

Gene clusters linked to insulin resistance identified in a genome-wide study of the Taiwan Biobank population

Supplementary Methods

Taiwan Biobank

The study cohort consisted of 147,880 Taiwanese subjects from the Taiwan Biobank.¹⁻⁷ Following individual quality control, there were 136,735 subjects having TyG index phenotypic data and 138,303 subjects having the TG:HDL-C ratio and the log(TG:HDL-C) ratio phenotypic data. The Taiwan Biobank recruited individuals from the general Taiwanese population across Taiwan between 2013 and 2022, gathering specimens and pertinent data through recruitment centers¹⁻⁷. Supported primarily by the Taiwanese government, the Taiwan Biobank aims to facilitate scientific investigations on a broad spectrum of public health concerns and foster collaborative opportunities for researchers focusing on prevalent local chronic illnesses². Inclusion criteria encompassed individuals aged 30 to 70 years, self-identified as Taiwanese descendants, and capable of performing daily activities independently at the time of recruitment⁸. Exclusion criteria pertained to individuals with a history of cancer or non-Taiwanese residency⁸. Prior to commencing the study, ethical approval was obtained from the Institutional Review Board of Taipei Veterans General Hospital (approval number: 2023-04-007CC#1), and all participants provided their informed consent in accordance with established guidelines and regulations.

Genotyping and imputation

DNA extraction from blood samples was carried out using the QIAamp DNA blood kit in accordance with the manufacturer's guidelines (Qiagen, Valencia, CA, USA). The quality of the

genomic DNA was assessed through agarose gel electrophoresis, while the quantity was determined using spectrophotometry^{9,10}. SNP genotyping was performed using the Axiom Genome-Wide Array Plate System (Affymetrix, Santa Clara, CA, USA) with custom Taiwan Biobank chips. To maximize genetic data acquisition from Taiwanese samples, the custom Taiwan Biobank chip was developed by incorporating SNPs with minor allele frequencies (MAFs) exceeding 10% from the Human Exome BeadChip (Illumina, Inc., San Diego, CA, USA), SNPs with MAFs of at least 5% from the Axiom Genome-Wide CHB 1 Array chip (Affymetrix, Inc., Santa Clara, CA, USA), and SNPs previously identified in cancer, pharmacogenomics, and genetic ancestry studies^{8,11}. To assess the performance of the custom Taiwan Biobank chip, genotyping was conducted on 70 unrelated Taiwanese individuals using both the Axiom Genome-Wide CHB 1 Array chip and the custom Taiwan Biobank chip. Notably, a high average concordance rate of 99.6% was achieved for the SNPs in these 70 subjects⁸.

In this investigation, stringent quality control measures were applied to eliminate unreliable SNPs from subsequent analysis^{4,12}. SNPs that deviated from Hardy-Weinberg equilibrium (HWE) with a P-value below 1×10^{-6} , exhibited a genotyping call rate below 95%, or possessed a MAF less than 1% were excluded. Initially, we had 686,370 directly genotyped SNPs and 15,851,039 imputed SNPs. Following the quality control process, a total of 7,604,854 SNPs were utilized as the foundation for SNP functional prediction.

Statistical analysis

We conducted a comprehensive GWAS to investigate the genetic underpinnings of three surrogate markers of IR including the TyG index¹³ and the TG:HDLC ratio¹⁴, and the log(TG:HDLC) ratio (i.e., the TG:HDLC ratio on a logarithmic scale). The TyG index was derived

using the formula $\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$, where this index is expressed on a logarithmic scale to capture the combined influence of fasting triglyceride and glucose levels on metabolic health. This GWAS analysis was performed using mixed linear models implemented in BOLT-LMM (version 2.4.1)¹⁵, a robust tool designed for large-scale genetic association studies. Our models were meticulously adjusted for sex and the top 10 principal components (PCs) to account for potential confounding factors such as population stratification and genetic ancestry. This adjustment ensures that the associations identified are more likely to reflect true genetic signals rather than artifacts arising from population structure. The BOLT-LMM for genetic association testing accounts for relatedness among participants through its random effects model. This method allows us to maintain all samples in our analyses without the necessity of excluding related individuals. In our GWAS analysis, age and age² were not included as covariates due to the minor correlation observed between the TyG index and age ($r = 0.22849$), suggesting that age adjustment would not significantly alter our findings. Additionally, we did not control for Body Mass Index (BMI) to examine the comprehensive genetic influences on insulin resistance, encompassing both direct effects and those mediated by BMI, as our goal was to understand the total genetic contribution to this trait¹⁶. The Manhattan and quantile-quantile (Q-Q) plots were generated utilizing the R package 'qqman' as part of the data visualization process. To address potential genomic inflation, we utilized linkage disequilibrium score regression (LDSC)¹⁷. For each trait—namely the TyG index, the TG:HDL ratio, and log(TG:HDL)—we calculated lambda Genomic Control (GC) and intercept values. These values were subsequently employed to adjust our QQ plots, thereby providing a more accurate evaluation of the significance of our genetic associations by correcting for inflation. This study adhered to the conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ commonly employed in GWASs.

To address comparisons with European ancestry-based analyses, we included a direct comparison of significant genome-wide results for insulin resistance-associated genes between the Taiwan Biobank and recent studies focusing on European ancestry. This comparison involved aligning significant loci and evaluating differences in effect size, allele frequencies, and sample size.

To assess parent-offspring pairs, we utilized the KING software¹⁸ with the command “king -related --degree 2” to identify the kinship relationships and calculate specific metrics, including the kinship coefficient and IBS0 values, between sample pairs. We then filtered the results to include only those with an inferred parent-offspring relationship type, a kinship coefficient between 0.1767 and 0.3535, and an IBS0 value below 0.0012^{18,19}. Using information on age and sex, we determined the roles of parents and offspring, excluding parent-offspring pairs with an age difference of 15 years or less. A total of 9,387 parent-offspring pairs were identified, including 2,815 trios and 6,572 duos. Phasing of related samples was conducted using SHAPEIT4²⁰.

To examine parent-of-origin effects (POE) of genetic variants on traits in family-based cohorts, we conducted a simplified parental asymmetry test²¹. This approach evaluated paternal and maternal effects by independently comparing the transmission of the minor allele from each parent. For the POE analysis, we assessed differences in paternal versus maternal minor allele transmission among heterozygous offspring.

Due to the absence of medication usage data in the Taiwan Biobank, we recognize this as a limitation in our analysis concerning potential confounders such as lipid-lowering or glucose-regulating medications. To address this partially, we performed a sensitivity analysis by excluding individuals with self-reported diabetes mellitus (DM). We reran the GWAS on this subset to ascertain if the genetic associations with the TyG index were influenced by the presence of DM,

which might indirectly reflect medication effects.

To identify and retain independent genetic variants associated with these traits, we employed the clumping method in PLINK¹². This method accounts for linkage disequilibrium (LD) patterns in the genome, reducing redundancy by filtering out SNPs in high LD. Clumping retains SNPs with an association p-value less than 5×10^{-5} , ensuring statistical significance, and an r^2 value less than 0.5, ensuring relative independence. The LD evaluation window is set at 250 kilobases (kb). The process starts with the most significantly associated SNP and excludes others within the 250 kb window that have an r^2 value of 0.5 or higher. This iterative process results in a set of SNPs that are independent markers for association with the trait, providing a clearer picture of the genetic variants truly associated with the trait. This approach improves the reliability of subsequent analyses, such as replication studies, fine-mapping, or functional assays.

We performed fine mapping using susieR (v.0.12.35)²², an R package for Bayesian variable selection in linear regression models, particularly useful for genetic fine mapping. The analysis focused on variants within a 1.5 megabase (Mb) radius of each identified genomic risk locus. Only genetic variants with a p-value less than 5×10^{-30} after clumping were included, indicating a robust association. Overlapping significant regions were merged into single regions for analysis, reducing redundancy and focusing on unique genomic areas likely to harbor causal variants. A total of 10 distinct regions were analyzed after merging overlapping areas. In this context, we utilized susieR (v.0.12.35) for fine mapping, leveraging two key metrics: Posterior Inclusion Probability (PIP) and Residual Sum of Squares Posterior Inclusion Probability (RSS PIP). PIP represents the probability that a genetic variant is included in the model given the observed data, thus quantifying the strength of evidence for the variant's association with the trait. Higher PIP values indicate a stronger likelihood that the variant is associated with the trait under investigation. RSS PIP, on the other

hand, integrates information from the residual sum of squares with the PIP to evaluate the importance of a genetic variant in explaining the variability of the trait after accounting for other variants in the model. Furthermore, in *susieR* (v.0.12.35), purity is characterized as the minimum absolute pairwise correlation, measured by Pearson's r , among SNPs within the credible set (CS). This metric assesses the level of independence and non-redundancy among the SNPs identified as credible contributors to the trait under investigation. A higher purity value indicates a lower level of correlation between the SNPs within the credible set, suggesting greater independence and non-redundancy among the selected genetic variants. On the other hand, the concept of "coverage" in credible sets pertains to the likelihood that the causal variant responsible for the trait is encompassed within the defined credible set. This measure quantifies the probability that the true causal variant is accurately captured and represented by the selected SNPs in the credible set, providing insights into the comprehensiveness and effectiveness of the genetic variant selection process. This comprehensive evaluation enhances our ability to pinpoint genetic variants that significantly contribute to the trait's genetic architecture, thereby improving the accuracy and relevance of our fine mapping efforts.

We estimated heritability and genetic correlations using LDSC v.1.0.1¹⁷. LDSC quantifies the contribution of genetic variants to a trait's heritability based on GWAS summary statistics, utilizing LD information to distinguish the signal from polygenic traits and confounding biases such as population stratification. Key statistics obtained from LDSC include:

1. **h^2 (Heritability)**: Represents the SNP heritability estimated by LDSC, quantifying the proportion of variance in a trait explained by the SNPs included in the GWAS.
2. **Lambda GC**: Measures inflation in test statistics due to population stratification or other confounding factors. A value close to 1 suggests minimal confounding.

3. **Mean Chi²**: The average chi-squared statistics across all SNPs, indicating overall signal strength in the GWAS data.
4. **Intercept**: Represents the component of Mean Chi² not attributed to polygenic signal. An intercept close to 1 indicates minimal confounding biases.
5. **Ratio (LD Score Regression Coefficient)**: The slope of the regression of chi-squared statistics on LD scores, estimating the contribution of polygenic effects to the inflation in test statistics.

We constructed polygenic risk scores (PRSs) using PRS-CS (v.1.1.0)²³ and a subset of 30% of the TWB population as the testing dataset. The process involved:

1. Conducting or obtaining GWAS summary statistics for the traits of interest.
2. Using PRS-CS to estimate SNP weights based on these summary statistics and a reference LD panel.
3. Applying these weights using PLINK's --score function¹² on the genotype data of the testing dataset to compute the PRS for each individual.
4. Analyzing the predictive power of the PRS on the testing dataset to assess its effectiveness in predicting the trait based on genetic data.

The metrics for evaluating the performance and accuracy of PRS models are as follows: R^2 , PRS SNPs, and $R^2 - R^2_{\text{Null}}$. R^2 represents the proportion of variance in the phenotype explained by the PRS model. It quantifies the predictive accuracy of the PRS in capturing the variability of the trait of interest based on the genetic information from the selected SNPs. A higher R^2 value indicates a greater proportion of the phenotype variance explained by the PRS model, reflecting its predictive strength. PRS SNPs refer to the number of SNPs included in the PRS calculation. The number of PRS SNPs influences the predictive power and specificity of the PRS model. $R^2 -$

R^2 Null represents the difference between the R^2 value of the PRS model and the null model. The null model typically includes no genetic information and serves as a baseline for comparison. The R^2 - R^2 Null metric assesses the incremental predictive value gained by incorporating genetic information through the PRS model compared to a model without genetic predictors. A higher R^2 - R^2 value indicates the added predictive utility of the PRS model over the null model in explaining the phenotype variance.

Sex-stratified and sex-differentiated analyses

In sex-stratified analyses, we repeated the mixed linear model analyses described above using BOLT-LMM software, separately for male (n=48,189) and female (n=88,564) subjects, adjusting for sex and the top 10 principal components (PCs). Subsequently, we conducted a sex-differentiated analysis²⁴ using the GWAMA software²⁵ with the "-sex" option to identify sex-specific allelic effects and test for heterogeneity between sexes.

Transcriptome-wide association studies

The TWAS were employed to investigate the relationship between gene expression and the TyG index. FUSION²⁶ was utilized to combine gene expression measurements with GWAS summary statistics. Precomputed expression reference weights in GTEx v7 were obtained from <http://gusevlab.org/projects/fusion/>, encompassing 11 human tissues: adipose subcutaneous, adipose visceral omentum, adrenal gland, brain cortex, brain hippocampus, brain hypothalamus, liver, muscle skeletal, pancreas, pituitary, and thyroid tissues. FUSION was then used to calculate TWAS Z-scores and P-values, identifying genes with significant associations between their expression levels and TyG index susceptibility.

Pathway analysis

First, we constructed protein-protein interaction (PPI) networks utilizing NDEx-The Network Data Exchange (<https://www.ndexbio.org/iquery/>)²⁷ with significant genes associated with the TyG index. Within NDEx, we employed the Human Integrated Protein–Protein Interaction rEference (HIPPIE) database²⁸ for the PPI analysis. Next, pathway analysis for the genes within the PPI network was conducted using ClueGO²⁹, a plugin in the Cytoscape software³⁰. ClueGO leverages ontology source databases such as GO, REACTOME, KEGG, and WikiPathways to identify gene ontology terms and pathway networks, elucidating the functional significance of identified genes within specific biological processes and pathways²⁹.

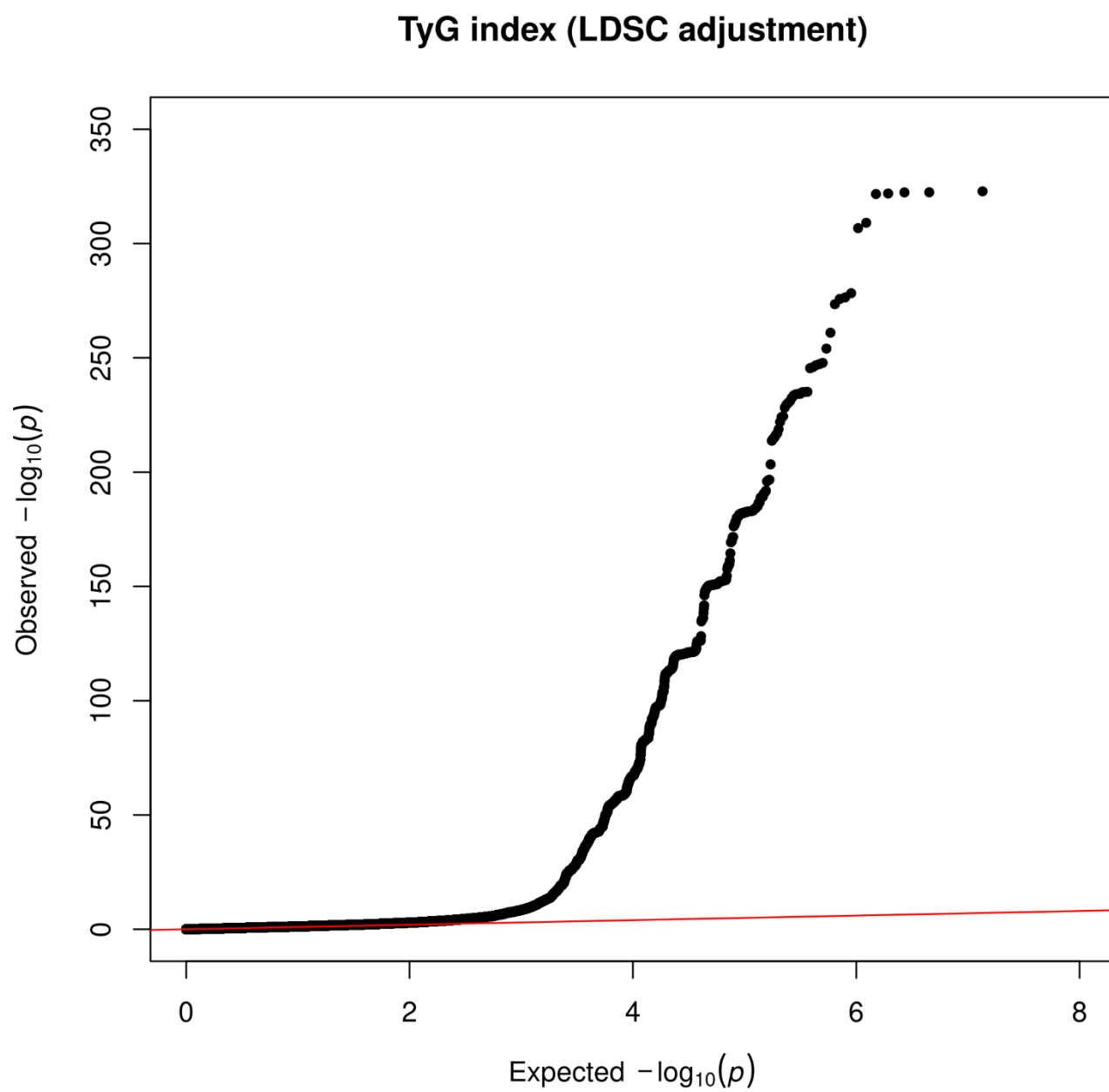
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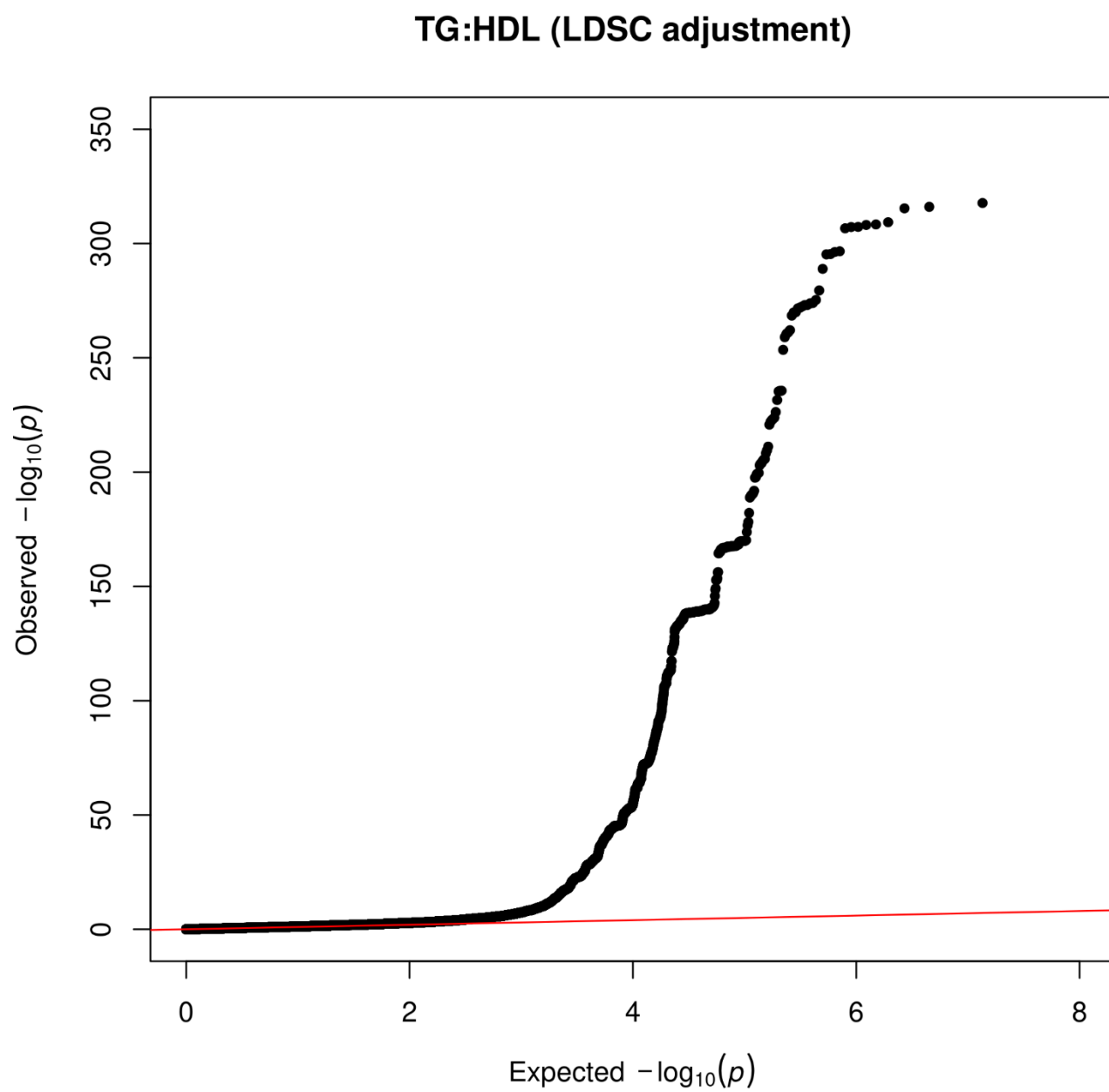
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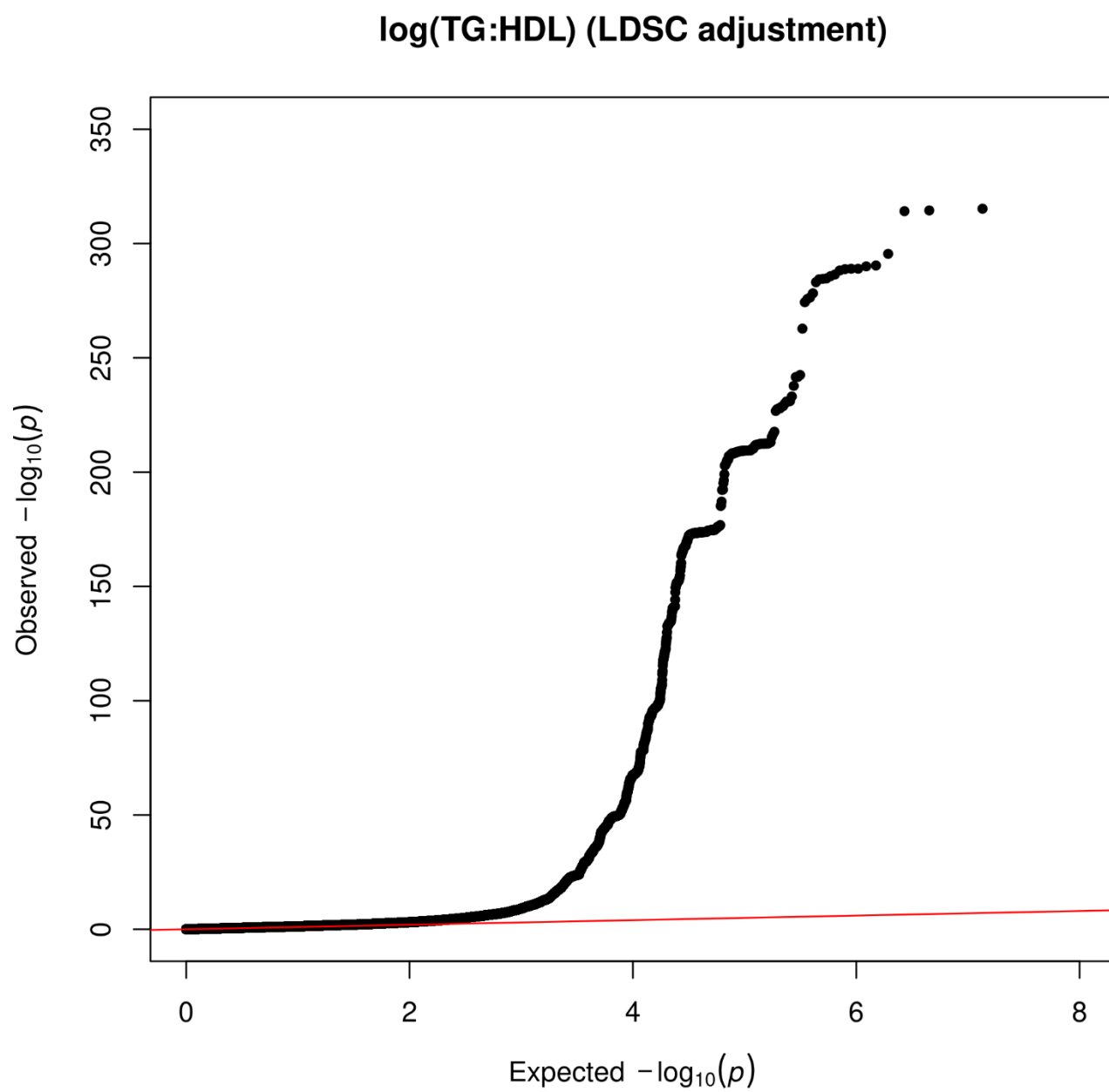
(a) Q-Q plot for TyG index



(b) Q-Q plot for TG:HDL-C

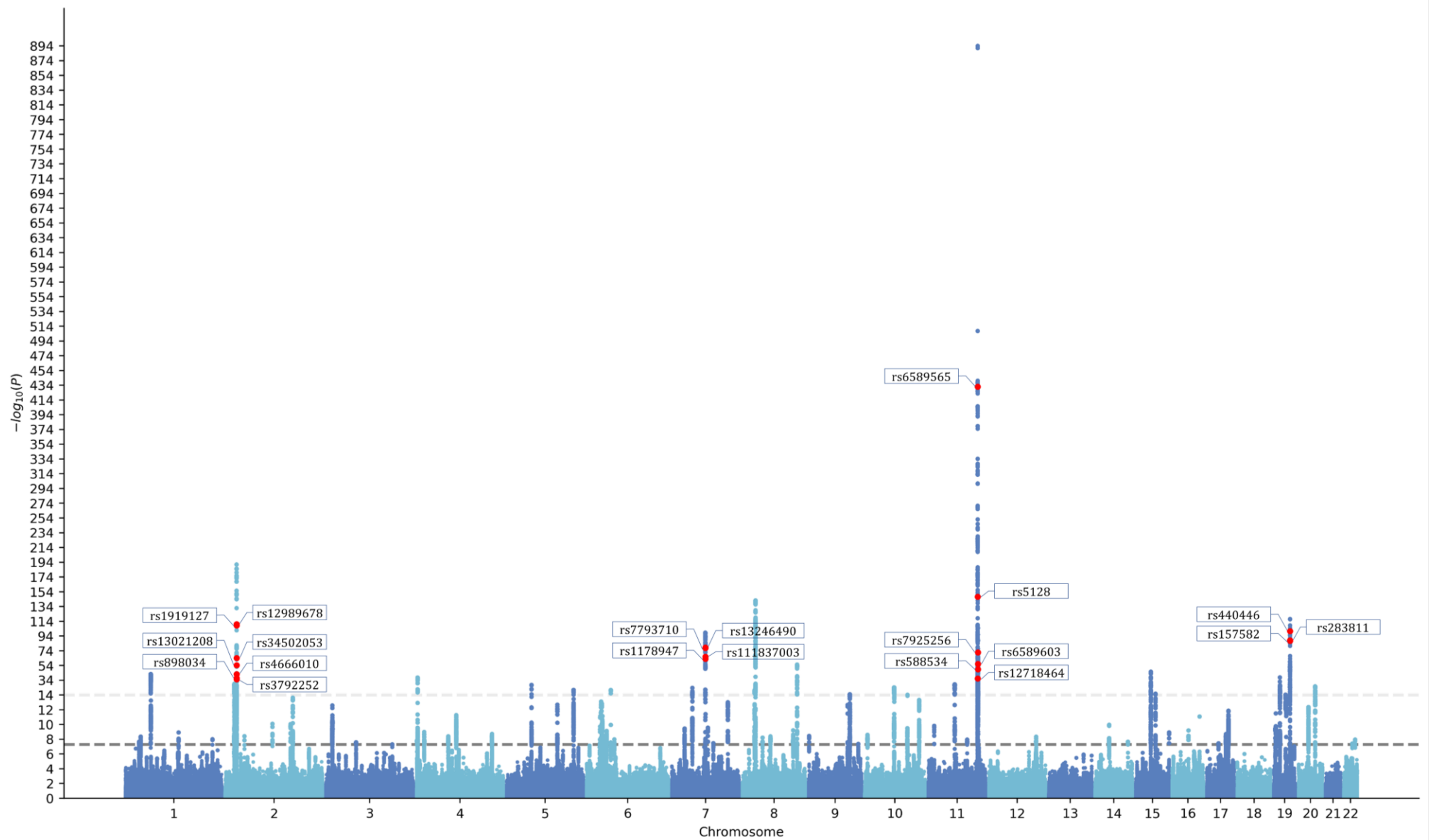


(c) Q-Q plot for $\log(\text{TG:HDL-C})$



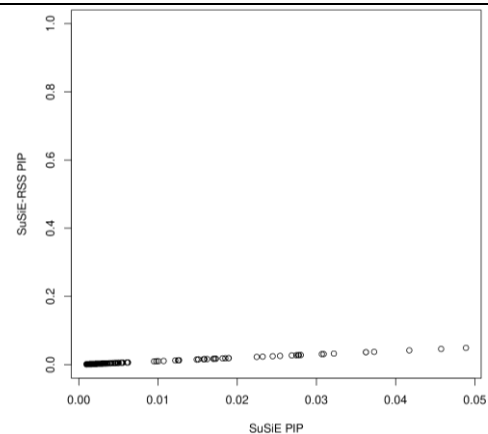
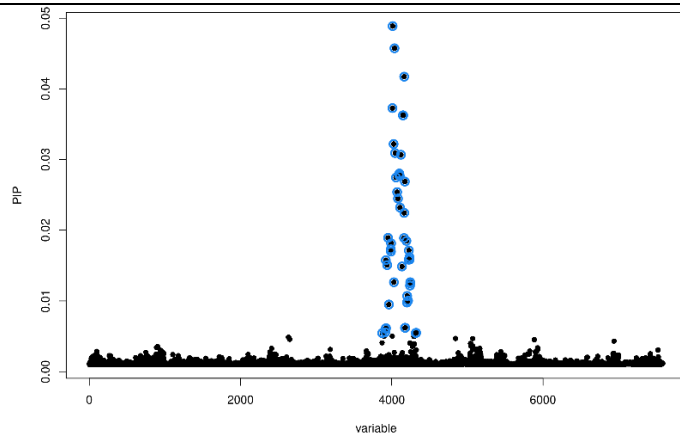
Supplementary Figure 1. The quantile-quantile (Q-Q) plots for the identified SNPs associated with the three IR surrogate markers, including (a) the TyG index, (b) TG:HDL-C ratio, and (c) log(TG:HDL-C) ratio.

IR = insulin resistance; LDSC = Linkage Disequilibrium Score Regression; TG:HDLC = the triglyceride to high-density lipoprotein cholesterol ratio; TyG = the product of fasting plasma glucose and triglycerides ($\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)/2}]$).

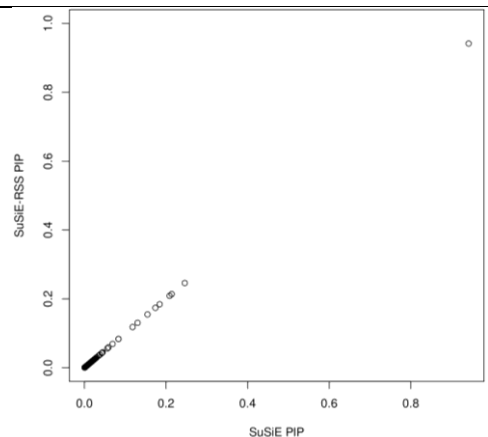
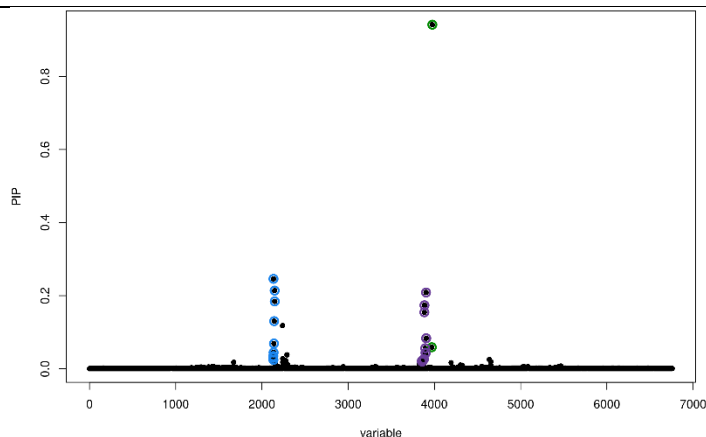


Supplementary Figure 2. Manhattan plot of TyG: Top 20 novel SNPs.

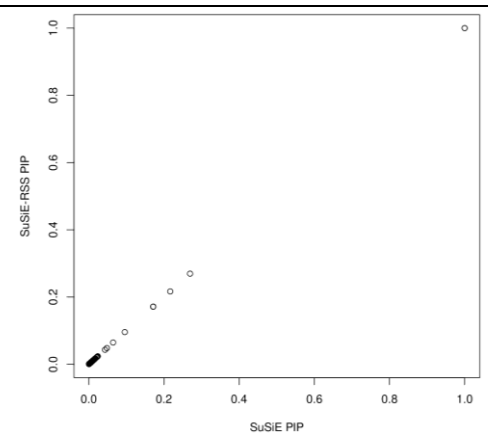
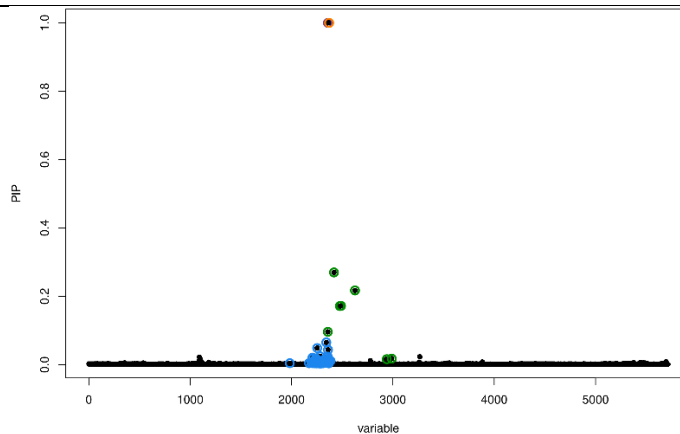
Chr1, BP: 61003238~ 64003238, N SNPs= 7,584



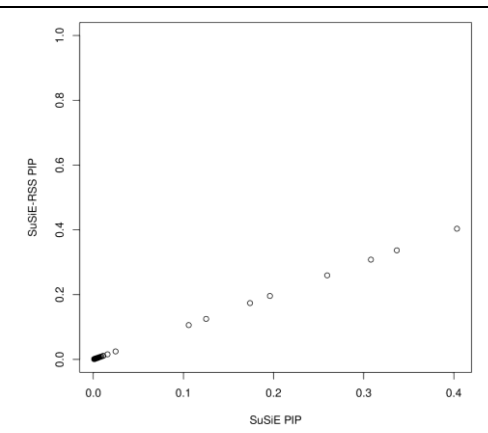
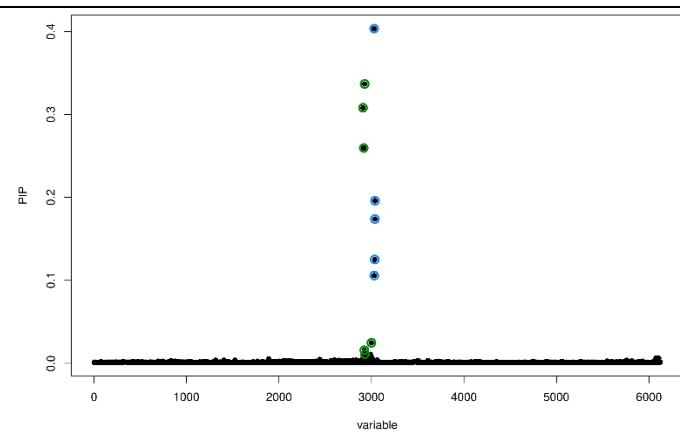
Chr2, BP: 19491280 ~ 22491280, N SNPs= 6,758



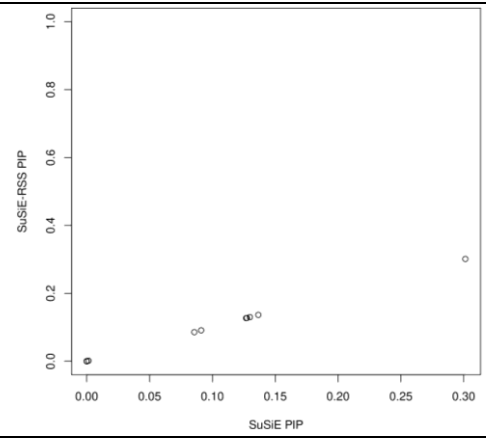
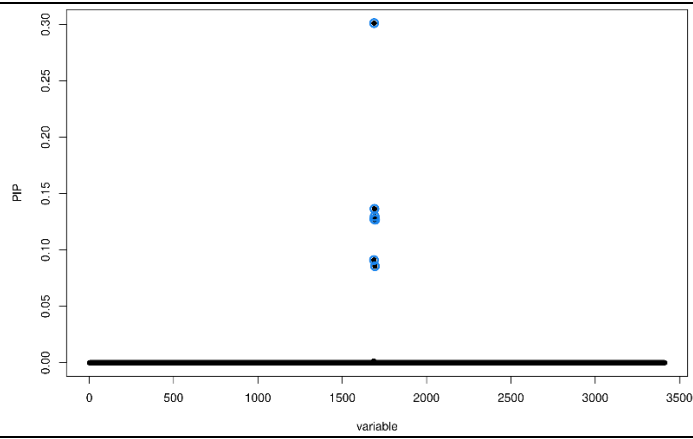
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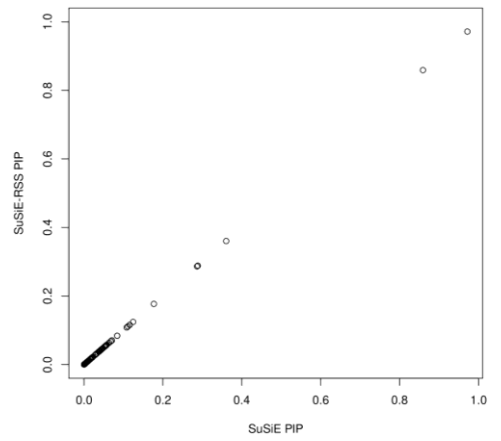
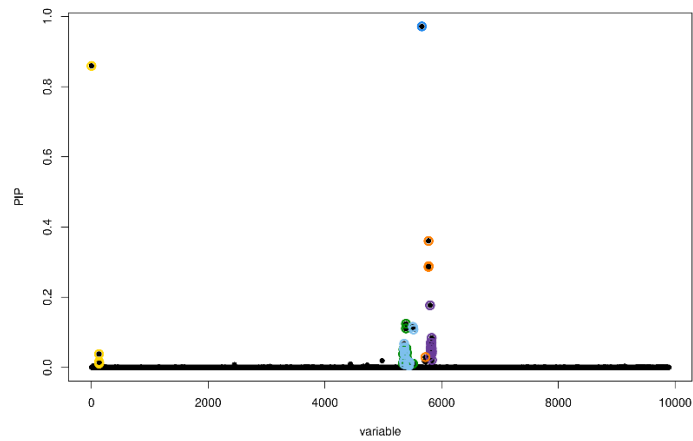
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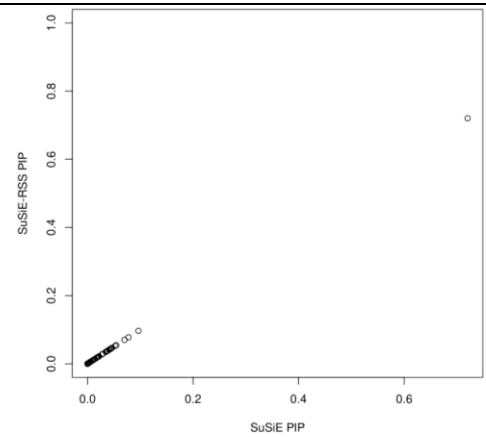
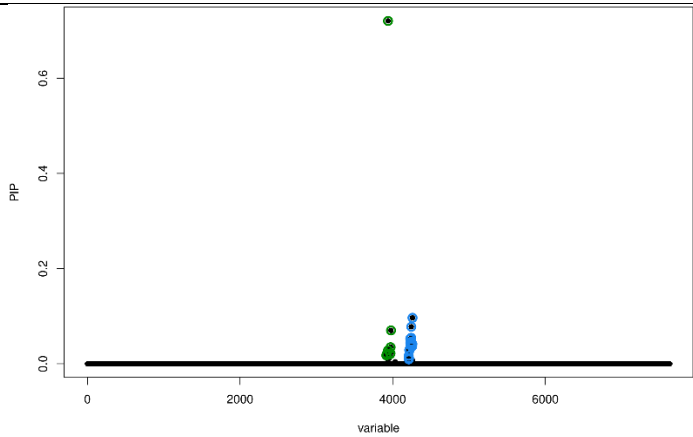
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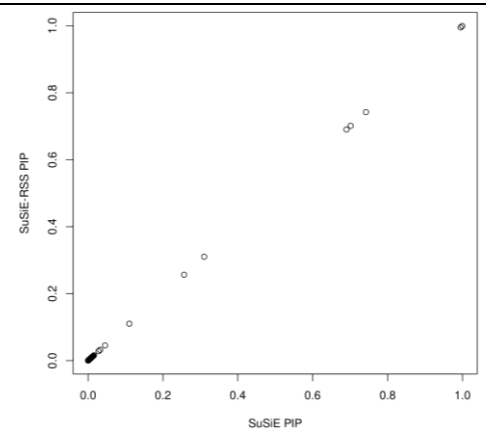
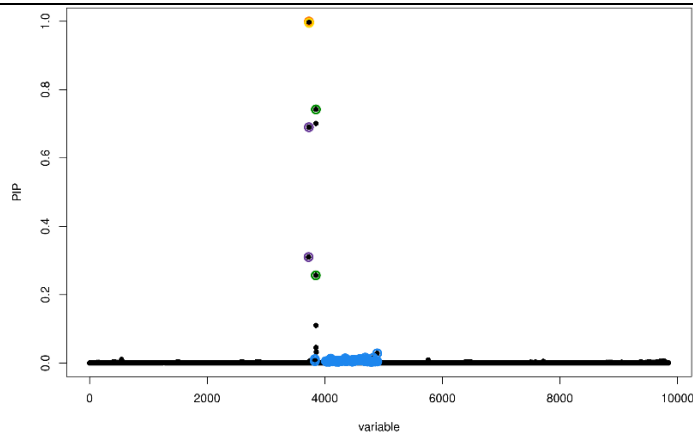
Chr8, BP: 18399789 ~ 21520643, N SNPs= 9,894



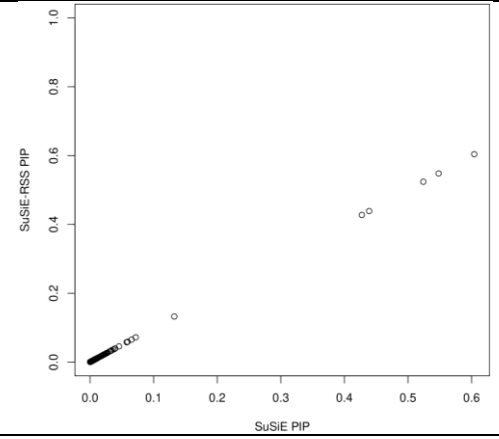
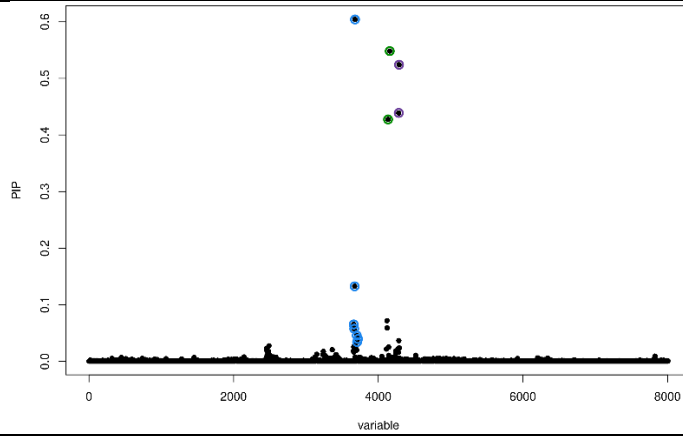
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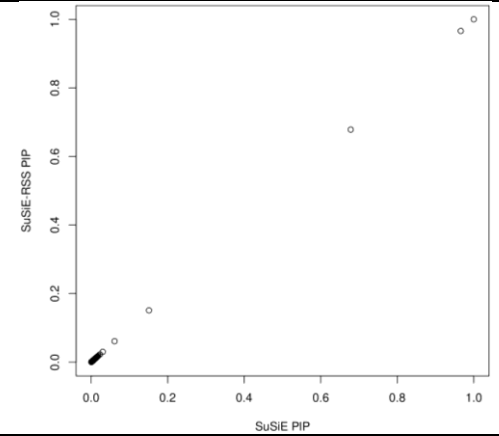
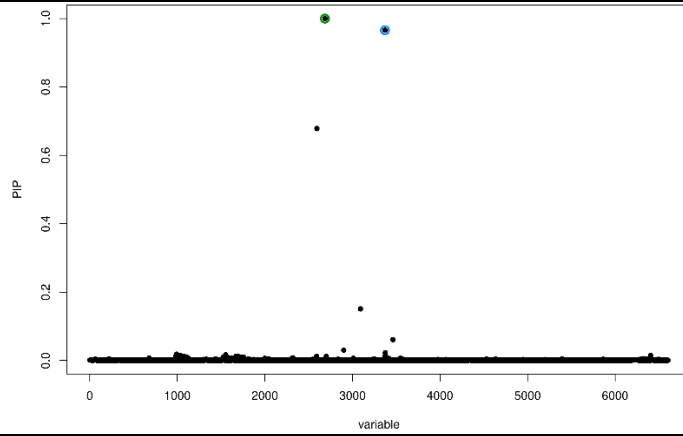
Chr11, BP: 115134723 ~ 118855903, N SNPs= 9,846



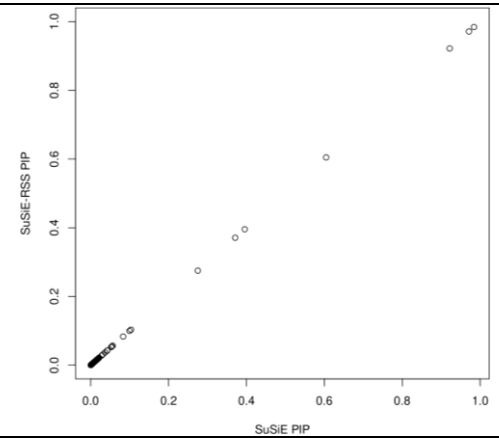
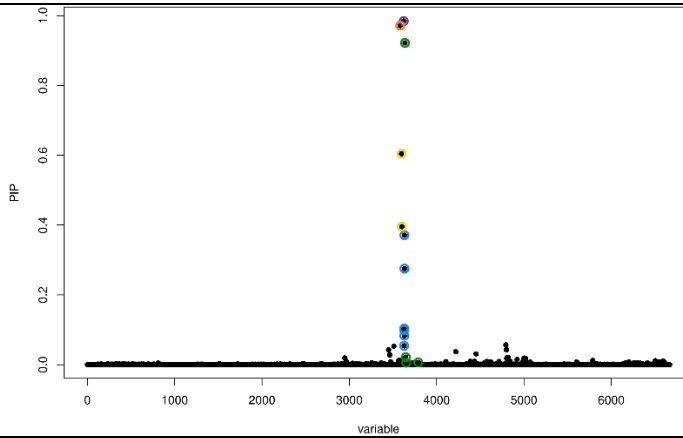
Chr15, BP: 56887979 ~ 59931740, N SNPs= 8,004



Chr19, BP: 17768740 ~ 20768740, N SNPs= 6,603

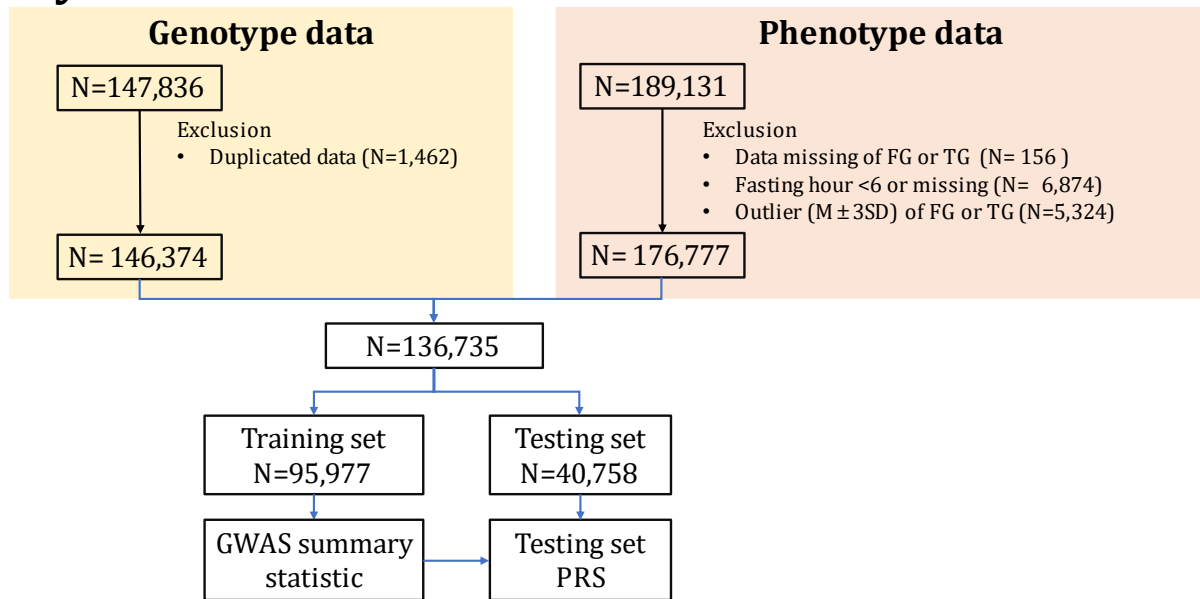


Chr19, BP: 43378777 ~ 46429300, N SNPs= 6,668



Supplementary Figure 3. Results of the fine mapping analysis in 10 distinct regions of interest for the TyG index. The fine mapping analysis identified 10 distinct genomic regions of interest using susieR (v.0.12.35). PIP = Posterior Inclusion Probability; RSS = Residual Sum of Squares.

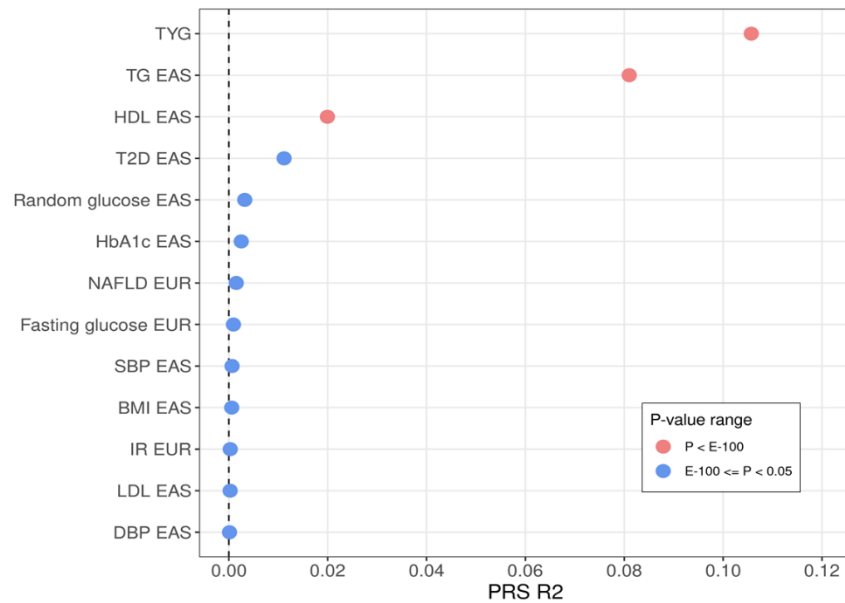
TyG index



FG: fasting glucose

Supplementary Figure 4. The flowchart for the association of IR-related polygenic risk scores (PRSs) with the TyG index in the testing set.

FG = fasting glucose; IR = insulin resistance; TyG index = the triglyceride-glucose index; TG = triglyceride. The TyG index was derived using the formula $\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$.



Supplementary Figure 5. The results for the association of IR-related polygenic risk scores (PRSs) with the TyG index in the testing set.

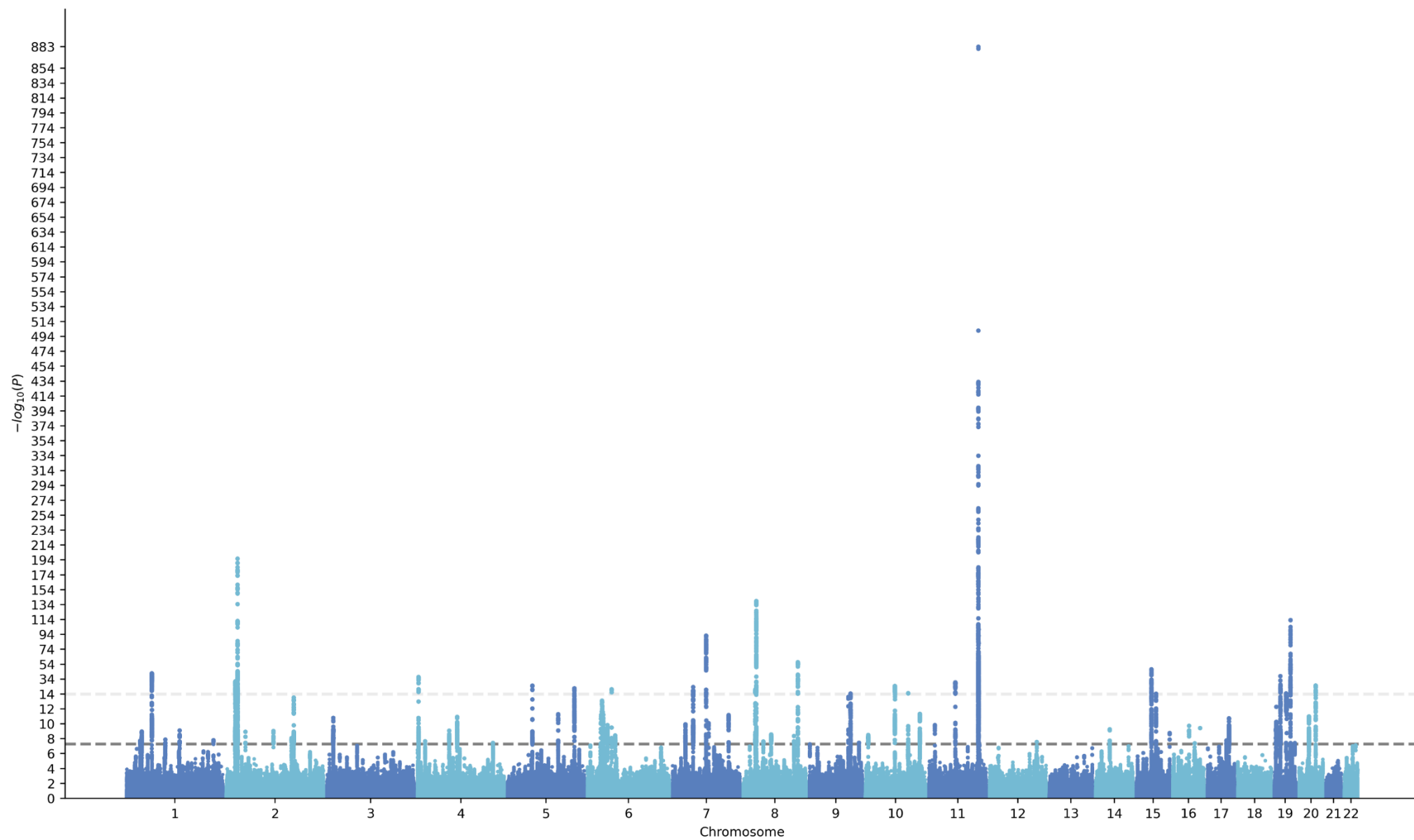
GWAS of the TyG index using the training set in the Taiwan Biobank.

null.model : TyG_index~SNPSEX+AGE+PC1- PC10

prs.model : TyG_index~**strSCORE** +SNPSEX+AGE+PC1- PC10

TyG index = the triglyceride-glucose index; R2 (R-squared) = the proportion of variance in the phenotype explained by the PRS model.

The TyG index was derived using the formula $\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$.



Supplementary Figure 6. Manhattan plot of TyG excluding self-reported diabetes mellitus (DM) cases.

Supplementary Table 1. Baseline characteristics of the Taiwanese population in the (A) whole, (B) female, and (C) male cohorts within the Taiwan Biobank.

A. Whole cohort

	Trait	Units	N	Median (Q1,Q3)	Frequency (%)
Demographics	Female	%	136,735	-	88,546 (64.76)
	Age	year	136,735	50 (40, 59)	-
Lipids	TyG	-	136,735	8.35 (7.97, 8.76)	-
	TG:HDL-C	-	136,735	1.69 (1.06, 2.79)	-
	log (TG:HDL-C)	-	136,735	0.52 (0.06, 1.03)	-
	TG	mg/dL	136,735	91 (64, 133)	-
	HDL-C	mg/dL	136,735	54 (45, 63)	-
	LDL-C	mg/dL	136,735	119 (99, 141)	-
Glycemic	Diabetes	%	136,735	-	5,615 (4.11)
	Glucose	mg/dL	136,735	92 (87, 98)	-
Cardiovascular	Valve heart disease	%	136,735	-	5,836 (4.27)
	Coronary artery disease	%	136,735	-	1,674 (1.22)
	Arrhythmia	%	136,735	-	6,064 (4.43)
	Cardiomyopathy	%	136,735	-	1,003 (0.73)
	Congenital heart disease	%	136,735	-	288 (0.21)
	Other heart disease	%	136,735	-	207 (0.15)
Hepatic	ALT (SGOT)	U/L	136,735	22 (19, 27)	-
Obesity	BMI	Kg/m2	136,650	23.71 (21.49, 26.28)	-
	WHR	-	136,652	0.86 (0.82, 0.91)	-
Circulation	Systolic BP	mmHg	136,707	117.5 (106.5, 130)	-

B. Female cohort

	Trait	Units	N	Median (Q1,Q3)	Frequency (N)
Demographics	Age	year	88,564	50 (40, 58)	-
	TyG	-	88,564	8.25 (7.89, 8.64)	-
Lipids	TG:HDL-C	-	88,564	1.43 (0.94, 2.31)	-
	log (TG:HDL-C)	-	88,564	0.36 (-0.06, 0.84)	-
	TG	mg/dL	88,564	83 (60, 121)	-
	HDL-C	mg/dL	88,564	58 (49, 67)	-
	LDL-C	mg/dL	88,564	118 (98, 140)	-
Glycemic	Diabetes	%	88,564	-	3,035 (3.43)
	Glucose	mg/dL	88,564	91 (86, 96)	-
Cardiovascular	Valve heart disease	%	88,564	-	4,555 (5.14)
	Coronary artery disease	%	88,564	-	561 (0.63)
	Arrhythmia	%	88,564	-	4,057 (4.58)
	Cardiomyopathy	%	88,564	-	499 (0.56)
	Congenital heart disease	%	88,564	-	196 (0.22)
	Other heart disease	%	88,564	-	130 (0.15)
Hepatic	ALT	U/L	88,564	22 (18, 26)	-
Obesity	BMI	Kg/m2	88,504	22.93 (20.91, 25.49)	-
	WHR	-	88,509	0.84 (0.8, 0.89)	-
Circulation	Systolic BP	mmHg	88,524	113 (103, 126.5)	-

C. Male cohort

	Trait	Units	N	Median (Q1,Q3)	Frequency (N)
Demographics	Age	year	48,189	50 (39, 60)	-
	TyG	-	48,189	8.55 (8.17, 8.93)	-
Lipids	TG:HDL-C	-	48,189	2.29 (1.44, 3.66)	-
	log (TG:HDL-C)	-	48,189	0.83 (0.37, 1.30)	-
	TG	mg/dL	48,189	108 (75, 156)	-
	HDL-C	mg/dL	48,189	47 (41, 55)	-
	LDL-C	mg/dL	48,189	121 (101, 143)	-
Glycemic	Diabetes	%	48,189	-	2,580 (5.35)
	Glucose	mg/dL	48,189	94 (89, 100)	-
Cardiovascular	Valve heart disease	%	48,189	-	1,281 (2.66)
	Coronary artery disease	%	48,189	-	1,113 (2.31)
	Arrhythmia	%	48,189	-	2,007 (4.16)
	Cardiomyopathy	%	48,189	-	504 (1.05)
	Congenital heart disease	%	48,189	-	92 (0.19)
	Other heart disease	%	48,189	-	77 (0.16)
Hepatic	ALT	U/L	48,189	24 (21, 29)	-
Obesity	BMI	Kg/m2	48,146	25 (22.99, 27.29)	-
	WHR	-	48,143	0.9 (0.86, 0.94)	-
Circulation	Systolic BP	mmHg	48,183	123.5 (114, 135)	-

Supplementary Table 2. The number of significant SNPs identified at various significance thresholds for GWASs of three IR surrogate markers, including the TyG index, TG:HDL-C ratio, and log(TG:HDL-C) ratio.

P	TyG index (N=136,735)	TG:HDL-C (N=138,303)	log(TG:HDL-C) (N=138,303)
5.00E-08	8,738	6,814	9,318
5.00E-10	5,864	4,867	6,534
5.00E-50	1,235	858	1,033
5.00E-100	414	396	433
5.00E-200	75	82	142
5.00E-300	42	39	43

IR = insulin resistance; TG:HDL-C = the ratio of triglycerides to high-density lipoprotein cholesterol; TyG index = the triglyceride-glucose index; log(TG:HDL-C) = the logarithm-transformed TG:HDL-C ratio.

The TyG index was derived using the formula $\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$. This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test. The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 3. GWAS results of the top 20 significant SNPs after clumping for three IR surrogate markers, including the TyG index, TG:HDL-C ratio, and log(TG:HDL-C) ratio.

TyG index (N=136,735)				TG:HDL (N=138,303)				log(TG:HDL) (N=138,303)			
N SNPs after clump=271				N SNPs after clump=238				N SNPs after clump=305			
CHR	SNP	Pos	P	CHR	SNP	Pos	P	CHR	SNP	Pos	P
11	rs7350481	116715567	<5E-300	11	rs7350481	116715567	<5E-300	11	rs7350481	116715567	<5E-300
11	chr11:116741689_AACACACACACAC_A	116741689	<5E-300	11	chr11:116741689_AACACACACACAC_A	116741689	<5E-300	11	rs61905084	116739578	<5E-300
11	rs61905084	116739578	1.10E-261	11	rs61905084	116739578	5.10E-310	11	chr11:116741689_AACACACACACAC_A	116741689	<5E-300
11	rs7927820	116811440	1.70E-248	11	rs6589573	116815050	1.90E-206	11	rs7927820	116811440	1.40E-229
11	rs603446	116783719	9.00E-225	11	rs603446	116783719	3.50E-200	11	rs603446	116783719	9.20E-214
2	rs1260326	27508073	4.30E-204	8	rs12679834	19962922	6.30E-171	8	rs12679834	19962922	1.60E-213
8	rs75278536	19963914	2.00E-153	2	rs1260326	27508073	7.40E-140	2	rs1260326	27508073	1.60E-177
19	rs483082	44912921	1.30E-123	19	rs438811	44913484	1.10E-115	11	rs1784127	116667859	6.00E-123
11	rs1784128	116667972	1.20E-112	11	rs1784127	116667859	4.70E-112	16	rs17231506	56960616	2.70E-122
11	chr11:117120044_G_GAAC	117120044	1.80E-109	11	rs182500870	116755846	1.90E-95	8	rs1534650	20020643	7.60E-108
7	rs3812316	73606007	8.50E-105	16	rs17231506	56960616	2.50E-94	19	rs429358	44908684	4.20E-100
11	rs75955612	116759802	7.10E-82	8	rs1534650	20020643	1.00E-90	7	rs3812316	73606007	8.20E-99
8	rs1534650	20020643	2.00E-72	11	rs200405951	116780493	6.10E-79	11	rs182500870	116755846	5.10E-93
11	rs182500870	116755846	7.90E-71	11	rs75955612	116759802	1.20E-78	11	chr11:117120044_G_GAAAC	117120044	1.30E-82
11	rs499563	116652244	1.90E-68	7	rs3812316	73606007	4.30E-78	11	rs75955612	116759802	1.50E-81
11	rs11216100	116701814	3.30E-67	11	rs141882698	116730622	2.80E-72	11	rs200405951	116780493	6.90E-79
19	rs157580	44892009	2.20E-64	11	chr11:117120044_G_GAAAC	117120044	8.80E-72	19	rs440446	44905910	9.50E-78
11	rs12276805	117008043	8.40E-61	11	rs199986368	117031627	3.40E-71	11	rs199986368	117031627	2.20E-73
11	rs141882698	116730622	2.90E-60	11	rs184616707	116639841	2.40E-66	11	rs141882698	116730622	4.80E-72
19	rs7259004	44929300	2.00E-59	11	rs567599	116651848	5.20E-65	11	rs499563	116652244	6.40E-70

IR = insulin resistance; TG:HDL-C = the ratio of triglycerides to high-density lipoprotein cholesterol; TyG index = the triglyceride-glucose index; log(TG:HDL-C) = the logarithm-transformed TG:HDL-C ratio.

The TyG index was derived using the formula $\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$.

CHR = chromosome, P = p-value, Pos = position

This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.

The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 4. Summary of variants exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SFPQ *	1	rs79395015	35,170,115	T	C	0.376865	0.011096	0.002100	2.9E-08
SFPQ *	1	rs77686522	35,171,992	T	A	0.392116	0.011195	0.002070	1.2E-08
SFPQ *	1	rs80099351	35,177,518	G	A	0.392388	0.011126	0.002067	1.6E-08
SFPQ *	1	rs3768339	35,184,401	C	T	0.390551	0.011028	0.002071	2.3E-08
SFPQ *	1	rs3738696	35,186,666	C	A	0.389461	0.011583	0.002070	4.1E-09
SFPQ *	1	rs12075530	35,188,306	T	C	0.389494	0.011564	0.002070	4.3E-09
SFPQ *	1	rs142470364	35,192,209	C	CAT	0.409919	0.011517	0.002064	5.1E-09
SFPQ *	1	rs12075169	35,193,419	G	C	0.410141	0.011518	0.002063	4.9E-09
SFPQ *	1	rs77084091	35,194,249	T	C	0.408525	0.010970	0.002077	2.5E-08
SFPQ *	1	rs77086052	35,197,007	G	A	0.410591	0.011373	0.002070	7.6E-09
SFPQ *	1	rs12083658	35,198,902	A	C	0.413097	0.010941	0.002080	3.0E-08
SFPQ *	1	rs80332318	35,199,001	G	A	0.404779	0.010837	0.002091	4.6E-08
SFPQ *	1	rs11264116	35,200,158	T	C	0.396434	0.011143	0.002075	1.7E-08
SFPQ *	1	chr1:35200449_A_ATTGGT	35,200,449	ATTGGT	A	0.396214	0.011229	0.002077	1.4E-08
SFPQ *	1	rs12081295	35,200,520	A	G	0.396548	0.011151	0.002076	1.6E-08
SFPQ *	1	rs7542630	35,202,061	C	T	0.408871	0.011057	0.002071	2.1E-08
SFPQ *	1	rs145536651	35,203,297	T	TATA	0.407079	0.010759	0.002076	4.7E-08
SFPQ *	1	chr1:35206901_C_CAA	35,206,901	C	CAA	0.499314	-0.011146	0.002053	1.5E-08
SFPQ *	1	rs35520620	35,207,155	T	C	0.498113	-0.011390	0.002059	8.7E-09
SFPQ *	1	rs28673907	35,207,726	T	C	0.411009	0.011442	0.002081	7.2E-09
SFPQ *	1	rs7512559	35,212,152	T	C	0.483345	-0.010723	0.002052	3.7E-08
SFPQ *	1	rs7520747	35,212,538	G	T	0.483316	-0.010733	0.002052	3.6E-08
SFPQ *	1	rs10752602	35,212,644	G	A	0.484273	-0.010825	0.002054	3.1E-08
SFPQ *	1	rs10796919	35,213,148	T	C	0.394521	0.011304	0.002087	9.5E-09
SFPQ *	1	rs60037734	35,213,586	T	G	0.488546	0.010729	0.002048	3.6E-08
SFPQ *	1	rs58482098	35,213,593	G	T	0.394110	0.011273	0.002087	1.1E-08
SFPQ *	1	rs12096175	35,215,884	C	T	0.413794	0.011439	0.002090	8.9E-09
SFPQ *	1	rs12568606	35,216,695	A	C	0.412996	0.011635	0.002087	4.1E-09
SFPQ *	1	rs74224909	35,218,456	G	A	0.415165	0.011469	0.002079	5.4E-09
SFPQ *	1	rs58534131	35,220,920	T	C	0.394636	0.011368	0.002086	7.7E-09
SFPQ *	1	rs78157661	35,221,488	C	T	0.394805	0.011441	0.002086	6.4E-09
SFPQ *	1	rs11264122	35,224,074	A	G	0.419580	0.010746	0.002066	2.8E-08
SFPQ *	1	rs75178217	35,226,309	A	G	0.421557	0.010797	0.002064	2.6E-08
ZMYM4 *	1	rs72910977	35,233,068	A	G	0.450750	0.010574	0.002062	3.7E-08
ZMYM4 *	1	rs72893303	35,233,650	T	C	0.452160	0.010638	0.002061	3.2E-08
ZMYM4 *	1	rs77968776	35,235,523	G	A	0.442374	0.010757	0.002066	3.4E-08
ZMYM4 *	1	rs74791659	35,236,875	G	A	0.442685	0.010874	0.002068	2.7E-08
ZMYM4 *	1	rs59854554	35,237,683	G	A	0.442225	0.010920	0.002071	2.6E-08
MACF1	1	rs61779308	39,472,585	T	C	0.145936	0.016507	0.002849	7.0E-09
MACF1	1	rs61779309	39,474,827	C	T	0.144566	0.016324	0.002869	1.3E-08
MACF1	1	rs61779313	39,478,577	C	T	0.147876	0.015559	0.002846	3.5E-08
MACF1	1	rs1386747518	39,480,077	AGTGAG	T	0.147639	0.015532	0.002848	4.0E-08
MACF1	1	chr1:39482510_TTTTG_T	39,482,510	TTTTG	T	0.148424	0.015394	0.002846	4.8E-08
MACF1	1	rs61779314	39,482,667	T	C	0.148174	0.015513	0.002843	3.7E-08
BMP8A	1	rs72663503	39,503,387	T	C	0.148374	0.015498	0.002835	3.9E-08
BMP8A	1	rs61779331	39,505,256	A	C	0.148005	0.015488	0.002842	4.6E-08
BMP8A, PPIEL	1	rs755249	39,529,402	T	C	0.136293	0.015755	0.002937	4.7E-08
PPIEL	1	rs12141058	39,534,682	T	C	0.141249	0.016115	0.002900	2.5E-08
PPIEL	1	rs143948354	39,536,713	G	GA	0.121807	0.018070	0.003086	2.3E-09
PPIEL	1	rs72663520	39,537,738	T	C	0.123151	0.018009	0.003071	2.3E-09
PPIEL	1	rs72663521	39,540,231	A	G	0.112513	0.017911	0.003187	1.0E-08
PPIEL	1	rs61779359	39,544,563	C	T	0.112879	0.017426	0.003182	2.4E-08
PPIEL	1	rs41270829	39,546,018	T	G	0.112822	0.017808	0.003181	1.2E-08
PPIEL	1	rs61781362	39,546,558	T	C	0.113320	0.017539	0.003174	1.8E-08
PPIEL	1	rs61781363	39,546,761	T	C	0.113184	0.017524	0.003175	1.9E-08
PPIEL	1	rs4660808	39,552,837	T	C	0.113250	0.017539	0.003175	1.9E-08
PPIEL	1	rs61781364	39,553,919	G	A	0.104384	0.018542	0.003315	1.0E-08
PPIEL	1	rs1180333	39,554,832	T	C	0.114994	0.017155	0.003155	3.6E-08
PPIEL	1	rs76207570	39,556,810	T	C	0.112065	0.017506	0.003192	2.2E-08
PPIEL	1	rs17264866	39,557,105	G	C	0.113184	0.017524	0.003175	1.9E-08
PPIEL	1	rs138909742	39,559,525	T	TG	0.113179	0.017522	0.003175	1.9E-08
PABPC4	1	rs4660293	39,562,508	G	A	0.113566	0.017593	0.003171	1.4E-08
PABPC4	1	rs58302493	39,568,233	A	G	0.110637	0.017509	0.003208	3.1E-08
PABPC4	1	rs17513135	39,570,014	T	C	0.110803	0.017462	0.003206	3.3E-08
PABPC4	1	rs3768321	39,570,256	T	G	0.110909	0.017275	0.003207	4.7E-08
PABPC4	1	rs2293476	39,571,175	C	G	0.110724	0.017330	0.003207	4.2E-08
PABPC4	1	rs41264487	39,571,682	G	C	0.113078	0.017688	0.003177	1.4E-08
PABPC4	1	rs2068663	39,572,899	T	C	0.113063	0.017559	0.003178	1.9E-08
PABPC4	1	rs79094524	39,575,699	GA	G	0.112792	0.017472	0.003182	2.3E-08
PABPC4	1	rs76113306	39,576,027	TCGGAGC	T	0.111634	0.018131	0.003195	7.9E-09
PABPC4 *	1	rs61781368	39,578,080	G	C	0.110695	0.017805	0.003210	2.0E-08
PABPC4 *	1	rs12064914	39,578,100	A	G	0.111287	0.017528	0.003206	3.7E-08
PABPC4 *	1	rs7520271	39,579,041	A	C	0.119465	0.017284	0.003110	1.7E-08
PABPC4 *	1	rs61781370	39,579,628	C	A	0.110473	0.017636	0.003212	2.2E-08
PABPC4 *	1	rs12740105	39,579,796	A	G	0.119047	0.017455	0.003108	1.2E-08
PABPC4 *	1	rs111768751	39,580,421	A	G	0.111677	0.018065	0.003194	9.0E-09
PABPC4 *	1	chr1:39580875_A_AT	39,580,875	A	AT	0.118941	0.017384	0.003109	1.4E-08
PABPC4 *	1	rs12037073	39,581,225	C	T	0.118776	0.017497	0.003110	1.1E-08
PABPC4 *	1	rs11206374	39,582,337	A	G	0.111262	0.018008	0.003199	1.1E-08
PABPC4 *	1	rs4660846	39,583,839	C	T	0.118905	0.017482	0.003108	1.0E-08
PABPC4 *	1	rs7539261	39,584,831	A	T	0.118926	0.017510	0.003107	1.0E-08
PABPC4 *	1	rs7539279	39,584,896	A	G	0.118926	0.017510	0.003107	1.0E-08
PABPC4 *	1	rs61781371	39,586,436	G	C	0.111151	0.017866	0.003201	1.3E-08
PABPC4 *	1	rs9729677	39,587,137	T	G	0.118457	0.017157	0.003116	2.3E-08
PABPC4 *	1	rs11206387	39,587,326	A	G	0.118416	0.017041	0.003116	2.8E-08
PABPC4 *	1	rs61781373	39,587,421	C	A	0.104168	0.017983	0.003321	3.5E-08
PABPC4 *	1	rs2695324	39,587,969	A	G	0.118428	0.017123	0.003116	2.4E-08
PABPC4 *	1	rs11206390	39,588,827	G	A	0.118428	0.017120	0.003116	2.4E-08
PABPC4 *	1	rs2695319	39,591,028	C	G	0.117244	0.017477	0.003133	1.5E-08
PABPC4 *	1	rs113825410	39,591,871	G	A	0.111155	0.017855	0.003201	1.4E-08
PABPC4 *	1	rs76841360	39,594,353	A	G	0.111153	0.017844	0.003201	1.5E-08
PABPC4 *	1	rs4660303	39,594,801	A	G	0.111148	0.017855	0.003202	1.4E-08
PABPC4 *	1	rs12037222	39,599,289	A	G	0.108696	0.017491	0.003230	4.6E-08
PABPC4 *	1	rs74504886	39,599,944	A	G	0.108118	0.018153	0.003237	1.5E-08
HEYL *	1	rs149794918	39,600,183	G	GT	0.106784	0.017912	0.003259	2.4E-08

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
HEYL *	1	rs3916164	39,604,267	A	G	0.108798	0.018042	0.003227	1.4E-08
HEYL *	1	rs113879410	39,607,339	C	G	0.108149	0.017856	0.003237	2.3E-08
HEYL *	1	rs61781377	39,609,786	T	C	0.111734	0.017882	0.003194	1.2E-08
HEYL *	1	rs61781390	39,610,222	A	G	0.111784	0.017834	0.003192	1.4E-08
HEYL *	1	rs61781391	39,611,865	A	G	0.111827	0.017732	0.003193	1.7E-08
HEYL *	1	rs61781392	39,617,969	A	C	0.113111	0.017892	0.003178	1.0E-08
HEYL *	1	rs61232586	39,620,685	T	G	0.112655	0.017867	0.003187	1.2E-08
HEYL *	1	rs61781393	39,622,092	A	G	0.112032	0.017678	0.003195	1.8E-08
HEYL *	1	rs17343290	39,622,371	A	G	0.112476	0.017872	0.003188	1.2E-08
USP1 *	1	rs1334806	62,409,642	A	G	0.446147	0.012921	0.002060	1.5E-10
USP1 *	1	rs72929768	62,416,932	T	C	0.449834	0.013730	0.002065	1.1E-11
USP1 *	1	rs12406266	62,426,154	A	G	0.336307	-0.018225	0.002133	2.4E-18
USP1 *	1	rs13375306	62,426,411	A	G	0.325680	-0.017956	0.002157	1.3E-17
USP1 *	1	rs584998	62,426,557	G	A	0.409825	-0.013849	0.002050	5.4E-12
USP1 *	1	rs11207965	62,427,445	A	C	0.336515	-0.018556	0.002129	4.3E-19
USP1 *	1	rs56941198	62,427,538	AT	A	0.409792	-0.014023	0.002048	2.7E-12
USP1 *	1	rs12023351	62,427,860	T	C	0.407580	-0.014520	0.002049	4.9E-13
USP1 *	1	rs12045584	62,429,211	T	A	0.336589	-0.018473	0.002128	5.4E-19
USP1 *	1	rs12025429	62,430,113	T	C	0.334186	-0.018936	0.002132	8.6E-20
USP1 *	1	rs635897	62,430,748	C	A	0.407859	-0.014610	0.002047	3.3E-13
USP1 *	1	rs662723	62,432,105	G	A	0.409580	-0.014098	0.002045	1.9E-12
USP1 *	1	rs10493324	62,432,471	T	C	0.324072	-0.020402	0.002170	7.5E-22
USP1 *	1	rs60500353	62,433,313	T	C	0.211408	-0.028577	0.002507	4.8E-32
USP1 *	1	rs624698	62,435,140	G	A	0.260173	-0.030297	0.002303	6.6E-43
USP1 *	1	rs624700	62,435,141	C	G	0.260173	-0.030297	0.002303	6.6E-43
USP1 *	1	rs626787	62,435,572	G	C	0.259766	-0.030527	0.002295	1.2E-43
USP1 *	1	rs631106	62,436,136	A	C	0.259620	-0.030431	0.002295	2.0E-43
USP1	1	rs646179	62,437,203	G	A	0.382925	-0.022791	0.002079	3.9E-30
USP1	1	rs9436221	62,437,688	C	T	0.254188	-0.030218	0.002310	3.1E-42
USP1	1	rs9436222	62,437,692	G	C	0.254188	-0.030218	0.002310	3.1E-42
USP1	1	rs9436223	62,437,876	T	C	0.254182	-0.030291	0.002310	1.9E-42
USP1	1	rs12029068	62,438,624	T	C	0.254182	-0.030291	0.002310	1.9E-42
USP1	1	rs9436661	62,438,904	G	T	0.254184	-0.030288	0.002310	1.9E-42
USP1	1	rs11588261	62,439,265	A	G	0.254186	-0.030288	0.002310	1.9E-42
USP1	1	rs10493322	62,440,222	T	C	0.212511	-0.033275	0.002456	1.0E-44
USP1	1	rs60688353	62,440,418	CAA	C	0.212509	-0.033342	0.002455	7.9E-45
USP1	1	rs187325430	62,440,427	T	C	0.051831	-0.026165	0.004556	8.5E-09
USP1	1	rs638714	62,440,818	T	G	0.253764	-0.030448	0.002311	9.4E-43
USP1	1	rs638305	62,440,866	T	G	0.254348	-0.030356	0.002308	1.4E-42
USP1	1	chr1:62441011_A_AT	62,441,011	AT	A	0.239677	-0.030562	0.002382	1.1E-40
USP1	1	rs637723	62,441,057	T	C	0.251645	-0.030884	0.002323	2.4E-43
USP1	1	rs656297	62,441,924	G	A	0.254348	-0.030356	0.002308	1.4E-42
USP1	1	rs642845	62,442,564	C	T	0.261748	-0.028901	0.002296	3.6E-39
USP1	1	rs641540	62,442,867	G	A	0.254348	-0.030356	0.002308	1.4E-42
USP1	1	rs527281380	62,444,278	A	AAAG	0.226059	-0.032067	0.002429	6.5E-43
USP1	1	rs1553145497	62,445,632	GTGTA	G	0.254395	-0.030138	0.002310	5.8E-42
USP1	1	rs10647753	62,445,634	GTA	G	0.254703	-0.030276	0.002310	3.0E-42
USP1	1	rs598253	62,445,670	C	T	0.254332	-0.030369	0.002309	1.3E-42
USP1	1	rs11207969	62,446,080	G	A	0.254332	-0.030369	0.002309	1.3E-42
USP1	1	rs659656	62,446,449	G	C	0.254332	-0.030369	0.002309	1.3E-42
USP1	1	rs150910573	62,447,199	G	A	0.023553	-0.038285	0.006659	1.8E-09
USP1	1	rs10158897	62,447,248	T	C	0.212528	-0.033332	0.002456	9.4E-45
USP1	1	rs783291	62,449,307	A	G	0.254350	-0.030373	0.002309	1.2E-42
USP1	1	rs11207970	62,449,802	T	C	0.211490	-0.033436	0.002463	8.7E-45
USP1	1	rs583609	62,451,125	C	T	0.254361	-0.030374	0.002309	1.2E-42
USP1 *	1	rs597470	62,452,125	G	T	0.254350	-0.030377	0.002309	1.2E-42
USP1 *	1	rs597078	62,452,186	A	G	0.253893	-0.030443	0.002311	1.1E-42
USP1 *	1	rs597076	62,452,194	A	T	0.253893	-0.030443	0.002311	1.1E-42
USP1 *	1	rs630144	62,453,193	G	A	0.254354	-0.030379	0.002309	1.2E-42
DOCK7 *	1	chr1:62453356_GT_G	62,453,356	G	GT	0.251615	-0.030982	0.002337	3.8E-43
DOCK7 *	1	rs79346928	62,454,307	CAT	C	0.212539	-0.033346	0.002455	7.2E-45
DOCK7 *	1	rs636523	62,454,337	G	A	0.212279	-0.033058	0.002457	3.4E-44
DOCK7 *	1	rs636497	62,454,358	G	A	0.254372	-0.030346	0.002308	1.4E-42
DOCK7 *	1	rs624660	62,454,717	A	C	0.254957	-0.030366	0.002309	1.3E-42
DOCK7	1	rs634341	62,455,751	C	T	0.251475	-0.030460	0.002324	2.2E-42
DOCK7	1	rs3913007	62,455,915	C	T	0.212540	-0.033366	0.002456	6.6E-45
DOCK7	1	rs4350231	62,456,989	A	G	0.210422	-0.033699	0.002465	3.6E-45
DOCK7	1	rs12023489	62,458,187	A	G	0.253832	-0.030380	0.002312	1.6E-42
DOCK7	1	rs12037659	62,458,192	T	C	0.211956	-0.033426	0.002460	7.0E-45
DOCK7	1	rs62932760	62,458,534	TG	T	0.237063	-0.029692	0.002391	9.8E-38
DOCK7	1	rs9988450	62,458,777	T	C	0.254376	-0.030360	0.002309	1.3E-42
DOCK7	1	rs77064258	62,460,056	T	C	0.176857	-0.031695	0.002650	2.0E-35
DOCK7	1	rs13055520	62,460,386	A	T	0.254560	-0.030454	0.002310	7.9E-43
DOCK7	1	rs7547965	62,460,700	G	A	0.254618	-0.030420	0.002310	9.4E-43
DOCK7	1	chr1:62462070_CA_C	62,462,070	C	CA	0.232320	-0.031687	0.002430	2.1E-41
DOCK7	1	rs1167996	62,462,126	T	G	0.251997	-0.030638	0.002317	4.7E-43
DOCK7	1	rs998403	62,462,878	A	G	0.210694	-0.033659	0.002463	2.5E-45
DOCK7	1	rs11356503	62,463,707	T	TA	0.210694	-0.033659	0.002463	2.5E-45
DOCK7	1	rs1177541	62,464,221	G	A	0.253005	-0.030660	0.002314	3.5E-43
DOCK7	1	rs77083979	62,464,435	A	G	0.202337	-0.033182	0.002501	6.5E-43
DOCK7	1	rs11207972	62,464,553	G	A	0.253023	-0.030644	0.002314	3.8E-43
DOCK7	1	rs1167998	62,465,961	C	A	0.259674	-0.029711	0.002293	9.7E-42
DOCK7	1	rs77907749	62,466,449	T	C	0.202368	-0.033068	0.002500	1.1E-42
DOCK7	1	rs1168001	62,468,087	G	A	0.253041	-0.030581	0.002314	5.2E-43
DOCK7	1	rs12124284	62,468,356	A	G	0.210957	-0.033691	0.002462	1.9E-45
DOCK7	1	rs1168002	62,468,637	A	G	0.253915	-0.030757	0.002316	1.9E-43
DOCK7	1	rs1168003	62,469,175	G	A	0.253041	-0.030581	0.002314	5.2E-43
DOCK7	1	rs12043877	62,469,328	T	C	0.202369	-0.033080	0.002500	1.0E-42
DOCK7	1	rs1007205	62,471,241	T	C	0.252975	-0.030578	0.002315	5.5E-43
DOCK7	1	rs10889330	62,473,795	C	G	0.253039	-0.030570	0.002314	5.4E-43
DOCK7	1	rs1979722	62,474,426	A	G	0.210736	-0.033562	0.002463	4.1E-45
DOCK7	1	rs11442941	62,474,595	T	TG	0.252958	-0.030543	0.002315	7.2E-43
DOCK7	1	chr1:62475497_GA_G	62,475,497	GA	G	0.256426	-0.030546	0.002323	4.0E-42
DOCK7	1	rs182487886	62,477,264	C	T	0.020717	-0.038907	0.007079	7.5E-09
DOCK7	1	rs10889331	62,477,336	G	T	0.253039	-0.030558	0.002314	5.8E-43
DOCK7	1	rs1168009	62,478,283	G	A	0.253249	-0.030567	0.002315	5.5E-43
DOCK7	1	rs1168010	62,478,308	G	A	0.253322	-0.030530	0.002315	7.0E-43

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
DOCK7	1	rs35913674	62,479,276	CA	C	0.253588	-0.030602	0.002314	5.4E-43
DOCK7	1	rs1183260	62,479,747	A	G	0.252796	-0.030489	0.002314	9.1E-43
DOCK7	1	rs6587976	62,479,960	T	C	0.252796	-0.030489	0.002314	9.1E-43
DOCK7	1	rs1305521	62,483,363	A	G	0.254021	-0.030485	0.002314	1.2E-42
DOCK7	1	rs11207974	62,484,289	C	T	0.252752	-0.030524	0.002314	7.7E-43
DOCK7	1	rs10889332	62,485,187	T	C	0.252708	-0.030576	0.002316	7.4E-43
DOCK7	1	rs2489835	62,489,300	T	C	0.252698	-0.030582	0.002315	5.2E-43
DOCK7	1	rs1690761	62,490,191	C	T	0.252689	-0.030530	0.002315	6.8E-43
DOCK7	1	rs10889333	62,491,359	A	G	0.210685	-0.033686	0.002463	2.1E-45
DOCK7	1	rs10889334	62,491,528	G	C	0.210675	-0.033684	0.002463	2.0E-45
DOCK7	1	rs10789112	62,492,087	C	T	0.210679	-0.033701	0.002464	2.0E-45
DOCK7	1	rs1183851	62,492,987	T	C	0.378240	-0.023056	0.002083	7.4E-31
DOCK7	1	rs10889335	62,494,430	G	A	0.202695	-0.032492	0.002513	1.0E-40
DOCK7	1	rs1168041	62,494,579	T	C	0.217490	-0.029252	0.002437	1.2E-35
DOCK7	1	chr1:62494664_T_TG	62,494,664	TG	T	0.156236	-0.032521	0.002829	1.0E-32
DOCK7	1	rs1168040	62,494,904	T	C	0.252588	-0.031099	0.002315	2.2E-44
DOCK7	1	rs1168036	62,497,063	A	G	0.251242	-0.030796	0.002317	2.6E-43
DOCK7	1	rs1002687	62,498,066	G	A	0.252803	-0.030615	0.002316	5.4E-43
DOCK7	1	chr1:62498080_A_AT	62,498,080	A	AT	0.260819	-0.030398	0.002335	2.0E-41
DOCK7	1	rs1168034	62,498,243	G	C	0.251423	-0.030834	0.002317	1.9E-43
DOCK7	1	chr1:62499937_GA_G	62,499,937	GA	G	0.252113	-0.030796	0.002320	3.1E-43
DOCK7	1	rs35529421	62,499,950	A	T	0.204911	-0.033955	0.002502	1.5E-44
DOCK7	1	rs1168032	62,502,076	A	G	0.251234	-0.030859	0.002317	1.8E-43
DOCK7	1	rs1168031	62,502,316	C	T	0.251423	-0.030834	0.002317	1.9E-43
DOCK7	1	chr1:62502762_A_AT	62,502,762	AT	A	0.209336	-0.033907	0.002469	1.4E-45
DOCK7	1	rs1168030	62,502,820	C	T	0.251563	-0.030895	0.002317	1.4E-43
DOCK7	1	rs56342264	62,503,238	T	TA	0.209468	-0.033947	0.002468	9.9E-46
DOCK7	1	rs1168029	62,503,731	G	A	0.252371	-0.030533	0.002316	8.9E-43
DOCK7	1	rs1168028	62,503,760	G	A	0.251421	-0.030829	0.002317	1.9E-43
DOCK7	1	rs1168027	62,504,513	T	C	0.251240	-0.030792	0.002317	2.7E-43
DOCK7	1	rs1168026	62,505,325	T	C	0.251421	-0.030829	0.002317	1.9E-43
DOCK7	1	chr1:62506471_CT_C	62,506,471	CT	C	0.254110	-0.030474	0.002320	2.2E-42
DOCK7	1	rs7527004	62,506,557	G	A	0.251473	-0.030824	0.002317	2.2E-43
DOCK7	1	rs12027778	62,507,642	G	C	0.192586	-0.033649	0.002547	2.6E-42
DOCK7	1	rs1184865	62,508,124	A	G	0.251417	-0.030831	0.002317	1.9E-43
DOCK7	1	rs1168042	62,508,479	A	T	0.251236	-0.030800	0.002317	2.5E-43
DOCK7	1	rs35836805	62,508,787	T	TTTAC	0.209095	-0.033905	0.002470	1.7E-45
DOCK7	1	rs11207976	62,511,080	A	G	0.251234	-0.030794	0.002317	2.6E-43
DOCK7	1	rs11207977	62,511,636	T	C	0.209683	-0.033711	0.002469	5.0E-45
DOCK7	1	rs11781212	62,511,748	G	A	0.253481	-0.030311	0.002326	6.1E-42
DOCK7	1	rs1168044	62,511,887	A	C	0.254500	-0.030474	0.002319	1.8E-42
DOCK7	1	rs1690755	62,514,490	A	G	0.251509	-0.030841	0.002317	1.7E-43
DOCK7	1	rs10557760	62,514,728	CACA	C	0.251578	-0.030847	0.002317	2.0E-43
DOCK7	1	rs10889336	62,514,739	C	T	0.209613	-0.033943	0.002468	1.2E-45
DOCK7	1	rs10889337	62,514,936	A	G	0.251417	-0.030831	0.002317	1.9E-43
DOCK7	1	rs12090886	62,515,769	G	A	0.251417	-0.030831	0.002317	1.9E-43
DOCK7	1	rs11207979	62,517,323	A	G	0.251240	-0.030757	0.002317	3.2E-43
DOCK7	1	rs1168046	62,518,022	A	C	0.251134	-0.030760	0.002318	3.3E-43
DOCK7	1	rs1168047	62,518,080	C	T	0.251240	-0.030757	0.002317	3.2E-43
DOCK7	1	rs10889338	62,519,226	T	C	0.209285	-0.033876	0.002469	1.7E-45
DOCK7	1	rs1168050	62,521,284	C	T	0.251275	-0.030732	0.002318	3.9E-43
DOCK7	1	rs1690766	62,521,618	T	C	0.251243	-0.030742	0.002317	3.6E-43
DOCK7	1	rs11781195	62,523,301	T	C	0.251829	-0.030590	0.002316	9.6E-43
DOCK7	1	rs1627591	62,524,136	C	T	0.251242	-0.030745	0.002317	3.6E-43
DOCK7	1	rs11577840	62,525,698	T	C	0.251242	-0.030745	0.002317	3.6E-43
DOCK7	1	rs12062275	62,526,234	T	C	0.251242	-0.030745	0.002317	3.6E-43
DOCK7	1	rs11207980	62,527,078	C	T	0.209585	-0.033868	0.002470	1.6E-45
DOCK7	1	rs4915838	62,527,397	G	A	0.251240	-0.030740	0.002317	3.7E-43
DOCK7	1	rs12403207	62,527,949	T	C	0.251891	-0.030854	0.002321	3.2E-43
DOCK7	1	rs12039115	62,529,592	T	C	0.200908	-0.033317	0.002507	6.5E-43
DOCK7	1	rs1168015	62,530,375	C	G	0.251236	-0.030742	0.002317	3.6E-43
DOCK7	1	rs1168013	62,531,167	C	G	0.251223	-0.030694	0.002317	4.5E-43
DOCK7	1	rs10458569	62,531,930	A	C	0.181609	-0.032324	0.002607	1.5E-37
DOCK7	1	rs35664253	62,532,065	C	CAG	0.251242	-0.030730	0.002317	3.7E-43
DOCK7	1	chr1:62533439_A_AT	62,533,439	A	AT	0.251354	-0.030833	0.002318	2.2E-43
DOCK7	1	rs4915840	62,533,924	C	G	0.251419	-0.030817	0.002318	2.5E-43
DOCK7	1	rs61393465	62,535,060	G	GC	0.209292	-0.033837	0.002469	2.0E-45
DOCK7	1	rs1168018	62,535,449	A	C	0.251223	-0.030746	0.002317	3.5E-43
DOCK7	1	rs1168017	62,536,880	A	G	0.251242	-0.030730	0.002317	3.7E-43
DOCK7	1	rs76176236	62,538,722	C	T	0.121218	-0.029502	0.003094	3.5E-23
DOCK7	1	rs56115463	62,540,080	A	C	0.200015	-0.033345	0.002514	9.7E-43
DOCK7	1	rs7548877	62,540,279	T	C	0.251258	-0.030709	0.002318	4.3E-43
DOCK7	1	rs11207981	62,540,416	C	A	0.251467	-0.030827	0.002319	2.5E-43
DOCK7	1	rs1168023	62,540,924	A	T	0.251260	-0.030704	0.002318	4.4E-43
DOCK7	1	rs66827188	62,541,132	TTATAG/	T	0.251774	-0.030604	0.002319	8.6E-43
DOCK7	1	rs11781221	62,541,171	A	C	0.251295	-0.030705	0.002318	4.3E-43
DOCK7	1	rs11207982	62,541,511	T	C	0.209307	-0.033833	0.002469	2.1E-45
DOCK7	1	rs1184547	62,541,557	G	A	0.251260	-0.030704	0.002318	4.4E-43
DOCK7	1	rs1168022	62,542,050	A	T	0.251253	-0.030711	0.002318	4.3E-43
DOCK7	1	rs76755357	62,542,503	A	G	0.052743	-0.026124	0.004515	4.6E-09
DOCK7	1	rs1168021	62,544,229	A	G	0.252147	-0.030476	0.002317	1.8E-42
DOCK7	1	rs1168020	62,544,285	C	T	0.252352	-0.030480	0.002319	2.3E-42
DOCK7	1	rs1179765	62,544,439	G	C	0.251260	-0.030725	0.002318	3.8E-43
DOCK7	1	rs12074528	62,545,200	T	C	0.251260	-0.030725	0.002318	3.8E-43
DOCK7	1	rs10889339	62,546,385	A	G	0.251494	-0.030768	0.002318	2.8E-43
DOCK7	1	rs10889340	62,546,400	A	C	0.251374	-0.030732	0.002318	3.5E-43
DOCK7	1	rs11207983	62,546,436	C	T	0.251260	-0.030725	0.002318	3.8E-43
DOCK7	1	rs2029763	62,547,463	G	A	0.209307	-0.033857	0.002469	1.8E-45
DOCK7	1	rs11207984	62,547,725	C	T	0.251260	-0.030725	0.002318	3.8E-43
DOCK7	1	rs11207985	62,548,115	A	G	0.251308	-0.030711	0.002318	4.2E-43
DOCK7	1	rs10789113	62,549,528	T	A	0.209325	-0.033860	0.002469	1.8E-45
DOCK7	1	chr1:62550719_AT_A	62,550,719	AT	A	0.262905	-0.029940	0.002335	1.2E-40
DOCK7	1	rs11207986	62,552,499	T	C	0.251275	-0.030732	0.002318	3.8E-43
DOCK7	1	rs10889342	62,553,181	T	C	0.207182	-0.034033	0.002482	1.7E-45
DOCK7	1	rs11207988	62,553,316	T	A	0.188948	-0.031820	0.002606	2.2E-36
DOCK7	1	rs7519785	62,554,248	G	A	0.251299	-0.030689	0.002317	5.1E-43
DOCK7	1	rs10159255	62,555,145	A	C	0.209355	-0.033821	0.002469	2.4E-45

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
DOCK7	1	rs2131925	62,560,271	G	T	0.252434	-0.030614	0.002316	7.0E-43
DOCK7	1	rs2131926	62,560,340	C	T	0.251466	-0.030761	0.002316	3.2E-43
DOCK7	1	rs10889343	62,560,758	T	G	0.251466	-0.030761	0.002316	3.2E-43
DOCK7	1	rs4329540	62,561,353	C	T	0.252096	-0.030593	0.002315	8.7E-43
DOCK7	1	chr1:62562233_CTTT_C	62,562,233	C	CTTT	0.209513	-0.033857	0.002468	1.9E-45
DOCK7	1	rs4915621	62,563,762	A	G	0.251415	-0.030767	0.002317	3.2E-43
DOCK7	1	rs12025714	62,565,940	A	C	0.197041	-0.032605	0.002532	3.4E-40
DOCK7	1	rs6693353	62,565,945	A	C	0.251404	-0.030794	0.002317	2.7E-43
DOCK7	1	rs139360475	62,566,892	AACAG	A	0.457553	-0.019540	0.002038	2.3E-23
DOCK7	1	rs10889344	62,568,270	C	C	0.251403	-0.030800	0.002317	2.6E-43
DOCK7	1	rs10789114	62,568,551	C	T	0.208125	-0.033851	0.002477	3.8E-45
DOCK7	1	rs7555577	62,568,692	A	C	0.251261	-0.030747	0.002322	4.2E-43
DOCK7	1	rs10789115	62,570,458	A	G	0.251397	-0.030809	0.002317	2.4E-43
DOCK7	1	rs12735272	62,571,136	G	A	0.251397	-0.030809	0.002317	2.4E-43
DOCK7	1	rs12116574	62,572,166	T	C	0.205699	-0.033309	0.002491	4.2E-43
DOCK7	1	rs142666378	62,572,632	T	TGG	0.251397	-0.030809	0.002317	2.4E-43
DOCK7	1	rs6696502	62,573,862	C	T	0.251392	-0.030830	0.002317	2.2E-43
DOCK7	1	rs12038768	62,575,057	T	G	0.209509	-0.033889	0.002468	1.6E-45
DOCK7	1	rs1207990	62,575,415	T	C	0.251386	-0.030839	0.002317	2.1E-43
DOCK7	1	rs11207992	62,576,129	G	T	0.209509	-0.033889	0.002468	1.6E-45
DOCK7	1	rs1472257	62,576,455	A	G	0.251381	-0.030837	0.002317	2.1E-43
DOCK7	1	rs10789116	62,577,067	G	A	0.209509	-0.033889	0.002468	1.6E-45
DOCK7	1	rs1748201	62,579,835	A	C	0.250203	-0.030956	0.002322	1.7E-43
DOCK7	1	rs1748200	62,580,368	T	C	0.251559	-0.030849	0.002317	2.0E-43
DOCK7	1	rs1629122	62,580,907	C	A	0.251656	-0.030746	0.002317	3.6E-43
DOCK7	1	chr1:62582603_C_CCCCA	62,582,603	CCCCA	C	0.206698	-0.033042	0.002527	4.6E-41
DOCK7	1	rs9436224	62,582,604	C	A	0.229541	-0.030208	0.002444	1.9E-37
DOCK7	1	rs34465969	62,582,605	C	A	0.227121	-0.030087	0.002446	3.0E-37
DOCK7	1	rs35194512	62,582,606	C	A	0.185915	-0.034011	0.002629	2.0E-40
DOCK7	1	rs11207995	62,583,880	C	A	0.211869	-0.033735	0.002466	2.4E-45
DOCK7	1	rs1748195	62,583,922	G	C	0.243851	-0.029750	0.002342	1.6E-39
DOCK7	1	rs12042319	62,584,148	A	G	0.209490	-0.033920	0.002468	1.3E-45
DOCK7	1	rs3850634	62,584,927	G	T	0.209567	-0.033793	0.002467	2.5E-45
DOCK7	1	rs12030293	62,586,017	T	C	0.201082	-0.033329	0.002506	6.0E-43
DOCK7	1	rs12048208	62,589,609	A	G	0.199653	-0.033542	0.002516	3.5E-43
DOCK7	1	rs11207996	62,589,799	A	G	0.209821	-0.033859	0.002470	2.5E-45
DOCK7	1	rs188174159	62,589,831	C	G	0.066423	-0.025845	0.004056	7.4E-11
DOCK7	1	rs1748197	62,590,441	A	G	0.221696	-0.032914	0.002417	1.7E-44
DOCK7	1	rs2366636	62,590,999	A	G	0.221696	-0.032914	0.002417	1.7E-44
DOCK7	1	rs1748199	62,591,465	C	T	0.221696	-0.032914	0.002417	1.7E-44
DOCK7	1	rs79439217	62,594,366	TAAGAA	T	0.251339	-0.030919	0.002319	1.7E-43
DOCK7	1	rs6690733	62,594,640	C	A	0.251299	-0.030777	0.002317	3.1E-43
DOCK7	1	rs79151558	62,595,131	G	A	0.036518	-0.034167	0.005402	9.0E-11
DOCK7	1	rs11207997	62,596,235	T	C	0.251335	-0.030806	0.002317	2.5E-43
ANGPTL3, DOCK7	1	rs34483103	62,604,866	A	TTAATG	0.209166	-0.033817	0.002472	2.8E-45
DOCK7	1	rs10789117	62,606,594	C	A	0.253192	-0.030428	0.002313	1.4E-42
DOCK7	1	rs59952505	62,607,196	C	CA	0.253216	-0.030540	0.002312	5.8E-43
DOCK7	1	rs6675401	62,608,304	T	C	0.252933	-0.030536	0.002312	8.1E-43
DOCK7	1	rs6678483	62,608,771	A	C	0.252935	-0.030539	0.002312	8.0E-43
DOCK7	1	rs71776858	62,608,856	C	CTCAT	0.209388	-0.033664	0.002470	5.7E-45
DOCK7	1	rs10889347	62,610,155	A	G	0.252930	-0.030554	0.002312	7.5E-43
DOCK7	1	rs10889348	62,612,551	T	A	0.209496	-0.033688	0.002470	4.9E-45
DOCK7	1	rs146535322	62,614,247	A	G	0.020540	-0.042372	0.007107	3.8E-10
DOCK7	1	rs10889349	62,616,248	G	A	0.246464	-0.031257	0.002341	4.9E-43
DOCK7	1	rs2031373	62,617,618	A	C	0.385613	-0.022925	0.002073	1.3E-30
DOCK7	1	rs61471917	62,618,359	A	G	0.252933	-0.030541	0.002312	8.2E-43
DOCK7	1	rs10889350	62,619,595	T	C	0.253200	-0.030459	0.002313	1.3E-42
DOCK7	1	chr1:62619812_T_TA	62,619,812	TA	T	0.376558	-0.022394	0.002107	1.8E-28
DOCK7	1	rs12239736	62,620,326	A	T	0.208492	-0.033779	0.002478	4.0E-45
DOCK7	1	rs12239737	62,620,330	A	T	0.153624	-0.032393	0.002846	1.7E-31
DOCK7	1	rs6587980	62,625,187	T	C	0.251259	-0.030729	0.002319	3.4E-43
DOCK7	1	rs11207998	62,625,800	C	G	0.200879	-0.033245	0.002507	1.1E-42
DOCK7	1	rs10157265	62,627,946	T	C	0.252908	-0.030546	0.002312	7.6E-43
DOCK7	1	rs34211669	62,627,990	G	GT	0.209284	-0.033755	0.002469	3.7E-45
DOCK7	1	rs11485618	62,628,536	G	A	0.209264	-0.033768	0.002469	3.3E-45
DOCK7	1	rs10789118	62,629,021	G	A	0.209257	-0.033753	0.002469	3.5E-45
DOCK7	1	rs7520810	62,630,040	T	C	0.252813	-0.030519	0.002313	8.3E-43
DOCK7	1	rs12025800	62,631,110	G	C	0.252912	-0.030555	0.002313	7.2E-43
DOCK7	1	rs141409973	62,631,753	AG	A	0.252912	-0.030555	0.002313	7.2E-43
DOCK7	1	rs10789119	62,632,564	A	G	0.209276	-0.033756	0.002469	3.4E-45
DOCK7	1	rs11207999	62,632,970	C	A	0.252912	-0.030555	0.002313	7.2E-43
DOCK7	1	rs10889352	62,633,352	C	T	0.209257	-0.033753	0.002469	3.5E-45
DOCK7	1	rs2366638	62,633,906	A	G	0.252912	-0.030554	0.002313	7.3E-43
DOCK7	1	rs377031118	62,634,374	GA	G	0.252422	-0.030535	0.002316	9.4E-43
DOCK7	1	rs10789120	62,635,452	A	G	0.208696	-0.033509	0.002473	1.6E-44
DOCK7	1	rs1570694	62,637,546	G	A	0.209241	-0.033701	0.002469	4.7E-45
DOCK7	1	rs6657050	62,639,582	G	A	0.252043	-0.030476	0.002317	1.4E-42
DOCK7	1	rs12047226	62,639,867	C	T	0.209234	-0.033709	0.002469	4.4E-45
DOCK7	1	rs113795489	62,640,503	A	AAAGC	0.209232	-0.033707	0.002469	4.4E-45
DOCK7	1	rs7538689	62,640,577	A	G	0.385976	-0.022667	0.002068	5.4E-30
DOCK7	1	rs7539035	62,641,096	A	C	0.252893	-0.030557	0.002313	6.8E-43
DOCK7	1	rs995000	62,641,855	T	C	0.208334	-0.033423	0.002474	3.2E-44
DOCK7	1	rs10789121	62,642,348	C	T	0.385878	-0.022777	0.002069	3.0E-30
DOCK7	1	rs11208000	62,642,703	G	A	0.249548	-0.030866	0.002329	3.8E-43
DOCK7	1	rs66531495	62,643,009	A	GGCCAC	0.249840	-0.030837	0.002331	6.6E-43
DOCK7	1	rs993013	62,645,398	G	T	0.254192	-0.030577	0.002310	5.2E-43
DOCK7	1	rs1168085	62,646,649	C	G	0.252908	-0.030577	0.002313	6.3E-43
DOCK7	1	rs1168086	62,646,718	A	G	0.252908	-0.030577	0.002313	6.3E-43
DOCK7	1	rs746735	62,647,840	C	A	0.253200	-0.030473	0.002314	1.1E-42
DOCK7	1	rs1168089	62,648,048	T	C	0.251840	-0.030232	0.002316	5.8E-42
DOCK7	1	rs33999917	62,650,370	GA	G	0.251869	-0.030286	0.002315	3.8E-42
DOCK7	1	rs1168093	62,650,556	G	A	0.251877	-0.030279	0.002315	4.0E-42
DOCK7	1	rs112957492	62,651,339	C	T	0.208197	-0.033484	0.002473	1.9E-44
DOCK7	1	rs35107877	62,651,507	A	AG	0.251887	-0.030283	0.002315	3.8E-42
DOCK7	1	rs10889353	62,652,525	C	A	0.208908	-0.033255	0.002472	6.8E-44
DOCK7	1	rs1168097	62,654,700	C	T	0.256311	-0.029851	0.002310	4.9E-41
DOCK7	1	rs60286666	62,655,430	T	TC	0.253112	-0.030688	0.002313	3.4E-43

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
DOCK7	1	rs1168098	62,655,623	G	A	0.252816	-0.030700	0.002315	3.4E-43
DOCK7	1	rs1168099	62,657,188	C	A	0.253144	-0.030577	0.002313	5.8E-43
DOCK7	1	rs4495740	62,658,794	G	T	0.208222	-0.033508	0.002473	1.6E-44
DOCK7	1	rs1168100	62,658,871	T	C	0.451796	-0.019479	0.002037	5.2E-23
DOCK7	1	rs1168102	62,662,034	C	T	0.251886	-0.030294	0.002315	3.9E-42
DOCK7	1	rs1168103	62,662,410	C	T	0.251982	-0.030241	0.002315	5.6E-42
DOCK7	1	rs1168104	62,662,654	A	G	0.251880	-0.030275	0.002315	4.5E-42
DOCK7	1	rs10889354	62,663,411	C	T	0.208282	-0.033575	0.002474	1.2E-44
DOCK7	1	rs11208001	62,664,760	T	C	0.251171	-0.029800	0.002332	5.0E-40
DOCK7	1	rs12024419	62,664,854	A	G	0.180849	-0.032287	0.002615	4.0E-37
DOCK7	1	rs2479464	62,665,320	G	A	0.251893	-0.030184	0.002316	9.1E-42
DOCK7	1	rs1168132	62,667,797	T	A	0.251856	-0.030190	0.002316	9.6E-42
DOCK7	1	rs4587594	62,668,259	A	G	0.208210	-0.033428	0.002474	3.1E-44
DOCK7	1	rs28399032	62,669,953	C	G	0.208160	-0.033521	0.002474	2.0E-44
DOCK7	1	rs1168128	62,670,175	C	G	0.251922	-0.030326	0.002318	4.7E-42
DOCK7	1	rs181835401	62,670,284	A	G	0.250533	-0.030297	0.002324	8.1E-42
DOCK7	1	rs1168124	62,674,059	C	T	0.251723	-0.030347	0.002317	3.8E-42
DOCK7	1	rs138271600	62,679,499	A	G	0.052311	-0.026413	0.004533	3.4E-09
DOCK7	1	rs11208004	62,679,768	A	G	0.208465	-0.033200	0.002476	9.1E-44
DOCK7	1	rs4459145	62,680,578	A	C	0.246719	-0.030015	0.002344	1.7E-40
DOCK7	1	rs7531579	62,681,369	C	A	0.207963	-0.033630	0.002476	1.3E-44
DOCK7	1	chr1:62686882_G_GA	62,686,882	GA	G	0.195389	-0.033102	0.002563	1.4E-40
DOCK7	1	rs56280080	62,687,528	T	TCAGAA	0.207453	-0.033630	0.002487	2.0E-44
DOCK7	1	rs4344355	62,688,282	T	C	0.208133	-0.033780	0.002487	9.2E-45
DOCK7 *	1	rs10889356	62,689,678	A	G	0.207614	-0.033615	0.002486	2.1E-44
DOCK7 *	1	rs1168114	62,690,372	A	G	0.216110	-0.032565	0.002455	2.2E-42
DOCK7 *	1	rs1168113	62,690,427	T	C	0.235798	-0.029703	0.002378	7.0E-38
DOCK7 *	1	rs35834397	62,693,541	TA	T	0.226444	-0.030229	0.002409	6.4E-38
DOCK7 *	1	rs10889357	62,694,611	T	C	0.193612	-0.033455	0.002552	1.2E-41
DOCK7 *	1	rs1168107	62,695,502	A	T	0.226477	-0.030205	0.002409	6.9E-38
DOCK7 *	1	rs12136083	62,697,402	C	T	0.193682	-0.033535	0.002551	7.2E-42
DOCK7 *	1	rs9659790	62,700,090	G	A	0.226473	-0.030220	0.002408	5.6E-38
DOCK7 *	1	rs11208006	62,704,195	T	C	0.226477	-0.030136	0.002408	9.1E-38
DOCK7 *	1	rs12041843	62,704,478	G	T	0.177990	-0.032148	0.002650	2.6E-36
DOCK7 *	1	rs6682423	62,705,392	C	T	0.226440	-0.030199	0.002408	6.6E-38
DOCK7 *	1	rs6666816	62,705,528	C	T	0.226440	-0.030193	0.002408	6.8E-38
DOCK7 *	1	rs880694	62,707,613	C	T	0.226529	-0.030211	0.002408	5.9E-38
DOCK7 *	1	rs10889360	62,708,247	T	C	0.193667	-0.033540	0.002551	6.6E-42
DOCK7 *	1	rs11208007	62,710,412	T	A	0.193719	-0.033540	0.002550	6.1E-42
DOCK7 *	1	rs4409689	62,711,694	C	T	0.226474	-0.030259	0.002408	4.8E-38
DOCK7 *	1	rs60152331	62,711,868	G	T	0.370903	-0.021967	0.002107	6.9E-27
DOCK7 *	1	rs7518497	62,712,025	C	A	0.193661	-0.033580	0.002551	5.0E-42
DOCK7 *	1	rs9787151	62,713,467	C	T	0.226546	-0.030250	0.002407	4.4E-38
DOCK7 *	1	rs9787156	62,713,541	G	A	0.226553	-0.030251	0.002407	4.3E-38
DOCK7 *	1	rs117487653	62,715,289	C	T	0.052752	-0.026074	0.004514	8.3E-09
DOCK7 *	1	rs12043910	62,715,877	A	G	0.185329	-0.033198	0.002595	7.5E-40
DOCK7 *	1	rs6686331	62,716,464	C	T	0.226492	-0.030359	0.002409	3.0E-38
DOCK7 *	1	rs75650238	62,717,743	C	CCA	0.184774	-0.033416	0.002600	4.0E-40
DOCK7 *	1	rs6661669	62,720,298	T	C	0.226771	-0.030492	0.002408	1.5E-38
DOCK7 *	1	rs76609868	62,720,544	C	A	0.183114	-0.033042	0.002611	4.3E-39
DOCK7 *	1	rs12031537	62,722,415	A	C	0.183609	-0.033218	0.002603	1.5E-39
DOCK7 *	1	rs7517372	62,723,893	G	A	0.212296	-0.029086	0.002469	6.9E-34
DOCK7 *	1	rs4915624	62,725,847	G	A	0.215902	-0.029723	0.002448	1.3E-35
DOCK7 *	1	rs76794398	62,725,894	A	G	0.183769	-0.032886	0.002600	6.1E-39
DOCK7 *	1	rs4915853	62,725,906	C	A	0.224779	-0.030111	0.002411	1.6E-37
DOCK7 *	1	rs199747920	62,727,151	ATTTC	A	0.216341	-0.029500	0.002446	3.2E-35
DOCK7 *	1	rs149188767	62,727,166	CTTTCT	C	0.224686	-0.028487	0.002444	4.3E-33
DOCK7 *	1	chr1:62727171_CT_C	62,727,171	C	CT	0.214293	-0.029457	0.002600	8.6E-35
DOCK7 *	1	rs12029452	62,727,599	C	A	0.183764	-0.032888	0.002600	5.9E-39
DOCK7 *	1	rs12026283	62,728,242	A	T	0.183764	-0.032888	0.002600	5.9E-39
DOCK7 *	1	rs2149116	62,728,301	G	A	0.374870	-0.021418	0.002110	2.6E-25
DOCK7 *	1	rs12023282	62,728,306	A	G	0.183802	-0.032849	0.002600	7.0E-39
DOCK7 *	1	rs6664692	62,729,989	C	T	0.212797	-0.029448	0.002462	1.1E-34
DOCK7 *	1	rs11208009	62,730,021	C	T	0.221232	-0.030041	0.002428	6.1E-37
DOCK7 *	1	rs10889364	62,731,143	T	C	0.183872	-0.032933	0.002599	4.4E-39
DOCK7 *	1	rs12049254	62,731,481	C	G	0.183897	-0.032940	0.002599	4.2E-39
DOCK7 *	1	rs76753312	62,733,237	C	G	0.183920	-0.032805	0.002597	6.2E-39
DOCK7 *	1	chr1:62733488_GA_G	62,733,488	GA	G	0.184982	-0.032955	0.002598	4.9E-39
DOCK7 *	1	rs4630152	62,733,601	C	T	0.213436	-0.029481	0.002456	6.2E-35
DOCK7 *	1	rs150990100	62,733,676	TG	T	0.222909	-0.030105	0.002430	5.4E-37
DOCK7 *	1	rs61775961	62,733,677	G	T	0.222533	-0.030072	0.002433	7.6E-37
DOCK7 *	1	rs61775962	62,733,679	A	G	0.222533	-0.030072	0.002433	7.6E-37
DOCK7 *	1	rs6679002	62,734,265	G	T	0.222056	-0.030066	0.002420	3.1E-37
DOCK7 *	1	rs12024044	62,734,645	A	G	0.184479	-0.032891	0.002593	4.5E-39
DOCK7 *	1	rs12025111	62,735,769	A	G	0.184378	-0.032959	0.002594	3.2E-39
DOCK7 *	1	rs12028944	62,735,867	A	T	0.184456	-0.032849	0.002594	5.5E-39
ATG4C *	1	chr1:62736501_AT_A	62,736,501	AT	A	0.195244	-0.031671	0.002595	3.7E-36
ATG4C *	1	rs12121288	62,736,790	G	A	0.213017	-0.029563	0.002462	5.8E-35
ATG4C *	1	rs72915166	62,736,922	A	G	0.212678	-0.029727	0.002466	2.9E-35
ATG4C *	1	rs78731792	62,736,973	A	G	0.183802	-0.033001	0.002606	5.3E-39
ATG4C *	1	rs66676942	62,737,728	A	AT	0.181146	-0.033192	0.002641	2.4E-38
ATG4C *	1	rs10789123	62,737,950	T	A	0.209539	-0.029896	0.002509	2.4E-34
ATG4C *	1	rs12027341	62,738,235	A	G	0.179391	-0.033157	0.002658	1.4E-37
ATG4C *	1	rs77870744	62,738,693	C	T	0.181167	-0.032550	0.002653	1.9E-36
ATG4C *	1	rs10889365	62,744,078	T	A	0.323051	-0.015892	0.002175	1.4E-14
ATG4C *	1	rs12124310	62,745,143	G	A	0.472345	-0.014078	0.002055	9.5E-13
ATG4C *	1	rs11208013	62,745,229	G	T	0.303204	-0.014919	0.002213	9.4E-13
ATG4C *	1	rs10889366	62,746,055	C	T	0.303363	-0.014851	0.002212	1.1E-12
ATG4C *	1	rs7517722	62,747,351	A	G	0.322981	-0.015801	0.002172	1.5E-14
ATG4C *	1	rs7546804	62,749,346	C	T	0.303729	-0.014636	0.002207	2.0E-12
ATG4C *	1	rs35245250	62,749,539	A	G	0.307233	-0.014672	0.002215	2.0E-12
ATG4C *	1	rs61765877	62,749,542	T	C	0.307552	-0.014640	0.002213	2.2E-12
ATG4C *	1	rs61765878	62,749,543	T	G	0.307565	-0.014546	0.002216	3.3E-12
ATG4C *	1	rs2149115	62,749,703	A	G	0.323849	-0.015649	0.002167	2.1E-14
ATG4C *	1	chr1:62750578_GT_G	62,750,578	GT	G	0.327027	-0.015356	0.002176	6.1E-14
ATG4C *	1	chr1:62750950_T_TA	62,750,950	T	TA	0.326091	-0.015363	0.002162	5.9E-14
ATG4C *	1	rs10789124	62,753,106	A	C	0.305256	-0.014429	0.002193	2.3E-12

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
ATG4C *	1	rs10749734	62,754,277	G	A	0.325344	-0.015291	0.002155	4.8E-14
ATG4C *	1	rs6663281	62,755,520	T	C	0.305289	-0.014451	0.002193	2.1E-12
ATG4C *	1	rs6702274	62,756,495	C	A	0.325105	-0.015389	0.002155	3.3E-14
ATG4C *	1	rs11208019	62,757,051	A	G	0.324993	-0.015402	0.002155	3.3E-14
ATG4C *	1	rs12085904	62,758,431	T	C	0.305299	-0.014480	0.002193	1.9E-12
ATG4C *	1	rs34837685	62,758,629	C	CG	0.305302	-0.014476	0.002193	1.9E-12
ATG4C *	1	rs12567340	62,759,440	T	C	0.325123	-0.015416	0.002154	2.9E-14
ATG4C *	1	rs6688416	62,759,580	A	C	0.325577	-0.015299	0.002156	4.6E-14
ATG4C *	1	rs6688417	62,759,584	A	G	0.325123	-0.015416	0.002154	2.9E-14
ATG4C *	1	rs11810184	62,759,727	A	G	0.470589	-0.013455	0.002049	6.6E-12
ATG4C *	1	rs6664372	62,759,780	C	G	0.305434	-0.014398	0.002193	2.5E-12
ATG4C *	1	rs11208021	62,759,863	T	C	0.325116	-0.015408	0.002154	3.0E-14
ATG4C *	1	rs6664677	62,760,028	C	T	0.325116	-0.015408	0.002154	3.0E-14
ATG4C *	1	rs11208023	62,760,152	C	T	0.325116	-0.015408	0.002154	3.0E-14
ATG4C *	1	rs11208024	62,760,241	T	C	0.325422	-0.015464	0.002155	2.8E-14
ATG4C *	1	rs10889371	62,760,321	T	C	0.305365	-0.014469	0.002193	1.9E-12
ATG4C *	1	rs35332757	62,760,475	T	TAA	0.325116	-0.015408	0.002154	3.0E-14
ATG4C *	1	rs10789125	62,761,091	T	C	0.325115	-0.015397	0.002154	3.1E-14
ATG4C *	1	rs10889372	62,761,709	C	T	0.325360	-0.015346	0.002156	4.2E-14
ATG4C *	1	rs34399640	62,762,493	G	GT	0.325573	-0.015245	0.002156	5.1E-14
ATG4C *	1	rs11208025	62,762,659	A	G	0.325001	-0.015366	0.002155	3.5E-14
ATG4C *	1	rs10889374	62,762,771	A	T	0.305289	-0.014462	0.002193	2.0E-12
ATG4C *	1	rs10889375	62,763,157	G	A	0.324919	-0.015393	0.002157	2.9E-14
ATG4C *	1	rs11208026	62,763,202	C	G	0.324567	-0.015181	0.002156	6.3E-14
ATG6C *	1	rs6656747	62,764,464	A	G	0.305286	-0.014493	0.002192	1.8E-12
ATG4C *	1	rs11208027	62,765,214	G	A	0.324830	-0.015369	0.002155	3.4E-14
ATG4C *	1	rs12138091	62,765,246	T	A	0.305165	-0.014518	0.002193	1.7E-12
ATG4C *	1	rs11807368	62,765,730	G	T	0.324846	-0.015409	0.002155	3.0E-14
ATG4C *	1	rs10889376	62,766,178	C	G	0.304704	-0.014281	0.002197	4.4E-12
ATG4C *	1	rs11579171	62,768,057	C	T	0.325910	-0.015122	0.002155	9.3E-14
ATG4C *	1	rs7543380	62,768,997	T	A	0.301671	-0.014946	0.002199	5.1E-13
ATG4C *	1	rs12044009	62,774,246	G	A	0.246036	-0.015124	0.002350	1.2E-11
ATG4C *	1	rs4396149	62,776,025	C	T	0.324558	-0.015210	0.002168	1.2E-13
ATG4C *	1	rs7540030	62,784,304	A	G	0.301312	-0.014889	0.002201	6.9E-13
ATG4C *	1	rs12750156	62,790,022	C	T	0.323352	-0.015445	0.002160	4.2E-14
ATG4C *	1	rs6657707	62,792,979	C	T	0.322156	-0.015656	0.002162	1.9E-14
ATG4C *	1	rs12129919	62,795,685	C	T	0.323369	-0.015431	0.002161	4.3E-14
ATG4C *	1	rs10736399	62,798,112	T	C	0.301206	-0.014930	0.002202	6.3E-13
ATG4C *	1	rs11208032	62,799,494	G	C	0.322160	-0.015653	0.002162	1.9E-14
ATG4C *	1	rs6587990	62,806,788	T	A	0.323454	-0.015392	0.002156	4.2E-14
ATG4C *	1	rs12752360	62,808,188	C	G	0.323452	-0.015386	0.002156	4.3E-14
ATG4C *	1	rs11579518	62,808,587	G	A	0.323814	-0.015209	0.002156	8.4E-14
ATG4C *	1	rs11208035	62,808,867	T	C	0.322459	-0.015551	0.002157	2.1E-14
ATG4C *	1	rs6683832	62,811,233	G	A	0.301554	-0.014806	0.002197	7.8E-13
ATG4C *	1	rs6686232	62,811,426	C	T	0.322436	-0.015561	0.002157	2.1E-14
ATG4C *	1	rs12120847	62,812,209	G	A	0.322235	-0.015559	0.002158	2.2E-14
ATG4C *	1	rs10749735	62,812,321	A	G	0.322235	-0.015559	0.002158	2.2E-14
ATG4C *	1	rs11208036	62,812,347	G	A	0.322235	-0.015559	0.002158	2.2E-14
ATG4C *	1	rs6665932	62,813,093	A	G	0.322237	-0.015557	0.002158	2.2E-14
ATG4C *	1	rs6657235	62,813,424	T	C	0.322237	-0.015557	0.002158	2.2E-14
ATG4C *	1	rs6660873	62,814,582	T	A	0.322238	-0.015554	0.002158	2.2E-14
ATG4C *	1	chr1:62815181_CT_C	62,815,181	CT	C	0.473014	-0.013522	0.002028	4.3E-12
ATG4C *	1	rs6682286	62,815,748	G	A	0.322238	-0.015554	0.002158	2.2E-14
ATG4C *	1	rs7539616	62,817,334	C	T	0.477165	-0.013415	0.002021	5.5E-12
ATG4C *	1	rs12134455	62,817,783	A	G	0.322251	-0.015559	0.002158	2.2E-14
ATG4C *	1	rs11208037	62,817,845	A	G	0.322733	-0.015545	0.002159	2.3E-14
ATG4C *	1	rs11208038	62,817,875	A	G	0.322252	-0.015559	0.002158	2.2E-14
ATG4C *	1	rs2366820	62,818,249	C	T	0.322394	-0.015620	0.002159	1.8E-14
ATG4C *	1	rs2366821	62,818,466	G	C	0.323067	-0.015512	0.002159	1.9E-14
ATG4C *	1	rs7528963	62,820,576	G	A	0.497097	0.014733	0.002042	3.3E-14
ATG4C *	1	rs11208040	62,821,867	T	A	0.322204	-0.015609	0.002159	1.8E-14
ATG4C *	1	rs7519205	62,824,457	G	A	0.332393	-0.014839	0.002142	3.5E-13
ATG4C *	1	rs6664673	62,824,892	G	C	0.302020	-0.014801	0.002196	8.5E-13
ATG4C *	1	rs6587991	62,825,003	C	A	0.322880	-0.015541	0.002157	2.5E-14
ATG4C *	1	rs7414021	62,826,201	A	G	0.302258	-0.014768	0.002199	1.1E-12
ATG4C *	1	rs10159426	62,827,199	C	G	0.309450	-0.014498	0.002185	2.5E-12
ATG4C *	1	rs10789129	62,827,786	T	C	0.300741	-0.014480	0.002200	3.2E-12
ATG4C *	1	rs34117354	62,827,807	T	TC	0.300741	-0.014480	0.002200	3.2E-12
ATG4C *	1	rs7512374	62,828,034	C	T	0.321914	-0.015295	0.002159	7.1E-14
ATG4C *	1	rs7512529	62,828,075	G	A	0.321491	-0.015236	0.002161	9.2E-14
ATG4C *	1	rs7524508	62,828,183	T	A	0.321906	-0.015286	0.002159	7.3E-14
ATG4C *	1	rs6663165	62,829,519	C	T	0.310974	-0.013819	0.002181	2.4E-11
ATG4C *	1	rs6687943	62,830,098	A	T	0.310598	-0.013772	0.002181	2.9E-11
ATG4C *	1	rs6679582	62,830,600	T	C	0.310527	-0.013751	0.002180	3.1E-11
ATG4C *	1	rs10889383	62,831,090	C	T	0.310492	-0.013789	0.002181	2.7E-11
ATG4C *	1	rs11587081	62,831,444	A	G	0.331406	-0.014541	0.002144	1.1E-12
ATG4C *	1	rs2366822	62,831,549	G	T	0.310528	-0.013750	0.002180	3.1E-11
ATG4C *	1	rs5774617	62,831,628	CT	C	0.283988	-0.014853	0.002254	3.3E-12
ATG4C *	1	rs56799376	62,832,193	G	GTTTTA	0.310623	-0.013667	0.002181	4.1E-11
ATG4C *	1	rs7527905	62,832,439	G	A	0.331403	-0.014560	0.002144	1.0E-12
ATG4C *	1	rs10889384	62,835,981	G	A	0.310544	-0.013780	0.002180	2.8E-11
ATG4C *	1	rs10889385	62,836,344	T	A	0.331433	-0.014537	0.002144	1.1E-12
ATG4C *	1	rs11208043	62,836,820	C	T	0.332570	-0.014371	0.002146	1.9E-12
ATG4C *	1	rs2886770	62,837,115	A	G	0.301073	-0.014528	0.002199	2.4E-12
ATG4C *	1	rs2886771	62,837,769	A	G	0.321945	-0.015259	0.002159	7.7E-14
ATG4C *	1	rs12567999	62,837,928	T	C	0.321945	-0.015259	0.002159	7.7E-14
ATG4C *	1	rs10493327	62,838,174	C	T	0.321945	-0.015259	0.002159	7.7E-14
ATG4C *	1	rs10889386	62,839,848	C	G	0.301073	-0.014528	0.002199	2.4E-12
ATG4C *	1	rs6695607	62,840,561	T	G	0.321945	-0.015259	0.002159	7.7E-14
ATG4C *	1	rs6683423	62,840,983	G	A	0.310557	-0.013749	0.002180	3.1E-11
ATG4C *	1	rs12743698	62,841,289	C	T	0.331431	-0.014533	0.002144	1.1E-12
ATG4C *	1	rs3737892	62,841,632	A	G	0.331431	-0.014533	0.002144	1.1E-12
ATG4C *	1	rs3737893	62,841,713	T	C	0.321941	-0.015257	0.002159	7.8E-14
ATG4C *	1	rs6665455	62,842,772	A	G	0.301075	-0.014527	0.002199	2.4E-12
ATG4C *	1	rs4448545	62,843,657	G	A	0.331433	-0.014532	0.002144	1.1E-12
ATG4C *	1	rs71045858	62,844,156	T	TG	0.301075	-0.014527	0.002199	2.4E-12
ATG4C *	1	rs11208045	62,844,194	A	G	0.321947	-0.015258	0.002159	7.8E-14

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
ATG4C	1	rs11208046	62,844,526	C	T	0.321947	-0.015258	0.002159	7.8E-14
ATG4C	1	rs71045859	62,845,712	AT	A	0.332199	-0.014563	0.002143	1.1E-12
ATG4C	1	rs12748640	62,846,102	T	C	0.331433	-0.014532	0.002144	1.1E-12
ATG4C	1	rs11208047	62,846,165	G	A	0.310559	-0.013748	0.002180	3.1E-11
ATG4C	1	rs71045860	62,847,231	A	AAAAC	0.331436	-0.014522	0.002144	1.1E-12
ATG4C	1	rs56692911	62,848,150	T	TTTTG	0.323624	-0.015005	0.002161	1.9E-13
ATG4C	1	rs6587992	62,849,801	A	G	0.331422	-0.014502	0.002144	1.2E-12
ATG4C	1	rs6587993	62,850,012	T	C	0.331422	-0.014502	0.002144	1.2E-12
ATG4C	1	rs6587994	62,850,077	G	A	0.331422	-0.014502	0.002144	1.2E-12
ATG4C	1	rs7529145	62,850,858	A	G	0.323972	-0.014619	0.002182	2.2E-12
ATG4C	1	rs7529146	62,850,860	A	G	0.312189	-0.013565	0.002195	8.7E-11
ATG4C	1	rs6699457	62,851,169	C	G	0.310562	-0.013688	0.002180	3.6E-11
ATG4C	1	rs6670072	62,852,531	T	C	0.331420	-0.014489	0.002144	1.2E-12
ATG4C	1	rs6676821	62,854,495	T	G	0.321939	-0.015212	0.002159	9.0E-14
ATG4C	1	rs6677051	62,854,650	T	C	0.321940	-0.015212	0.002159	8.9E-14
ATG4C	1	rs1333733	62,856,890	A	G	0.310585	-0.013773	0.002179	3.1E-11
ATG4C	1	rs1981067	62,857,072	C	T	0.331351	-0.014566	0.002143	1.0E-12
ATG4C	1	rs6587996	62,857,413	G	A	0.331443	-0.014589	0.002143	9.5E-13
ATG4C	1	rs6656119	62,857,582	C	G	0.331443	-0.014589	0.002143	9.5E-13
ATG4C	1	rs7527423	62,859,046	T	A	0.331443	-0.014589	0.002143	9.5E-13
ATG4C	1	rs71045861	62,859,699	CT	C	0.331990	-0.014274	0.002145	3.3E-12
ATG4C	1	rs6676637	62,860,283	T	G	0.321960	-0.015302	0.002158	7.1E-14
ATG4C	1	rs7521483	62,860,645	C	A	0.331443	-0.014589	0.002143	9.5E-13
ATG4C	1	rs2184192	62,861,191	T	G	0.472212	-0.013357	0.002026	9.0E-12
ATG4C	1	rs1333736	62,861,764	T	A	0.321960	-0.015302	0.002158	7.1E-14
ATG4C	1	rs6670694	62,862,187	G	A	0.321960	-0.015302	0.002158	7.1E-14
ATG4C	1	rs6683732	62,862,408	T	C	0.321992	-0.015287	0.002158	7.4E-14
ATG4C	1	rs7540205	62,863,117	T	C	0.322433	-0.015368	0.002158	5.3E-14
ATG4C	1	rs1360677	62,863,273	T	C	0.301302	-0.014447	0.002198	3.3E-12
ATG4C	1	rs1360678	62,863,380	T	C	0.321993	-0.015282	0.002158	7.6E-14
ATG4C	1	rs7531329	62,863,788	G	A	0.301294	-0.014500	0.002197	2.9E-12
ATG4C	1	rs3211074	62,864,546	G	A	0.331482	-0.014577	0.002143	9.9E-13
ATG4C *	1	rs17097064	62,865,621	T	G	0.331482	-0.014577	0.002143	9.9E-13
ATG4C *	1	rs5774621	62,866,019	TA	T	0.310756	-0.013680	0.002179	4.1E-11
ATG4C *	1	rs1413242	62,866,193	C	T	0.310622	-0.013751	0.002179	3.3E-11
ATG4C *	1	rs998096	62,866,234	A	C	0.331412	-0.014566	0.002143	1.0E-12
ATG4C *	1	rs12128286	62,866,524	A	C	0.331476	-0.014557	0.002143	1.1E-12
ATG4C *	1	rs1931079	62,866,953	G	A	0.331490	-0.014568	0.002143	1.0E-12
ATG4C *	1	rs2803245	62,867,539	C	T	0.290972	-0.014237	0.002225	1.4E-11
ATG4C *	1	rs11803404	62,867,652	T	C	0.331576	-0.014601	0.002143	8.9E-13
ATG4C *	1	rs10640020	62,867,798	C	CTCTT	0.310756	-0.013825	0.002179	2.8E-11
ATG4C *	1	rs1333730	62,868,437	G	A	0.331517	-0.014612	0.002143	8.9E-13
ATG4C *	1	rs11208049	62,868,614	G	A	0.331579	-0.014535	0.002143	1.2E-12
ATG4C *	1	rs7553110	62,869,374	A	G	0.322027	-0.015336	0.002158	6.5E-14
ATG4C *	1	rs7555606	62,869,525	A	G	0.322236	-0.015405	0.002158	5.0E-14
ATG4C *	1	rs11584363	62,870,392	A	G	0.322027	-0.015336	0.002158	6.5E-14
ATG4C *	1	rs11208050	62,870,600	T	C	0.322027	-0.015336	0.002158	6.5E-14
ATG4C *	1	chr1:62870674_A_AT	62,870,674	A	AT	0.323487	-0.014843	0.002163	3.4E-13
ATG4C *	1	rs11208051	62,870,957	C	T	0.331517	-0.014612	0.002143	8.9E-13
ATG4C *	1	rs28793284	62,871,200	G	T	0.334125	-0.014561	0.002140	1.0E-12
ATG4C *	1	rs12756081	62,871,663	G	A	0.331514	-0.014614	0.002143	8.9E-13
ATG4C *	1	rs2050248	62,872,447	A	T	0.310636	-0.013775	0.002179	3.1E-11
ATG4C *	1	rs6587997	62,872,515	T	G	0.331492	-0.014568	0.002143	1.0E-12
ATG4C *	1	rs11208052	62,873,126	A	G	0.331537	-0.014545	0.002143	1.1E-12
ATG4C *	1	rs36019631	62,873,148	CT	C	0.331504	-0.014564	0.002143	1.0E-12
ATG4C *	1	rs6657552	62,873,981	T	C	0.310459	-0.013844	0.002180	2.6E-11
ATG4C *	1	rs6693530	62,873,985	G	A	0.331312	-0.014621	0.002144	9.0E-13
ATG4C *	1	rs10889387	62,875,174	C	T	0.310293	-0.013855	0.002180	2.6E-11
ATG4C *	1	rs12725996	62,876,411	T	A	0.331480	-0.014735	0.002146	6.2E-13
ATG4C *	1	rs7515960	62,876,535	A	G	0.331156	-0.014629	0.002143	8.8E-13
ATG4C *	1	rs6587998	62,876,798	C	T	0.331156	-0.014629	0.002143	8.8E-13
ATG4C *	1	rs6685784	62,877,152	C	A	0.331156	-0.014629	0.002143	8.8E-13
ATG4C *	1	rs1333734	62,877,305	C	T	0.310295	-0.013851	0.002180	2.6E-11
ATG4C *	1	rs12749904	62,877,674	C	A	0.331156	-0.014629	0.002143	8.8E-13
ATG4C *	1	rs1537496	62,878,769	A	T	0.332560	-0.014495	0.002146	1.4E-12
ATG4C *	1	rs7522726	62,878,835	A	G	0.310295	-0.013851	0.002180	2.6E-11
ATG4C *	1	rs7526246	62,880,316	A	T	0.326744	-0.014261	0.002150	3.2E-12
ATG4C *	1	rs12728111	62,880,901	C	T	0.326744	-0.014261	0.002150	3.2E-12
ATG4C *	1	rs12742537	62,881,305	G	A	0.326483	-0.014231	0.002151	3.5E-12
ATG4C *	1	rs11580642	62,882,427	T	A	0.326744	-0.014261	0.002150	3.2E-12
ATG4C *	1	rs7535496	62,882,885	A	T	0.306736	-0.013686	0.002187	3.9E-11
ATG4C *	1	rs11804568	62,885,930	T	C	0.325758	-0.014062	0.002167	6.2E-12
ATG4C *	1	rs11208056	62,887,038	C	T	0.326008	-0.014143	0.002168	4.3E-12
ATG4C *	1	rs12564421	62,887,759	G	T	0.291981	-0.015153	0.002245	3.5E-12
ATG4C *	1	rs2780871	62,889,202	T	C	0.278740	-0.015588	0.002267	1.0E-12
ATG4C *	1	rs7512480	62,893,145	C	T	0.297964	-0.016691	0.002221	1.1E-14
ATG4C *	1	rs2803238	62,893,889	G	A	0.284797	-0.014837	0.002240	8.8E-12
ATG4C *	1	rs55924040	62,894,308	C	T	0.269218	-0.014819	0.002276	1.4E-11
SMG5	1	rs12128955	156,274,030	T	C	0.475160	-0.011420	0.002017	4.2E-08
SMG5	1	rs9943105	156,275,454	C	T	0.475269	-0.011443	0.002015	4.0E-08
SMG5	1	rs7542045	156,276,682	C	G	0.475269	-0.011443	0.002015	4.0E-08
SMG5	1	rs6701440	156,279,714	G	A	0.475445	-0.011450	0.002016	3.9E-08
VHLL *	1	rs12072638	156,297,689	G	T	0.474319	-0.011624	0.002018	2.3E-08
VHLL *	1	rs949464	156,302,480	T	C	0.473031	-0.011554	0.002022	3.3E-08
CCT3 *	1	rs7522860	156,305,490	A	G	0.472395	-0.011551	0.002023	3.5E-08
CCT3	1	rs2296374	156,317,612	C	T	0.475292	-0.011492	0.002016	3.5E-08
CCT3	1	rs11264472	156,322,575	G	A	0.475251	-0.011514	0.002016	3.3E-08
CCT3	1	rs3762281	156,334,991	G	A	0.475676	-0.011411	0.002018	4.5E-08
TSACC	1	chr1:156339262_CA_C	156,339,262	C	CA	0.480746	-0.012512	0.002058	6.2E-09
GALNT2	1	rs4631704	230,157,783	T	C	0.199889	-0.013738	0.002529	5.7E-09
GALNT2	1	rs4846913	230,158,968	A	C	0.191140	-0.014628	0.002570	1.4E-09
GALNT2	1	rs2144300	230,159,169	T	C	0.191637	-0.014681	0.002563	1.1E-09
GALNT2	1	rs6143660	230,159,329	T	TTGTTCA	0.193473	-0.014584	0.002558	1.2E-09
SDC1 *	2	rs907868	20,171,406	T	C	0.374393	-0.011525	0.002090	2.7E-08
SDC1 *	2	rs907867	20,171,540	G	T	0.374289	-0.011665	0.002089	1.8E-08
SDC1 *	2	rs907866	20,171,619	A	G	0.373547	-0.011737	0.002092	1.6E-08
SDC1 *	2	rs1107851	20,171,852	C	T	0.384324	-0.012279	0.002080	4.1E-09

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
SDC1 *	2	rs1107850	20,172,011	A	G	0.372399	-0.011837	0.002093	1.3E-08
SDC1 *	2	rs2090034	20,172,648	A	G	0.382356	-0.011850	0.002079	1.4E-08
SDC1 *	2	rs2090032	20,172,786	C	G	0.383527	-0.012044	0.002076	7.1E-09
SDC1 *	2	rs11096641	20,174,397	A	G	0.383657	-0.012223	0.002080	4.7E-09
SDC1 *	2	rs12478327	20,174,488	C	A	0.383448	-0.012163	0.002079	5.3E-09
C2orf43 *	2	rs6732741	20,894,274	A	T	0.158785	-0.014784	0.002778	8.4E-09
C2orf43 *	2	rs60220193	20,894,620	A	G	0.158727	-0.014848	0.002778	7.3E-09
C2orf43 *	2	rs55775005	20,898,194	T	C	0.161998	-0.014764	0.002766	1.3E-08
C2orf43 *	2	rs13008369	20,900,678	T	G	0.150463	-0.016012	0.002819	4.8E-10
C2orf43 *	2	rs7583126	20,901,107	G	A	0.150356	-0.016475	0.002822	2.0E-10
C2orf43 *	2	rs13015995	20,901,187	T	C	0.150350	-0.016481	0.002822	2.0E-10
C2orf43 *	2	rs6722139	20,901,622	A	C	0.150175	-0.016478	0.002824	2.0E-10
APOB *	2	rs113780557	20,920,505	C	T	0.141609	-0.017702	0.002938	7.3E-11
APOB *	2	rs114851711	20,921,082	A	C	0.139759	-0.017804	0.002957	1.1E-10
APOB *	2	rs7580543	20,921,560	A	G	0.142194	-0.018024	0.002930	3.0E-11
APOB *	2	chr2:20921764_C_CA	20,921,764	CA	C	0.141940	-0.018011	0.002934	3.2E-11
APOB *	2	rs7588415	20,923,901	A	G	0.142252	-0.018464	0.002930	1.3E-11
APOB *	2	rs7586740	20,925,873	C	T	0.142246	-0.018561	0.002930	1.1E-11
APOB *	2	rs7596102	20,926,088	A	G	0.142217	-0.018519	0.002930	1.1E-11
APOB *	2	rs7594084	20,927,845	C	T	0.143234	-0.018305	0.002922	1.6E-11
APOB *	2	rs4479392	20,928,382	T	C	0.143356	-0.018256	0.002923	2.0E-11
APOB *	2	rs111471227	20,929,266	T	C	0.143599	-0.018149	0.002920	2.6E-11
APOB *	2	rs6731905	20,929,669	C	T	0.143655	-0.018136	0.002919	2.7E-11
APOB *	2	rs6732027	20,929,774	G	T	0.143655	-0.018136	0.002919	2.7E-11
APOB *	2	rs7565511	20,930,030	G	C	0.142595	-0.018386	0.002930	1.6E-11
APOB *	2	rs72888845	20,931,957	A	C	0.138449	-0.017502	0.002968	2.5E-10
APOB *	2	rs74358761	20,935,300	A	G	0.139874	-0.016335	0.002960	1.1E-09
APOB *	2	chr2:20936344_CA_C	20,936,344	C	CA	0.046059	0.025683	0.004787	1.1E-08
APOB *	2	rs5013879	20,936,353	C	A	0.046220	0.025688	0.004779	1.1E-08
APOB *	2	rs12710748	20,936,567	C	T	0.046217	0.025727	0.004779	1.1E-08
APOB *	2	rs12710749	20,936,790	C	A	0.046138	0.026220	0.004787	5.8E-09
APOB *	2	rs12710750	20,936,804	T	C	0.045729	0.025763	0.004804	1.0E-08
APOB *	2	rs76203970	20,937,176	A	C	0.149616	-0.018034	0.002868	5.2E-12
APOB *	2	rs9306897	20,938,306	T	C	0.081577	0.031161	0.003718	5.0E-17
APOB *	2	rs72888868	20,938,435	A	G	0.150767	-0.017740	0.002860	1.0E-11
APOB *	2	rs75509845	20,940,759	A	G	0.151021	-0.017923	0.002857	6.9E-12
APOB *	2	rs11096689	20,940,780	C	T	0.079717	0.032811	0.003750	2.7E-18
APOB *	2	rs13414987	20,942,072	A	C	0.146548	-0.018118	0.002898	1.4E-11
APOB *	2	rs4072815	20,942,098	T	G	0.146514	-0.018054	0.002898	1.6E-11
APOB *	2	rs4296389	20,943,234	C	T	0.095673	0.033556	0.003459	1.2E-22
APOB *	2	rs4507059	20,943,569	G	A	0.083641	0.031989	0.003655	8.9E-19
APOB *	2	rs10201379	20,943,917	C	A	0.130143	0.030691	0.003023	2.2E-25
APOB *	2	rs4426495	20,944,222	C	T	0.130179	0.030683	0.003022	2.3E-25
APOB *	2	rs10180633	20,945,069	G	T	0.126882	0.030997	0.003059	2.5E-25
APOB *	2	rs13020417	20,945,074	T	G	0.049306	0.039142	0.004664	1.3E-16
APOB *	2	rs10183548	20,945,739	G	A	0.125487	0.031582	0.003064	3.3E-26
APOB *	2	rs5829761	20,946,172	AC	A	0.125495	0.031590	0.003064	3.3E-26
APOB *	2	rs6732011	20,946,761	G	T	0.125454	0.031574	0.003065	2.7E-26
APOB *	2	rs35424228	20,947,933	T	C	0.049030	0.039406	0.004676	1.3E-16
APOB *	2	rs3923037	20,948,514	A	C	0.123491	0.031362	0.003085	1.5E-25
APOB *	2	rs149034253	20,951,648	A	G	0.049396	0.039073	0.004658	1.2E-16
APOB *	2	rs4076525	20,952,157	T	C	0.032209	0.029962	0.005739	3.1E-08
APOB *	2	rs141074569	20,952,398	C	G	0.036447	0.029696	0.005402	5.8E-09
APOB *	2	rs1477526787	20,953,510	T	TTATG	0.046030	0.040549	0.004815	8.7E-17
APOB *	2	rs1323575780	20,954,023	T	TGTGTG	0.039173	0.030647	0.005218	8.0E-10
APOB *	2	chr2:20954030_TGTG_T	20,954,030	T	TGTG	0.039233	0.030904	0.005212	5.3E-10
APOB *	2	chr2:20954889_AGT_A	20,954,889	AGT	A	0.040729	0.029654	0.005117	1.7E-09
APOB *	2	rs148458076	20,955,854	C	T	0.123042	0.033098	0.003079	2.6E-28
APOB *	2	rs36145916	20,956,506	T	C	0.122383	0.033468	0.003086	1.0E-28
APOB *	2	rs143375141	20,956,554	T	C	0.161621	-0.018738	0.002758	8.6E-14
APOB *	2	rs36187918	20,958,070	G	A	0.122567	0.033057	0.003082	3.0E-28
APOB *	2	rs141232528	20,958,693	T	C	0.040982	0.029135	0.005090	2.7E-09
APOB *	2	rs36190370	20,958,814	A	C	0.046058	0.041423	0.004809	2.2E-17
APOB *	2	rs199556826	20,958,937	C	CT	0.041056	0.029202	0.005084	2.4E-09
APOB *	2	rs147436013	20,959,450	T	G	0.162746	-0.018757	0.002743	7.5E-14
APOB *	2	rs36191919	20,960,266	G	A	0.041898	0.028726	0.005032	2.6E-09
APOB *	2	rs1344063	20,961,673	T	C	0.125960	0.032337	0.003041	1.2E-27
APOB *	2	rs2337382	20,961,892	A	G	0.089181	0.036792	0.003535	1.4E-25
APOB *	2	rs17397667	20,961,975	A	G	0.041970	0.028790	0.005026	2.2E-09
APOB *	2	rs12999441	20,963,235	C	T	0.044423	0.044671	0.004883	2.8E-19
APOB *	2	rs2337381	20,963,249	A	C	0.041976	0.028756	0.005026	2.3E-09
APOB *	2	rs4665639	20,964,019	A	G	0.122370	0.033472	0.003073	6.4E-29
APOB *	2	rs62120837	20,964,499	A	G	0.042037	0.028785	0.005024	2.2E-09
APOB *	2	rs62120838	20,964,641	C	T	0.042361	0.029933	0.005006	4.8E-10
APOB *	2	rs17393586	20,964,727	A	G	0.044423	0.044671	0.004883	2.8E-19
APOB *	2	rs6707950	20,964,769	T	C	0.086983	0.038401	0.003575	4.4E-27
APOB *	2	rs4665788	20,965,616	T	C	0.041976	0.028756	0.005026	2.3E-09
APOB *	2	rs4665790	20,965,698	T	A	0.122879	0.033855	0.003066	1.3E-29
APOB *	2	rs17041662	20,966,196	C	T	0.122820	0.033889	0.003067	1.3E-29
APOB *	2	rs17397826	20,966,219	T	C	0.044423	0.044671	0.004883	2.8E-19
APOB *	2	rs56142315	20,966,511	A	C	0.041976	0.028756	0.005026	2.3E-09
APOB *	2	rs68093099	20,967,235	T	G	0.041976	0.028756	0.005026	2.3E-09
APOB *	2	rs17041663	20,967,366	G	T	0.122276	0.033420	0.003073	7.8E-29
APOB *	2	rs35695820	20,967,415	G	GCGCC	0.132493	0.029453	0.002987	3.2E-24
APOB *	2	rs79490663	20,968,191	G	A	0.159860	-0.018419	0.002753	2.3E-13
APOB *	2	rs6706783	20,968,537	A	T	0.086902	0.038356	0.003575	5.0E-27
APOB *	2	rs1320144	20,969,240	A	C	0.122190	0.033509	0.003074	5.7E-29
APOB *	2	rs1320145	20,969,490	G	A	0.122649	0.033861	0.003070	1.4E-29
APOB *	2	rs35893087	20,969,651	A	G	0.122227	0.033511	0.003074	5.3E-29
APOB *	2	rs72788558	20,971,996	C	T	0.159452	-0.018397	0.002757	2.6E-13
APOB *	2	rs17041679	20,972,540	T	C	0.122755	0.033146	0.003067	1.9E-28
APOB *	2	rs72788559	20,972,650	T	G	0.158797	-0.018955	0.002762	6.9E-14
APOB *	2	rs10495712	20,973,240	A	G	0.042176	0.028249	0.005013	4.1E-09
APOB *	2	rs34335269	20,973,378	A	G	0.121822	0.033531	0.003077	5.2E-29
APOB *	2	rs62120842	20,973,575	A	G	0.042176	0.028249	0.005013	4.1E-09
APOB *	2	rs62120843	20,973,812	G	T	0.042185	0.028400	0.005013	3.4E-09
APOB *	2	rs938848	20,973,975	G	C	0.042499	0.029392	0.004995	9.3E-10

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
APOB *	2	rs201349382	20,974,609	T	TC	0.152329	-0.021578	0.002805	1.0E-16
APOB *	2	rs6733447	20,975,264	G	A	0.123005	0.034067	0.003064	4.0E-30
APOB *	2	rs55664492	20,975,554	T	C	0.044716	0.044511	0.004869	2.0E-19
APOB *	2	rs10495713	20,977,647	A	G	0.121303	0.034231	0.003083	6.7E-30
APOB *	2	rs7608123	20,980,007	T	G	0.121285	0.034261	0.003083	6.1E-30
APOB *	2	rs112097204	20,980,087	A	C	0.042179	0.028328	0.005012	3.9E-09
APOB *	2	rs7571469	20,981,609	G	C	0.121292	0.034296	0.003082	5.5E-30
APOB *	2	rs10172650	20,982,585	A	G	0.156989	-0.020307	0.002768	1.7E-15
APOB *	2	rs10164442	20,982,691	G	A	0.156705	-0.020311	0.002769	1.6E-15
APOB *	2	rs35131127	20,983,042	C	T	0.087433	0.038525	0.003564	2.8E-27
APOB *	2	rs62120847	20,983,048	C	T	0.042504	0.029261	0.004993	1.1E-09
APOB *	2	rs9789416	20,983,180	A	G	0.121219	0.034316	0.003083	5.9E-30
APOB *	2	rs11124924	20,983,403	C	G	0.173760	-0.019347	0.002660	1.5E-15
APOB *	2	rs56327713	20,983,964	T	G	0.087480	0.038897	0.003567	8.1E-28
APOB *	2	rs56403064	20,984,034	C	T	0.121802	0.034812	0.003076	7.1E-31
APOB *	2	rs56213756	20,984,123	G	C	0.121442	0.034887	0.003081	5.8E-31
APOB *	2	rs67212568	20,985,612	G	T	0.044359	0.044818	0.004885	2.2E-19
APOB *	2	rs55938327	20,986,670	C	T	0.042529	0.028841	0.004993	1.9E-09
APOB *	2	rs34059329	20,986,894	T	C	0.087528	0.038090	0.003565	9.2E-27
APOB *	2	chr2:20986987_TG_T	20,986,987	TG	T	0.172272	0.026300	0.002733	2.3E-23
APOB *	2	rs1320143	20,989,476	G	A	0.120226	0.034793	0.003102	2.0E-30
APOB *	2	rs6721844	20,989,699	T	G	0.087035	0.037992	0.003579	1.9E-26
APOB *	2	rs6722374	20,990,190	T	G	0.119606	0.034812	0.003110	2.5E-30
APOB *	2	rs13014683	20,990,254	T	C	0.049359	0.041154	0.004647	3.0E-18
APOB *	2	rs4665642	20,990,313	G	A	0.119618	0.034805	0.003111	2.5E-30
APOB *	2	rs62120852	20,990,672	T	C	0.042242	0.027177	0.005008	1.6E-08
APOB *	2	rs1318006	20,991,280	G	A	0.120337	0.035241	0.003105	5.1E-31
APOB *	2	rs1318005	20,991,336	G	A	0.120041	0.034999	0.003110	1.3E-30
APOB *	2	rs1318004	20,991,337	C	T	0.120041	0.034999	0.003110	1.3E-30
APOB *	2	rs72780134	20,991,960	A	G	0.167929	-0.020243	0.002708	4.2E-16
APOB *	2	rs12992267	20,992,773	T	C	0.071282	0.038455	0.003922	1.6E-22
APOB *	2	rs34776010	20,993,375	G	C	0.071287	0.038460	0.003922	1.6E-22
APOB *	2	rs79823619	20,993,415	C	G	0.164415	-0.019727	0.002735	2.8E-15
APOB *	2	rs62122481	20,993,943	A	C	0.042315	0.027046	0.005001	2.0E-08
APOB *	2	rs57947200	20,994,357	A	T	0.069202	0.038226	0.003999	2.3E-21
APOB *	2	rs56984418	20,994,358	G	A	0.071272	0.038236	0.003923	1.9E-22
APOB *	2	rs74580781	20,994,558	A	G	0.038139	0.028004	0.005265	4.5E-08
APOB *	2	rs6756501	20,995,933	T	C	0.066624	0.037445	0.004051	2.4E-20
APOB *	2	rs6725189	20,996,129	T	G	0.066927	0.037269	0.004043	2.3E-20
APOB *	2	rs4665709	20,998,083	A	G	0.071372	0.037695	0.003921	6.4E-22
APOB *	2	rs4371387	20,998,261	A	G	0.071285	0.038036	0.003923	2.7E-22
APOB *	2	rs952274	20,998,485	T	G	0.066947	0.037150	0.004042	2.8E-20
APOB *	2	rs952275	20,998,527	G	T	0.043288	0.029558	0.004948	6.3E-10
APOB *	2	rs62122484	21,000,700	A	G	0.039361	0.044421	0.005183	4.5E-17
APOB *	2	rs369226260	21,001,217	A	T	0.036324	0.044911	0.005434	5.7E-16
APOB *	2	rs371445178	21,001,218	T	A	0.036329	0.044906	0.005434	5.6E-16
APOB *	2	rs551038752	21,001,219	A	T	0.036324	0.044911	0.005434	5.7E-16
APOB *	2	rs1042031	21,002,881	T	C	0.044415	0.044446	0.004884	5.9E-19
APOB *	2	rs1800479	21,004,511	G	C	0.042961	0.045179	0.004972	5.0E-19
APOB *	2	rs693	21,009,323	A	G	0.048642	0.030812	0.004681	6.8E-12
APOB *	2	rs1041968	21,009,932	A	G	0.048181	0.030050	0.004698	2.4E-11
APOB *	2	rs3749054	21,014,366	T	A	0.044515	0.044608	0.004880	3.6E-19
APOB *	2	rs2854725	21,014,914	G	T	0.155434	-0.021878	0.002787	1.5E-17
APOB *	2	rs12713868	21,016,712	T	C	0.028424	0.035368	0.006083	4.2E-08
APOB *	2	rs76622701	21,017,012	T	A	0.042485	0.031675	0.005022	3.3E-11
APOB *	2	rs13003321	21,017,014	C	T	0.038333	0.042203	0.005289	1.1E-15
APOB *	2	rs12720828	21,018,872	T	C	0.043231	0.044995	0.004952	4.4E-19
APOB *	2	rs10199768	21,021,128	T	G	0.047782	0.032121	0.004719	8.7E-13
APOB *	2	rs57825321	21,024,193	A	T	0.146942	-0.027130	0.002858	2.8E-24
APOB *	2	rs679899	21,028,042	G	A	0.148598	0.014842	0.002833	2.7E-08
APOB *	2	rs13306194	21,029,662	A	G	0.143167	-0.028420	0.002901	1.4E-25
APOB *	2	rs520354	21,036,740	A	G	0.148024	0.015132	0.002831	9.8E-09
APOB *	2	rs597331	21,039,555	G	A	0.146098	0.015095	0.002875	2.6E-08
APOB *	2	rs374763462	21,045,951	A	T	0.033843	0.032339	0.005645	2.9E-08
APOB *	2	rs11893021	21,050,706	G	T	0.177571	-0.020273	0.002687	9.2E-16
APOB *	2	rs58612563	21,051,291	G	A	0.177914	-0.020223	0.002682	8.0E-16
APOB *	2	rs75022238	21,052,006	C	T	0.177991	-0.020259	0.002681	6.3E-16
APOB *	2	rs111397565	21,052,832	CA	C	0.178059	-0.020157	0.002679	7.5E-16
APOB *	2	chr2:21054688_TTTG_T	21,054,688	T	TTTG	0.177251	-0.019390	0.002697	9.8E-15
APOB *	2	rs57922105	21,055,341	T	C	0.172801	-0.020093	0.002704	1.5E-15
APOB *	2	rs75565290	21,055,810	G	A	0.172797	-0.020141	0.002703	1.3E-15
APOB *	2	rs1003177	21,057,947	A	G	0.076525	-0.024767	0.003866	7.0E-12
APOB *	2	rs35750610	21,059,021	C	T	0.041734	0.037873	0.005071	3.4E-13
APOB *	2	rs75208098	21,060,292	C	T	0.173481	-0.020051	0.002697	1.4E-15
APOB *	2	rs60857806	21,061,227	G	T	0.173180	-0.020088	0.002699	1.3E-15
APOB *	2	rs56885855	21,061,405	T	C	0.173192	-0.020104	0.002699	1.3E-15
APOB *	2	rs75953246	21,061,841	A	G	0.173186	-0.020112	0.002699	1.2E-15
APOB *	2	rs77257367	21,062,230	T	C	0.172249	-0.020365	0.002707	6.4E-16
APOB *	2	rs11894096	21,062,695	G	A	0.171008	-0.020058	0.002716	2.0E-15
APOB *	2	chr2:21062703_C_CA	21,062,703	CA	C	0.173473	-0.020142	0.002697	1.1E-15
APOB *	2	rs11894310	21,063,145	G	A	0.173866	-0.019951	0.002694	1.9E-15
APOB *	2	rs57024468	21,064,771	C	T	0.173891	-0.019887	0.002693	2.3E-15
APOB *	2	rs67608778	21,067,028	A	AAG	0.171811	-0.019349	0.002711	1.5E-14
APOB *	2	rs75207863	21,068,360	A	G	0.174140	-0.019696	0.002692	3.6E-15
APOB *	2	rs79662771	21,068,361	G	A	0.174140	-0.019696	0.002692	3.6E-15
APOB *	2	rs113414662	21,068,827	T	TAAG	0.174144	-0.019723	0.002692	3.3E-15
APOB *	2	rs17041755	21,069,695	A	G	0.174152	-0.019724	0.002692	3.2E-15
APOB *	2	rs1897084	21,074,114	G	A	0.173655	-0.019436	0.002684	7.2E-15
APOB *	2	rs7422168	21,074,322	C	G	0.173657	-0.019473	0.002684	6.5E-15
APOB *	2	rs58420813	21,077,134	C	T	0.173953	-0.019573	0.002680	4.8E-15
APOB *	2	rs80196520	21,078,435	A	C	0.174161	-0.019582	0.002678	4.2E-15
APOB *	2	rs59263713	21,079,390	T	G	0.174196	-0.019507	0.002677	5.0E-15
APOB *	2	rs11886946	21,082,715	C	A	0.174590	-0.019777	0.002673	2.3E-15
APOB *	2	rs79721590	21,083,359	C	G	0.174571	-0.019641	0.002673	3.4E-15
APOB *	2	rs112680646	21,084,238	A	G	0.174612	-0.019472	0.002672	5.1E-15
APOB *	2	rs138654155	21,091,983	A	ATATCT	0.176145	-0.018787	0.002651	2.2E-14
APOB *	2	rs57666320	21,093,675	T	C	0.175501	-0.019003	0.002651	1.1E-14

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
APOB *	2	rs11899839	21,095,586	A	T	0.176390	-0.018568	0.002642	3.1E-14
APOB *	2	rs13019377	21,096,429	A	T	0.133593	0.015535	0.002962	4.8E-08
APOB *	2	rs1544977	21,097,940	G	C	0.176420	-0.018659	0.002640	2.2E-14
APOB *	2	rs76234631	21,101,118	A	C	0.176570	-0.018467	0.002639	3.7E-14
APOB *	2	rs77449706	21,104,188	T	C	0.176568	-0.018556	0.002641	3.1E-14
APOB *	2	rs77809614	21,105,146	A	C	0.176388	-0.018641	0.002640	2.4E-14
APOB *	2	rs57334943	21,105,494	GCTTC	G	0.176188	-0.018601	0.002643	2.6E-14
APOB *	2	rs6757883	21,107,738	G	A	0.176504	-0.018593	0.002639	2.5E-14
APOB *	2	rs2337384	21,110,978	G	A	0.176518	-0.018555	0.002639	2.8E-14
APOB *	2	rs78943787	21,111,867	A	T	0.176518	-0.018555	0.002639	2.8E-14
APOB *	2	rs74367604	21,112,857	C	T	0.176518	-0.018555	0.002639	2.8E-14
APOB *	2	rs112223447	21,113,105	CACTG	C	0.176518	-0.018555	0.002639	2.8E-14
APOB *	2	rs61086479	21,114,871	T	C	0.176460	-0.018511	0.002640	3.2E-14
APOB *	2	rs12172886	21,116,332	G	C	0.176458	-0.018500	0.002640	3.3E-14
APOB *	2	rs11892905	21,116,651	G	A	0.176478	-0.018482	0.002640	3.6E-14
APOB *	2	rs74957119	21,118,017	C	T	0.176478	-0.018509	0.002640	3.3E-14
APOB *	2	rs72207140	21,118,375	T	TA	0.176458	-0.018527	0.002640	3.1E-14
APOB *	2	rs312955	21,119,021	G	A	0.272353	0.014531	0.002267	1.3E-11
APOB *	2	rs79542263	21,121,389	G	A	0.176515	-0.018571	0.002639	2.7E-14
APOB *	2	rs76885666	21,121,682	C	A	0.176515	-0.018571	0.002639	2.7E-14
APOB *	2	rs78051902	21,122,133	A	C	0.171404	-0.018568	0.002676	6.6E-14
APOB *	2	rs2059972	21,123,923	G	T	0.083985	-0.022791	0.003685	3.1E-11
APOB *	2	rs61517696	21,126,306	C	T	0.176546	-0.018550	0.002639	2.8E-14
APOB *	2	rs113135613	21,126,367	C	CT	0.171748	-0.018456	0.002682	1.3E-13
APOB *	2	rs74582026	21,127,869	C	T	0.176646	-0.018633	0.002639	2.2E-14
APOB *	2	rs61142046	21,129,214	C	T	0.175983	-0.018506	0.002644	3.7E-14
APOB *	2	rs77258720	21,129,410	A	G	0.176541	-0.018545	0.002639	2.9E-14
APOB *	2	rs79909173	21,129,857	C	T	0.176541	-0.018545	0.002639	2.9E-14
APOB *	2	rs61437001	21,131,249	A	G	0.176645	-0.018436	0.002639	3.8E-14
APOB *	2	rs11903814	21,133,608	C	T	0.176205	-0.018326	0.002642	6.1E-14
APOB *	2	rs59537367	21,134,007	A	T	0.175902	-0.018571	0.002644	3.3E-14
APOB *	2	rs79538365	21,136,575	G	C	0.176349	-0.018551	0.002641	3.1E-14
APOB *	2	rs312966	21,137,711	A	G	0.283629	0.013796	0.002244	5.8E-11
APOB *	2	rs58411268	21,145,373	A	G	0.078010	-0.024374	0.003817	6.0E-12
APOB *	2	rs79783818	21,147,375	A	T	0.171215	-0.018762	0.002689	4.5E-14
APOB *	2	rs78059021	21,148,150	T	C	0.176318	-0.018598	0.002641	2.8E-14
APOB *	2	rs11685909	21,149,673	T	C	0.042795	0.032298	0.004995	2.8E-10
APOB *	2	rs11689541	21,149,675	C	T	0.042707	0.032426	0.005000	2.7E-10
APOB *	2	rs140043113	21,149,823	T	G	0.176354	-0.018594	0.002641	2.8E-14
APOB *	2	rs11900335	21,150,887	C	T	0.176328	-0.018559	0.002641	3.1E-14
APOB *	2	rs113725991	21,151,946	T	C	0.174824	-0.018150	0.002653	1.4E-13
APOB *	2	rs35112647	21,152,185	A	G	0.044608	0.031113	0.004891	4.7E-10
APOB *	2	rs11893753	21,152,259	G	A	0.176308	-0.018572	0.002641	3.0E-14
APOB *	2	rs60403956	21,153,184	G	A	0.175923	-0.018398	0.002644	5.1E-14
APOB *	2	rs58658975	21,153,912	T	C	0.175742	-0.018465	0.002645	4.6E-14
APOB *	2	rs60132502	21,153,937	A	G	0.175742	-0.018465	0.002645	4.6E-14
APOB *	2	rs74369686	21,154,770	G	T	0.176604	-0.018506	0.002640	3.2E-14
APOB *	2	rs12997242	21,158,305	A	G	0.271955	0.014349	0.002269	2.4E-11
APOB *	2	rs34468875	21,160,481	T	C	0.272881	0.014374	0.002269	2.1E-11
APOB *	2	rs114624425	21,162,078	G	A	0.176337	-0.018752	0.002643	1.9E-14
APOB *	2	rs117023568	21,163,502	T	C	0.156179	-0.017132	0.002792	9.5E-11
APOB *	2	rs11683495	21,163,615	G	C	0.036741	0.031398	0.005377	2.4E-08
APOB *	2	rs61407223	21,164,291	G	A	0.158396	-0.016648	0.002772	1.7E-10
APOB *	2	rs34054060	21,164,823	G	A	0.044420	0.031007	0.004904	6.7E-10
APOB *	2	rs36068322	21,167,459	C	T	0.044366	0.031151	0.004910	4.9E-10
APOB *	2	rs75499894	21,167,669	T	C	0.156274	-0.016272	0.002798	5.6E-10
APOB *	2	rs17041973	21,178,363	G	T	0.156202	-0.016880	0.002798	1.3E-10
APOB *	2	rs140618521	21,178,492	G	A	0.031132	0.034288	0.005809	2.7E-08
APOB *	2	rs75691153	21,179,519	C	G	0.157555	-0.016522	0.002786	2.7E-10
APOB *	2	rs13022408	21,180,306	G	A	0.041118	0.028559	0.005088	4.8E-08
APOB *	2	rs75249613	21,191,561	G	T	0.156032	-0.017003	0.002807	1.1E-10
DPYSL5	2	rs3769134	26,928,023	A	G	0.324564	0.011178	0.002163	3.9E-08
DPYSL5	2	rs7579579	26,928,974	T	C	0.324657	0.011175	0.002162	3.9E-08
DPYSL5	2	rs6547317	26,929,051	A	G	0.324654	0.011177	0.002162	3.9E-08
DPYSL5	2	rs7599286	26,929,530	T	C	0.325164	0.011204	0.002162	3.7E-08
DPYSL5	2	rs2384511	26,929,867	G	A	0.325281	0.011264	0.002162	3.2E-08
DPYSL5	2	rs56956849	26,930,227	G	GAGAGC	0.325034	0.011333	0.002162	2.7E-08
DPYSL5	2	rs6547318	26,930,613	A	C	0.331827	0.011229	0.002154	4.0E-08
DPYSL5	2	rs3820821	26,932,980	C	T	0.331496	0.012055	0.002155	4.3E-09
DPYSL5	2	rs4665929	26,932,981	T	G	0.332583	0.011812	0.002152	7.5E-09
DPYSL5	2	rs3820822	26,932,994	A	G	0.332558	0.011812	0.002152	7.6E-09
DPYSL5	2	rs4665363	26,933,548	G	T	0.332707	0.011989	0.002154	4.9E-09
DPYSL5	2	rs920437	26,934,528	A	G	0.332788	0.011999	0.002155	5.0E-09
DPYSL5	2	rs920435	26,934,920	C	T	0.332029	0.012031	0.002157	4.6E-09
DPYSL5	2	rs12615423	26,935,755	T	G	0.332568	0.012026	0.002156	4.6E-09
DPYSL5	2	rs11992311	26,936,473	G	A	0.332539	0.012070	0.002156	4.2E-09
DPYSL5	2	rs7589627	26,936,918	C	T	0.335545	0.012361	0.002162	1.6E-09
DPYSL5	2	rs6759548	26,938,192	A	G	0.332528	0.012056	0.002156	4.4E-09
DPYSL5	2	rs72804857	26,938,608	C	G	0.166268	0.017104	0.002718	7.8E-11
DPYSL5	2	rs6718978	26,938,723	G	A	0.332503	0.012073	0.002156	4.2E-09
DPYSL5	2	rs3739085	26,940,176	T	C	0.328610	0.011971	0.002164	5.2E-09
DPYSL5	2	rs3820823	26,941,938	G	A	0.328250	0.011993	0.002164	5.5E-09
DPYSL5	2	rs3739086	26,942,334	C	T	0.334977	0.013196	0.002162	1.5E-10
DPYSL5	2	rs6707735	26,943,954	T	C	0.327873	0.012372	0.002164	1.7E-09
DPYSL5	2	rs6708148	26,944,452	A	G	0.328067	0.012289	0.002163	2.2E-09
DPYSL5	2	rs3739088	26,944,916	T	C	0.328668	0.012170	0.002162	3.1E-09
MAPRE3 *	2	rs10181777	26,964,386	A	G	0.191435	0.014424	0.002565	1.2E-08
MAPRE3 *	2	rs62130501	26,966,629	T	C	0.154602	0.015763	0.002787	7.7E-09
MAPRE3 *	2	rs12471037	26,968,343	T	C	0.154595	0.015775	0.002787	8.2E-09
MAPRE3 *	2	rs7564363	26,968,605	A	G	0.154598	0.015771	0.002787	8.2E-09
MAPRE3 *	2	rs12714026	26,969,333	T	C	0.154561	0.015725	0.002788	9.2E-09
MAPRE3 *	2	rs7568733	26,970,140	A	T	0.154614	0.015771	0.002788	8.1E-09
MAPRE3	2	rs17005732	26,976,555	C	A	0.153791	0.015503	0.002795	1.6E-08
MAPRE3	2	chr2:26996115_A_AATTTT	26,996,113	AATTTT	A	0.157671	0.015211	0.002777	3.2E-08
MAPRE3	2	rs10207573	27,020,067	C	G	0.155224	0.016002	0.002783	4.0E-09
MAPRE3	2	rs10865456	27,023,417	C	T	0.155495	0.015793	0.002781	6.1E-09
TMEM214 *	2	rs34732613	27,031,928	T	C	0.236641	0.012717	0.002382	4.1E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
TMEM214	2	rs2304714	27,035,383	G	T	0.161598	0.016952	0.002746	3.6E-10
TMEM214	2	rs2304713	27,035,893	G	C	0.161647	0.016965	0.002745	3.5E-10
TMEM214 *	2	rs7584145	27,044,380	A	C	0.237003	0.012644	0.002375	4.8E-08
TMEM214 *	2	rs4665940	27,046,646	C	G	0.143702	0.016108	0.002923	4.1E-08
AGBL5 *	2	rs11679069	27,047,443	G	A	0.237340	0.012702	0.002374	4.2E-08
AGBL5-AS1	2	rs11126836	27,050,260	C	T	0.237349	0.012724	0.002374	4.0E-08
AGBL5 *	2	rs11680096	27,050,703	T	C	0.235124	0.012846	0.002389	3.7E-08
AGBL5	2	rs3806520	27,053,334	G	A	0.237374	0.012666	0.002374	4.4E-08
AGBL5	2	rs2278593	27,056,145	G	A	0.161732	0.016876	0.002743	4.0E-10
AGBL5	2	rs7560144	27,057,592	A	G	0.235240	0.012764	0.002381	4.1E-08
AGBL5	2	rs6547401	27,061,977	A	G	0.237501	0.012917	0.002376	2.4E-08
AGBL5	2	rs3832065	27,063,380	CTCG	C	0.237632	0.013030	0.002377	1.9E-08
AGBL5	2	rs13014240	27,063,530	G	C	0.236944	0.013078	0.002379	1.7E-08
AGBL5	2	rs70953845	27,064,781	GTC	G	0.161356	0.017140	0.002748	2.1E-10
AGBL5	2	rs1078809	27,066,047	C	T	0.236805	0.013004	0.002377	2.1E-08
AGBL5	2	rs35874715	27,068,193	G	A	0.159244	0.017084	0.002761	3.3E-10
AGBL5	2	rs7575465	27,068,793	G	A	0.234801	0.012996	0.002384	2.4E-08
AGBL5	2	rs10865461	27,069,783	T	C	0.234751	0.013018	0.002384	2.3E-08
AGBL5	2	rs1053609	27,070,282	G	T	0.236808	0.013032	0.002377	1.9E-08
OST4 *	2	rs4665943	27,073,017	T	C	0.234667	0.013152	0.002385	1.8E-08
OST4 *	2	rs11126857	27,074,889	A	G	0.234891	0.013025	0.002384	2.3E-08
EMILIN1 *	2	rs11679681	27,075,611	C	A	0.241172	0.013240	0.002382	1.2E-08
EMILIN1 *	2	rs3754734	27,076,730	G	T	0.237305	0.013075	0.002377	1.8E-08
EMILIN1	2	rs2011616	27,079,693	A	G	0.233844	0.013554	0.002388	6.5E-09
EMILIN1	2	rs2304682	27,084,901	G	C	0.233984	0.014017	0.002381	1.8E-09
KHK	2	rs2119026	27,087,525	G	A	0.233977	0.014015	0.002380	1.8E-09
KHK	2	rs6547413	27,090,014	A	G	0.234920	0.013997	0.002375	2.0E-09
KHK	2	rs12714092	27,092,014	A	G	0.244073	0.014797	0.002344	9.7E-11
KHK	2	rs6754356	27,092,153	G	A	0.244428	0.014656	0.002343	1.4E-10
KHK	2	rs6754371	27,092,196	G	A	0.244084	0.014804	0.002344	9.6E-11
KHK	2	rs2304681	27,092,384	A	G	0.243880	0.014826	0.002344	8.9E-11
KHK	2	rs3769139	27,092,846	C	T	0.243864	0.014908	0.002345	6.9E-11
KHK	2	rs6714547	27,098,338	T	G	0.246979	0.015040	0.002342	6.2E-11
KHK	2	rs10185736	27,098,356	C	T	0.247031	0.014954	0.002343	7.7E-11
CGREF1, KHK	2	rs1131375	27,100,517	T	C	0.244499	0.014785	0.002346	1.1E-10
CGREF1	2	rs34400677	27,101,068	G	GC	0.244493	0.014815	0.002346	1.1E-10
CGREF1	2	rs1057394	27,101,168	G	A	0.244737	0.014778	0.002347	1.2E-10
CGREF1	2	rs2384571	27,101,856	G	C	0.244282	0.014874	0.002347	9.2E-11
CGREF1	2	rs2384572	27,101,883	G	T	0.246378	0.014906	0.002342	7.3E-11
CGREF1	2	rs4665372	27,102,969	A	T	0.243483	0.014975	0.002352	7.1E-11
CGREF1	2	rs1866560	27,105,685	T	G	0.242859	0.014977	0.002355	7.7E-11
CGREF1	2	rs11691465	27,111,471	G	A	0.241669	0.014941	0.002375	1.2E-10
CGREF1	2	rs2891550	27,111,756	C	T	0.241577	0.015037	0.002376	9.6E-11
CGREF1	2	rs13423359	27,112,032	T	G	0.243004	0.014948	0.002373	1.1E-10
CGREF1	2	rs1866559	27,112,718	C	T	0.241207	0.015242	0.002377	5.7E-11
CGREF1	2	rs7582361	27,113,508	C	T	0.241428	0.015116	0.002377	8.2E-11
CGREF1	2	rs12714094	27,113,564	C	A	0.241432	0.015115	0.002377	8.3E-11
CGREF1	2	rs12617392	27,113,959	A	C	0.239056	0.015090	0.002391	1.1E-10
CGREF1	2	chr2:27116037_AC_A	27,116,037	A	AC	0.240381	0.015385	0.002385	5.3E-11
CGREF1	2	rs6749216	27,117,951	C	T	0.239331	0.015660	0.002389	2.7E-11
CGREF1	2	rs6746337	27,118,195	T	A	0.239347	0.015700	0.002390	2.6E-11
CGREF1 *	2	rs7560633	27,119,199	C	G	0.239393	0.015518	0.002392	3.9E-11
ABHD1 *	2	rs11126871	27,121,589	A	T	0.238658	0.015965	0.002396	1.6E-11
ABHD1 *	2	rs7605526	27,122,616	A	G	0.236931	0.016001	0.002415	2.1E-11
ABHD1	2	rs4665946	27,125,063	A	C	0.299935	0.020584	0.002211	2.3E-21
ABHD1	2	rs4665947	27,125,161	C	T	0.301075	0.020724	0.002216	2.3E-21
ABHD1	2	rs6741646	27,125,330	T	C	0.307646	0.020331	0.002187	3.1E-21
ABHD1	2	rs12467319	27,125,819	C	T	0.299538	0.019646	0.002198	9.0E-20
ABHD1	2	rs1866561	27,128,411	G	A	0.299587	0.020194	0.002195	6.8E-21
ABHD1	2	rs2304678	27,130,639	C	G	0.163268	0.021184	0.002735	2.5E-15
PREB	2	rs71401560	27,131,111	TA	T	0.163373	0.021355	0.002736	1.6E-15
PREB	2	rs11695930	27,132,103	T	C	0.162272	0.021031	0.002745	6.1E-15
PREB	2	rs2289358	27,133,123	T	G	0.162720	0.021215	0.002746	2.7E-15
PREB	2	rs2289359	27,133,410	C	T	0.162791	0.021284	0.002746	2.1E-15
PREB *	2	rs11678061	27,134,751	T	C	0.162779	0.021266	0.002748	2.5E-15
PRR30	2	rs11121	27,137,019	C	T	0.294392	0.017540	0.002230	1.3E-15
PRR30	2	rs2304680	27,138,378	T	C	0.157753	0.020732	0.002783	3.4E-14
PRR30	2	rs3795961	27,139,079	A	G	0.157892	0.020689	0.002784	3.7E-14
PRR30 *	2	rs11691585	27,139,503	G	A	0.160123	0.021159	0.002769	6.9E-15
PRR30 *	2	rs7574004	27,140,243	C	T	0.295179	0.018123	0.002231	1.5E-16
PRR30 *	2	chr2:27141287_CT_C	27,141,287	C	CT	0.291462	0.019658	0.002255	1.2E-18
PRR30 *	2	rs2439076	27,142,694	T	C	0.294701	0.018026	0.002228	2.0E-16
PRR30 *	2	rs1659677	27,142,747	A	G	0.294752	0.018036	0.002228	1.9E-16
PRR30 *	2	rs1659711	27,143,540	C	A	0.298767	0.018142	0.002221	8.7E-17
TCF23 *	2	rs1298360	27,144,930	T	C	0.157821	0.020993	0.002784	1.7E-14
TCF23 *	2	rs4665950	27,145,435	A	G	0.157818	0.020977	0.002784	1.8E-14
TCF23 *	2	rs1275518	27,145,623	G	A	0.160180	0.021388	0.002769	3.7E-15
TCF23 *	2	rs1275515	27,147,364	C	T	0.160168	0.021475	0.002770	2.9E-15
TCF23 *	2	rs1275514	27,147,662	C	T	0.158784	0.021559	0.002793	2.8E-15
TCF23 *	2	rs7606672	27,147,737	C	G	0.160165	0.021429	0.002770	3.4E-15
TCF23 *	2	rs1275513	27,148,102	T	C	0.295831	0.018856	0.002228	7.9E-18
TCF23	2	rs1275511	27,150,802	T	C	0.305759	0.016661	0.002217	2.9E-14
TCF23	2	rs1275510	27,150,871	A	G	0.157043	0.021516	0.002796	6.0E-15
TCF23	2	rs1275509	27,151,141	G	A	0.307092	0.016272	0.002213	1.1E-13
TCF23	2	rs1275508	27,151,551	C	A	0.156786	0.021500	0.002797	5.8E-15
SLCSA6 *	2	rs74684611	27,191,771	C	T	0.104577	-0.030955	0.003361	2.3E-21
CAD *	2	rs118130043	27,245,399	G	A	0.043899	0.035039	0.004997	3.8E-13
TRIM54	2	rs76147177	27,286,115	C	T	0.042929	0.029700	0.005020	4.4E-09
TRIM54	2	rs189387480	27,292,538	T	A	0.025387	-0.041120	0.006443	5.9E-12
MPV17	2	rs146502189	27,322,314	T	G	0.031976	-0.039853	0.005727	3.3E-13
GTF3C2	2	rs201232671	27,348,271	G	A	0.040449	0.038281	0.005205	6.4E-14
PPM1G	2	rs140391935	27,387,603	T	C	0.044801	0.038113	0.004933	1.1E-15
PPM1G	2	rs17006049	27,389,375	A	G	0.070626	0.021476	0.003945	4.1E-08
PPM1G	2	rs79803862	27,399,271	A	T	0.066680	-0.037880	0.004107	4.0E-22
PPM1G	2	rs150374069	27,402,962	ATAT	A	0.017655	0.045327	0.007662	4.2E-10
PPM1G *	2	rs1728918	27,412,596	A	G	0.208816	0.026660	0.002476	5.9E-28
NRBP1 *	2	rs147530299	27,419,228	A	AGTGGC	0.158097	0.027357	0.002781	2.2E-23

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
NRBP1 *	2	rs147558391	27,427,727	T	A	0.019467	-0.045181	0.007314	6.5E-10
IFT172	2	rs117414910	27,455,222	T	C	0.047282	0.039239	0.004799	1.8E-17
IFT172	2	rs140257887	27,456,289	T	C	0.027198	-0.044315	0.006201	4.9E-14
IFT172	2	rs141875753	27,478,462	G	A	0.020805	0.044549	0.007060	2.7E-11
IFT172	2	rs150202539	27,489,531	T	A	0.026183	-0.037633	0.006331	8.6E-09
GCKR	2	rs201393954	27,500,983	T	TC	0.025491	-0.043925	0.006407	2.1E-13
GCKR	2	rs1260326	27,508,073	T	C	0.492771	0.059432	0.002013	4.3E-204
GCKR	2	rs3817588	27,508,345	C	T	0.357550	-0.055891	0.002100	3.7E-165
GCKR	2	rs146716184	27,508,726	C	T	0.069804	0.028718	0.003991	9.1E-14
GCKR	2	rs148527487	27,509,703	AT	A	0.353087	-0.055333	0.002120	2.4E-158
GCKR	2	rs6547692	27,512,105	G	A	0.491544	0.058653	0.002018	2.3E-197
GCKR	2	rs780096	27,518,205	C	G	0.490821	0.058582	0.002014	3.8E-197
GCKR	2	rs780095	27,518,238	A	G	0.489481	0.058567	0.002016	1.2E-196
GCKR	2	rs780094	27,518,370	T	C	0.480495	0.057737	0.002014	9.1E-192
GCKR	2	rs780093	27,519,736	T	C	0.483161	0.057039	0.002014	1.8E-187
GCKR	2	rs780092	27,520,287	G	A	0.359919	-0.055058	0.002095	1.3E-160
GCKR	2	rs814295	27,520,348	G	A	0.361670	-0.054865	0.002093	1.0E-159
GCKR	2	rs74928908	27,521,222	G	A	0.358819	-0.054936	0.002098	2.5E-159
GCKR *	2	rs1260334	27,525,730	C	A	0.486595	0.057323	0.002024	2.6E-187
GCKR *	2	rs1260333	27,525,757	A	G	0.485797	0.056595	0.002011	6.1E-185
GCKR *	2	rs1313566	27,526,037	G	A	0.483452	0.057067	0.002026	8.4E-186
GCKR *	2	rs11336847	27,526,125	AT	A	0.483741	0.056952	0.002032	1.2E-183
GCKR *	2	rs6744393	27,527,272	T	C	0.359156	-0.054485	0.002122	1.7E-153
GCKR *	2	rs2950835	27,527,678	A	G	0.485082	0.056467	0.002041	4.0E-179
GCKR *	2	rs2911711	27,527,679	T	A	0.485086	0.056453	0.002041	4.8E-179
GCKR *	2	rs78680773	27,528,695	C	A	0.357286	-0.054342	0.002123	1.7E-152
GCKR *	2	rs6753534	27,530,004	C	T	0.485827	0.050123	0.002046	4.9E-141
GCKR *	2	rs74450311	27,531,758	C	CAT	0.375247	-0.039484	0.002081	5.0E-84
GCKR *	2	rs62131879	27,532,245	G	T	0.375962	-0.039574	0.002080	1.8E-84
GCKR *	2	rs4665986	27,532,301	G	A	0.150726	-0.014977	0.002818	4.1E-08
GCKR *	2	rs7606605	27,532,849	T	A	0.210882	0.027045	0.002507	2.7E-29
GCKR *	2	rs4665987	27,532,958	A	G	0.472462	0.044819	0.002019	1.3E-114
GCKR *	2	rs4665381	27,534,283	A	C	0.148752	-0.015743	0.002829	8.7E-09
GCKR *	2	rs10181342	27,534,476	G	A	0.375851	-0.039567	0.002080	2.0E-84
GCKR *	2	chr2:27535170_CA_C	27,535,170	CA	C	0.152290	-0.015068	0.002813	3.1E-08
GCKR *	2	rs149454845	27,536,953	C	T	0.021761	-0.044969	0.006926	3.4E-11
GCKR *	2	rs4665988	27,538,569	A	C	0.472629	0.044843	0.002018	9.3E-115
GCKR *	2	rs116443177	27,541,255	T	C	0.377609	-0.039373	0.002078	1.2E-83
GCKR *	2	rs34162673	27,541,597	GTT	G	0.148792	-0.015681	0.002829	9.8E-09
GCKR *	2	rs62131881	27,541,914	T	G	0.375722	-0.039574	0.002080	1.8E-84
GCKR *	2	rs62131882	27,542,613	C	T	0.377298	-0.039402	0.002077	6.7E-84
GCKR *	2	rs12473139	27,542,720	C	T	0.473538	0.045119	0.002017	2.8E-116
GCKR *	2	rs4665991	27,543,417	A	G	0.473113	0.045010	0.002019	1.5E-115
GCKR *	2	rs1972669	27,544,240	T	G	0.148798	-0.015684	0.002829	9.8E-09
GCKR *	2	rs67080990	27,544,621	G	GC	0.473677	0.045054	0.002018	7.4E-116
GCKR *	2	rs4493210	27,545,205	G	T	0.150276	-0.015516	0.002819	1.3E-08
GCKR *	2	rs62141278	27,545,514	T	C	0.378041	-0.039248	0.002078	2.6E-83
GCKR *	2	rs1080060	27,545,941	T	A	0.148802	-0.015688	0.002829	9.7E-09
GCKR *	2	rs61185615	27,546,345	C	T	0.146895	-0.015462	0.002848	2.0E-08
GCKR *	2	rs59210625	27,546,607	C	A	0.211089	0.027012	0.002506	2.6E-29
GCKR *	2	rs62141279	27,548,548	T	C	0.376719	-0.039451	0.002079	6.6E-84
GCKR *	2	rs6749052	27,550,012	A	T	0.150348	-0.015058	0.002822	3.3E-08
C2orf16 *	2	chr2:27550224_C_CT	27,550,224	CT	C	0.372562	-0.039098	0.002097	1.2E-80
C2orf16 *	2	rs2384626	27,550,781	A	G	0.148825	-0.015722	0.002829	8.8E-09
C2orf16 *	2	rs2384627	27,551,582	A	G	0.375911	-0.039106	0.002079	2.5E-82
C2orf16 *	2	rs1820297	27,552,057	A	G	0.151051	-0.015206	0.002811	2.6E-08
C2orf16 *	2	rs202103665	27,553,764	A	AT	0.471712	0.044874	0.002017	8.6E-115
C2orf16 *	2	rs70953865	27,554,571	T	TTTGTTT	0.155629	-0.015808	0.002790	6.8E-09
C2orf16 *	2	rs62141281	27,554,784	T	G	0.376692	-0.039208	0.002076	5.4E-83
C2orf16 *	2	rs6750943	27,555,037	T	G	0.151329	-0.015012	0.002809	3.8E-08
C2orf16 *	2	rs6761095	27,555,143	G	T	0.151095	-0.015195	0.002810	2.6E-08
C2orf16 *	2	rs6751087	27,555,149	C	T	0.376693	-0.039208	0.002076	5.3E-83
C2orf16 *	2	rs6706610	27,555,224	G	A	0.151098	-0.015200	0.002810	2.6E-08
C2orf16 *	2	rs12995461	27,555,300	C	A	0.472051	0.044816	0.002016	1.7E-114
C2orf16 *	2	rs10169065	27,555,693	G	A	0.472051	0.044816	0.002016	1.7E-114
C2orf16 *	2	rs10179872	27,555,705	A	G	0.470849	0.044596	0.002018	2.1E-113
C2orf16 *	2	rs79414972	27,558,930	G	A	0.364267	-0.037970	0.002114	2.9E-75
C2orf16 *	2	rs62141288	27,560,331	A	G	0.354775	-0.037243	0.002129	3.4E-71
C2orf16 *	2	rs200969564	27,560,335	GAC	G	0.354775	-0.037243	0.002129	3.4E-71
C2orf16 *	2	rs62141290	27,560,525	C	T	0.374975	-0.039162	0.002082	2.3E-82
C2orf16 *	2	rs6547709	27,560,551	G	A	0.151220	-0.015310	0.002809	2.1E-08
C2orf16 *	2	rs4665382	27,560,934	C	T	0.472066	0.044804	0.002017	2.1E-114
C2orf16 *	2	rs62141291	27,561,167	T	C	0.376712	-0.039137	0.002076	1.1E-82
C2orf16 *	2	rs62141292	27,561,433	C	A	0.376707	-0.039142	0.002076	1.1E-82
C2orf16 *	2	rs7570476	27,561,791	T	C	0.471999	0.044775	0.002017	3.2E-114
C2orf16 *	2	rs10208529	27,563,321	T	A	0.472007	0.044767	0.002017	3.6E-114
C2orf16 *	2	rs60854669	27,564,062	C	T	0.376686	-0.039144	0.002076	1.0E-82
C2orf16 *	2	rs12714204	27,564,673	T	C	0.151183	-0.015167	0.002809	2.8E-08
C2orf16 *	2	rs965813	27,566,994	A	T	0.376663	-0.039132	0.002076	1.2E-82
C2orf16 *	2	rs4665383	27,568,688	G	C	0.472011	0.044768	0.002017	3.5E-114
C2orf16 *	2	rs59876138	27,569,456	C	A	0.376673	-0.039138	0.002076	1.1E-82
C2orf16 *	2	rs7577311	27,571,054	T	G	0.472218	0.044780	0.002017	3.5E-114
C2orf16 *	2	rs4260197	27,571,283	C	G	0.151198	-0.015202	0.002809	2.5E-08
C2orf16 *	2	rs10205364	27,571,366	C	T	0.151219	-0.015203	0.002809	2.5E-08
C2orf16 *	2	rs10165098	27,573,659	C	T	0.151191	-0.015174	0.002809	2.7E-08
C2orf16 *	2	rs6704596	27,574,060	G	A	0.376681	-0.039139	0.002076	1.1E-82
C2orf16	2	rs1919125	27,578,536	C	G	0.151560	-0.014975	0.002807	3.8E-08
C2orf16	2	rs1919126	27,578,551	C	A	0.151562	-0.014979	0.002807	3.7E-08
C2orf16	2	rs1919127	27,578,626	C	T	0.471991	0.044690	0.002016	6.9E-114
C2orf16	2	rs1919128	27,578,892	G	A	0.472037	0.044668	0.002016	8.3E-114
C2orf16	2	rs3811644	27,579,938	G	A	0.376664	-0.039164	0.002076	7.9E-83
ZNF512	2	rs145957642	27,583,926	GT	G	0.148599	-0.015101	0.002830	4.3E-08
ZNF512	2	rs62138961	27,584,547	G	C	0.148968	-0.015214	0.002826	3.4E-08
ZNF512	2	rs13026621	27,584,757	G	A	0.150497	-0.015045	0.002814	3.7E-08
ZNF512	2	rs6734059	27,585,287	C	T	0.376765	-0.039172	0.002076	7.5E-83
ZNF512	2	rs12478841	27,588,855	G	A	0.472824	0.044668	0.002016	8.6E-114
ZNF512	2	rs6760250	27,589,385	A	G	0.472824	0.044668	0.002016	8.6E-114

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
ZNF512	2	rs4665995	27,590,960	T	G	0.150497	-0.015045	0.002814	3.7E-08
ZNF512	2	rs4665996	27,591,476	T	C	0.150497	-0.015045	0.002814	3.7E-08
ZNF512	2	rs62138963	27,591,507	T	C	0.376648	-0.039171	0.002076	7.4E-83
ZNF512	2	rs62138964	27,591,571	T	C	0.376648	-0.039171	0.002076	7.4E-83
ZNF512	2	rs145275920	27,591,660	T	C	0.057846	-0.044924	0.004336	4.7E-27
ZNF512	2	rs6738089	27,592,411	A	G	0.150497	-0.015045	0.002814	3.7E-08
ZNF512	2	rs13022873	27,592,643	C	A	0.472761	0.044601	0.002017	2.2E-113
ZNF512	2	rs76013440	27,593,448	A	G	0.375635	-0.039137	0.002080	3.9E-82
ZNF512	2	rs62138965	27,593,726	C	T	0.375817	-0.038928	0.002079	1.5E-81
ZNF512	2	rs4665997	27,594,122	T	C	0.150497	-0.015045	0.002814	3.7E-08
ZNF512	2	rs13010586	27,594,950	A	G	0.472837	0.044661	0.002016	9.1E-114
ZNF512	2	rs1919129	27,595,854	G	C	0.376644	-0.039164	0.002076	8.1E-83
ZNF512	2	rs62138966	27,596,305	A	G	0.376388	-0.039224	0.002076	5.3E-83
ZNF512	2	rs12989678	27,598,155	T	C	0.472286	0.045241	0.002022	1.3E-115
ZNF512	2	rs78378018	27,599,416	GAC	G	0.376755	-0.039164	0.002076	8.8E-83
ZNF512	2	rs117655217	27,600,099	C	T	0.057622	-0.044994	0.004338	5.6E-27
ZNF512	2	rs56725354	27,601,301	C	G	0.376643	-0.039167	0.002076	7.9E-83
ZNF512	2	rs62138968	27,601,618	G	C	0.376641	-0.039172	0.002076	7.6E-83
ZNF512	2	rs12927528	27,601,644	TTTTTG	T	0.375468	-0.039453	0.002080	1.4E-83
ZNF512	2	rs7604798	27,602,073	T	C	0.150517	-0.014959	0.002814	4.3E-08
ZNF512	2	rs12467476	27,602,848	C	T	0.471495	0.044394	0.002017	2.1E-112
ZNF512	2	rs12464616	27,604,225	T	C	0.472781	0.044648	0.002016	1.1E-113
ZNF512	2	rs2141372	27,604,329	T	G	0.376666	-0.039172	0.002076	8.6E-83
ZNF512	2	rs66497975	27,604,459	T	GTCATGT	0.471374	0.044820	0.002019	3.8E-114
ZNF512	2	rs62138969	27,605,425	G	A	0.150514	-0.014996	0.002814	3.9E-08
ZNF512	2	rs6719960	27,607,200	G	A	0.376629	-0.039199	0.002076	6.3E-83
ZNF512	2	rs6547734	27,608,123	G	T	0.150878	-0.015019	0.002811	3.7E-08
ZNF512	2	rs6547735	27,608,740	C	T	0.376625	-0.039224	0.002076	5.1E-83
ZNF512	2	rs2384656	27,609,188	G	A	0.472792	0.044691	0.002016	6.4E-114
ZNF512	2	rs1881397	27,609,418	G	A	0.377062	-0.039265	0.002077	4.2E-83
ZNF512	2	chr2:27609869_CA_C	27,609,869	C	CA	0.395960	-0.037243	0.002099	2.8E-73
ZNF512	2	rs12427483	27,610,460	T	TATATAT	0.331958	-0.041816	0.002179	4.6E-85
ZNF512	2	rs74175068	27,610,635	C	T	0.459228	0.044264	0.002060	2.2E-107
ZNF512	2	rs34016998	27,610,820	T	C	0.472149	0.044629	0.002016	1.3E-113
ZNF512	2	rs12987055	27,611,285	C	T	0.472459	0.044492	0.002016	6.8E-113
ZNF512	2	rs4665999	27,611,577	T	C	0.150896	-0.014932	0.002811	4.4E-08
ZNF512	2	rs13405762	27,611,748	C	A	0.374292	-0.038848	0.002084	5.1E-81
ZNF512	2	rs78170284	27,612,215	A	G	0.376951	-0.038889	0.002076	1.2E-81
ZNF512	2	rs13020949	27,613,738	T	C	0.472270	0.044399	0.002017	2.0E-112
ZNF512	2	chr2:27614806_CT_C	27,614,806	C	CT	0.376630	-0.038943	0.002079	1.1E-81
ZNF512	2	rs11127071	27,615,191	C	A	0.150518	-0.014979	0.002817	4.2E-08
ZNF512	2	rs1881395	27,615,682	A	G	0.376571	-0.038926	0.002079	1.4E-81
ZNF512	2	rs6737921	27,616,240	T	C	0.150446	-0.014986	0.002818	4.2E-08
ZNF512	2	rs4666000	27,616,502	C	T	0.472148	0.044367	0.002018	2.8E-112
ZNF512	2	rs2068834	27,616,672	C	T	0.471784	0.044424	0.002018	1.9E-112
ZNF512	2	rs7571558	27,616,965	G	C	0.376647	-0.038910	0.002079	1.5E-81
ZNF512	2	rs4666001	27,617,672	G	A	0.156551	0.023590	0.002774	4.9E-18
ZNF512	2	rs4666002	27,617,773	C	G	0.471553	0.044548	0.002200	7.5E-113
ZNF512	2	rs62138971	27,617,887	A	G	0.375501	-0.039175	0.002089	4.4E-82
ZNF512	2	rs6756238	27,618,438	G	A	0.150421	-0.014896	0.002819	4.7E-08
ZNF512	2	rs1881396	27,621,734	G	T	0.371524	-0.039765	0.002093	8.8E-84
GPN1	2	rs3749147	27,629,051	A	G	0.313819	0.036325	0.002172	1.5E-65
GPN1	2	rs146892484	27,629,283	C	CG	0.417381	0.028347	0.002049	3.9E-45
GPN1	2	rs34502053	27,631,657	A	G	0.316429	0.036840	0.002168	7.9E-68
GPN1	2	rs10173720	27,632,530	A	T	0.418805	0.028115	0.002044	1.1E-44
GPN1	2	rs6719175	27,636,484	A	T	0.314964	0.036904	0.002179	3.3E-67
GPN1	2	rs77350364	27,643,272	A	G	0.418271	0.027855	0.002050	1.8E-43
GPN1	2	rs12474585	27,648,726	C	T	0.418299	0.028121	0.002049	1.9E-44
GPN1	2	rs35605899	27,649,445	A	AATAT	0.335323	0.032846	0.002141	8.7E-56
GPN1	2	rs8731	27,650,459	C	G	0.417856	0.028189	0.002049	1.3E-44
SUPT7L	2	chr2:27652149_AAAAT_A	27,652,149	AAAAT	A	0.417080	0.028059	0.002053	3.9E-44
SUPT7L	2	rs67775899	27,652,169	TAAA	T	0.417713	0.027863	0.002056	1.7E-43
SUPT7L	2	rs10202364	27,652,175	T	A	0.418235	0.027911	0.002053	1.1E-43
SUPT7L	2	rs4666010	27,655,819	T	C	0.417773	0.028211	0.002049	9.9E-45
SLC4A1AP	2	rs2272406	27,669,156	T	A	0.335271	0.032828	0.002139	9.0E-56
SLC4A1AP	2	rs76586169	27,674,968	G	A	0.417473	0.028160	0.002048	1.5E-44
SLC4A1AP	2	rs13021208	27,678,861	T	C	0.335345	0.033421	0.002140	1.6E-57
SLC4A1AP	2	rs72613829	27,680,120	C	T	0.416616	0.028528	0.002050	1.6E-45
SLC4A1AP	2	rs13023094	27,687,839	C	A	0.335411	0.032790	0.002138	9.6E-56
SLC4A1AP	2	rs12998770	27,690,321	C	T	0.335627	0.032793	0.002139	9.5E-56
SLC4A1AP *	2	rs80322731	27,697,569	G	A	0.208356	0.026665	0.002519	3.7E-28
SLC4A1AP *	2	rs13030973	27,705,930	C	T	0.332559	0.032915	0.002139	4.5E-56
SLC4A1AP *	2	rs4665385	27,707,970	C	T	0.413128	0.028202	0.002048	1.1E-44
SLC4A1AP *	2	rs6727388	27,709,720	G	A	0.331812	0.033213	0.002140	6.8E-57
SLC4A1AP *	2	rs4616435	27,710,775	T	C	0.332519	0.032919	0.002139	4.6E-56
SLC4A1AP *	2	rs58199976	27,711,657	T	C	0.412244	0.028559	0.002048	1.0E-45
SLC4A1AP *	2	rs6727215	27,711,864	A	G	0.331778	0.033223	0.002140	6.2E-57
SLC4A1AP *	2	rs4665386	27,712,485	C	A	0.413698	0.028443	0.002047	2.4E-45
SLC4A1AP *	2	rs6742571	27,719,021	G	A	0.419392	0.028207	0.002048	7.5E-45
SLC4A1AP *	2	chr2:27724905_CT_C	27,724,905	C	CT	0.411803	0.027107	0.002078	2.6E-40
SLC4A1AP *	2	rs1881394	27,726,185	G	A	0.415470	0.027977	0.002065	1.7E-43
SLC4A1AP *	2	rs143611256	27,726,613	A	G	0.034079	0.032108	0.005561	8.3E-09
SLC4A1AP *	2	rs10432705	27,727,970	A	G	0.331615	0.033487	0.002163	1.8E-56
SLC4A1AP *	2	rs867282	27,728,791	C	T	0.415285	0.027841	0.002064	4.4E-43
SLC4A1AP *	2	rs2384655	27,729,368	T	A	0.415329	0.027798	0.002064	6.0E-43
SLC4A1AP *	2	rs12994085	27,729,539	T	C	0.415338	0.027806	0.002064	5.8E-43
SLC4A1AP *	2	rs12993377	27,729,900	C	G	0.415333	0.027806	0.002064	5.9E-43
MRPL33 *	2	rs12624148	27,733,614	C	T	0.415533	0.027792	0.002067	1.2E-42
MRPL33 *	2	rs6753736	27,735,988	G	C	0.420708	0.026428	0.002062	4.8E-39
MRPL33 *	2	rs75429814	27,738,747	T	C	0.411148	0.025919	0.002079	3.4E-37
MRPL33 *	2	rs111938697	27,740,266	C	T	0.415296	0.025951	0.002071	2.6E-37
MRPL33 *	2	rs12714223	27,740,463	A	G	0.414297	0.025517	0.002071	3.4E-36
MRPL33 *	2	rs36017854	27,740,804	AAT	A	0.413450	0.025633	0.002074	2.2E-36
MRPL33 *	2	rs9678824	27,741,461	G	C	0.414520	0.025366	0.002069	8.7E-36
MRPL33 *	2	rs13023194	27,744,393	C	G	0.333573	0.029051	0.002157	8.0E-43
MRPL33 *	2	rs9967838	27,745,587	C	A	0.414526	0.025169	0.002057	9.2E-36
MRPL33 *	2	chr2:27747209_A_AT	27,747,209	AT	A	0.402836	0.024382	0.002069	3.0E-33

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
MRPL33 *	2	rs9677663	27,749,578	A	G	0.409755	0.025461	0.002050	6.2E-37
MRPL33 *	2	rs57238885	27,751,393	C	G	0.409843	0.025681	0.002049	1.9E-37
MRPL33 *	2	rs10201247	27,752,104	G	A	0.409843	0.025681	0.002049	1.9E-37
MRPL33 *	2	rs6547796	27,752,527	C	T	0.410132	0.025606	0.002050	2.9E-37
MRPL33 *	2	rs4666011	27,758,045	G	C	0.409875	0.025669	0.002049	1.7E-37
MRPL33 *	2	rs10209020	27,758,077	T	C	0.410121	0.025634	0.002050	2.3E-37
MRPL33 *	2	rs12471347	27,758,788	G	C	0.409963	0.025630	0.002048	2.0E-37
MRPL33 *	2	rs77154381	27,759,252	A	G	0.408163	0.025699	0.002052	1.3E-37
MRPL33 *	2	rs12477908	27,764,179	C	A	0.411035	0.025437	0.002048	6.9E-37
MRPL33 *	2	rs13006480	27,764,354	G	C	0.326285	0.028651	0.002166	1.4E-41
MRPL33 *	2	rs140124512	27,764,951	T	A	0.042755	-0.035544	0.005090	4.2E-12
MRPL33 *	2	rs13013484	27,765,954	A	G	0.410004	0.025618	0.002048	2.2E-37
MRPL33 *	2	rs146796793	27,766,610	G	A	0.053044	-0.041000	0.004552	4.8E-21
MRPL33 *	2	rs4665390	27,767,042	C	T	0.411047	0.025378	0.002049	1.2E-36
MRPL33 *	2	rs74429612	27,770,976	C	T	0.411139	0.025417	0.002048	8.2E-37
MRPL33	2	rs3736594	27,772,914	C	A	0.411138	0.025540	0.002048	3.3E-37
MRPL33	2	rs3792252	27,773,064	A	G	0.409967	0.025607	0.002048	2.2E-37
MRPL33	2	rs139682392	27,776,317	A	G	0.029487	0.035110	0.005949	2.8E-09
MRPL33	2	rs35463245	27,777,857	C	G	0.408066	0.025376	0.002054	1.4E-36
MRPL33	2	rs17006242	27,778,184	C	A	0.410985	0.025472	0.002048	5.2E-37
MRPL33	2	rs3792253	27,779,135	T	C	0.409868	0.025619	0.002049	2.3E-37
MRPL33 *	2	rs13030345	27,780,307	T	G	0.306598	0.027149	0.002203	5.3E-36
RBKS	2	rs74327441	27,784,205	G	A	0.403848	0.024941	0.002081	2.2E-34
RBKS	2	rs192918024	27,787,093	T	A	0.029314	-0.040147	0.006037	1.1E-12
RBKS	2	rs7596967	27,789,917	T	G	0.389860	0.022991	0.002087	4.8E-29
RBKS	2	rs7593136	27,794,925	A	G	0.411352	0.025012	0.002048	1.0E-35
RBKS	2	rs6744348	27,795,158	A	C	0.411367	0.025017	0.002048	1.0E-35
RBKS	2	rs36035825	27,795,264	T	G	0.411364	0.025021	0.002048	9.8E-36
RBKS	2	rs4666012	27,795,426	A	G	0.411362	0.025021	0.002048	9.7E-36
RBKS	2	rs11322614	27,796,225	AT	A	0.410072	0.025070	0.002053	8.2E-36
RBKS	2	rs4666013	27,796,239	C	T	0.411364	0.025023	0.002047	9.1E-36
RBKS	2	rs4666014	27,796,308	G	A	0.411459	0.024926	0.002047	1.5E-35
RBKS	2	rs4666015	27,796,500	G	A	0.411384	0.025010	0.002047	9.7E-36
RBKS	2	rs34181670	27,796,989	T	C	0.411384	0.025012	0.002047	9.6E-36
RBKS	2	rs35679500	27,797,099	T	C	0.411384	0.025012	0.002047	9.6E-36
RBKS	2	rs12623170	27,797,290	C	T	0.411810	0.024690	0.002047	7.6E-35
RBKS	2	rs3935148	27,798,099	T	A	0.408517	0.025201	0.002051	3.7E-36
RBKS	2	rs13027427	27,798,176	G	T	0.379866	0.022703	0.002080	3.8E-29
RBKS	2	rs6745545	27,798,978	C	G	0.379798	0.022687	0.002080	4.2E-29
RBKS	2	rs7570730	27,799,808	G	A	0.379735	0.022628	0.002082	7.2E-29
RBKS	2	rs11127125	27,800,253	T	C	0.379006	0.022521	0.002084	1.4E-28
RBKS	2	rs11127126	27,800,417	C	T	0.379756	0.022553	0.002083	1.1E-28
RBKS	2	rs12473340	27,800,930	G	A	0.379693	0.022535	0.002083	1.2E-28
RBKS	2	rs12473400	27,801,157	G	T	0.380546	0.022516	0.002083	1.5E-28
RBKS	2	rs4630723	27,801,464	T	C	0.389752	0.021126	0.002100	4.6E-25
RBKS	2	rs13019037	27,801,775	C	T	0.379812	0.022420	0.002085	2.2E-28
RBKS	2	rs4632296	27,802,117	T	C	0.380991	0.022344	0.002091	4.5E-28
RBKS	2	rs13001060	27,802,194	T	C	0.382657	0.022100	0.002090	1.5E-27
RBKS	2	rs12995865	27,802,199	A	C	0.382657	0.022100	0.002090	1.5E-27
RBKS	2	rs11891769	27,802,713	G	C	0.379895	0.022339	0.002085	3.9E-28
RBKS	2	rs12465012	27,805,324	C	T	0.359118	0.019771	0.002109	1.0E-21
RBKS	2	rs4665392	27,806,782	A	G	0.358937	0.019534	0.002109	2.7E-21
RBKS	2	rs12986980	27,807,570	A	G	0.358156	0.019736	0.002109	1.1E-21
RBKS	2	rs13023003	27,809,270	G	C	0.358541	0.019712	0.002107	1.1E-21
RBKS	2	rs4233716	27,811,517	C	T	0.379153	0.017365	0.002085	2.1E-17
RBKS	2	rs4233717	27,811,813	A	T	0.379153	0.017365	0.002085	2.1E-17
RBKS	2	chr2:27813039_TAA_T	27,813,039	TAA	T	0.378779	0.017344	0.002085	2.2E-17
RBKS	2	rs4666016	27,814,273	T	A	0.377551	0.017465	0.002086	1.4E-17
RBKS	2	rs4464229	27,815,213	C	T	0.379228	0.017321	0.002087	2.5E-17
RBKS	2	rs12617171	27,815,932	C	T	0.378183	0.017285	0.002085	2.7E-17
RBKS	2	rs4420671	27,816,433	G	C	0.378268	0.017368	0.002085	2.0E-17
RBKS	2	rs4493211	27,816,605	G	T	0.378740	0.017349	0.002086	2.3E-17
RBKS	2	rs4665393	27,817,409	G	A	0.378278	0.017362	0.002085	2.0E-17
RBKS	2	rs4666017	27,817,658	C	A	0.378278	0.017362	0.002085	2.0E-17
RBKS	2	rs12478766	27,818,333	T	C	0.378241	0.017299	0.002085	2.7E-17
RBKS	2	rs13026758	27,818,406	A	G	0.378261	0.017340	0.002085	2.3E-17
RBKS	2	rs4666018	27,819,192	C	T	0.383333	0.017237	0.002083	4.1E-17
RBKS	2	rs66523005	27,822,746	TAGAA	T	0.387053	0.017407	0.002081	2.9E-17
RBKS	2	rs4666020	27,823,161	G	A	0.387020	0.017534	0.002081	1.7E-17
RBKS	2	chr2:27825136_CA_C	27,825,136	CA	C	0.388379	0.017140	0.002085	9.4E-17
RBKS	2	rs9679543	27,828,084	C	T	0.381916	0.017517	0.002075	1.2E-17
RBKS	2	rs10531773	27,831,894	GAA	G	0.382123	0.017536	0.002076	1.1E-17
RBKS	2	rs148824274	27,832,605	G	T	0.023549	-0.037285	0.006670	1.8E-08
RBKS	2	rs4666021	27,833,014	A	G	0.381402	0.017274	0.002076	3.6E-17
RBKS	2	rs9678430	27,834,262	G	C	0.381410	0.017296	0.002076	3.3E-17
RBKS	2	rs12463914	27,834,492	C	T	0.381473	0.017281	0.002076	3.5E-17
RBKS	2	rs7560060	27,834,657	T	C	0.381402	0.017274	0.002076	3.6E-17
RBKS	2	rs4666022	27,834,956	T	C	0.381321	0.017351	0.002076	2.5E-17
RBKS	2	rs12464988	27,835,359	C	T	0.379731	0.017095	0.002086	1.1E-16
RBKS	2	rs13027666	27,835,566	T	C	0.380260	0.016949	0.002082	1.8E-16
RBKS	2	rs11885959	27,836,033	C	G	0.381321	0.017351	0.002076	2.5E-17
RBKS	2	rs4665394	27,836,155	T	C	0.381252	0.017290	0.002076	3.3E-17
RBKS	2	rs12617110	27,837,044	A	G	0.381378	0.017399	0.002076	2.1E-17
RBKS	2	rs12617113	27,837,070	A	G	0.381378	0.017399	0.002076	2.1E-17
RBKS	2	rs12992890	27,837,964	T	C	0.381321	0.017351	0.002076	2.5E-17
RBKS	2	rs34096628	27,838,123	A	C	0.381321	0.017351	0.002076	2.5E-17
RBKS	2	rs4275987	27,840,089	A	G	0.386153	0.017675	0.002084	6.7E-18
RBKS	2	rs4462754	27,841,127	C	T	0.381897	0.017545	0.002075	1.1E-17
RBKS	2	rs9678336	27,842,537	A	G	0.381357	0.017348	0.002076	2.6E-17
RBKS	2	rs74446114	27,843,255	C	T	0.300086	0.020525	0.002213	5.0E-21
RBKS	2	rs4233718	27,843,493	A	G	0.381417	0.017341	0.002076	2.7E-17
RBKS	2	rs11127127	27,844,037	G	T	0.382009	0.017528	0.002075	1.1E-17
RBKS	2	rs11127128	27,844,103	T	A	0.381417	0.017341	0.002076	2.7E-17
RBKS	2	rs77853892	27,844,692	A	C	0.165512	0.023859	0.002759	3.1E-19
RBKS	2	rs4564736	27,846,676	A	T	0.381322	0.017351	0.002076	2.5E-17
RBKS	2	rs11901133	27,846,846	T	G	0.381351	0.017352	0.002076	2.5E-17
RBKS	2	rs4555299	27,848,323	A	G	0.381322	0.017351	0.002076	2.5E-17

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
RBKS	2	rs35841453	27,849,835	T	C	0.381402	0.017353	0.002076	2.6E-17
RBKS	2	rs4666024	27,850,112	C	G	0.379054	0.017395	0.002080	2.3E-17
RBKS	2	rs4666025	27,851,027	C	T	0.381402	0.017353	0.002076	2.6E-17
RBKS	2	rs4313931	27,851,834	C	T	0.381402	0.017353	0.002076	2.6E-17
RBKS	2	rs4583413	27,851,957	C	T	0.381322	0.017351	0.002076	2.5E-17
RBKS	2	rs4419196	27,852,431	A	G	0.381322	0.017351	0.002076	2.5E-17
RBKS	2	rs4447576	27,853,381	T	C	0.384953	0.017256	0.002085	3.9E-17
RBKS	2	rs11127129	27,853,841	C	G	0.381683	0.017646	0.002080	8.5E-18
RBKS	2	rs7426295	27,856,127	G	A	0.375981	0.017264	0.002083	8.6E-17
RBKS	2	rs4233719	27,856,477	C	A	0.375981	0.017264	0.002083	8.6E-17
RBKS	2	rs4233720	27,856,908	A	G	0.376072	0.017177	0.002083	1.3E-16
RBKS	2	rs13025314	27,857,347	G	A	0.376072	0.017177	0.002083	1.3E-16
RBKS	2	rs4578808	27,858,763	G	T	0.376072	0.017177	0.002083	1.3E-16
RBKS	2	rs4578809	27,859,627	G	A	0.376072	0.017177	0.002083	1.3E-16
RBKS	2	chr2:27860975_C_CT	27,860,975	C	CT	0.376067	0.017210	0.002083	1.1E-16
RBKS	2	rs6714106	27,860,977	C	T	0.378680	0.017226	0.002085	1.5E-16
RBKS	2	rs7595986	27,862,444	A	G	0.375919	0.017294	0.002083	7.5E-17
RBKS	2	rs13021285	27,862,480	T	C	0.376010	0.017207	0.002083	1.1E-16
RBKS	2	rs77353560	27,862,677	A	C	0.284816	0.019235	0.002252	9.2E-18
RBKS	2	rs11902158	27,863,898	A	G	0.376010	0.017207	0.002083	1.1E-16
RBKS	2	rs13004096	27,864,338	C	T	0.376010	0.017207	0.002083	1.1E-16
RBKS	2	rs1973116	27,865,051	C	T	0.375044	0.017599	0.002088	3.1E-17
RBKS	2	rs4666028	27,865,713	T	A	0.377126	0.016971	0.002082	2.7E-16
RBKS	2	rs71441095	27,866,981	A	G	0.471656	-0.026153	0.002040	2.1E-38
RBKS	2	rs10171517	27,867,192	T	C	0.471815	-0.026146	0.002040	2.1E-38
RBKS	2	rs898034	27,867,953	T	C	0.471922	-0.026189	0.002040	1.5E-38
RBKS	2	rs2337373	27,870,055	C	T	0.375985	0.017238	0.002083	9.4E-17
RBKS	2	rs13016573	27,871,403	C	G	0.377268	0.017372	0.002086	6.8E-17
RBKS	2	rs4665398	27,871,903	A	T	0.376069	0.017185	0.002083	1.2E-16
RBKS	2	rs12466687	27,873,840	C	A	0.377013	0.017350	0.002085	7.3E-17
RBKS	2	rs12466717	27,873,925	G	A	0.375910	0.017309	0.002083	7.1E-17
RBKS	2	rs4666030	27,874,355	C	T	0.375907	0.017312	0.002083	7.0E-17
RBKS	2	rs13411592	27,875,857	A	G	0.375909	0.017316	0.002083	6.9E-17
RBKS	2	rs35445284	27,878,028	A	AT	0.376618	0.017311	0.002085	8.6E-17
RBKS	2	rs6706209	27,879,071	T	C	0.375853	0.017441	0.002082	4.1E-17
RBKS	2	rs12620151	27,879,837	T	A	0.375932	0.017441	0.002082	4.3E-17
RBKS	2	rs6547814	27,880,131	G	A	0.375853	0.017440	0.002082	4.1E-17
RBKS	2	rs763594764	27,881,051	A	AAACC	0.036799	0.030066	0.005354	3.2E-08
RBKS	2	rs11886463	27,881,670	C	T	0.375939	0.017361	0.002082	5.9E-17
RBKS	2	rs13413962	27,881,699	A	G	0.375851	0.017446	0.002082	4.0E-17
RBKS	2	rs6708889	27,884,825	T	C	0.375840	0.017367	0.002082	5.4E-17
RBKS	2	chr2:27888789_TA_T	27,888,789	T	TA	0.375553	0.017409	0.002083	4.6E-17
BABAM2	2	rs7607546	27,895,795	A	G	0.375681	0.017257	0.002079	6.4E-17
BABAM2	2	rs141361525	27,896,053	G	C	0.055586	-0.036713	0.004461	8.7E-18
BABAM2	2	rs7592580	27,898,323	C	T	0.376610	0.017035	0.002078	2.0E-16
BABAM2	2	rs17006365	27,900,507	G	T	0.376550	0.017233	0.002079	6.7E-17
BABAM2	2	rs6709765	27,900,893	T	A	0.375807	0.017250	0.002078	6.1E-17
BABAM2	2	rs10177845	27,901,304	A	G	0.375883	0.017211	0.002078	7.3E-17
BABAM2	2	rs34483784	27,906,524	G	A	0.389669	0.015239	0.002068	2.6E-13
BABAM2	2	rs10201105	27,908,366	C	G	0.389677	0.015228	0.002068	2.7E-13
BABAM2	2	rs10190494	27,908,376	G	A	0.389918	0.015029	0.002068	5.4E-13
BABAM2	2	rs10204488	27,909,383	A	G	0.386746	0.015571	0.002068	5.9E-14
BABAM2	2	rs2016616	27,911,170	G	A	0.390736	0.015468	0.002071	1.1E-13
BABAM2	2	rs1458396	27,913,484	G	A	0.389616	0.015306	0.002068	2.0E-13
BABAM2	2	rs35177396	27,916,281	TA	T	0.393525	0.014860	0.002071	1.2E-12
BABAM2	2	rs2337372	27,917,482	G	A	0.389649	0.015287	0.002068	2.3E-13
BABAM2	2	rs10173848	27,920,150	T	G	0.386536	0.015673	0.002068	3.9E-14
BABAM2	2	rs1870325	27,921,200	A	G	0.386570	0.015611	0.002068	4.9E-14
BABAM2	2	rs117290132	27,923,697	A	G	0.040453	-0.037743	0.005186	8.7E-14
BABAM2	2	rs6745379	27,924,674	C	T	0.387502	0.015779	0.002068	2.8E-14
BABAM2	2	rs13026003	27,927,931	C	T	0.390014	0.015309	0.002069	2.0E-13
BABAM2	2	rs111357701	27,928,463	TTTCTC	T	0.387909	0.015473	0.002075	1.3E-13
BABAM2	2	rs10185472	27,928,487	A	G	0.389129	0.015342	0.002070	1.8E-13
BABAM2	2	rs6547815	27,932,328	A	T	0.387340	0.015463	0.002069	9.9E-14
BABAM2	2	rs11886375	27,932,881	A	C	0.387207	0.015471	0.002068	9.7E-14
BABAM2	2	rs10174070	27,933,753	G	A	0.388351	0.015082	0.002082	8.6E-13
BABAM2	2	rs191742408	27,935,145	A	G	0.031089	0.033526	0.005790	5.9E-09
BABAM2	2	rs10194283	27,936,212	A	G	0.387333	0.015676	0.002066	4.3E-14
BABAM2	2	rs10184052	27,936,777	G	A	0.387431	0.015673	0.002066	4.4E-14
BABAM2	2	rs13400398	27,939,242	T	C	0.387096	0.015690	0.002066	4.5E-14
BABAM2	2	rs13416434	27,939,407	C	T	0.387097	0.015690	0.002066	4.5E-14
BABAM2	2	rs4390729	27,939,994	C	T	0.390424	0.015341	0.002065	2.0E-13
BABAM2	2	rs11274834	27,940,623	GCTAAC.	C	0.383781	0.015556	0.002077	1.2E-13
BABAM2	2	rs10170872	27,941,686	T	C	0.387043	0.015755	0.002066	3.7E-14
BABAM2	2	rs57403744	27,942,131	A	G	0.158298	0.022079	0.002788	4.5E-16
BABAM2	2	chr2:27942534_AT_A	27,942,534	A	AT	0.033479	0.035589	0.005684	9.8E-10
BABAM2	2	rs13399709	27,944,583	T	C	0.387209	0.015655	0.002065	5.2E-14
BABAM2	2	rs7577437	27,945,548	G	A	0.387404	0.015644	0.002065	5.0E-14
BABAM2	2	rs6547816	27,946,730	C	T	0.388758	0.015361	0.002071	1.8E-13
BABAM2	2	rs12165240	27,949,258	T	A	0.389334	0.015556	0.002069	8.7E-14
BABAM2	2	rs13382482	27,949,426	C	T	0.389711	0.015682	0.002067	5.5E-14
BABAM2	2	rs7595847	27,950,176	A	T	0.389894	0.015643	0.002067	5.9E-14
BABAM2	2	rs1506535	27,951,214	G	A	0.390009	0.015624	0.002067	6.4E-14
BABAM2	2	rs13008539	27,951,540	A	C	0.390009	0.015624	0.002067	6.4E-14
BABAM2	2	rs7584462	27,953,189	T	A	0.390423	0.015413	0.002067	1.5E-13
BABAM2	2	rs7587180	27,953,242	G	A	0.390826	0.015303	0.002067	2.1E-13
BABAM2	2	rs10205313	27,953,660	C	A	0.389178	0.014989	0.002073	8.6E-13
BABAM2	2	rs188363080	27,953,699	T	A	0.035585	0.032359	0.005442	3.0E-09
BABAM2	2	chr2:27955981_G_GT	27,955,981	GT	G	0.388375	0.015534	0.002075	1.3E-13
BABAM2	2	rs10559599	27,958,465	TTA	T	0.390573	0.015371	0.002067	1.8E-13
BABAM2	2	rs1506537	27,959,034	C	G	0.387492	0.015508	0.002067	9.9E-14
BABAM2	2	rs1506536	27,959,139	C	T	0.390123	0.015349	0.002068	2.0E-13
BABAM2	2	rs2012704	27,961,899	A	T	0.387151	0.015391	0.002068	1.4E-13
BABAM2	2	rs1350481	27,962,941	C	G	0.386783	0.015336	0.002068	1.7E-13
BABAM2	2	rs3056502	27,966,214	T	TTTC	0.384347	0.015475	0.002071	1.0E-13
BABAM2	2	rs1902966	27,966,413	A	G	0.384347	0.015475	0.002071	1.0E-13
BABAM2	2	rs1841068	27,968,762	T	C	0.387106	0.015703	0.002066	4.3E-14

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BABAM2	2	rs10188108	27,969,688	G	C	0.387558	0.015485	0.002065	8.9E-14
BABAM2	2	rs10198257	27,973,444	C	T	0.375985	0.014980	0.002108	3.2E-12
BABAM2	2	rs12465000	27,976,557	A	G	0.387375	0.015654	0.002065	4.9E-14
BABAM2	2	rs12465103	27,976,869	C	G	0.387400	0.015632	0.002065	5.2E-14
BABAM2	2	rs2337374	27,977,285	A	G	0.387399	0.015628	0.002065	5.3E-14
BABAM2	2	rs898032	27,980,069	G	C	0.387910	0.015356	0.002065	1.6E-13
BABAM2	2	rs898031	27,980,427	T	C	0.246737	0.015477	0.002357	1.7E-11
BABAM2	2	rs7577342	27,982,714	T	C	0.388157	0.015621	0.002066	6.1E-14
BABAM2	2	rs28662360	27,986,053	G	A	0.387395	0.015603	0.002065	5.8E-14
BABAM2	2	rs10209126	27,986,416	T	C	0.387096	0.015661	0.002066	5.0E-14
BABAM2	2	rs13029008	27,990,023	A	G	0.386876	0.015448	0.002066	1.1E-13
BABAM2	2	rs10175508	27,990,557	T	C	0.386971	0.015583	0.002066	6.9E-14
BABAM2	2	rs12470614	27,994,460	C	T	0.387907	0.015344	0.002065	1.7E-13
BABAM2	2	rs1458397	27,996,741	C	T	0.389157	0.015257	0.002065	2.4E-13
BABAM2	2	rs1458398	27,997,074	G	A	0.388579	0.015342	0.002064	1.7E-13
BABAM2	2	rs10204513	27,998,058	C	G	0.388726	0.015170	0.002064	3.2E-13
BABAM2	2	rs10196483	27,998,315	T	A	0.388726	0.015170	0.002064	3.2E-13
BABAM2	2	rs11127131	28,001,249	T	G	0.136358	0.017266	0.002941	2.7E-09
BABAM2	2	rs10204832	28,005,541	A	T	0.388728	0.015163	0.002064	3.3E-13
BABAM2	2	rs10168171	28,009,220	G	A	0.388734	0.015169	0.002064	3.2E-13
BABAM2	2	rs2839791	28,009,412	C	A	0.388290	0.015399	0.002064	1.5E-13
BABAM2	2	rs145058190	28,010,531	T	C	0.040653	-0.037779	0.005168	6.7E-14
BABAM2	2	rs58258810	28,011,829	GA	G	0.387312	0.014810	0.002072	1.3E-12
BABAM2	2	rs56046821	28,011,834	A	T	0.388729	0.015169	0.002064	3.2E-13
BABAM2	2	rs7602328	28,012,317	A	G	0.388583	0.015339	0.002064	1.8E-13
BABAM2	2	rs13003383	28,012,896	C	T	0.388517	0.015112	0.002064	4.1E-13
BABAM2	2	rs10495761	28,013,088	T	C	0.388184	0.015196	0.002064	3.1E-13
BABAM2	2	rs11127132	28,013,253	C	T	0.388456	0.015220	0.002064	2.9E-13
BABAM2	2	rs6547817	28,015,118	T	C	0.388289	0.015391	0.002064	1.6E-13
BABAM2	2	rs35526001	28,017,352	A	ATGT	0.386188	0.015462	0.002069	1.5E-13
BABAM2	2	rs10180107	28,017,658	C	T	0.387626	0.015543	0.002064	8.5E-14
BABAM2	2	rs4616436	28,019,441	A	G	0.387477	0.015705	0.002065	4.8E-14
BABAM2	2	rs6725627	28,019,585	G	T	0.387646	0.015546	0.002064	8.6E-14
BABAM2	2	rs12997202	28,027,522	A	G	0.386848	0.015561	0.002065	7.8E-14
BABAM2	2	rs6727432	28,028,123	G	T	0.387685	0.015426	0.002065	1.3E-13
BABAM2	2	rs17006439	28,031,825	A	G	0.182471	0.018335	0.002660	7.5E-13
BABAM2	2	rs4666032	28,031,902	C	T	0.148544	0.018979	0.002852	8.3E-12
BABAM2	2	rs937812	28,032,435	T	C	0.387411	0.015690	0.002065	5.2E-14
BABAM2	2	rs9309658	28,033,964	G	A	0.387396	0.015686	0.002065	5.2E-14
BABAM2	2	rs7593127	28,035,160	A	G	0.387396	0.015686	0.002065	5.2E-14
BABAM2	2	rs6731650	28,038,296	A	C	0.387054	0.015795	0.002066	3.7E-14
BABAM2	2	rs10175826	28,038,517	A	G	0.386384	0.015563	0.002068	8.6E-14
BABAM2	2	rs10200337	28,038,807	T	C	0.245315	0.015908	0.002365	6.4E-12
BABAM2	2	rs6547819	28,043,177	G	A	0.384228	0.014571	0.002085	4.5E-12
BABAM2	2	rs7580274	28,043,202	T	C	0.384381	0.015483	0.002078	1.3E-13
BABAM2	2	rs6738887	28,045,600	T	C	0.387881	0.015363	0.002065	1.5E-13
BABAM2	2	rs12614744	28,046,835	T	A	0.388338	0.015363	0.002067	1.5E-13
BABAM2	2	rs13402420	28,048,568	G	T	0.401897	0.013840	0.002052	2.1E-11
BABAM2	2	rs4133152	28,052,962	A	T	0.041864	-0.038436	0.005096	1.4E-14
BABAM2	2	rs1395324	28,053,776	G	C	0.387322	0.015725	0.002065	4.2E-14
BABAM2	2	rs1911128	28,056,782	G	T	0.402023	0.013919	0.002052	1.5E-11
BABAM2	2	rs1911127	28,056,826	A	G	0.402028	0.013908	0.002052	1.6E-11
BABAM2	2	rs6547820	28,058,678	A	G	0.387256	0.015765	0.002065	3.4E-14
BABAM2	2	rs6758799	28,061,766	C	T	0.386982	0.015639	0.002066	5.1E-14
BABAM2	2	rs10173528	28,065,525	T	C	0.246012	0.016007	0.002362	4.8E-12
BABAM2	2	rs13414801	28,067,480	C	T	0.401797	0.013919	0.002053	1.5E-11
BABAM2	2	rs13409819	28,070,432	A	C	0.386002	0.016033	0.002101	4.2E-14
BABAM2	2	rs11691385	28,076,117	G	A	0.469986	0.017101	0.002058	1.1E-16
BABAM2	2	rs6737313	28,076,400	G	A	0.470819	0.017171	0.002058	8.5E-17
BABAM2	2	rs11363251	28,078,343	G	GC	0.442036	0.016944	0.002029	1.3E-16
BABAM2	2	rs2337699	28,080,846	T	C	0.444895	0.016835	0.002024	1.9E-16
BABAM2	2	rs11682011	28,081,194	A	G	0.293343	0.016755	0.002225	3.2E-14
BABAM2	2	chr2:28082112_GA_G	28,082,112	G	GA	0.293069	0.016883	0.002228	2.3E-14
BABAM2	2	rs13415164	28,082,796	T	C	0.293895	0.016335	0.002224	1.4E-13
BABAM2	2	rs2337700	28,084,076	G	A	0.461600	0.014987	0.002015	1.5E-13
BABAM2	2	rs12614949	28,084,924	A	G	0.442716	0.016692	0.002025	4.2E-16
BABAM2	2	rs10173426	28,086,710	G	A	0.312538	0.014228	0.002184	3.5E-11
BABAM2	2	rs13402525	28,091,991	T	G	0.295683	0.016252	0.002217	1.4E-13
BABAM2	2	rs13405377	28,092,277	T	G	0.294570	0.016960	0.002222	1.2E-14
BABAM2	2	rs13431542	28,092,278	T	C	0.294570	0.016960	0.002222	1.2E-14
BABAM2	2	rs11678963	28,092,691	G	A	0.312599	0.014313	0.002184	2.4E-11
BABAM2	2	rs6710214	28,094,574	G	A	0.321553	0.015073	0.002169	1.3E-12
BABAM2	2	rs10182585	28,094,942	G	A	0.318961	0.015920	0.002178	1.3E-13
BABAM2	2	rs7578052	28,096,012	G	A	0.304343	0.016842	0.002196	1.0E-14
BABAM2	2	rs6757405	28,096,049	T	C	0.303246	0.017080	0.002200	5.2E-15
BABAM2	2	rs3863	28,096,267	G	A	0.302894	0.016905	0.002200	8.4E-15
BABAM2	2	rs13395259	28,096,429	T	C	0.452127	0.017453	0.002027	1.9E-17
BABAM2	2	rs11679638	28,096,872	T	C	0.304808	0.016924	0.002191	6.1E-15
BABAM2	2	rs7581813	28,097,094	G	T	0.451406	0.017252	0.002019	2.8E-17
BABAM2	2	rs7572644	28,097,166	T	C	0.451208	0.017188	0.002019	3.6E-17
BABAM2	2	rs7558946	28,097,314	T	C	0.450371	0.017321	0.002021	1.9E-17
BABAM2	2	rs10209559	28,099,593	A	G	0.293978	0.016843	0.002217	1.9E-14
BABAM2	2	rs10187665	28,101,263	G	A	0.319035	0.015760	0.002171	1.5E-13
BABAM2	2	rs80259585	28,101,619	T	C	0.030715	0.032512	0.005846	3.4E-08
BABAM2	2	rs118163881	28,101,775	C	A	0.027665	0.035568	0.006161	3.4E-09
BABAM2	2	rs77252308	28,101,842	T	TC	0.293582	0.016696	0.002221	3.4E-14
BABAM2	2	rs6705961	28,102,334	T	C	0.441347	0.016700	0.002031	4.6E-16
BABAM2	2	rs9309659	28,103,391	C	G	0.451981	0.017467	0.002032	1.8E-17
BABAM2	2	rs10186196	28,104,963	G	C	0.293469	0.015740	0.002232	1.1E-12
BABAM2	2	rs55796876	28,107,028	G	A	0.459192	0.014552	0.002054	1.6E-12
BABAM2	2	rs13000292	28,112,486	C	T	0.450987	0.013808	0.002049	1.3E-11
BABAM2	2	rs1948922	28,119,286	A	G	0.441606	0.012787	0.002050	4.0E-10
BABAM2	2	rs13030032	28,125,303	A	T	0.478688	0.010939	0.002044	4.2E-08
BABAM2	2	rs56115343	28,125,617	C	T	0.332310	0.012971	0.002160	6.2E-10
BABAM2	2	rs6707054	28,127,353	T	C	0.321352	0.012513	0.002170	3.5E-09
BABAM2	2	rs7559383	28,127,876	T	C	0.322138	0.011957	0.002171	1.5E-08
BABAM2	2	rs7585476	28,128,055	A	G	0.323308	0.011733	0.002167	2.8E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BABAM2	2	rs6712135	28,129,014	T	C	0.323658	0.011979	0.002164	1.4E-08
BABAM2	2	rs6720961	28,132,428	G	A	0.324171	0.012035	0.002162	1.1E-08
BABAM2	2	rs11692928	28,133,519	T	G	0.324095	0.012061	0.002162	1.1E-08
BABAM2	2	rs7581912	28,134,403	G	T	0.323588	0.011976	0.002163	1.4E-08
BABAM2	2	rs7579101	28,134,460	G	A	0.323586	0.011964	0.002163	1.4E-08
BABAM2	2	rs11689563	28,134,841	G	A	0.323583	0.011967	0.002163	1.4E-08
BABAM2	2	rs10189434	28,135,884	T	C	0.324361	0.011768	0.002162	2.5E-08
BABAM2	2	rs13431389	28,137,361	C	T	0.324506	0.011821	0.002163	1.9E-08
BABAM2	2	rs7594162	28,138,594	G	A	0.323691	0.012023	0.002163	1.2E-08
BABAM2	2	rs13384961	28,139,127	C	T	0.322979	0.011974	0.002165	1.6E-08
BABAM2	2	rs7581221	28,139,135	A	C	0.323714	0.012167	0.002164	8.5E-09
BABAM2	2	rs13393848	28,139,147	A	G	0.322474	0.012252	0.002169	7.0E-09
BABAM2	2	rs11691530	28,139,451	G	C	0.323690	0.012029	0.002163	1.1E-08
BABAM2	2	rs10170879	28,140,730	T	A	0.324298	0.011948	0.002162	1.4E-08
BABAM2	2	rs7575930	28,142,797	T	C	0.324587	0.011603	0.002148	3.0E-08
BABAM2	2	rs141106979	28,145,437	A	T	0.020655	-0.046571	0.007108	2.2E-11
BABAM2	2	rs6741499	28,146,569	T	C	0.324613	0.011535	0.002147	3.2E-08
BABAM2	2	rs11886621	28,150,033	T	C	0.323807	0.012112	0.002149	6.8E-09
BABAM2	2	rs11423536	28,152,010	AG	A	0.325032	0.011574	0.002147	2.8E-08
BABAM2	2	rs60751755	28,155,692	C	T	0.324567	0.011879	0.002151	1.4E-08
BABAM2	2	rs60039280	28,156,576	G	A	0.324614	0.011627	0.002156	3.0E-08
BABAM2	2	rs11685351	28,157,109	C	A	0.324677	0.011586	0.002156	3.4E-08
BABAM2	2	rs56104185	28,160,820	G	T	0.322175	0.011850	0.002168	2.1E-08
BABAM2	2	rs10173507	28,161,265	C	T	0.323569	0.011898	0.002161	1.7E-08
BABAM2	2	rs143037086	28,218,937	T	G	0.025248	-0.039933	0.006413	2.7E-10
SIX3 *	2	rs895636	44,961,214	T	C	0.421410	0.011528	0.002032	3.9E-09
SIX3 *	2	rs340515	44,961,231	G	T	0.437080	0.011961	0.002031	1.3E-09
SIX3 *	2	rs5830819	44,962,917	AC	A	0.427659	0.011048	0.002039	1.1E-08
SIX3 *	2	rs12712928	44,964,941	C	G	0.433108	0.011111	0.002050	1.5E-08
INHBB *	2	rs2311597	120,548,195	A	G	0.487025	-0.011280	0.002031	1.1E-08
INHBB *	2	rs17050272	120,548,864	A	G	0.478144	-0.011445	0.002013	7.8E-09
INHBB *	2	rs6724056	120,549,811	T	G	0.481436	0.012025	0.002036	1.7E-09
INHBB *	2	rs7578604	120,551,084	T	G	0.299953	0.014481	0.002229	2.9E-11
INHBB *	2	rs954244	120,551,655	G	C	0.301320	0.014110	0.002221	5.8E-11
INHBB *	2	rs2030745	120,551,706	A	G	0.479026	0.012096	0.002204	1.1E-09
INHBB *	2	rs2030746	120,551,912	T	C	0.480750	0.012145	0.002021	8.7E-10
INHBB *	2	rs11686154	120,553,361	A	G	0.479851	0.011340	0.002029	1.3E-08
INHBB *	2	rs940688	120,553,424	C	G	0.480671	0.011258	0.002028	1.4E-08
INHBB *	2	rs3843846	120,554,223	A	G	0.478100	0.011241	0.002032	1.6E-08
GRB14 *	2	rs12692735	164,648,055	T	G	0.102874	-0.020870	0.003310	7.1E-10
GRB14 *	2	rs10930133	164,650,214	A	T	0.106432	-0.019742	0.003264	4.5E-09
COBLL1 *	2	rs6754919	164,651,333	T	C	0.103165	-0.021192	0.003305	3.2E-10
COBLL1 *	2	rs6713419	164,651,790	C	T	0.103175	-0.021175	0.003305	3.3E-10
COBLL1 *	2	rs10184004	164,651,879	T	C	0.103064	-0.021037	0.003305	4.6E-10
COBLL1 *	2	rs10179126	164,655,284	G	C	0.103144	-0.021014	0.003304	4.8E-10
COBLL1 *	2	rs34271465	164,656,555	C	CA	0.103620	-0.020937	0.003301	4.7E-10
COBLL1 *	2	rs10195252	164,656,581	C	T	0.103295	-0.020767	0.003302	8.2E-10
COBLL1 *	2	rs36105243	164,668,241	G	C	0.103140	-0.021111	0.003304	3.9E-10
COBLL1 *	2	rs7592412	164,669,828	C	T	0.103130	-0.021119	0.003304	3.9E-10
COBLL1 *	2	rs13432797	164,670,077	C	G	0.080572	-0.022336	0.003693	5.5E-09
COBLL1 *	2	rs1128249	164,672,114	T	G	0.103276	-0.021070	0.003302	4.4E-10
COBLL1 *	2	rs13389219	164,672,366	T	C	0.103380	-0.021424	0.003304	2.1E-10
COBLL1 *	2	rs10187501	164,675,944	G	A	0.080271	-0.022269	0.003701	6.5E-09
COBLL1 *	2	rs6717858	164,683,151	C	T	0.103859	-0.021080	0.003297	3.5E-10
COBLL1	2	rs6753142	164,687,561	C	T	0.103551	-0.020863	0.003300	5.5E-10
COBLL1	2	rs6738627	164,687,940	A	G	0.103819	-0.021020	0.003296	3.9E-10
COBLL1	2	rs10601676	164,688,063	G	GAA	0.102876	-0.021353	0.003311	2.4E-10
COBLL1	2	rs10630427	164,688,863	CAA	C	0.103302	-0.020966	0.003305	4.9E-10
COBLL1	2	rs10649609	164,696,196	AAAAAT	A	0.113541	-0.017968	0.003192	2.6E-08
COBLL1	2	rs12692737	164,697,799	A	C	0.078247	-0.021173	0.003743	3.8E-08
COBLL1	2	rs9653282	164,698,148	T	A	0.078042	-0.020983	0.003747	4.8E-08
COBLL1	2	chr2:164698386_T_TTA	164,698,386	TTA	T	0.078038	-0.021000	0.003748	4.6E-08
COBLL1	2	rs7609045	164,698,697	A	G	0.078038	-0.021000	0.003748	4.6E-08
COBLL1	2	rs34704590	164,699,087	A	AT	0.077966	-0.021154	0.003750	3.8E-08
COBLL1	2	rs2198550	164,700,250	C	A	0.077915	-0.021111	0.003752	4.1E-08
COBLL1	2	rs6712203	164,700,808	T	C	0.114206	-0.018330	0.003168	1.1E-08
NOSTRIN	2	rs2947934	168,839,020	G	A	0.322658	0.011433	0.002195	4.5E-08
NOSTRIN	2	rs560952	168,847,977	T	C	0.417743	0.011145	0.002077	1.7E-08
NOSTRIN	2	rs497808	168,848,527	T	G	0.420476	0.010949	0.002068	2.3E-08
NOSTRIN	2	rs11354593	168,848,560	CA	C	0.419850	0.011098	0.002068	1.4E-08
NOSTRIN	2	rs566465	168,848,594	A	T	0.354392	0.011325	0.002136	1.4E-08
NOSTRIN	2	rs540652	168,850,918	C	T	0.418174	0.011089	0.002070	1.3E-08
NOSTRIN	2	rs488621	168,851,042	A	G	0.418015	0.011017	0.002070	1.6E-08
NOSTRIN	2	rs546146	168,852,687	C	G	0.352872	0.011453	0.002137	8.9E-09
NOSTRIN	2	rs527393	168,853,247	G	A	0.418179	0.011146	0.002069	1.1E-08
NOSTRIN	2	rs2685799	168,854,794	T	C	0.414609	0.011304	0.002073	7.6E-09
NOSTRIN	2	rs2632380	168,857,840	T	C	0.413523	0.011498	0.002074	4.3E-09
NOSTRIN	2	rs569997	168,858,383	T	C	0.415210	0.011571	0.002072	3.5E-09
NOSTRIN	2	rs576062	168,859,176	A	G	0.413886	0.011628	0.002073	3.0E-09
NOSTRIN	2	rs2632372	168,861,031	T	C	0.350509	0.011519	0.002118	4.4E-09
NOSTRIN	2	rs143166986	168,862,756	C	TTCTTTA	0.415326	0.011373	0.002060	4.0E-09
SPC25 *	2	rs9751269	168,869,393	A	G	0.419279	0.011241	0.002054	5.7E-09
SPC25	2	rs6734923	168,871,220	G	C	0.418551	0.011197	0.002055	6.2E-09
SPC25	2	rs554494	168,873,053	G	A	0.419605	0.011196	0.002054	5.9E-09
SPC25	2	rs506273	168,875,025	T	C	0.412971	0.011191	0.002060	6.7E-09
SPC25	2	rs543727	168,879,788	A	T	0.437139	0.011576	0.002066	2.8E-09
SPC25	2	rs524586	168,881,341	A	G	0.373724	0.011845	0.002108	1.7E-09
SPC25	2	rs493816	168,881,727	C	T	0.440580	0.011825	0.002066	1.0E-09
G6PC2 *	2	rs34177044	168,897,975	A	G	0.407277	0.012501	0.002072	1.3E-09
G6PC2 *	2	rs13387347	168,898,336	C	T	0.454410	0.012588	0.002045	2.3E-10
G6PC2 *	2	rs1402837	168,900,844	T	C	0.403825	0.012391	0.002055	1.1E-09
G6PC2	2	rs2232326	168,907,981	C	T	0.040310	-0.033658	0.005155	3.8E-11
G6PC2 *	2	rs12053049	168,910,638	C	T	0.289853	0.016296	0.002254	6.9E-14
G6PC2 *	2	rs16856187	168,913,876	C	A	0.293402	0.016413	0.002249	7.2E-14
G6PC2 *	2	rs60415045	168,914,614	C	A	0.288613	0.015823	0.002258	7.3E-13
G6PC2 *	2	rs10497347	168,914,704	C	T	0.284481	0.015981	0.002269	7.3E-13
G6PC2 *	2	rs66629516	168,914,874	T	TG	0.282954	0.015897	0.002271	8.8E-13

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
G6PC2 *	2	rs13419326	168,914,910	C	A	0.282965	0.015886	0.002271	9.2E-13
G6PC2 *	2	rs4144857	168,914,996	C	G	0.282988	0.015870	0.002271	9.8E-13
G6PC2 *	2	rs4144858	168,915,008	T	C	0.283000	0.015900	0.002271	8.8E-13
G6PC2 *	2	rs504979	168,915,349	T	C	0.345693	0.012827	0.002149	5.6E-10
ABCB11 *	2	rs71676177	168,919,036	A	ATTTG	0.288613	0.017001	0.002246	8.5E-15
ABCB11 *	2	rs73972707	168,919,250	G	A	0.288752	0.016897	0.002245	1.2E-14
ABCB11 *	2	rs28819151	168,919,319	G	A	0.288751	0.016889	0.002245	1.2E-14
ABCB11 *	2	rs74870851	168,919,713	G	A	0.288831	0.016913	0.002245	1.2E-14
ABCB11 *	2	chr2:168920546_AT_A	168,920,546	AT	A	0.348389	0.012495	0.002158	2.4E-09
ABCB11 *	2	rs78529720	168,920,787	G	A	0.290862	0.017071	0.002238	6.7E-15
ABCB11 *	2	rs147578319	168,921,847	TTTTT	T	0.376937	0.012486	0.002110	7.0E-10
ABCB11 *	2	rs192788039	168,922,071	G	A	0.039614	-0.028624	0.005225	3.1E-08
ABCB11 *	2	rs478333	168,922,646	G	A	0.361529	0.012466	0.002124	1.5E-09
ABCB11 *	2	rs4148804	168,922,695	T	C	0.278742	0.016332	0.002278	2.9E-13
ABCB11	2	rs496550	168,923,202	T	C	0.373196	0.012317	0.002081	6.7E-10
ABCB11	2	rs495714	168,923,254	C	T	0.373317	0.012417	0.002080	5.0E-10
ABCB11	2	rs579275	168,923,856	T	C	0.373018	0.012375	0.002081	5.8E-10
ABCB11	2	rs519887	168,924,375	T	C	0.372999	0.012396	0.002082	5.4E-10
ABCB11	2	rs519035	168,924,451	T	C	0.372998	0.012401	0.002082	5.4E-10
ABCB11	2	rs484066	168,925,971	A	T	0.349616	0.012851	0.002112	2.8E-10
ABCB11	2	rs16856247	168,927,903	T	C	0.291290	0.015915	0.002217	1.3E-13
ABCB11	2	rs503931	168,928,939	A	C	0.372770	0.012096	0.002083	1.2E-09
ABCB11	2	rs551754	168,931,176	C	T	0.372838	0.012246	0.002081	7.8E-10
ABCB11	2	rs527150	168,931,529	A	G	0.372783	0.012242	0.002081	7.6E-10
ABCB11	2	rs497692	168,932,506	T	C	0.373222	0.012164	0.002080	9.7E-10
ABCB11	2	rs13389076	168,933,002	A	G	0.315323	0.013029	0.002174	4.2E-10
ABCB11	2	rs16856252	168,933,210	C	T	0.342110	0.012781	0.002127	3.7E-10
ABCB11	2	rs555975	168,934,425	G	A	0.375930	0.012197	0.002089	1.3E-09
ABCB11	2	rs3755157	168,935,661	T	C	0.314627	0.015179	0.002167	5.8E-13
ABCB11	2	rs3755158	168,935,678	G	C	0.344791	0.012492	0.002119	5.9E-10
ABCB11	2	rs472614	168,935,911	A	G	0.372266	0.012038	0.002084	1.9E-09
ABCB11	2	rs565412	168,937,773	A	G	0.372117	0.012004	0.002089	2.2E-09
ABCB11	2	rs567074	168,937,921	T	C	0.372074	0.011973	0.002089	2.6E-09
ABCB11	2	rs479682	168,938,177	T	C	0.369879	0.012076	0.002095	2.2E-09
ABCB11	2	rs480562	168,938,261	T	A	0.371933	0.011942	0.002090	2.9E-09
ABCB11	2	rs482508	168,938,473	A	G	0.370294	0.012122	0.002093	1.8E-09
ABCB11	2	rs508743	168,938,777	C	G	0.370673	0.012212	0.002096	1.4E-09
ABCB11	2	rs58512362	168,938,957	G	A	0.344633	0.012343	0.002129	1.0E-09
ABCB11	2	rs79933700	168,939,085	CTGTT	C	0.370992	0.011997	0.002096	2.6E-09
ABCB11	2	rs2544360	168,939,677	T	C	0.357876	0.012111	0.002110	1.8E-09
ABCB11	2	rs2685803	168,939,775	A	G	0.371788	0.012096	0.002097	1.9E-09
ABCB11	2	rs2544367	168,939,778	T	C	0.371788	0.012096	0.002097	1.9E-09
ABCB11	2	rs2685804	168,940,262	A	G	0.371370	0.012111	0.002095	1.7E-09
ABCB11	2	rs2685805	168,940,550	A	G	0.371401	0.012090	0.002096	1.8E-09
ABCB11	2	rs2685806	168,940,794	A	G	0.371313	0.012098	0.002095	1.8E-09
ABCB11	2	rs2685807	168,941,016	C	T	0.371297	0.012089	0.002095	1.8E-09
ABCB11	2	rs2685808	168,941,130	G	T	0.371445	0.012028	0.002096	2.2E-09
ABCB11	2	rs1581397	168,941,142	T	C	0.371529	0.011991	0.002096	2.5E-09
ABCB11	2	rs2685810	168,941,222	T	C	0.371312	0.012064	0.002095	1.9E-09
ABCB11	2	rs2685811	168,941,417	A	G	0.371298	0.012094	0.002096	1.8E-09
ABCB11	2	rs77601801	168,941,523	G	A	0.321801	0.012895	0.002173	4.3E-10
ABCB11	2	rs2685812	168,941,661	A	G	0.372662	0.012176	0.002096	1.2E-09
ABCB11	2	rs2685813	168,941,929	T	C	0.372662	0.012193	0.002096	1.1E-09
ABCB11	2	rs2685814	168,942,109	T	C	0.372633	0.012193	0.002097	1.1E-09
ABCB11	2	rs3084063	168,942,222	C	CATATTA	0.377487	0.012114	0.002108	2.3E-09
ABCB11	2	rs2250677	168,942,778	C	T	0.372830	0.012171	0.002097	1.3E-09
ABCB11	2	rs2307959	168,943,763	A	ACGTG	0.374088	0.012144	0.002098	1.3E-09
ABCB11	2	rs5836215	168,943,792	G	GT	0.372883	0.012077	0.002098	1.6E-09
ABCB11	2	rs853791	168,943,918	A	G	0.372867	0.012084	0.002098	1.6E-09
ABCB11	2	rs853790	168,943,931	A	T	0.374251	0.012038	0.002100	1.8E-09
ABCB11	2	chr2:168944282_TG_T	168,944,282	TG	T	0.373286	0.012015	0.002099	1.9E-09
ABCB11	2	rs860510	168,945,118	A	C	0.372863	0.012102	0.002099	1.5E-09
ABCB11	2	rs853788	168,945,395	T	C	0.372835	0.012086	0.002099	1.6E-09
ABCB11	2	rs853786	168,945,800	G	A	0.373099	0.012051	0.002101	1.8E-09
ABCB11	2	rs862662	168,945,819	C	A	0.373083	0.012044	0.002101	1.9E-09
ABCB11	2	rs853785	168,946,084	C	T	0.373040	0.012084	0.002104	1.7E-09
ABCB11	2	rs16856261	168,947,058	T	C	0.310459	0.015038	0.002206	1.8E-12
ABCB11	2	rs853784	168,947,164	C	T	0.372590	0.011721	0.002120	7.2E-09
ABCB11	2	rs853783	168,949,001	A	C	0.368074	0.011123	0.002128	3.3E-08
ABCB11	2	rs55700007	168,949,511	G	T	0.342056	0.011980	0.002165	3.8E-09
ABCB11	2	rs853782	168,949,788	C	T	0.370232	0.011423	0.002127	1.5E-08
ABCB11	2	rs853781	168,949,811	A	G	0.367993	0.011363	0.002131	2.0E-08
ABCB11	2	rs139014876	168,950,218	A	G	0.037205	-0.031902	0.005393	1.9E-09
ABCB11	2	rs72886761	168,950,228	A	G	0.341076	0.012092	0.002166	2.8E-09
ABCB11	2	rs853780	168,950,972	C	G	0.370211	0.011452	0.002129	1.4E-08
SYN2 *	3	rs7615580	11,985,766	C	T	0.036049	-0.031118	0.005409	1.2E-09
SYN2 *	3	rs2623897	11,989,795	G	A	0.034700	-0.032378	0.005506	8.3E-10
SYN2 *	3	rs2600268	11,991,338	G	A	0.034700	-0.032378	0.005506	8.3E-10
SYN2 *	3	chr3:11992441_TA_T	11,992,441	TA	T	0.034710	-0.032437	0.005505	7.6E-10
SYN2 *	3	rs2600269	11,992,486	C	T	0.034710	-0.032437	0.005505	7.6E-10
SYN2 *	3	rs2600271	11,994,702	T	C	0.034627	-0.032594	0.005510	7.2E-10
SYN2 *	3	rs11295397	11,995,298	CA	C	0.034707	-0.032456	0.005505	7.3E-10
SYN2 *	3	rs10560475	11,995,304	TCA	T	0.034731	-0.032732	0.005504	5.2E-10
SYN2 *	3	rs199870642	11,995,302	A	T	0.034718	-0.032360	0.005505	8.3E-10
SYN2 *	3	rs5846736	11,995,538	GT	G	0.034707	-0.032456	0.005505	7.3E-10
SYN2 *	3	rs2600229	11,996,979	A	T	0.034707	-0.032459	0.005505	7.3E-10
SYN2 *	3	rs2600230	11,997,155	T	A	0.034707	-0.032459	0.005505	7.3E-10
SYN2 *	3	rs2618404	11,997,191	A	C	0.034707	-0.032459	0.005505	7.3E-10
SYN2 *	3	rs2618403	11,997,989	C	T	0.034711	-0.032647	0.005505	5.8E-10
SYN2 *	3	rs2618402	11,998,325	C	A	0.034768	-0.031994	0.005500	1.1E-09
SYN2	3	rs2923857	12,004,864	G	C	0.034486	-0.033011	0.005522	4.0E-10
SYN2	3	rs2600235	12,004,945	T	G	0.034486	-0.033011	0.005522	4.0E-10
SYN2	3	rs2623879	12,004,946	T	C	0.034503	-0.033098	0.005521	3.7E-10
SYN2	3	rs2618389	12,007,234	C	T	0.034476	-0.032900	0.005523	4.5E-10
SYN2	3	rs2618387	12,007,963	T	A	0.033622	-0.034547	0.005593	1.2E-10
SYN2	3	rs217049	12,019,417	C	T	0.034440	-0.032797	0.005526	5.2E-10
SYN2	3	rs59306735	12,020,503	C	T	0.034440	-0.032797	0.005526	5.2E-10

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
SYN2	3	rs307611	12,021,844	G	C	0.034440	-0.032797	0.005526	5.2E-10
SYN2	3	rs307608	12,023,291	G	A	0.035523	-0.030419	0.005448	6.3E-09
SYN2	3	rs394945	12,033,617	T	C	0.034442	-0.032811	0.005526	5.1E-10
SYN2	3	rs402149	12,033,844	G	A	0.034442	-0.032811	0.005526	5.1E-10
SYN2	3	rs373827	12,034,975	G	A	0.034442	-0.032811	0.005526	5.1E-10
SYN2	3	rs6767059	12,035,062	G	A	0.034442	-0.032811	0.005526	5.1E-10
SYN2	3	rs454615	12,035,510	T	C	0.034442	-0.032811	0.005526	5.1E-10
SYN2	3	rs10510409	12,041,804	T	C	0.034407	-0.032962	0.005530	4.3E-10
SYN2	3	rs167408	12,046,948	A	G	0.034442	-0.032810	0.005526	5.1E-10
SYN2	3	rs2030150	12,050,190	T	C	0.034442	-0.032806	0.005526	5.1E-10
SYN2	3	rs307560	12,051,905	T	C	0.034442	-0.032806	0.005526	5.1E-10
SYN2	3	rs71304084	12,077,400	T	C	0.115255	-0.018361	0.003170	1.2E-09
SYN2	3	rs148566174	12,078,193	C	CTT	0.114998	-0.018197	0.003174	2.0E-09
SYN2	3	rs147433183	12,078,502	G	A	0.034418	-0.032839	0.005526	4.8E-10
SYN2	3	rs112143125	12,085,373	A	G	0.072982	-0.023138	0.003940	1.5E-09
SYN2	3	rs1587385	12,087,736	G	C	0.034415	-0.032795	0.005526	5.1E-10
SYN2	3	rs35416561	12,088,199	T	TCAAA	0.034415	-0.032795	0.005526	5.1E-10
SYN2	3	rs61156889	12,088,662	TAA	T	0.034415	-0.032795	0.005526	5.1E-10
SYN2	3	rs2119812	12,090,187	T	C	0.034393	-0.032765	0.005528	5.3E-10
SYN2	3	rs34389637	12,090,516	CT	C	0.034393	-0.032765	0.005528	5.3E-10
SYN2	3	rs184262	12,093,240	A	G	0.034392	-0.032772	0.005528	5.3E-10
SYN2	3	rs13061425	12,095,404	G	T	0.034392	-0.032770	0.005528	5.3E-10
SYN2	3	rs143095555	12,095,450	A	AGG	0.035215	-0.032825	0.005481	3.1E-10
SYN2	3	rs6798755	12,097,592	T	C	0.033051	-0.034383	0.005639	2.0E-10
SYN2	3	rs58683249	12,098,765	C	T	0.034392	-0.032766	0.005528	5.3E-10
SYN2	3	rs453131	12,099,453	C	G	0.034391	-0.032757	0.005528	5.4E-10
SYN2	3	rs6442307	12,101,855	C	A	0.034391	-0.032757	0.005528	5.4E-10
SYN2	3	rs160113	12,103,739	T	C	0.115525	-0.018138	0.003165	1.6E-09
SYN2	3	rs34206487	12,103,849	G	A	0.034391	-0.032754	0.005528	5.4E-10
SYN2	3	rs11715886	12,105,736	G	C	0.034390	-0.032758	0.005528	5.4E-10
SYN2	3	rs73813125	12,106,763	C	T	0.034390	-0.032758	0.005528	5.4E-10
SYN2	3	rs13079332	12,107,348	A	G	0.034390	-0.032758	0.005528	5.4E-10
SYN2	3	rs117621918	12,108,368	C	T	0.028273	-0.033131	0.006084	1.7E-08
SYN2	3	rs13064800	12,110,157	A	C	0.032997	-0.031352	0.005639	4.2E-09
SYN2	3	rs35544543	12,112,767	CA	C	0.120014	-0.017224	0.003123	6.0E-09
SYN2	3	rs71628735	12,113,377	AG	A	0.034401	-0.032657	0.005527	6.1E-10
SYN2	3	rs35814004	12,114,537	C	CTA	0.034410	-0.032725	0.005527	5.7E-10
SYN2	3	rs11720130	12,114,816	A	G	0.115864	-0.018027	0.003160	1.9E-09
SYN2	3	rs71628736	12,115,035	A	C	0.034401	-0.032657	0.005527	6.1E-10
SYN2	3	rs66822996	12,115,142	C	CAT	0.034425	-0.032646	0.005526	6.3E-10
SYN2	3	rs71624931	12,125,648	A	G	0.034318	-0.032614	0.005534	6.8E-10
SYN2	3	chr3:12127953_A_AT	12,127,953	AT	A	0.034328	-0.032562	0.005533	7.0E-10
SYN2	3	rs13064956	12,128,751	C	T	0.115809	-0.017734	0.003162	2.4E-09
SYN2	3	chr3:12132044_C_CTT	12,132,044	CTT	C	0.043588	-0.027055	0.004996	8.2E-09
SYN2	3	rs34831171	12,132,155	C	T	0.115969	-0.018217	0.003159	1.1E-09
SYN2	3	rs7647950	12,139,096	T	G	0.034325	-0.032723	0.005535	5.9E-10
SYN2	3	rs71304088	12,139,633	C	T	0.034325	-0.032723	0.005535	5.9E-10
SYN2	3	rs4488811	12,140,528	T	C	0.034257	-0.032779	0.005540	5.7E-10
SYN2	3	rs7621569	12,143,057	G	A	0.115202	-0.018258	0.003170	9.2E-10
SYN2	3	rs11721223	12,143,660	G	A	0.034247	-0.032628	0.005541	6.7E-10
SYN2	3	rs1039247	12,144,804	G	T	0.034247	-0.032628	0.005541	6.7E-10
SYN2	3	rs1867012	12,146,743	C	T	0.034243	-0.032842	0.005541	5.4E-10
SYN2	3	rs11708978	12,146,995	G	A	0.034243	-0.032842	0.005541	5.4E-10
SYN2	3	rs35522627	12,147,066	A	C	0.034243	-0.032842	0.005541	5.4E-10
SYN2	3	rs71628739	12,147,193	G	TGTGTGT	0.035170	-0.031207	0.005472	2.3E-09
SYN2	3	chr3:12147956_C_CA	12,147,956	CA	C	0.111756	-0.018227	0.003218	2.4E-09
SYN2	3	rs6768568	12,148,318	A	G	0.034126	-0.031853	0.005551	1.8E-09
SYN2	3	rs6792867	12,148,400	C	A	0.034126	-0.031853	0.005551	1.8E-09
SYN2	3	rs7629805	12,150,894	G	A	0.034212	-0.033233	0.005544	3.5E-10
SYN2	3	rs117082374	12,150,945	C	T	0.028070	-0.033901	0.006107	9.3E-09
SYN2	3	rs7652520	12,151,127	C	G	0.034212	-0.033233	0.005544	3.5E-10
SYN2, TIMP4	3	rs17035945	12,153,128	T	C	0.114740	-0.018163	0.003178	1.6E-09
SYN2, TIMP4	3	rs71304089	12,155,463	T	C	0.034213	-0.033162	0.005543	3.8E-10
SYN2, TIMP4	3	rs71304090	12,155,999	G	A	0.034209	-0.033202	0.005543	3.6E-10
SYN2, TIMP4	3	rs10433537	12,156,985	T	A	0.034209	-0.033198	0.005543	3.6E-10
SYN2	3	rs146888519	12,163,301	ATTAT	A	0.034026	-0.033267	0.005558	4.7E-10
SYN2	3	rs186275353	12,165,221	A	G	0.028471	-0.033786	0.006064	7.8E-09
SYN2	3	rs78518024	12,165,961	C	T	0.034661	-0.033264	0.005508	2.6E-10
SYN2	3	chr3:12168855_AT_A	12,168,855	AT	A	0.116417	-0.018709	0.003157	4.5E-10
SYN2	3	rs13064273	12,174,631	A	G	0.034664	-0.033228	0.005507	2.8E-10
SYN2	3	rs6781687	12,174,760	G	A	0.050799	-0.029168	0.004621	2.1E-11
SYN2	3	rs34189310	12,175,017	A	AT	0.034681	-0.033281	0.005508	2.6E-10
SYN2	3	rs13070993	12,176,297	T	C	0.034940	-0.033383	0.005487	2.1E-10
SYN2	3	rs6805092	12,179,924	T	C	0.044783	-0.032513	0.004877	4.2E-12
SYN2	3	rs34646613	12,187,872	A	AC	0.034643	-0.033073	0.005510	3.0E-10
SYN2	3	rs310763	12,189,204	T	C	0.116495	-0.017980	0.003154	1.6E-09
SYN2 *	3	rs71304092	12,195,065	A	G	0.044799	-0.032117	0.004878	6.4E-12
SYN2 *	3	rs13077227	12,200,266	G	A	0.044804	-0.032101	0.004878	6.9E-12
SYN2 *	3	rs7637403	12,200,988	A	G	0.116268	-0.018169	0.003157	1.1E-09
SYN2 *	3	rs13079837	12,209,346	A	T	0.117316	-0.017763	0.003143	1.7E-09
SYN2 *	3	rs13099882	12,209,388	G	A	0.117406	-0.017856	0.003142	1.4E-09
SYN2 *	3	rs35000292	12,213,022	C	CAA	0.034414	-0.033119	0.005530	2.7E-10
SYN2 *	3	rs11718525	12,213,765	T	C	0.034001	-0.034028	0.005566	1.2E-10
SYN2 *	3	rs34733382	12,214,747	T	TA	0.033395	-0.034900	0.005616	5.0E-11
SYN2 *	3	rs34562457	12,214,750	C	T	0.033395	-0.034900	0.005616	5.0E-11
SYN2 *	3	rs74280642	12,221,434	A	G	0.033318	-0.036371	0.005624	6.9E-12
SYN2 *	3	rs6786675	12,223,962	C	G	0.033442	-0.036556	0.005611	4.8E-12
SYN2 *	3	rs35355828	12,225,005	A	G	0.046238	-0.035198	0.004814	1.0E-14
SYN2 *	3	rs11720578	12,225,584	T	G	0.046274	-0.034667	0.004813	2.3E-14
SYN2 *	3	rs35146940	12,229,787	T	A	0.033321	-0.035968	0.005620	1.1E-11
SYN2 *	3	rs310749	12,232,268	G	T	0.136630	-0.016411	0.002954	4.2E-09
SYN2 *	3	rs13065423	12,233,092	A	G	0.034339	-0.035310	0.005534	1.1E-11
SYN2 *	3	rs13088452	12,233,461	C	T	0.034343	-0.035329	0.005534	1.1E-11
SYN2 *	3	rs13066157	12,233,494	A	G	0.034346	-0.035251	0.005533	1.2E-11
SYN2 *	3	rs71304093	12,233,820	T	C	0.034349	-0.035294	0.005533	1.1E-11
SYN2 *	3	rs13071168	12,233,947	A	G	0.034351	-0.035278	0.005533	1.1E-11
SYN2 *	3	rs11709119	12,234,993	T	G	0.034458	-0.034742	0.005523	2.0E-11

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
SYN2 *	3	rs36086545	12,235,690	A	G	0.034500	-0.034795	0.005517	1.9E-11
SYN2 *	3	rs112560967	12,236,156	A	C	0.034561	-0.034300	0.005512	3.1E-11
SYN2 *	3	rs113205156	12,236,157	C	T	0.034470	-0.033856	0.005520	6.0E-11
SYN2 *	3	rs17036101	12,236,345	A	G	0.034896	-0.034254	0.005489	2.9E-11
SYN2 *	3	rs34780220	12,236,613	G	A	0.034558	-0.034393	0.005512	2.7E-11
SYN2 *	3	rs11715362	12,236,964	G	T	0.034509	-0.034302	0.005517	3.3E-11
SYN2 *	3	rs11719082	12,237,028	G	A	0.034509	-0.034305	0.005517	3.3E-11
SYN2 *	3	rs35551471	12,237,709	A	G	0.034517	-0.034463	0.005516	2.7E-11
SYN2 *	3	rs67201468	12,238,506	G	GT	0.034518	-0.034468	0.005516	2.7E-11
PPARG *	3	rs35220653	12,242,071	G	C	0.034541	-0.034451	0.005513	2.6E-11
PPARG *	3	rs1562040	12,243,905	A	G	0.034550	-0.034495	0.005513	2.4E-11
PPARG *	3	rs17036130	12,246,788	A	G	0.034601	-0.034293	0.005508	3.3E-11
PPARG *	3	rs13081389	12,248,301	G	A	0.035075	-0.033370	0.005475	7.0E-11
PPARG *	3	rs7628899	12,249,014	A	T	0.034608	-0.034411	0.005508	2.8E-11
PPARG *	3	rs34835192	12,249,293	C	CA	0.034608	-0.034411	0.005508	2.8E-11
PPARG *	3	rs1596417	12,249,399	T	A	0.034679	-0.033899	0.005503	4.8E-11
PPARG *	3	rs34881099	12,250,003	A	C	0.034608	-0.034411	0.005508	2.8E-11
PPARG *	3	rs35577339	12,254,847	A	G	0.034536	-0.034450	0.005517	2.7E-11
PPARG *	3	rs71304095	12,255,014	A	G	0.034537	-0.034455	0.005517	2.7E-11
PPARG *	3	rs35252428	12,255,654	T	C	0.034540	-0.034462	0.005517	2.7E-11
PPARG *	3	rs773846047	12,256,287	G	A	0.034493	-0.032276	0.005528	3.0E-10
PPARG *	3	rs66615477	12,256,815	T	G	0.032060	-0.032347	0.005777	9.7E-09
PPARG *	3	rs35316189	12,257,068	A	G	0.034531	-0.034364	0.005518	2.9E-11
PPARG *	3	rs35099296	12,257,139	C	CATA	0.034530	-0.034354	0.005518	2.9E-11
PPARG *	3	rs71304096	12,257,866	G	A	0.034527	-0.034415	0.005518	2.7E-11
PPARG *	3	rs71304097	12,258,116	A	C	0.034527	-0.034414	0.005518	2.7E-11
PPARG *	3	rs35877199	12,258,161	A	G	0.034527	-0.034414	0.005518	2.7E-11
PPARG *	3	rs35057507	12,258,223	A	G	0.034859	-0.033949	0.005501	4.1E-11
PPARG *	3	rs13067702	12,258,446	C	G	0.034521	-0.034445	0.005519	2.6E-11
PPARG *	3	rs34685612	12,258,484	A	G	0.034521	-0.034445	0.005519	2.6E-11
PPARG *	3	rs71304098	12,258,559	A	G	0.034521	-0.034440	0.005519	2.6E-11
PPARG *	3	rs13088598	12,259,564	T	C	0.034443	-0.034689	0.005527	2.2E-11
PPARG *	3	rs13088608	12,259,617	G	A	0.034443	-0.034689	0.005527	2.2E-11
PPARG *	3	rs13089415	12,259,861	T	G	0.034438	-0.034788	0.005528	2.0E-11
PPARG *	3	rs6771792	12,259,973	T	C	0.034438	-0.034789	0.005528	2.0E-11
PPARG *	3	rs34430055	12,260,072	C	T	0.034438	-0.034789	0.005528	2.0E-11
PPARG *	3	rs35541642	12,260,763	T	C	0.034439	-0.034803	0.005528	1.9E-11
PPARG *	3	rs11715261	12,275,733	C	G	0.035786	-0.032597	0.005421	1.0E-10
PPARG *	3	rs11715234	12,275,811	A	C	0.035787	-0.032598	0.005421	1.0E-10
PPARG *	3	rs2920502	12,287,696	G	C	0.219171	-0.014498	0.002478	9.7E-10
PPARG	3	rs17036160	12,288,284	T	C	0.038518	-0.033821	0.005239	5.9E-12
PPARG	3	rs11709077	12,295,008	A	G	0.039900	-0.034881	0.005147	6.0E-13
PPARG	3	rs11712037	12,303,231	G	C	0.037132	-0.032911	0.005333	6.1E-11
PPARG	3	rs117937053	12,305,918	G	A	0.033441	-0.030776	0.005630	3.5E-09
PPARG	3	rs35000407	12,310,022	G	T	0.039628	-0.033903	0.005163	3.0E-12
PPARG	3	rs2067819	12,317,550	A	G	0.039691	-0.033390	0.005160	5.3E-12
PPARG	3	chr3:12318858_G_GT	12,318,858	GT	G	0.038768	-0.036000	0.005230	2.8E-13
PPARG	3	rs150732434	12,319,385	T	TG	0.039608	-0.034035	0.005164	2.5E-12
PPARG	3	rs13083375	12,323,809	T	G	0.039608	-0.034035	0.005164	2.5E-12
PPARG	3	rs13064760	12,327,902	T	C	0.039608	-0.034035	0.005164	2.5E-12
PPARG	3	rs2012444	12,334,457	T	C	0.039601	-0.033936	0.005165	3.4E-12
PPARG	3	rs35240997	12,337,852	G	A	0.039697	-0.033159	0.005160	8.3E-12
PPARG	3	rs13085211	12,341,766	A	G	0.040154	-0.034193	0.005130	1.4E-12
PPARG	3	rs7638903	12,342,215	A	G	0.039554	-0.034365	0.005166	1.6E-12
PPARG	3	rs11128603	12,344,329	G	A	0.039602	-0.034073	0.005163	2.3E-12
PPARG	3	rs4684847	12,344,838	T	C	0.039409	-0.034318	0.005175	1.8E-12
PPARG	3	rs7610055	12,346,910	A	G	0.037419	-0.032441	0.005310	8.1E-11
PPARG	3	rs35788455	12,347,409	C	CTTG	0.039627	-0.033894	0.005161	2.8E-12
PPARG	3	rs17036326	12,347,814	G	A	0.039762	-0.033590	0.005153	4.3E-12
PPARG	3	rs17036328	12,348,985	C	T	0.039667	-0.034009	0.005159	2.4E-12
PPARG	3	rs6802898	12,349,708	T	C	0.039693	-0.033939	0.005156	2.6E-12
PPARG	3	rs2197423	12,350,084	A	G	0.039712	-0.034037	0.005156	2.3E-12
PPARG	3	rs7647481	12,350,314	A	G	0.039627	-0.033894	0.005161	2.8E-12
PPARG	3	rs7649970	12,350,773	T	C	0.039742	-0.034036	0.005153	2.2E-12
PPARG	3	rs1801282	12,351,626	G	C	0.039741	-0.033670	0.005153	3.6E-12
PPARG	3	rs17036342	12,352,183	G	A	0.039604	-0.033652	0.005162	4.3E-12
PPARG	3	rs1899951	12,353,341	T	C	0.039641	-0.033764	0.005160	3.5E-12
PPARG	3	rs4684848	12,354,146	A	G	0.039600	-0.033647	0.005162	4.3E-12
PPARG	3	rs4135250	12,355,346	G	A	0.039599	-0.033652	0.005162	4.3E-12
PPARG	3	rs71304101	12,355,414	A	G	0.039599	-0.033652	0.005162	4.3E-12
PPARG	3	rs2881654	12,355,456	A	G	0.039599	-0.033652	0.005162	4.3E-12
PPARG	3	rs2120825	12,371,840	G	T	0.030319	-0.031433	0.005902	2.0E-08
KBTBD8 *	3	rs13078428	66,802,660	T	C	0.377766	-0.010979	0.002126	7.9E-09
KBTBD8 *	3	rs9813067	66,812,220	T	C	0.470648	-0.011274	0.002035	3.3E-09
KBTBD8 *	3	rs7638057	66,812,294	C	T	0.471142	-0.011305	0.002035	3.0E-09
KBTBD8 *	3	rs7645370	66,812,469	T	G	0.470692	-0.011320	0.002035	2.6E-09
KBTBD8 *	3	rs7642618	66,812,578	A	G	0.470531	-0.011235	0.002035	3.4E-09
KBTBD8 *	3	rs7629637	66,812,641	G	C	0.475234	-0.011294	0.002039	2.5E-09
KBTBD8 *	3	rs34113192	66,813,244	A	G	0.470407	-0.011328	0.002037	2.7E-09
KBTBD8 *	3	rs11342763	66,814,250	GA	G	0.466327	-0.011008	0.002043	7.6E-09
KBTBD8 *	3	rs4856967	66,814,463	T	C	0.467957	-0.010681	0.002041	1.7E-08
KBTBD8 *	3	rs4856968	66,814,508	A	G	0.468407	-0.010613	0.002043	2.1E-08
KBTBD8 *	3	rs9682765	66,815,451	C	T	0.474438	-0.010981	0.002045	7.4E-09
KBTBD8 *	3	rs6549423	66,816,248	G	A	0.472992	-0.011101	0.002036	4.2E-09
KBTBD8 *	3	rs6549424	66,816,324	T	C	0.473308	-0.011180	0.002038	3.2E-09
KBTBD8 *	3	rs6549425	66,816,387	T	A	0.473049	-0.010992	0.002035	5.4E-09
KBTBD8 *	3	rs7641377	66,816,670	T	C	0.466503	-0.010467	0.002041	3.1E-08
KBTBD8 *	3	rs4856827	66,817,179	A	G	0.472383	-0.011350	0.002040	2.2E-09
SPON2	4	rs872894	1,195,420	T	C	0.166380	-0.015356	0.002745	3.1E-08
LOC100130872, SPON2	4	rs4974570	1,202,805	T	C	0.164895	-0.015579	0.002755	3.4E-08
MSANTD1 *	4	rs6446731	3,283,024	G	A	0.417205	-0.012950	0.002068	1.0E-09
RGS12 *	4	rs3129316	3,286,179	A	G	0.379264	-0.012456	0.002094	3.9E-09
RGS12 *	4	rs2071666	3,288,676	A	G	0.378120	-0.012359	0.002095	5.0E-09
RGS12 *	4	rs3129314	3,291,312	G	T	0.378326	-0.012126	0.002097	9.4E-09
RGS12 *	4	rs3135145	3,297,777	T	C	0.344318	-0.012129	0.002136	1.8E-08
RGS12 *	4	rs73193354	3,298,808	G	T	0.336500	0.013564	0.002150	1.2E-09
RGS12 *	4	rs3129310	3,299,661	T	G	0.377188	-0.012684	0.002089	1.6E-09

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
RGS12 *	4	rs2239725	3,304,012	C	T	0.347773	-0.012345	0.002122	7.7E-09
RGS12 *	4	rs910568	3,305,646	A	G	0.346150	-0.012465	0.002124	6.0E-09
RGS12 *	4	rs76334211	3,305,705	G	GC	0.334413	0.012933	0.002141	5.8E-09
RGS12 *	4	rs3135146	3,305,911	C	G	0.347473	-0.012481	0.002121	6.1E-09
RGS12 *	4	rs73193357	3,306,228	G	C	0.333971	0.012979	0.002141	5.1E-09
RGS12 *	4	rs3129308	3,307,545	G	A	0.381445	-0.012597	0.002078	1.5E-09
RGS12 *	4	rs2749786	3,313,239	C	T	0.336225	0.013269	0.002134	2.2E-09
RGS12	4	rs2236052	3,316,686	A	G	0.348366	-0.012809	0.002114	2.2E-09
RGS12	4	rs2281470	3,317,826	T	C	0.333789	0.012909	0.002136	5.6E-09
RGS12	4	rs12643903	3,319,967	A	G	0.336224	0.012963	0.002134	4.2E-09
RGS12	4	rs2857859	3,320,413	T	C	0.334997	0.012979	0.002136	4.7E-09
RGS12	4	rs2857861	3,322,040	C	T	0.440888	-0.012409	0.002037	1.8E-09
RGS12	4	rs2051558	3,323,159	G	A	0.408335	-0.014196	0.002051	8.6E-12
RGS12	4	rs2749785	3,323,452	G	C	0.349390	-0.012658	0.002115	2.9E-09
RGS12	4	rs2749783	3,324,371	A	C	0.382146	-0.012963	0.002075	5.5E-10
RGS12	4	rs2857860	3,328,062	G	A	0.328715	0.013372	0.002155	2.9E-09
RGS12	4	rs3129336	3,333,174	T	C	0.326069	0.013285	0.002165	3.2E-09
RGS12	4	rs2748447	3,336,104	G	A	0.351616	-0.012727	0.002118	2.3E-09
RGS12	4	rs12640526	3,338,001	T	C	0.334035	0.012886	0.002139	6.2E-09
RGS12	4	rs2749782	3,338,034	T	C	0.350448	-0.012573	0.002121	4.0E-09
RGS12	4	chr4:3340762_A_AGGTGCAGGCC	3,340,762	A	GTGCAGC	0.381451	-0.013102	0.002078	3.7E-10
RGS12	4	rs2073286	3,343,164	C	T	0.337133	0.013004	0.002133	4.7E-09
RGS12	4	rs2749781	3,344,890	T	C	0.350959	-0.012522	0.002121	4.9E-09
RGS12	4	rs2749780	3,347,365	T	A	0.380918	-0.012855	0.002080	9.3E-10
RGS12	4	rs2749779	3,348,521	G	A	0.336954	0.013073	0.002133	3.7E-09
RGS12	4	rs76078669	3,349,544	A	ACT	0.334893	0.013077	0.002139	3.6E-09
RGS12	4	rs2749778	3,349,778	T	C	0.349403	-0.012687	0.002119	2.6E-09
RGS12	4	rs2749776	3,353,308	G	A	0.334881	0.012946	0.002138	6.0E-09
RGS12	4	rs2749775	3,353,811	T	C	0.334844	0.012957	0.002138	5.0E-09
RGS12	4	rs2857982	3,356,938	G	A	0.357461	-0.012445	0.002107	4.8E-09
RGS12	4	rs149402347	3,362,478	G	GTGTA	0.312704	0.012682	0.002219	3.9E-08
RGS12	4	rs60181496	3,362,661	C	G	0.362227	-0.011651	0.002124	4.5E-08
RGS12	4	rs60208975	3,362,803	A	G	0.393267	-0.012184	0.002091	7.0E-09
RGS12	4	rs881817	3,363,654	A	G	0.388538	-0.012490	0.002085	3.0E-09
RGS12	4	rs881818	3,363,680	C	G	0.322925	0.012676	0.002174	1.9E-08
RGS12	4	rs16844197	3,364,833	G	T	0.325017	0.012747	0.002169	1.5E-08
RGS12	4	rs62274923	3,365,109	G	A	0.325730	0.012400	0.002168	3.2E-08
RGS12	4	rs16844201	3,365,141	C	G	0.325728	0.012397	0.002168	3.2E-08
RGS12	4	rs13104157	3,365,223	T	C	0.355633	-0.011810	0.002123	3.5E-08
RGS12	4	rs13150241	3,365,554	A	G	0.354992	-0.012014	0.002120	1.8E-08
RGS12	4	rs6819202	3,366,537	G	A	0.356022	-0.012097	0.002122	1.2E-08
RGS12	4	rs3129334	3,366,799	T	C	0.354627	-0.012194	0.002123	1.0E-08
RGS12	4	rs10155132	3,367,773	A	G	0.352755	-0.012662	0.002127	3.1E-09
RGS12	4	rs7435601	3,367,918	T	C	0.351780	-0.012663	0.002130	3.6E-09
RGS12	4	rs12640721	3,372,448	G	A	0.337239	0.013034	0.002147	6.1E-09
RGS12	4	rs12640186	3,372,812	T	C	0.334239	0.012680	0.002152	1.9E-08
RGS12	4	rs10937924	3,373,171	T	C	0.373483	-0.014071	0.002107	4.8E-11
RGS12	4	rs73193372	3,373,261	T	C	0.333572	0.012740	0.002153	1.6E-08
RGS12	4	rs3129333	3,373,271	A	G	0.334107	0.012672	0.002153	2.0E-08
RGS12	4	rs3129332	3,374,041	A	G	0.336249	0.012967	0.002152	9.6E-09
RGS12	4	rs2343799	3,375,007	C	T	0.334162	0.012679	0.002163	2.1E-08
RGS12	4	rs138391629	3,375,752	GC	G	0.334008	0.012814	0.002170	1.8E-08
RGS12	4	rs3129331	3,375,947	A	G	0.333232	0.012873	0.002170	1.4E-08
RGS12	4	rs3129330	3,377,653	T	C	0.332022	0.012985	0.002182	1.4E-08
RGS12	4	rs1894442	3,384,588	T	C	0.459550	-0.026360	0.002039	5.5E-37
RGS12	4	rs16844249	3,385,421	T	C	0.120197	0.017573	0.003149	2.5E-09
RGS12	4	rs12644442	3,385,844	A	G	0.495182	0.025747	0.002048	1.8E-35
RGS12	4	rs4690090	3,387,800	T	C	0.441754	-0.025372	0.002058	4.2E-34
RGS12	4	rs6828057	3,388,084	A	G	0.444263	-0.025577	0.002059	2.1E-34
RGS12	4	rs2269496	3,388,419	C	T	0.287228	0.019854	0.002279	1.9E-17
RGS12	4	rs13127597	3,388,545	C	A	0.464262	-0.026243	0.002028	3.5E-37
RGS12	4	rs73193383	3,390,547	T	C	0.276099	0.022002	0.002298	8.8E-21
RGS12	4	rs17797467	3,390,588	G	C	0.466862	-0.025550	0.002041	5.5E-35
RGS12	4	rs13152128	3,390,623	A	C	0.460754	-0.025564	0.002037	6.0E-35
RGS12	4	rs12510769	3,392,647	C	T	0.282254	0.021952	0.002273	6.9E-21
RGS12	4	rs115019205	3,396,341	A	G	0.109484	0.019350	0.003233	4.9E-10
RGS12	4	rs73193388	3,399,951	T	C	0.143407	0.015817	0.002880	2.6E-08
RGS12	4	rs9995777	3,403,748	T	C	0.447668	0.023916	0.002076	6.4E-30
RGS12	4	rs16844280	3,407,297	T	C	0.107589	0.019819	0.003258	3.9E-10
RGS12	4	rs10027926	3,412,927	A	G	0.262363	0.022644	0.002348	7.4E-21
RGS12	4	rs62274930	3,413,609	T	C	0.473250	-0.025832	0.002053	1.8E-35
RGS12	4	rs16844301	3,413,651	A	G	0.498865	0.023616	0.002050	6.6E-30
RGS12	4	rs3213506	3,415,757	A	G	0.472750	-0.026033	0.002056	5.3E-36
RGS12	4	rs3213507	3,416,118	C	G	0.498911	-0.023734	0.002053	3.1E-30
RGS12	4	rs17190954	3,416,357	G	A	0.265551	0.022730	0.002334	2.7E-21
RGS12	4	rs16844307	3,416,438	T	C	0.473419	-0.026155	0.002057	3.4E-36
RGS12	4	rs16844309	3,416,539	A	G	0.472999	-0.026361	0.002057	8.2E-37
RGS12	4	rs12641989	3,418,113	A	G	0.265109	0.022573	0.002336	7.0E-21
RGS12	4	rs3748037	3,418,544	A	G	0.265152	0.022676	0.002336	4.2E-21
RGS12	4	rs3748036	3,418,644	T	C	0.473269	-0.026314	0.002059	1.2E-36
RGS12	4	rs4690095	3,419,582	C	T	0.487297	0.025991	0.002065	8.3E-36
RGS12	4	rs3088231	3,420,484	A	G	0.263768	0.022518	0.002346	1.1E-20
RGS12	4	rs3789739	3,421,715	T	C	0.475474	-0.026397	0.002066	1.8E-36
RGS12	4	rs16844330	3,422,504	T	C	0.105435	0.021649	0.003302	2.3E-11
RGS12	4	rs58143210	3,423,303	T	C	0.472041	-0.026112	0.002068	8.7E-36
RGS12	4	rs3804348	3,429,615	A	C	0.104082	0.020853	0.003328	1.3E-10
HGFAC	4	rs2073505	3,442,776	A	G	0.092945	0.025872	0.003488	2.7E-14
HGFAC *	4	rs28766336	3,452,024	T	G	0.474155	-0.025939	0.002062	2.4E-36
HGFAC *	4	rs4690099	3,452,727	T	C	0.464836	-0.025265	0.002063	1.6E-34
DOK7 *	4	rs2091626	3,460,173	T	G	0.466697	-0.025333	0.002064	9.9E-35
DOK7 *	4	rs1076903	3,460,467	G	A	0.466729	-0.025435	0.002064	5.3E-35
DOK7 *	4	rs28478452	3,461,750	A	G	0.465547	-0.025520	0.002068	4.8E-35
DOK7	4	rs56738936	3,468,759	T	TGTGA	0.340124	0.018873	0.002159	9.5E-19
DOK7	4	rs36205397	3,468,877	G	A	0.380466	0.019116	0.002089	1.5E-20
DOK7	4	chr4:3469063_A_AGT	3,469,063	AGT	A	0.378890	0.018968	0.002091	4.2E-20
DOK7	4	rs10007119	3,471,339	G	A	0.381509	0.019051	0.002079	1.7E-20
DOK7	4	rs6831256	3,471,412	G	A	0.381961	0.018959	0.002077	2.2E-20

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
LRPAP1	4	rs56358267	3,504,455	G	A	0.417099	0.011574	0.002056	2.2E-08
LRPAP1	4	rs2093098	3,512,107	C	T	0.421421	0.011652	0.002051	1.5E-08
LRPAP1	4	rs6789	3,512,968	G	A	0.417527	0.011270	0.002056	4.9E-08
LRPAP1	4	rs2285088	3,514,721	T	C	0.475089	0.012621	0.002054	8.1E-10
LRPAP1	4	rs1741550	3,515,322	C	T	0.420771	0.011562	0.002053	2.0E-08
LRPAP1	4	rs1730778	3,516,720	C	T	0.417109	0.011314	0.002056	4.6E-08
LRPAP1	4	rs1805167	3,518,370	AGGCGA	C	0.386358	0.012341	0.002118	6.8E-09
FAM184B *	4	rs73096946	17,787,092	C	T	0.352798	0.010944	0.002122	4.5E-08
FAM184B *	4	rs16895735	17,787,560	C	T	0.137156	0.015904	0.002946	4.1E-08
DCAF16 *	4	rs60258355	17,791,257	A	T	0.284030	0.011926	0.002245	1.9E-08
DCAF16 *	4	rs118071982	17,791,701	A	G	0.137931	0.015677	0.002935	4.9E-08
DCAF16 *	4	rs77992809	17,792,298	C	G	0.138295	0.015692	0.002934	4.9E-08
DCAF16 *	4	rs7672919	17,795,832	T	G	0.283860	0.011722	0.002243	3.2E-08
DCAF16 *	4	rs113241654	17,798,521	G	A	0.283061	0.011868	0.002247	2.1E-08
DCAF16	4	rs7690457	17,803,756	A	G	0.137948	0.015770	0.002935	4.2E-08
DCAF16	4	rs140064399	17,807,029	GA	G	0.138209	0.015989	0.002936	2.7E-08
NCAPG	4	rs11941723	17,810,905	G	A	0.143028	0.017605	0.002885	4.3E-10
NCAPG	4	rs16895792	17,811,173	T	C	0.126844	0.016488	0.003045	2.8E-08
NCAPG	4	rs16895796	17,811,596	A	T	0.142337	0.017298	0.002891	8.8E-10
NCAPG	4	rs16895802	17,814,266	G	C	0.143005	0.017178	0.002881	1.1E-09
NCAPG	4	rs139724825	17,822,441	T	C	0.141607	0.017392	0.002896	6.6E-10
LCORL, NCAPG	4	rs59037741	17,843,847	T	C	0.141216	0.016953	0.002898	2.4E-09
LCORL	4	rs16895882	17,847,141	G	T	0.142788	0.016903	0.002886	1.8E-09
LCORL	4	rs75878186	17,855,630	G	A	0.287564	0.012773	0.002233	1.6E-09
LCORL	4	rs79334166	17,857,843	G	A	0.287804	0.012698	0.002233	1.8E-09
LCORL	4	rs145087631	17,860,695	T	C	0.140742	0.016965	0.002906	1.8E-09
LCORL	4	rs58854324	17,862,391	C	T	0.350955	0.011244	0.002126	2.3E-08
LCORL	4	rs113476736	17,862,651	C	T	0.287120	0.012612	0.002239	2.3E-09
LCORL	4	rs61504083	17,862,990	TATAAC	T	0.350971	0.011164	0.002126	2.9E-08
LCORL	4	rs74619517	17,863,938	A	G	0.284534	0.012747	0.002248	2.7E-09
LCORL	4	rs73098804	17,864,242	A	T	0.279887	0.012564	0.002262	4.2E-09
LCORL	4	rs16895917	17,867,611	C	T	0.144979	0.015571	0.002862	1.3E-08
LCORL	4	rs78439738	17,873,012	C	T	0.144874	0.015769	0.002862	8.0E-09
LCORL	4	rs13131350	17,875,864	G	A	0.291497	0.012399	0.002220	2.8E-09
LCORL	4	rs76264386	17,876,967	G	A	0.144336	0.015621	0.002869	1.3E-08
LCORL	4	rs78994908	17,876,968	C	A	0.144336	0.015621	0.002869	1.3E-08
LCORL	4	rs7700107	17,878,793	C	A	0.294009	0.011852	0.002215	1.3E-08
LCORL	4	rs16895971	17,883,363	C	T	0.294387	0.012107	0.002213	6.5E-09
LCORL	4	rs144629949	17,902,432	GT	G	0.143588	0.015537	0.002874	2.0E-08
LCORL	4	rs78993313	17,916,447	T	C	0.140435	0.015647	0.002901	2.3E-08
LCORL	4	rs78471813	17,921,045	A	G	0.140422	0.015402	0.002900	3.8E-08
LCORL	4	rs116870149	17,926,197	C	T	0.144593	0.015762	0.002865	1.1E-08
LCORL	4	rs80043981	17,939,923	T	C	0.143909	0.016073	0.002873	5.6E-09
LCORL	4	chr4:17940116_G_GTA	17,940,116	GTA	G	0.146139	0.016021	0.002860	5.3E-09
LCORL	4	rs76828425	17,971,670	T	C	0.138707	0.015491	0.002936	2.9E-08
LCORL	4	rs111370140	17,983,602	A	G	0.140081	0.015685	0.002906	2.0E-08
LCORL	4	rs575272182	17,990,115	C	T	0.131518	0.016864	0.003003	4.1E-09
LCORL	4	rs868271938	17,999,017	C	T	0.140404	0.015386	0.002924	3.6E-08
LCORL	4	rs113214641	17,999,270	A	G	0.144885	0.016139	0.002862	4.0E-09
LCORL	4	rs79032496	18,000,844	A	T	0.144663	0.016110	0.002864	4.6E-09
LCORL	4	rs77093246	18,011,664	C	T	0.145463	0.015911	0.002856	6.4E-09
LCORL	4	rs78015869	18,016,706	T	C	0.141941	0.015889	0.002889	9.7E-09
UGT2B15 *	4	rs2168049	68,699,757	C	G	0.463908	-0.011276	0.002040	2.5E-08
UGT2B15 *	4	rs147532404	68,700,487	C	T	0.461440	-0.011440	0.002039	1.8E-08
UGT2B15 *	4	rs293460	68,705,431	A	T	0.454162	-0.011388	0.002049	3.3E-08
UGT2B15 *	4	rs293453	68,709,640	G	T	0.455610	-0.011567	0.002054	2.2E-08
UGT2B15 *	4	rs17146664	68,710,233	T	C	0.455062	-0.011477	0.002052	2.9E-08
UGT2B15 *	4	rs17146671	68,712,705	T	C	0.451718	-0.011760	0.002049	1.4E-08
UGT2B15 *	4	rs293449	68,714,467	C	T	0.454128	-0.011481	0.002050	2.7E-08
UGT2B15 *	4	rs17146678	68,715,901	G	A	0.454104	-0.011459	0.002050	2.8E-08
UGT2B15 *	4	rs293443	68,717,375	T	C	0.453996	-0.011335	0.002050	3.9E-08
UGT2B15 *	4	rs293442	68,717,837	C	T	0.453997	-0.011352	0.002050	3.7E-08
UGT2B15 *	4	rs293439	68,719,447	A	T	0.451567	-0.011573	0.002050	2.5E-08
UGT2B15 *	4	rs293438	68,720,647	A	G	0.451849	-0.011404	0.002049	4.0E-08
UGT2B15 *	4	rs141200334	68,722,470	A	G	0.451658	-0.011525	0.002048	2.7E-08
UGT2B15 *	4	chr4:68725553_G_GT	68,725,553	G	GT	0.453900	-0.011436	0.002054	4.2E-08
UGT2B15 *	4	rs139502240	68,726,315	G	T	0.451549	-0.011601	0.002048	2.3E-08
UGT2B15 *	4	rs293422	68,726,929	A	G	0.452125	-0.011542	0.002051	2.8E-08
UGT2B15 *	4	rs12644441	68,727,085	G	T	0.453878	-0.012149	0.002066	6.9E-09
UGT2B15 *	4	rs293420	68,727,115	C	T	0.452502	-0.011873	0.002051	1.1E-08
UGT2B15 *	4	rs1708574	68,728,368	T	C	0.451664	-0.011596	0.002049	2.5E-08
AFF1 *	4	chr4:86917330_T_TGAAG	86,917,330	T	TGAAG	0.365090	-0.011541	0.002133	3.1E-08
AFF1	4	rs7660883	87,061,724	G	C	0.407389	-0.011589	0.002050	4.7E-09
AFF1	4	rs10597574	87,061,855	A	ATG	0.407434	-0.011718	0.002051	3.2E-09
AFF1	4	rs3035539	87,062,748	C	CAT	0.407442	-0.011805	0.002051	2.5E-09
AFF1	4	rs28432336	87,063,179	G	A	0.407831	-0.011879	0.002052	2.1E-09
AFF1	4	rs11946481	87,063,458	T	C	0.407679	-0.011571	0.002051	5.2E-09
AFF1	4	rs3775228	87,064,014	T	C	0.404093	0.011734	0.002063	4.4E-09
AFF1	4	rs17668131	87,064,378	T	G	0.405681	0.011917	0.002060	2.7E-09
AFF1	4	rs72877984	87,064,569	A	G	0.407439	-0.011738	0.002051	3.1E-09
AFF1	4	rs10018904	87,065,054	C	G	0.405790	0.011820	0.002061	3.6E-09
AFF1	4	rs28677145	87,065,229	A	G	0.407387	-0.011814	0.002056	2.3E-09
AFF1	4	rs13120301	87,065,243	T	C	0.405686	0.011851	0.002061	3.3E-09
AFF1	4	rs236679	87,065,449	C	A	0.405499	0.011530	0.002063	9.4E-09
AFF1	4	rs236681	87,067,356	G	T	0.407414	0.012342	0.002058	7.4E-10
AFF1	4	rs2280952	87,067,388	C	T	0.405573	0.012028	0.002058	1.8E-09
AFF1	4	rs2280953	87,067,438	T	C	0.405122	0.011942	0.002059	2.4E-09
AFF1	4	rs2280954	87,067,710	G	A	0.405192	0.011841	0.002059	3.2E-09
AFF1	4	rs3775226	87,068,313	A	G	0.402590	0.011782	0.002065	3.9E-09
AFF1	4	rs11097127	87,069,182	T	G	0.407428	-0.011758	0.002057	2.9E-09
AFF1	4	rs11461770	87,069,713	CA	C	0.409403	-0.011723	0.002056	3.0E-09
AFF1	4	rs3736668	87,071,058	C	T	0.403560	0.011957	0.002062	2.3E-09
AFF1	4	rs3736669	87,071,601	A	G	0.413550	-0.012159	0.002055	8.9E-10
AFF1	4	rs17012368	87,074,967	G	T	0.415401	-0.012451	0.002054	3.6E-10
AFF1	4	rs2125787	87,075,471	G	A	0.415954	-0.012378	0.002050	3.9E-10
AFF1	4	rs17605615	87,075,593	A	G	0.395778	0.012521	0.002065	4.1E-10
AFF1	4	rs11408312	87,076,256	CT	C	0.416505	-0.012341	0.002045	3.8E-10

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
AFF1	4	rs9998251	87,077,903	A	G	0.414815	-0.012605	0.002047	1.8E-10
AFF1	4	rs236995	87,079,271	G	C	0.416085	-0.012505	0.002044	2.2E-10
AFF1	4	rs3775223	87,079,294	T	A	0.414820	-0.012618	0.002047	1.7E-10
AFF1	4	rs3836602	87,083,662	ATT	A	0.415311	-0.012433	0.002047	3.1E-10
AFF1	4	rs236996	87,084,051	A	G	0.416623	-0.012418	0.002044	3.2E-10
AFF1	4	rs151451	87,085,215	T	C	0.395212	0.012308	0.002065	7.9E-10
AFF1	4	rs4693156	87,086,075	C	T	0.415311	-0.012411	0.002047	3.3E-10
AFF1	4	rs236984	87,087,462	A	G	0.416563	-0.012292	0.002044	4.3E-10
AFF1	4	rs236985	87,087,630	A	G	0.416539	-0.012325	0.002044	3.8E-10
AFF1	4	rs3836601	87,087,885	C	CATT	0.415283	-0.012438	0.002047	2.9E-10
AFF1	4	rs236676	87,088,468	A	G	0.395338	0.012358	0.002064	6.8E-10
AFF1	4	chr4:87088605_AT_A	87,088,605	A	AT	0.413557	-0.012796	0.002050	1.2E-10
AFF1	4	rs236987	87,088,627	T	C	0.415990	-0.012310	0.002046	4.1E-10
AFF1	4	rs3775221	87,090,641	G	T	0.415313	-0.012434	0.002047	2.9E-10
AFF1	4	rs2045592	87,093,194	G	C	0.414847	-0.012413	0.002049	3.2E-10
AFF1	4	rs3775220	87,093,601	G	A	0.415036	-0.012343	0.002048	3.8E-10
AFF1	4	rs151450	87,095,362	A	G	0.396231	0.012573	0.002063	3.2E-10
AFF1	4	rs236992	87,095,587	A	G	0.415893	-0.012360	0.002045	3.3E-10
AFF1	4	rs236993	87,095,722	G	T	0.415812	-0.012403	0.002045	2.9E-10
AFF1	4	rs342452	87,097,256	A	G	0.415791	-0.012382	0.002045	3.1E-10
AFF1	4	rs342453	87,097,337	C	G	0.415870	-0.012382	0.002045	3.1E-10
AFF1	4	rs2035403	87,097,839	G	A	0.396451	0.012664	0.002063	2.4E-10
AFF1	4	rs3775217	87,098,315	G	A	0.414609	-0.012573	0.002048	1.8E-10
AFF1	4	rs342454	87,100,348	T	A	0.415783	-0.012394	0.002046	3.0E-10
AFF1	4	rs60695258	87,101,557	T	C	0.396892	0.012711	0.002078	2.3E-10
AFF1	4	rs3836600	87,102,076	A	AT	0.415570	-0.012367	0.002046	3.2E-10
AFF1	4	rs3775214	87,102,147	G	A	0.415566	-0.012366	0.002046	3.2E-10
AFF1	4	rs342456	87,102,718	T	C	0.413764	-0.012378	0.002048	2.9E-10
AFF1	4	rs3755985	87,103,586	G	A	0.399216	0.012740	0.002062	1.6E-10
AFF1	4	rs1674999	87,106,498	G	A	0.414043	-0.012498	0.002047	2.1E-10
AFF1	4	rs3841987	87,107,093	A	AG	0.414096	-0.012480	0.002047	2.3E-10
AFF1	4	rs3733377	87,108,330	G	C	0.398885	0.012563	0.002062	3.0E-10
AFF1	4	rs42177	87,109,109	G	T	0.414166	-0.012595	0.002045	1.4E-10
AFF1	4	rs75921854	87,110,944	A	T	0.399634	0.012336	0.002066	8.0E-10
AFF1	4	rs3755983	87,116,640	A	G	0.398690	0.013147	0.002072	7.3E-11
AFF1	4	rs3836599	87,117,848	T	TC	0.415643	-0.013101	0.002048	3.5E-11
AFF1	4	rs3775211	87,117,939	C	T	0.398745	0.013120	0.002072	7.9E-11
AFF1	4	rs2307789	87,118,309	C	CAT	0.415638	-0.013098	0.002048	3.5E-11
AFF1	4	rs11280827	87,119,033	T	CCAGCT	0.416244	-0.013059	0.002050	4.5E-11
AFF1	4	rs342438	87,119,254	A	G	0.415627	-0.013101	0.002047	3.5E-11
AFF1	4	rs342437	87,119,757	A	G	0.415346	-0.013165	0.002047	2.6E-11
AFF1	4	rs2307788	87,121,026	CAG	C	0.415348	-0.013091	0.002048	3.7E-11
AFF1	4	rs3755980	87,121,099	T	C	0.397836	0.013089	0.002075	1.0E-10
AFF1	4	rs342435	87,122,054	G	A	0.415972	-0.013071	0.002047	4.2E-11
AFF1	4	rs16930	87,122,793	G	A	0.417330	-0.012972	0.002051	5.9E-11
AFF1	4	rs3775209	87,125,794	A	G	0.398477	0.013018	0.002070	9.4E-11
AFF1	4	rs1037814	87,128,698	T	C	0.414522	-0.013369	0.002045	1.1E-11
AFF1	4	rs342469	87,129,402	G	A	0.414458	-0.013328	0.002045	1.4E-11
AFF1	4	rs342468	87,130,756	G	A	0.414489	-0.013255	0.002046	1.7E-11
AFF1	4	rs342467	87,131,067	T	C	0.414489	-0.013255	0.002046	1.7E-11
AFF1	4	rs342466	87,131,933	C	T	0.414476	-0.013263	0.002046	1.6E-11
AFF1	4	chr4:87135567_GT_G	87,135,567	GT	G	0.414280	-0.013410	0.002047	1.1E-11
AFF1	4	rs1408	87,136,201	G	A	0.414306	-0.013307	0.002047	1.5E-11
AFF1	4	rs3841986	87,137,491	CT	C	0.401897	0.013702	0.002071	1.5E-11
AFF1	4	rs10029915	87,138,465	C	G	0.401880	0.013812	0.002072	1.0E-11
AFF1	4	rs1842685	87,139,680	C	T	0.403713	0.013669	0.002077	1.9E-11
AFF1	4	chr4:87140472_ATATAT_A	87,140,472	ATATAT	A	0.414774	-0.014201	0.002060	1.1E-12
AFF1 *	4	rs2926511	87,141,459	A	G	0.412435	-0.013968	0.002054	2.4E-12
AFF1 *	4	rs66477840	87,142,207	A	G	0.400945	0.013832	0.002077	1.2E-11
AFF1 *	4	rs10023050	87,143,279	G	A	0.411000	-0.014032	0.002058	2.2E-12
AFF1 *	4	rs10023056	87,143,314	G	A	0.402848	0.013925	0.002075	7.0E-12
AFF1 *	4	rs10032710	87,145,107	A	G	0.387117	0.013811	0.002098	2.5E-11
AFF1 *	4	rs17012512	87,146,352	C	T	0.389361	0.013378	0.002099	1.5E-10
AFF1 *	4	rs17012517	87,149,332	G	A	0.455027	0.012027	0.002066	1.1E-09
KLHL8 *	4	rs28734493	87,151,541	T	A	0.451693	0.012305	0.002066	3.9E-10
KLHL8 *	4	chr4:87152570_C_CA	87,152,570	CA	C	0.451641	0.012373	0.002066	3.3E-10
KLHL8 *	4	rs28882732	87,154,824	G	A	0.449159	0.012188	0.002074	5.9E-10
KLHL8 *	4	rs55747890	87,155,474	G	A	0.361847	0.012910	0.002137	2.0E-10
KLHL8 *	4	rs7437661	87,156,860	C	A	0.451749	0.012348	0.002066	3.3E-10
KLHL8 *	4	rs1021104	87,157,017	A	G	0.451749	0.012372	0.002066	3.0E-10
KLHL8 *	4	rs28670747	87,157,327	G	C	0.451732	0.012345	0.002066	3.3E-10
KLHL8 *	4	rs111686783	87,158,018	A	G	0.450697	0.012325	0.002069	4.1E-10
KLHL8 *	4	rs1481947	87,159,990	T	C	0.450839	0.012351	0.002066	3.3E-10
KLHL8 *	4	rs3209390	87,161,300	C	T	0.468849	0.011843	0.002060	1.1E-09
KLHL8 *	4	rs3193672	87,161,955	C	T	0.450844	0.012048	0.002064	7.1E-10
KLHL8 *	4	rs10000784	87,166,331	G	A	0.467667	0.010962	0.002059	1.4E-08
KLHL8 *	4	rs28505236	87,172,309	G	C	0.449813	0.011306	0.002065	5.8E-09
KLHL8 *	4	rs1552144	87,173,498	T	C	0.450216	0.011176	0.002064	9.1E-09
KLHL8 *	4	rs66527077	87,188,846	A	G	0.467426	0.010821	0.002061	1.9E-08
KLHL8 *	4	rs11946293	87,191,788	A	C	0.467750	0.010974	0.002058	1.3E-08
KLHL8 *	4	rs4577539	87,202,806	G	T	0.467872	0.011136	0.002058	8.9E-09
KLHL8 *	4	rs10025704	87,207,192	A	G	0.468006	0.011070	0.002057	1.1E-08
KLHL8 *	4	rs35624376	87,237,936	C	T	0.449526	0.011102	0.002049	2.3E-08
KLHL8 *	4	rs35844368	87,238,219	T	C	0.447937	0.011252	0.002049	1.8E-08
KLHL8 *	4	rs13137873	87,238,277	T	C	0.448313	0.011101	0.002047	2.5E-08
KLHL8 *	4	rs13113529	87,238,292	C	T	0.448314	0.011101	0.002047	2.5E-08
KLHL8 *	4	rs10006766	87,238,866	G	A	0.448391	0.011146	0.002047	2.3E-08
KLHL8 *	4	rs10029254	87,238,988	T	C	0.448409	0.011142	0.002047	2.3E-08
KLHL8 *	4	rs35469118	87,247,026	T	C	0.355437	0.012875	0.002148	1.0E-09
KLHL8 *	4	rs7656630	87,252,540	C	T	0.450907	0.011078	0.002043	2.4E-08
TLL1 *	4	rs17634465	166,206,230	C	T	0.462485	-0.012086	0.002040	3.2E-09
TLL1 *	4	rs17691028	166,209,275	G	A	0.435355	-0.012055	0.002043	1.5E-08
TLL1 *	4	rs59649146	166,211,072	G	A	0.456809	-0.011379	0.002025	3.3E-08
TLL1 *	4	rs74718730	166,225,287	G	T	0.457400	-0.011833	0.002026	1.1E-08
TLL1 *	4	rs78889045	166,227,270	A	G	0.434324	-0.012227	0.002037	8.5E-09
TLL1 *	4	rs17634553	166,230,796	T	C	0.433333	-0.011938	0.002037	2.0E-08
TLL1 *	4	rs10517883	166,232,518	T	C	0.433796	-0.011864	0.002037	2.4E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
TLL1 *	4	rs149723812	166,235,572	G	A	0.456717	-0.011588	0.002026	2.3E-08
TLL1 *	4	rs184793585	166,238,504	T	C	0.432790	-0.011930	0.002039	2.0E-08
TLL1 *	4	rs11941421	166,239,949	C	G	0.439568	-0.011908	0.002040	2.3E-08
TLL1 *	4	rs58933593	166,244,458	G	C	0.434740	-0.012061	0.002036	1.5E-08
TLL1 *	4	rs58312036	166,249,069	A	G	0.434166	-0.011974	0.002042	1.9E-08
TLL1 *	4	rs7657081	166,252,496	G	A	0.455773	-0.011556	0.002038	3.3E-08
TLL1 *	4	rs78510747	166,254,179	T	A	0.454063	-0.012104	0.002043	8.5E-09
TLL1 *	4	rs78093495	166,256,202	A	G	0.455842	-0.011724	0.002031	2.0E-08
TLL1 *	4	rs76273838	166,256,725	G	A	0.455919	-0.011689	0.002031	2.1E-08
TLL1 *	4	rs421948	166,264,239	G	A	0.455021	-0.011406	0.002030	4.8E-08
TLL1 *	4	rs143526433	166,269,713	C	T	0.455009	-0.011434	0.002030	4.4E-08
TLL1 *	4	rs144318493	166,270,896	G	C	0.455015	-0.011433	0.002030	4.3E-08
TLL1 *	4	rs13144379	166,272,560	A	G	0.454894	-0.011525	0.002030	3.4E-08
TLL1 *	4	rs59688821	166,274,447	G	A	0.455214	-0.011457	0.002031	4.6E-08
TLL1 *	4	rs12511044	166,299,482	A	T	0.440612	-0.011471	0.002058	4.7E-08
ANKRD55 *	5	rs157504	56,498,248	C	T	0.293571	-0.012385	0.002267	1.7E-08
ANKRD55 *	5	rs3074482	56,498,680	T	TGG	0.294514	-0.012575	0.002258	9.9E-09
ANKRD55 *	5	rs151837	56,498,732	T	C	0.294568	-0.012560	0.002257	1.0E-08
ANKRD55 *	5	rs151838	56,498,738	T	C	0.294587	-0.012570	0.002257	1.0E-08
ANKRD55 *	5	rs157505	56,498,801	T	C	0.294479	-0.012706	0.002257	6.5E-09
ANKRD55 *	5	rs30351	56,498,805	A	G	0.237318	0.013877	0.002403	1.7E-09
ANKRD55 *	5	rs16885581	56,500,345	G	A	0.135636	-0.018131	0.002961	1.7E-10
ANKRD55 *	5	rs40271	56,500,492	T	C	0.239122	0.013716	0.002364	1.8E-09
ANKRD55 *	5	rs6881312	56,500,733	T	G	0.287146	0.014158	0.002233	9.5E-11
ANKRD55 *	5	rs157845	56,500,812	C	T	0.239777	0.013736	0.002363	1.6E-09
ANKRD55 *	5	rs588898	56,501,555	A	G	0.297965	-0.013187	0.002210	7.4E-10
ANKRD55 *	5	rs245109	56,501,758	C	T	0.297985	-0.013153	0.002210	8.0E-10
ANKRD55 *	5	rs173443	56,501,772	C	T	0.297922	-0.013153	0.002210	8.2E-10
ANKRD55 *	5	rs73132727	56,502,276	G	C	0.289362	0.014527	0.002223	2.5E-11
ANKRD55 *	5	rs157843	56,503,357	A	C	0.238802	0.013876	0.002366	1.4E-09
ANKRD55 *	5	rs73132728	56,504,012	G	A	0.290451	0.014427	0.002219	2.9E-11
ANKRD55 *	5	rs60762814	56,504,882	T	C	0.289369	0.014539	0.002223	2.4E-11
ANKRD55 *	5	rs25789	56,504,897	T	C	0.238341	0.013644	0.002368	2.4E-09
ANKRD55 *	5	rs73132731	56,505,331	G	A	0.290464	0.014424	0.002219	2.9E-11
ANKRD55 *	5	rs73132735	56,505,759	T	A	0.289732	0.014385	0.002225	3.8E-11
ANKRD55 *	5	rs27984	56,506,592	T	C	0.239118	0.013751	0.002364	1.7E-09
ANKRD55 *	5	rs56198135	56,507,151	A	G	0.284458	0.013494	0.002237	5.3E-10
ANKRD55 *	5	rs30000	56,507,706	A	G	0.239180	0.013743	0.002363	1.6E-09
ANKRD55 *	5	rs42392	56,508,102	G	A	0.298792	-0.013353	0.002205	3.9E-10
ANKRD55 *	5	rs25757	56,508,377	G	C	0.298773	-0.013347	0.002205	3.9E-10
ANKRD55 *	5	rs467022	56,509,812	T	C	0.237839	0.013823	0.002371	1.5E-09
ANKRD55 *	5	rs16885608	56,510,081	T	G	0.290119	0.014545	0.002219	1.9E-11
ANKRD55 *	5	rs459193	56,510,924	A	G	0.470542	-0.022128	0.002020	1.8E-29
C5orf67	5	rs464605	56,511,543	C	T	0.470819	-0.022198	0.002021	1.1E-29
C5orf67	5	rs458741	56,512,010	C	T	0.239188	0.013687	0.002366	2.1E-09
C5orf67	5	rs245143	56,512,322	G	A	0.296522	-0.013310	0.002220	4.8E-10
C5orf67	5	rs157507	56,512,451	T	C	0.330996	-0.015496	0.002144	7.3E-14
C5orf67	5	rs392794	56,512,515	C	T	0.470704	-0.022210	0.002021	9.6E-30
C5orf67	5	rs465002	56,512,648	C	T	0.470702	-0.022230	0.002021	8.6E-30
C5orf67	5	rs157510	56,513,139	C	A	0.330932	-0.015486	0.002144	7.7E-14
C5orf67	5	rs157512	56,513,300	C	T	0.435990	-0.020025	0.002037	1.7E-24
C5orf67	5	rs256903	56,513,311	C	A	0.469986	-0.022244	0.002023	8.5E-30
C5orf67	5	rs173964	56,513,638	A	G	0.469726	-0.022334	0.002024	5.3E-30
C5orf67	5	rs256904	56,514,478	A	T	0.470266	-0.022156	0.002024	1.6E-29
C5orf67	5	rs245142	56,514,622	A	G	0.330627	-0.015457	0.002144	9.1E-14
C5orf67	5	rs456867	56,515,265	T	C	0.330727	-0.015432	0.002142	1.0E-13
C5orf67	5	rs459447	56,515,514	A	G	0.329474	-0.015469	0.002146	9.4E-14
C5orf67	5	rs465983	56,516,303	G	A	0.439061	-0.019756	0.002038	7.2E-24
C5orf67	5	rs61142999	56,516,795	A	G	0.282761	0.013776	0.002245	2.0E-10
C5orf67	5	rs2448427	56,516,855	T	C	0.295755	-0.011974	0.002227	3.2E-08
C5orf67	5	rs405176	56,517,885	G	A	0.369679	-0.016063	0.002096	3.5E-15
C5orf67	5	rs60202005	56,518,728	T	C	0.284491	0.013924	0.002240	1.3E-10
C5orf67	5	rs56411612	56,519,256	T	G	0.284529	0.013946	0.002240	1.2E-10
C5orf67	5	rs36098873	56,520,044	AG	A	0.236945	0.013729	0.002381	2.1E-09
C5orf67	5	rs458356	56,520,065	G	A	0.237490	0.013767	0.002379	1.8E-09
C5orf67	5	rs458036	56,520,254	C	A	0.236888	0.013743	0.002381	2.0E-09
C5orf67	5	rs455660	56,521,061	T	C	0.381592	-0.016641	0.002076	1.0E-16
C5orf67	5	rs76721602	56,522,121	A	C	0.282004	0.014056	0.002278	1.5E-10
C5orf67	5	rs76878791	56,522,574	G	A	0.282281	0.013971	0.002287	2.7E-10
C5orf67	5	rs3843467	56,560,548	T	G	0.113402	0.018223	0.003182	4.6E-09
C5orf67	5	rs11429307	56,561,198	GT	G	0.112273	0.017541	0.003199	1.9E-08
C5orf67	5	chr5:56561721_A_AT	56,561,721	AT	A	0.112590	0.018522	0.003195	3.0E-09
C5orf67	5	rs11743303	56,564,125	G	A	0.114468	0.017942	0.003169	5.3E-09
C5orf67	5	rs3936511	56,564,954	G	A	0.114363	0.018051	0.003170	4.3E-09
C5orf67	5	rs3936510	56,565,039	T	G	0.114393	0.018018	0.003169	4.5E-09
C5orf67	5	rs5868014	56,565,080	G	GC	0.114324	0.017951	0.003170	5.0E-09
C5orf67	5	rs13173241	56,565,532	A	G	0.114470	0.018149	0.003169	3.6E-09
C5orf67	5	rs28650790	56,565,637	T	C	0.114351	0.018209	0.003170	3.5E-09
C5orf67	5	rs9687832	56,565,768	A	G	0.115659	0.017972	0.003154	4.4E-09
C5orf67	5	rs9687833	56,565,774	A	G	0.115702	0.017873	0.003153	5.3E-09
C5orf67	5	rs9687846	56,566,067	A	G	0.115025	0.018082	0.003162	3.8E-09
TNFAIP8	5	rs145778841	119,363,651	T	C	0.038650	-0.030245	0.005246	4.2E-08
TNFAIP8	5	rs143932930	119,364,483	T	G	0.038650	-0.030243	0.005246	4.2E-08
TNFAIP8	5	rs150800682	119,365,445	G	C	0.038664	-0.030661	0.005249	2.8E-08
TNFAIP8	5	rs9327100	119,366,180	G	A	0.039713	-0.029838	0.005184	3.7E-08
TNFAIP8	5	rs141199457	119,370,335	T	TC	0.038430	-0.031414	0.005265	1.3E-08
TNFAIP8	5	rs143225937	119,370,413	G	C	0.038431	-0.031412	0.005265	1.3E-08
TNFAIP8	5	rs151300053	119,374,385	A	G	0.038188	-0.030807	0.005279	3.2E-08
TNFAIP8	5	rs5870855	119,377,761	AT	A	0.158705	-0.020359	0.002773	3.7E-13
TNFAIP8	5	rs59406275	119,379,517	A	G	0.038221	-0.031321	0.005277	1.3E-08
TNFAIP8	5	rs140403040	119,381,339	G	A	0.037911	-0.030796	0.005294	2.1E-08
TNFAIP8	5	rs143744864	119,383,503	A	G	0.038078	-0.030015	0.005279	4.1E-08
TNFAIP8	5	rs12332329	119,385,999	A	G	0.144573	-0.020480	0.002872	8.6E-13
TNFAIP8	5	rs6882000	119,387,339	A	G	0.039204	-0.029648	0.005205	3.4E-08
TNFAIP8	5	rs6595187	119,387,914	G	A	0.159791	-0.020012	0.002757	5.8E-13
TNFAIP8	5	rs139299785	119,389,092	C	T	0.038100	-0.029868	0.005277	4.7E-08
TNFAIP8	5	rs9764678	119,390,967	C	T	0.158996	-0.019820	0.002762	9.8E-13

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
TNFAIP8	5	rs7720409	119,392,561	A	G	0.157548	-0.019539	0.002767	2.6E-12
TNFAIP8	5	rs3203922	119,393,258	C	G	0.157555	-0.019549	0.002767	2.6E-12
TNFAIP8	5	rs1045241	119,393,591	T	C	0.157669	-0.019515	0.002765	2.9E-12
TNFAIP8	5	rs1045242	119,393,632	G	A	0.157721	-0.019789	0.002768	1.4E-12
TNFAIP8 *	5	rs1105769	119,395,372	C	A	0.202994	-0.014571	0.002524	5.1E-09
TNFAIP8 *	5	rs1105770	119,395,552	G	T	0.202997	-0.014544	0.002524	4.9E-09
TNFAIP8 *	5	rs7703744	119,396,492	G	C	0.152554	-0.019470	0.002814	4.2E-12
TNFAIP8 *	5	rs56017758	119,404,998	A	G	0.148464	-0.018714	0.002858	6.6E-11
HSD17B4 *	5	rs35401573	119,543,023	T	G	0.040203	-0.027571	0.005144	4.7E-08
HSD17B4 *	5	rs139384974	119,572,531	T	C	0.035551	-0.028224	0.005473	4.4E-08
TIMD4	5	rs143642966	156,933,144	G	T	0.055744	-0.027025	0.004443	2.1E-10
TIMD4	5	rs11134462	156,933,172	G	C	0.345314	-0.012210	0.002151	1.8E-08
TIMD4	5	rs10062458	156,940,081	T	C	0.168303	-0.019710	0.002718	1.3E-13
TIMD4	5	rs7717984	156,942,160	C	T	0.158887	-0.020555	0.002770	2.3E-14
TIMD4	5	rs13167071	156,946,626	G	C	0.158908	-0.020344	0.002768	4.2E-14
TIMD4	5	rs11361881	156,950,119	CT	C	0.159485	-0.019825	0.002760	1.5E-13
TIMD4	5	rs4704727	156,953,056	T	G	0.159524	-0.020129	0.002759	6.2E-14
TIMD4	5	rs7724832	156,954,359	G	A	0.159563	-0.020018	0.002759	8.0E-14
TIMD4	5	rs4704825	156,955,297	A	G	0.210390	-0.018176	0.002496	3.7E-14
TIMD4	5	rs1363232	156,956,411	A	G	0.159607	-0.019911	0.002759	1.1E-13
TIMD4	5	rs2862059	156,957,504	G	C	0.164601	-0.019752	0.002742	1.2E-13
TIMD4	5	rs6878680	156,960,126	G	C	0.211185	-0.018262	0.002490	1.9E-14
TIMD4	5	rs4407617	156,960,425	C	G	0.159450	-0.020147	0.002763	5.7E-14
TIMD4	5	chr5:156962408_TA_T	156,962,408	TA	T	0.070085	-0.021332	0.003952	1.2E-08
TIMD4 *	5	rs6882076	156,963,286	T	C	0.271745	-0.021557	0.002272	4.9E-23
TIMD4 *	5	rs17054099	156,963,969	A	G	0.057160	-0.024900	0.004387	1.8E-09
TIMD4 *	5	rs68714202	156,964,617	T	C	0.271667	-0.021530	0.002273	5.7E-23
TIMD4 *	5	rs62382402	156,964,807	T	C	0.153121	-0.019589	0.002809	1.0E-12
TIMD4 *	5	rs4704826	156,965,071	C	A	0.271737	-0.021482	0.002273	7.3E-23
TIMD4 *	5	rs4704827	156,965,078	T	C	0.271666	-0.021531	0.002273	5.6E-23
TIMD4 *	5	rs12517431	156,965,237	C	T	0.271652	-0.021557	0.002273	5.1E-23
TIMD4 *	5	rs28735189	156,967,082	C	T	0.271007	-0.021515	0.002281	8.8E-23
TIMD4 *	5	rs9715911	156,967,430	G	A	0.270964	-0.021628	0.002282	5.9E-23
TIMD4 *	5	rs11745603	156,967,507	C	T	0.270955	-0.021634	0.002282	5.9E-23
TIMD4 *	5	rs12657266	156,968,992	C	T	0.270644	-0.021693	0.002286	4.7E-23
TIMD4 *	5	rs10043150	156,969,464	A	C	0.152076	-0.019611	0.002825	1.0E-12
TIMD4 *	5	rs1393207	156,970,529	T	A	0.270483	-0.021759	0.002288	3.6E-23
TIMD4 *	5	rs6882345	156,970,662	G	A	0.270479	-0.021742	0.002288	3.9E-23
TIMD4 *	5	rs6883317	156,971,242	A	G	0.151952	-0.019815	0.002827	6.0E-13
TIMD4 *	5	rs58198139	156,972,028	C	T	0.270465	-0.021758	0.002289	3.9E-23
TIMD4 *	5	rs11134475	156,972,939	A	G	0.270438	-0.021714	0.002290	4.9E-23
TIMD4 *	5	rs28722027	156,973,514	T	C	0.264021	-0.021032	0.002308	3.0E-21
TIMD4 *	5	rs6891318	156,973,733	C	A	0.264116	-0.020961	0.002308	4.2E-21
TIMD4 *	5	rs55776147	156,973,797	A	G	0.270842	-0.021590	0.002290	9.3E-23
TIMD4 *	5	rs7715848	156,974,467	G	C	0.151598	-0.019832	0.002832	6.1E-13
TIMD4 *	5	rs7702004	156,974,719	C	T	0.262357	-0.020995	0.002316	5.7E-21
TIMD4 *	5	chr5:156975081_A_AGAGG	156,975,081	AGAGG	A	0.252040	-0.018704	0.002384	3.3E-16
TIMD4 *	5	rs7707200	156,975,624	C	T	0.132413	-0.019527	0.003038	7.0E-11
TIMD4 *	5	rs7379358	156,976,582	T	A	0.392068	-0.013855	0.002113	2.4E-11
TIMD4 *	5	rs10055656	156,977,360	C	T	0.258926	-0.020726	0.002324	2.5E-20
TIMD4 *	5	rs28575973	156,977,576	A	C	0.258784	-0.020640	0.002325	3.7E-20
TIMD4 *	5	rs110062571	156,977,625	T	G	0.145919	-0.019684	0.002880	2.8E-12
TIMD4 *	5	chr5:156978231_C_CT	156,978,231	CT	C	0.195472	-0.017375	0.002567	3.0E-12
TIMD4 *	5	rs10059560	156,978,773	C	T	0.196804	-0.017220	0.002555	3.9E-12
TIMD4 *	5	rs10050384	156,978,935	T	C	0.196235	-0.017064	0.002557	6.4E-12
TIMD4 *	5	rs12187385	156,979,446	C	A	0.196733	-0.017112	0.002555	5.3E-12
TIMD4 *	5	rs4704728	156,979,597	G	C	0.388425	-0.014103	0.002096	5.1E-12
TIMD4 *	5	rs4704830	156,979,708	G	A	0.388491	-0.014071	0.002096	5.9E-12
TIMD4 *	5	rs4704831	156,979,709	C	G	0.388643	-0.014076	0.002096	6.1E-12
TIMD4 *	5	rs1973491	156,982,536	T	C	0.130526	-0.021632	0.003020	2.1E-13
TIMD4 *	5	rs55682810	156,984,036	GA	G	0.194480	-0.017815	0.002564	7.3E-13
TIMD4 *	5	rs56308765	156,984,044	A	C	0.192597	-0.017783	0.002580	9.2E-13
TIMD4 *	5	rs7736899	156,984,196	A	C	0.377823	-0.014040	0.002104	9.1E-12
TIMD4 *	5	rs10059263	156,984,250	C	T	0.196746	-0.016903	0.002556	8.5E-12
TIMD4 *	5	rs10039097	156,984,874	C	T	0.194486	-0.017811	0.002564	7.4E-13
TIMD4 *	5	rs6866930	156,985,611	C	G	0.377867	-0.014048	0.002105	8.8E-12
TIMD4 *	5	rs55875237	156,988,018	T	C	0.143619	-0.020916	0.002899	1.7E-13
TIMD4 *	5	rs111273781	156,989,163	T	C	0.131449	-0.021213	0.003010	5.2E-13
TIMD4 *	5	rs10044267	156,989,418	A	G	0.143626	-0.020911	0.002899	1.8E-13
TIMD4 *	5	rs12659077	156,989,695	G	T	0.384083	-0.014815	0.002099	4.0E-13
TIMD4 *	5	chr5:156995894_CAA_C	156,995,894	C	CAA	0.145324	-0.021027	0.002892	1.3E-13
HAVCR1 *	5	rs10075548	156,997,238	C	T	0.144719	-0.020849	0.002890	1.9E-13
HAVCR1 *	5	rs66891562	156,998,368	C	T	0.408715	-0.013208	0.002068	3.9E-11
HAVCR1 *	5	rs10079422	156,998,650	A	T	0.196528	-0.017841	0.002554	5.1E-13
HAVCR1 *	5	rs1501906	157,000,648	G	A	0.409586	-0.013019	0.002053	5.9E-11
HAVCR1 *	5	rs67899516	157,001,721	G	A	0.409428	-0.013061	0.002053	4.8E-11
HAVCR1 *	5	rs7714118	157,001,727	G	T	0.402889	-0.012453	0.002058	4.9E-10
HAVCR1 *	5	rs111847148	157,001,777	GACAA	G	0.403174	-0.012584	0.002059	3.1E-10
HAVCR1 *	5	rs1546288	157,003,694	G	A	0.409429	-0.013044	0.002054	5.1E-11
HAVCR1 *	5	rs66512776	157,004,261	C	T	0.409962	-0.012998	0.002056	6.9E-11
HAVCR1 *	5	rs6870058	157,004,262	A	G	0.403059	-0.012433	0.002060	5.4E-10
HAVCR1 *	5	rs2102151	157,005,007	T	C	0.197715	-0.017726	0.002538	6.3E-13
HAVCR1 *	5	rs7721033	157,005,512	T	C	0.197716	-0.017682	0.002538	7.2E-13
HAVCR1 *	5	rs10036890	157,006,640	A	T	0.197746	-0.017699	0.002538	6.9E-13
HAVCR1 *	5	rs10076109	157,007,151	T	C	0.197743	-0.017684	0.002538	7.2E-13
HAVCR1 *	5	rs9791162	157,007,697	C	T	0.409638	-0.013083	0.002056	5.9E-11
HAVCR1 *	5	rs10062923	157,008,228	A	G	0.145560	-0.020655	0.002874	2.5E-13
HAVCR1 *	5	rs56012634	157,008,942	A	G	0.409665	-0.013034	0.002057	6.9E-11
HAVCR1 *	5	rs55892205	157,009,022	G	A	0.409660	-0.013032	0.002057	7.0E-11
HAVCR1 *	5	rs4704833	157,009,347	A	T	0.409663	-0.013034	0.002057	7.0E-11
HAVCR1 *	5	rs1995376	157,009,447	A	T	0.197846	-0.017451	0.002537	1.4E-12
HAVCR1 *	5	rs76296718	157,009,493	G	A	0.145473	-0.020248	0.002876	7.4E-13
HAVCR1 *	5	rs140842228	157,011,602	G	T	0.405539	-0.012800	0.002060	1.5E-10
HAVCR1 *	5	rs6555788	157,011,656	C	T	0.193857	-0.017273	0.002555	2.5E-12
HAVCR1 *	5	rs6555789	157,011,856	T	C	0.193864	-0.017268	0.002555	2.5E-12
HAVCR1 *	5	rs141319343	157,011,963	A	G	0.048828	-0.027354	0.004716	1.2E-09
HAVCR1 *	5	rs7715158	157,012,073	A	G	0.194029	-0.017149	0.002554	3.5E-12

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
HAVCR1 *	5	rs113879698	157,012,840	T	A	0.405823	-0.012730	0.002060	1.7E-10
HAVCR1 *	5	rs80050550	157,013,424	C	G	0.406068	-0.012685	0.002060	2.1E-10
HAVCR1 *	5	rs7736117	157,013,824	T	C	0.193851	-0.017309	0.002555	2.3E-12
HAVCR1 *	5	rs187399190	157,014,301	G	A	0.408462	-0.012347	0.002064	6.2E-10
HAVCR1 *	5	rs6862070	157,014,453	T	C	0.190787	-0.016922	0.002581	1.0E-11
HAVCR1 *	5	rs4704834	157,016,055	A	G	0.262189	-0.020798	0.002299	3.6E-21
HAVCR1 *	5	chr5:157016890_C_CT	157,016,890	C	CT	0.406043	-0.012640	0.002060	2.2E-10
HAVCR1 *	5	rs4704836	157,017,430	G	A	0.407521	-0.012643	0.002064	2.3E-10
HAVCR1 *	5	rs9885146	157,017,750	T	C	0.141285	-0.020472	0.002907	6.1E-13
HAVCR1 *	5	rs6555801	157,018,625	A	C	0.141466	-0.020693	0.002905	3.5E-13
HAVCR1 *	5	rs56330860	157,019,393	GA	G	0.405877	-0.012682	0.002060	1.9E-10
HAVCR1 *	5	rs10462973	157,022,494	G	A	0.405924	-0.012642	0.002060	2.2E-10
HAVCR1 *	5	rs7707445	157,022,737	A	G	0.194013	-0.017300	0.002551	2.2E-12
HAVCR1 *	5	rs35242034	157,025,733	C	T	0.405846	-0.012654	0.002061	2.2E-10
HAVCR1 *	5	rs6866758	157,028,101	T	C	0.255438	-0.020206	0.002319	1.3E-19
HAVCR1	5	rs2134230	157,029,946	C	G	0.194086	-0.017074	0.002550	3.7E-12
HAVCR1	5	rs68145045	157,031,185	G	A	0.406150	-0.012405	0.002062	5.4E-10
HAVCR1	5	rs61047347	157,032,570	T	TC	0.197515	-0.015988	0.002535	4.7E-11
HAVCR1	5	rs2277025	157,033,084	T	C	0.406380	-0.012418	0.002063	5.3E-10
HAVCR1	5	rs3842063	157,033,162	T	TA	0.255934	-0.020046	0.002318	2.9E-19
HAVCR1	5	rs6896306	157,034,265	G	T	0.193916	-0.016808	0.002555	8.7E-12
HAVCR1	5	chr5:157038023_GA_G	157,038,023	G	GA	0.214558	-0.018225	0.002472	4.0E-14
HAVCR1	5	rs10213795	157,038,032	T	A	0.194773	-0.016602	0.002596	4.8E-11
HAVCR1	5	rs6878732	157,038,245	A	T	0.216767	-0.018616	0.002457	8.6E-15
HAVCR1	5	rs10059699	157,039,143	C	T	0.192715	-0.017175	0.002563	4.3E-12
HAVCR1	5	rs200212405	157,040,297	TC	T	0.190392	-0.017348	0.002580	3.6E-12
HAVCR1	5	rs56182597	157,040,299	C	A	0.186301	-0.018136	0.002626	1.1E-12
HAVCR1	5	rs17054133	157,040,380	C	T	0.192730	-0.017125	0.002562	4.8E-12
HAVCR1	5	rs6555819	157,041,528	A	G	0.193318	-0.016913	0.002560	7.4E-12
HAVCR1	5	rs6874311	157,041,787	T	G	0.193323	-0.016895	0.002560	7.8E-12
HAVCR1	5	rs9313418	157,042,213	T	C	0.193280	-0.016834	0.002560	9.1E-12
HAVCR1	5	rs2270926	157,042,772	A	G	0.140596	-0.020628	0.002914	5.5E-13
HAVCR1	5	rs10038271	157,043,390	T	C	0.140502	-0.020701	0.002914	4.3E-13
HAVCR1	5	rs11374500	157,045,224	TA	T	0.192894	-0.016897	0.002564	8.7E-12
HAVCR1	5	rs17054136	157,045,814	A	G	0.062742	0.021476	0.004169	4.5E-08
HAVCR1	5	rs35931650	157,046,505	G	A	0.192442	-0.016567	0.002561	1.9E-11
HAVCR1	5	rs62382456	157,046,893	A	G	0.192240	-0.016595	0.002562	1.8E-11
HAVCR1	5	rs7706174	157,048,387	G	T	0.192262	-0.016487	0.002563	2.5E-11
HAVCR1	5	rs1553318	157,052,312	G	C	0.197922	-0.017222	0.002537	1.6E-12
HAVCR1	5	chr5:157052432_CTTG_C	157,052,432	C	CTTG	0.191289	-0.016717	0.002569	1.8E-11
HAVCR1	5	rs77147640	157,052,557	CGTT	C	0.215817	-0.018068	0.002463	7.0E-14
HAVCR1	5	rs11134525	157,053,637	A	T	0.197066	-0.017026	0.002550	3.8E-12
HAVCR1	5	rs2270925	157,055,088	T	C	0.187464	-0.016600	0.002633	8.7E-11
HAVCR1	5	rs2270924	157,055,090	A	T	0.187464	-0.016600	0.002633	8.7E-11
HAVCR1	5	rs139106057	157,055,287	AT	A	0.134083	-0.019434	0.003020	7.3E-11
RREB1	6	rs9328401	7,225,441	C	A	0.203673	0.013344	0.002539	2.9E-08
RREB1	6	rs9505085	7,226,726	T	C	0.202103	0.013724	0.002548	1.5E-08
RREB1	6	rs9328402	7,227,278	T	C	0.202012	0.013706	0.002549	1.7E-08
TRIM27	6	rs9368581	28,914,454	T	C	0.055077	-0.024712	0.004552	1.2E-08
OR10C1 *	6	rs9368601	29,444,646	T	C	0.086247	-0.021414	0.003748	1.4E-08
MAS1L *	6	rs9393967	29,501,712	T	C	0.081131	-0.024133	0.003874	6.0E-10
UBD *	6	rs9391895	29,534,259	A	G	0.087180	-0.022954	0.003758	8.0E-10
UBD *	6	rs79289376	29,539,661	T	TA	0.092524	-0.020318	0.003673	1.7E-08
GABBR1	6	rs150971595	29,632,584	T	C	0.095512	-0.024841	0.003661	9.3E-12
MOG *	6	rs9380134	29,653,999	C	G	0.112135	-0.021637	0.003398	1.4E-10
HLA-F *	6	rs75791723	29,756,751	T	C	0.109305	-0.023348	0.003446	1.1E-11
HCG4 *	6	rs9368611	29,772,040	C	A	0.105552	-0.024038	0.003509	3.2E-12
ZNRD1ASP	6	rs9380151	30,052,051	C	T	0.110844	-0.023924	0.003419	2.0E-12
TRIM31 *	6	rs9261395	30,097,521	A	C	0.226078	0.015518	0.002675	1.2E-08
TRIM31	6	rs3132680	30,105,418	A	C	0.194676	0.015611	0.002840	4.1E-08
TRIM40 *	6	rs9393991	30,134,864	A	G	0.112228	-0.024611	0.003402	6.8E-13
TRIM15 *	6	rs9380156	30,173,265	G	A	0.313343	-0.012524	0.002289	3.1E-08
TRIM15 *	6	rs60776308	30,177,951	GT	G	0.312519	-0.012447	0.002290	3.4E-08
TRIM15 *	6	rs9391677	30,178,030	A	G	0.312402	-0.012318	0.002291	4.5E-08
TRIM26 *	6	rs9366754	30,184,256	C	G	0.312469	-0.012497	0.002290	3.0E-08
TRIM26	6	rs12175655	30,187,133	T	C	0.312444	-0.012498	0.002290	2.9E-08
TRIM26	6	rs2239531	30,201,052	T	C	0.312371	-0.012488	0.002290	3.2E-08
TRIM26	6	rs2284167	30,201,796	T	C	0.312230	-0.012545	0.002291	3.0E-08
TRIM26	6	rs28730510	30,202,280	G	C	0.312466	-0.012435	0.002289	3.5E-08
TRIM26	6	rs117565607	30,204,594	A	T	0.111312	-0.025120	0.003424	3.5E-13
TRIM26	6	rs2284171	30,205,173	A	G	0.312505	-0.012478	0.002290	3.2E-08
TRIM26	6	rs9391802	30,206,355	A	G	0.313170	-0.012399	0.002289	4.5E-08
TRIM26 *	6	rs9378221	30,214,057	C	T	0.312967	-0.012382	0.002289	4.0E-08
TRIM26 *	6	rs9378189	30,220,745	T	C	0.312378	-0.012534	0.002291	3.0E-08
TRIM26 *	6	rs9348838	30,221,422	T	A	0.311360	-0.012454	0.002293	3.4E-08
HCG17 *	6	rs12660499	30,227,096	A	G	0.312136	-0.012549	0.002291	2.9E-08
HCG17	6	rs62407543	30,243,396	A	G	0.344147	-0.012227	0.002286	4.2E-08
HCG17	6	rs72841870	30,246,234	C	G	0.334234	-0.012463	0.002303	4.0E-08
HCG17	6	rs9391803	30,247,600	A	T	0.334808	-0.012475	0.002298	3.8E-08
HCG17	6	rs77916299	30,253,390	A	AT	0.334171	-0.012756	0.002304	2.1E-08
HCG17	6	rs9405046	30,254,114	C	G	0.336037	-0.012580	0.002302	3.7E-08
HCG17, HCG18	6	rs117416277	30,288,213	C	T	0.111764	-0.025593	0.003425	1.5E-13
RPP21 *	6	rs9391681	30,383,227	C	T	0.109521	-0.025695	0.003471	1.4E-13
RPP21 *	6	rs3131113	30,398,865	T	C	0.368335	-0.012211	0.002276	3.3E-08
RPP21 *	6	rs78860372	30,412,589	T	A	0.353300	-0.012446	0.002301	2.4E-08
ABCF1	6	rs143982339	30,586,413	C	CAT	0.112856	-0.024104	0.003409	1.2E-12
ABCF1 *	6	rs9380181	30,595,202	T	A	0.116499	-0.024330	0.003364	5.5E-13
PPPIR10	6	rs9348841	30,610,096	C	T	0.113965	-0.023882	0.003380	1.3E-12
ATAT1	6	rs143128695	30,635,406	G	A	0.115202	-0.024939	0.003385	2.1E-13
DHX16 *	6	rs151195028	30,673,581	C	G	0.115302	-0.024610	0.003381	3.4E-13
FLOT1	6	rs9380182	30,735,848	C	A	0.113577	-0.024543	0.003396	2.4E-13
IER3 *	6	rs9391634	30,807,802	G	C	0.110377	-0.024401	0.003449	1.0E-12
DDR1 *	6	rs117589205	30,844,646	G	A	0.242935	-0.014308	0.002521	1.6E-08
DDR1 *	6	rs9295929	30,878,319	C	G	0.405907	0.012983	0.002289	3.1E-08
DDR1 *	6	rs9357102	30,880,222	C	T	0.405985	0.013018	0.002289	2.8E-08
DDR1 *	6	rs7756521	30,880,476	T	C	0.405920	0.013044	0.002289	2.6E-08
DDR1 *	6	rs9501032	30,882,414	T	C	0.405968	0.013098	0.002289	2.3E-08

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
DDR1 *	6	rs11334273	30,882,971	GT	G	0.405920	0.013045	0.002289	2.7E-08
DDR1 *	6	rs9380200	30,883,417	C	G	0.405942	0.013001	0.002289	2.9E-08
DDR1 *	6	rs9461638	30,883,528	G	C	0.405832	0.013037	0.002289	2.7E-08
DDR1	6	rs9468842	30,884,970	C	T	0.405887	0.012920	0.002289	3.6E-08
DDR1	6	rs6901464	30,886,313	G	T	0.405912	0.013003	0.002289	2.9E-08
DDR1	6	rs4618569	30,887,474	G	A	0.406110	0.013056	0.002288	2.5E-08
DDR1	6	rs2229933	30,889,295	G	C	0.405921	0.013016	0.002289	2.8E-08
DDR1	6	rs6924600	30,889,765	G	A	0.406165	0.013180	0.002288	1.9E-08
DDR1	6	rs6457282	30,890,211	T	C	0.406213	0.012900	0.002289	3.3E-08
DDR1	6	rs7761589	30,890,470	C	G	0.406945	0.012999	0.002289	2.2E-08
DDR1 *	6	rs7743661	30,890,477	T	C	0.406147	0.012920	0.002289	3.2E-08
DDR1	6	rs1049622	30,891,080	C	T	0.406149	0.012917	0.002289	3.4E-08
DDR1	6	rs41288940	30,891,526	A	ACT	0.436174	0.013855	0.002294	3.8E-09
DDR1	6	rs9366761	30,891,743	C	T	0.434434	0.012787	0.002264	2.8E-08
DDR1	6	rs3213644	30,893,448	G	A	0.434445	0.012829	0.002264	2.5E-08
DDR1	6	rs9366762	30,896,283	T	C	0.242573	-0.014391	0.002524	1.2E-08
DDR1	6	rs2239517	30,897,338	G	A	0.414707	0.013072	0.002274	1.7E-08
DDR1	6	rs2239518	30,897,948	C	T	0.434735	0.012758	0.002263	3.1E-08
DDR1	6	rs1049628	30,899,329	C	T	0.414641	0.013062	0.002274	1.8E-08
DDR1	6	rs8408	30,899,889	T	C	0.414638	0.013071	0.002274	1.8E-08
DDR1 *	6	rs9468844	30,900,456	G	C	0.414583	0.013054	0.002274	1.7E-08
DDR1 *	6	rs4713400	30,901,623	T	C	0.414423	0.013105	0.002274	1.6E-08
DDR1 *	6	rs9468845	30,901,816	G	A	0.414868	0.013079	0.002274	1.8E-08
DDR1 *	6	rs9378150	30,901,916	G	A	0.242549	-0.014259	0.002524	1.7E-08
DDR1 *	6	rs9295931	30,901,937	C	T	0.414638	0.013051	0.002274	1.9E-08
DDR1 *	6	rs3869085	30,902,336	G	A	0.414641	0.013062	0.002274	1.8E-08
DDR1 *	6	rs3869086	30,902,391	G	T	0.414638	0.013071	0.002274	1.8E-08
DDR1 *	6	rs9295932	30,902,686	A	G	0.414641	0.013082	0.002274	1.7E-08
DDR1 *	6	rs9468846	30,902,986	T	C	0.414638	0.013071	0.002274	1.8E-08
DDR1 *	6	rs12206075	30,903,223	T	C	0.414656	0.013104	0.002274	1.6E-08
DDR1 *	6	rs10947111	30,903,408	G	A	0.415123	0.013048	0.002275	2.0E-08
DDR1 *	6	rs41288539	30,903,672	G	C	0.414893	0.012926	0.002275	2.5E-08
DDR1 *	6	rs13215246	30,903,732	C	T	0.414638	0.013071	0.002274	1.8E-08
DDR1 *	6	rs13215409	30,903,842	C	A	0.414660	0.013078	0.002274	1.7E-08
DDR1 *	6	rs9404935	30,904,041	G	T	0.242546	-0.014301	0.002524	1.6E-08
DDR1 *	6	rs9295933	30,904,093	C	T	0.435037	0.012822	0.002266	2.6E-08
DDR1 *	6	rs9391636	30,904,155	A	T	0.342233	-0.013680	0.002252	1.1E-09
GTF2H4 *	6	rs9380201	30,904,922	T	C	0.414744	0.013086	0.002274	1.7E-08
GTF2H4 *	6	rs9501342	30,904,955	G	A	0.414744	0.013086	0.002274	1.7E-08
GTF2H4 *	6	rs9378191	30,905,781	C	T	0.413773	0.013356	0.002275	8.8E-09
GTF2H4 *	6	rs3757339	30,906,109	T	C	0.414291	0.013416	0.002277	8.1E-09
GTF2H4 *	6	rs3909130	30,906,388	T	C	0.413830	0.013471	0.002275	6.5E-09
GTF2H4 *	6	rs11456335	30,906,607	A	AC	0.414065	0.013278	0.002275	1.0E-08
GTF2H4 *	6	chr6:30906712_AT_A	30,906,712	AT	A	0.415909	0.013673	0.002274	5.0E-09
GTF2H4 *	6	rs9295934	30,906,736	A	G	0.415098	0.013539	0.002275	6.6E-09
GTF2H4 *	6	rs3835361	30,907,317	GTA	G	0.413807	0.013310	0.002274	9.9E-09
GTF2H4 *	6	rs2284175	30,907,368	T	C	0.413822	0.013271	0.002274	1.1E-08
GTF2H4 *	6	rs2284176	30,907,845	T	C	0.415117	0.013312	0.002275	9.1E-09
GTF2H4 *	6	rs3218806	30,907,887	G	T	0.413804	0.013316	0.002274	9.6E-09
GTF2H4	6	rs2074510	30,908,257	G	T	0.413804	0.013302	0.002274	1.0E-08
GTF2H4	6	rs1052693	30,908,375	C	T	0.413800	0.013312	0.002274	9.7E-09
GTF2H4	6	rs2074509	30,908,461	G	A	0.413808	0.013310	0.002274	9.7E-09
GTF2H4	6	rs2074508	30,908,661	G	A	0.413815	0.013318	0.002274	9.6E-09
GTF2H4	6	rs1362123	30,909,219	G	C	0.413804	0.013327	0.002274	9.4E-09
GTF2H4	6	rs1362122	30,909,277	G	A	0.433583	0.013037	0.002264	1.5E-08
GTF2H4	6	rs916920	30,909,425	T	C	0.413585	0.013353	0.002275	9.4E-09
GTF2H4	6	rs1419693	30,909,983	A	C	0.413819	0.013298	0.002275	1.0E-08
GTF2H4	6	rs3218814	30,910,802	A	T	0.413804	0.013316	0.002274	9.6E-09
GTF2H4	6	rs3218815	30,910,992	C	T	0.413895	0.013246	0.002275	1.1E-08
GTF2H4	6	rs2074512	30,911,142	T	C	0.413778	0.013278	0.002274	1.1E-08
VARS2	6	rs9468847	30,918,341	C	T	0.433564	0.013049	0.002264	1.5E-08
VARS2	6	rs3869091	30,919,272	T	G	0.242497	-0.014351	0.002525	1.4E-08
VARS2	6	rs2285319	30,920,195	C	T	0.429820	0.012541	0.002259	4.7E-08
VARS2	6	rs9357103	30,920,561	A	G	0.242529	-0.014339	0.002525	1.4E-08
VARS2	6	rs2074511	30,921,612	T	C	0.433710	0.013087	0.002264	1.4E-08
VARS2	6	rs35056976	30,925,222	AC	A	0.429361	0.012746	0.002260	2.7E-08
VARS2 *	6	rs3873332	30,928,213	A	G	0.433572	0.013048	0.002264	1.5E-08
VARS2 *	6	rs3873333	30,928,275	C	T	0.428845	0.012767	0.002262	3.0E-08
VARS2 *	6	rs3873334	30,928,370	G	A	0.429824	0.012548	0.002259	4.7E-08
SFTA2 *	6	rs9368646	30,931,300	C	T	0.433777	0.013130	0.002264	1.2E-08
SFTA2	6	rs4713402	30,931,456	C	T	0.433770	0.013113	0.002264	1.3E-08
SFTA2	6	rs2286655	30,931,969	G	A	0.433762	0.013123	0.002264	1.3E-08
SFTA2 *	6	rs117295261	30,934,590	T	G	0.113073	-0.021206	0.003434	6.2E-10
MUC21	6	rs9348845	30,984,584	A	C	0.358365	-0.012440	0.002225	3.0E-08
MUC21	6	chr6:30984996_CAATAA_C	30,984,996	C	CAATAA	0.403361	-0.013057	0.002177	3.1E-09
MUC22 *	6	rs3873343	31,001,550	T	C	0.358100	-0.012450	0.002225	2.5E-08
MUC22 *	6	rs2894050	31,001,580	T	G	0.358100	-0.012450	0.002225	2.5E-08
MUC22 *	6	rs9394024	31,005,311	A	C	0.132903	-0.017590	0.003183	1.5E-08
MUC22	6	rs9278834	31,011,107	A	T	0.357142	-0.012295	0.002229	3.6E-08
MUC22	6	rs9378112	31,011,275	T	C	0.357997	-0.012297	0.002225	3.5E-08
MUC22	6	rs9391700	31,011,301	A	G	0.358001	-0.012292	0.002225	3.6E-08
MUC22	6	rs9378113	31,011,321	T	C	0.358001	-0.012292	0.002225	3.6E-08
MUC22	6	rs9378151	31,011,395	A	C	0.358335	-0.012395	0.002224	2.7E-08
MUC22	6	rs9394025	31,011,702	T	C	0.358317	-0.012388	0.002224	2.7E-08
MUC22	6	rs9366764	31,012,016	A	G	0.358335	-0.012387	0.002224	2.7E-08
MUC22	6	rs9380204	31,012,156	C	T	0.358319	-0.012394	0.002224	2.7E-08
MUC22	6	rs9380205	31,013,584	G	C	0.358332	-0.012326	0.002224	3.1E-08
MUC22	6	rs9380206	31,013,978	T	C	0.358332	-0.012373	0.002224	2.8E-08
MUC22	6	rs9380207	31,014,946	T	C	0.358332	-0.012373	0.002224	2.8E-08
MUC22	6	rs9391701	31,015,486	A	G	0.358310	-0.012389	0.002224	2.7E-08
MUC22	6	chr6:31015863_A_AT	31,015,863	AT	A	0.358329	-0.012379	0.002224	2.8E-08
MUC22	6	rs3871466	31,015,906	C	T	0.358328	-0.012389	0.002224	2.7E-08
MUC22	6	rs3869096	31,016,627	G	T	0.358354	-0.012382	0.002224	2.7E-08
MUC22	6	rs9348846	31,016,941	G	C	0.358320	-0.012392	0.002224	2.6E-08
MUC22	6	rs9368652	31,017,226	G	A	0.357874	-0.012306	0.002225	3.2E-08
MUC22	6	rs13194580	31,017,238	T	C	0.357874	-0.012306	0.002225	3.2E-08
MUC22	6	rs9348848	31,017,827	T	C	0.358156	-0.012472	0.002225	2.2E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
MUC22	6	rs9348849	31,017,828	T	C	0.358156	-0.012472	0.002225	2.2E-08
MUC22	6	rs28993414	31,017,915	C	CTT	0.358310	-0.012389	0.002224	2.7E-08
MUC22	6	rs9394027	31,018,108	C	G	0.358307	-0.012383	0.002224	2.7E-08
MUC22	6	rs9295941	31,018,887	A	C	0.356065	-0.012563	0.002222	1.8E-08
MUC22	6	rs9295942	31,019,233	T	G	0.358488	-0.012278	0.002225	3.5E-08
MUC22	6	rs4713416	31,019,800	A	G	0.358285	-0.012369	0.002224	2.8E-08
MUC22	6	rs13207269	31,020,129	G	C	0.358284	-0.012373	0.002224	2.8E-08
MUC22	6	rs9391703	31,020,534	C	T	0.357114	-0.012273	0.002228	3.8E-08
MUC22	6	rs9391704	31,020,560	T	G	0.358058	-0.012368	0.002225	2.8E-08
MUC22	6	rs9501343	31,021,704	A	T	0.358160	-0.012376	0.002226	2.8E-08
MUC22	6	rs9501345	31,021,883	T	C	0.358169	-0.012373	0.002226	2.8E-08
MUC22	6	rs9501346	31,021,966	T	C	0.358248	-0.012337	0.002226	3.1E-08
MUC22	6	rs13201420	31,022,070	C	T	0.358102	-0.012430	0.002227	2.5E-08
MUC22	6	rs9394029	31,022,280	G	C	0.358242	-0.012371	0.002226	2.9E-08
MUC22	6	rs28894975	31,022,442	C	T	0.357465	-0.012181	0.002229	4.4E-08
MUC22	6	rs28894976	31,022,443	T	C	0.357465	-0.012181	0.002229	4.4E-08
MUC22	6	rs13220447	31,023,472	G	A	0.358180	-0.012476	0.002227	2.3E-08
MUC22	6	rs9394031	31,023,866	C	T	0.358182	-0.012548	0.002227	1.9E-08
MUC22	6	rs4713417	31,024,957	T	G	0.357393	-0.012542	0.002233	2.0E-08
MUC22	6	rs4713418	31,024,964	C	G	0.357393	-0.012542	0.002233	2.0E-08
MUC22	6	rs4713419	31,025,459	G	A	0.354713	-0.012778	0.002238	1.1E-08
MUC22	6	rs3094672	31,025,600	T	A	0.360372	-0.014443	0.002222	7.4E-11
MUC22	6	rs4713420	31,025,790	T	G	0.354251	-0.013347	0.002222	1.1E-09
MUC22	6	rs6457300	31,030,965	G	T	0.326723	0.016165	0.002232	6.8E-13
MUC22	6	rs6457301	31,031,102	C	T	0.326548	0.016171	0.002232	6.2E-13
MUC22	6	rs6457302	31,031,288	T	C	0.475853	-0.012904	0.002213	6.6E-09
MUC22	6	rs6457303	31,031,401	A	G	0.475861	-0.012912	0.002213	6.4E-09
MUC22	6	rs11330895	31,031,830	C	CA	0.281468	0.014121	0.002333	1.9E-09
MUC22	6	rs4713421	31,031,850	A	C	0.475482	-0.012869	0.002213	7.3E-09
MUC22	6	rs4713422	31,032,125	G	C	0.476034	-0.013039	0.002211	4.4E-09
MUC22	6	rs10947121	31,032,220	T	C	0.475866	-0.012916	0.002212	6.3E-09
MUC22	6	rs10807077	31,033,690	G	A	0.326859	0.016356	0.002232	3.7E-13
MUC22	6	rs10947124	31,033,719	T	G	0.326782	0.016280	0.002232	4.7E-13
MUC22	6	rs11969581	31,033,729	T	A	0.263140	0.013261	0.002334	1.2E-08
MUC22	6	rs11964623	31,033,742	T	C	0.263140	0.013261	0.002334	1.2E-08
MUC22	6	rs10947125	31,033,856	G	A	0.326796	0.016276	0.002232	4.7E-13
MUC22	6	rs10947126	31,033,891	A	G	0.328172	0.016397	0.002219	2.7E-13
MUC22	6	rs28360042	31,034,004	T	C	0.372728	0.014117	0.002353	1.1E-09
MUC22 *	6	rs9357105	31,036,146	A	G	0.129038	-0.018166	0.003237	1.9E-08
HCG22 *	6	rs9380213	31,074,619	A	G	0.125433	-0.017824	0.003285	4.1E-08
HCG22 *	6	rs9263460	31,077,336	T	C	0.223706	-0.014109	0.002625	2.8E-08
HCG22 *	6	rs9295949	31,078,024	A	C	0.225828	-0.013916	0.002614	3.3E-08
HCG22 *	6	rs9295950	31,078,025	T	C	0.225828	-0.013916	0.002614	3.3E-08
HCG22 *	6	rs9380215	31,081,878	A	G	0.225904	-0.013797	0.002614	4.1E-08
HCG22 *	6	rs4713431	31,083,231	A	G	0.225896	-0.013797	0.002614	4.1E-08
HCG22 *	6	rs9380217	31,083,776	T	C	0.225900	-0.013791	0.002614	4.2E-08
C6orf15 *	6	rs12527394	31,087,241	A	G	0.226072	-0.013729	0.002613	4.9E-08
C6orf15 *	6	rs1554329737	31,088,094	AT	A	0.126603	-0.018208	0.003274	2.3E-08
C6orf15 *	6	rs4947296	31,090,401	C	T	0.226065	-0.013747	0.002613	4.5E-08
C6orf15 *	6	rs12529288	31,091,198	A	G	0.226063	-0.013755	0.002613	4.6E-08
C6orf15 *	6	rs9263508	31,098,542	A	G	0.393784	-0.013634	0.002317	2.2E-09
C6orf15 *	6	rs9263512	31,098,900	T	G	0.226389	-0.013710	0.002612	4.9E-08
C6orf15 *	6	rs2394416	31,099,491	A	C	0.393795	-0.013648	0.002317	2.2E-09
C6orf15 *	6	rs74992754	31,100,249	A	C	0.393791	-0.013592	0.002317	2.4E-09
C6orf15 *	6	rs9263560	31,101,565	A	G	0.395197	-0.013419	0.002318	4.9E-09
C6orf15 *	6	rs9263572	31,101,972	A	C	0.226446	-0.013730	0.002612	4.7E-08
C6orf15 *	6	rs9394037	31,102,745	A	G	0.226157	-0.013861	0.002613	3.7E-08
C6orf15 *	6	rs9348854	31,102,747	T	C	0.226157	-0.013861	0.002613	3.7E-08
C6orf15 *	6	rs9357108	31,103,183	T	A	0.226157	-0.013861	0.002613	3.7E-08
C6orf15 *	6	rs9405049	31,103,676	A	G	0.226409	-0.013802	0.002610	4.4E-08
C6orf15 *	6	rs34209658	31,105,560	G	T	0.226397	-0.013778	0.002610	4.6E-08
C6orf15 *	6	rs35802713	31,105,592	T	G	0.225895	-0.013851	0.002614	4.1E-08
C6orf15 *	6	rs4947297	31,105,760	A	T	0.226397	-0.013778	0.002610	4.6E-08
C6orf15 *	6	rs4947298	31,105,879	A	T	0.217399	-0.014573	0.002666	1.8E-08
C6orf15 *	6	rs4947299	31,105,995	A	G	0.226401	-0.013787	0.002610	4.5E-08
C6orf15 *	6	rs4947302	31,106,351	T	C	0.226405	-0.013785	0.002610	4.5E-08
C6orf15 *	6	rs4947246	31,106,371	T	G	0.226396	-0.013799	0.002610	4.5E-08
C6orf15 *	6	rs9263625	31,107,384	A	G	0.393762	-0.013574	0.002318	2.6E-09
C6orf15 *	6	rs9295951	31,109,869	T	C	0.393685	-0.013537	0.002318	2.9E-09
C6orf15	6	rs2233978	31,111,926	G	C	0.393390	-0.013443	0.002318	3.9E-09
C6orf15	6	rs2233977	31,112,117	G	A	0.393575	-0.013566	0.002318	2.9E-09
C6orf15 *	6	rs2233969	31,112,655	G	A	0.388448	-0.012835	0.002324	1.8E-08
C6orf15 *	6	rs1265051	31,112,927	G	T	0.284650	-0.015100	0.002423	1.2E-10
C6orf15 *	6	rs4495304	31,112,941	C	T	0.225931	-0.013814	0.002614	4.1E-08
C6orf15 *	6	rs4486065	31,112,956	G	C	0.284331	-0.015250	0.002423	8.8E-11
C6orf15 *	6	rs2233967	31,113,051	G	C	0.283007	-0.015742	0.002429	2.1E-11
C6orf15 *	6	rs2233965	31,113,122	G	T	0.282843	-0.015740	0.002429	2.1E-11
C6orf15 *	6	rs2233964	31,113,142	G	A	0.284328	-0.015105	0.002423	1.3E-10
C6orf15 *	6	rs2233962	31,113,204	C	T	0.284282	-0.015197	0.002426	1.2E-10
C6orf15 *	6	rs1265047	31,113,687	G	A	0.398256	-0.014422	0.002301	2.3E-10
HCG27 *	6	rs7742179	31,191,243	A	T	0.403957	0.012410	0.002178	2.9E-08
HCG27	6	rs6921948	31,203,480	C	A	0.424420	0.014964	0.002261	3.3E-12
HCG27 *	6	rs3887381	31,204,574	T	C	0.311367	0.015077	0.002264	5.5E-12
HCG27 *	6	rs3998077	31,205,656	A	G	0.423952	0.014900	0.002260	4.2E-12
HCG27 *	6	rs6930065	31,205,892	C	T	0.367996	0.014279	0.002404	2.4E-10
HCG27 *	6	rs6930462	31,206,156	G	T	0.424387	0.014954	0.002261	3.4E-12
HCG27 *	6	rs9281253	31,206,206	CAAAG	C	0.427366	0.014613	0.002268	1.4E-11
HCG27 *	6	rs6930643	31,206,258	C	T	0.410499	0.014471	0.002309	2.5E-11
HCG27 *	6	rs2894181	31,206,750	G	A	0.424899	0.015149	0.002260	1.8E-12
HCG27 *	6	rs6936604	31,207,149	C	T	0.367840	0.014228	0.002405	2.8E-10
HCG27 *	6	rs6936825	31,207,267	C	T	0.424249	0.014907	0.002262	4.1E-12
HCG27 *	6	rs6914215	31,207,401	A	C	0.424247	0.014927	0.002262	3.8E-12
HCG27 *	6	rs6914076	31,207,429	G	A	0.424247	0.014927	0.002262	3.8E-12
HCG27 *	6	rs4249311	31,207,831	C	T	0.422904	0.014644	0.002267	9.0E-12
HCG27 *	6	rs9263911	31,207,890	G	A	0.408467	0.014185	0.002297	1.4E-10
HCG27 *	6	rs6919603	31,208,135	G	A	0.358504	0.014389	0.002429	4.5E-10
HCG27 *	6	rs4410769	31,208,469	T	C	0.424672	0.014945	0.002261	3.5E-12

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
HCG27 *	6	rs4457201	31,209,595	C	T	0.439408	0.014570	0.002243	7.6E-12
HCG27 *	6	rs9263927	31,210,456	T	C	0.439023	0.014488	0.002244	9.8E-12
HCG27 *	6	rs9263928	31,210,547	G	T	0.439449	0.014576	0.002243	7.4E-12
HCG27 *	6	rs9263929	31,210,551	A	G	0.439445	0.014591	0.002243	7.1E-12
HCG27 *	6	rs9263931	31,210,770	G	A	0.438863	0.014550	0.002245	8.5E-12
HCG27 *	6	rs9263933	31,210,849	G	A	0.438358	0.014483	0.002246	1.1E-11
HCG27 *	6	rs9263936	31,211,382	C	A	0.439445	0.014591	0.002243	7.1E-12
HCG27 *	6	rs9263938	31,211,601	T	C	0.439534	0.014612	0.002243	6.8E-12
HCG27 *	6	rs9263940	31,211,715	T	C	0.439530	0.014636	0.002243	6.4E-12
HCG27 *	6	rs34606125	31,212,574	C	CA	0.393260	0.014521	0.002337	5.3E-11
HCG27 *	6	rs9263944	31,212,646	G	A	0.439520	0.014636	0.002243	6.3E-12
HCG27 *	6	rs9263947	31,212,903	G	T	0.439520	0.014636	0.002243	6.3E-12
HCG27 *	6	rs9263953	31,213,931	C	T	0.439520	0.014635	0.002243	6.3E-12
HCG27 *	6	rs9281259	31,214,946	AG	A	0.439522	0.014639	0.002243	6.2E-12
HCG27 *	6	rs9263956	31,215,194	T	C	0.439515	0.014646	0.002243	6.1E-12
HCG27 *	6	rs3869109	31,216,419	G	A	0.439920	0.014548	0.002243	8.3E-12
HCG27 *	6	rs9263960	31,217,100	C	T	0.439350	0.014533	0.002243	8.9E-12
HCG27 *	6	rs9281263	31,217,872	AC	A	0.439678	0.014563	0.002242	8.1E-12
HCG27 *	6	rs9263964	31,218,262	T	C	0.422316	0.013254	0.002283	1.1E-09
HCG27 *	6	rs9263967	31,218,468	G	A	0.439693	0.014566	0.002243	7.9E-12
HCG27 *	6	rs9263968	31,218,591	A	G	0.439568	0.014550	0.002243	8.3E-12
HCG27 *	6	chr6:31218845_C_CTT	31,218,845	CTT	C	0.428727	0.014187	0.002259	5.7E-11
HCG27 *	6	rs9263978	31,219,791	G	A	0.439654	0.014618	0.002243	6.8E-12
HCG27 *	6	rs9281266	31,220,375	T	AAAATA	0.361036	-0.011329	0.002225	4.1E-08
HCG27 *	6	rs9263980	31,220,620	G	A	0.440403	0.014491	0.002242	9.0E-12
HCG27 *	6	rs6928399	31,227,441	T	C	0.288533	0.013285	0.002322	4.7E-09
HCG27 *	6	rs6934133	31,228,026	A	G	0.305266	0.014840	0.002281	2.1E-11
HCG27 *	6	rs6933818	31,228,027	T	C	0.305266	0.014840	0.002281	2.1E-11
HCG27 *	6	rs10807083	31,228,164	A	G	0.305880	0.014591	0.002279	4.0E-11
HCG27 *	6	rs7769211	31,228,241	C	T	0.355444	-0.011963	0.002235	1.1E-08
HCG27 *	6	rs3130522	31,229,063	C	T	0.358731	-0.011946	0.002222	8.9E-09
HCG27 *	6	rs3130943	31,229,070	G	A	0.358731	-0.011946	0.002222	8.9E-09
HCG27 *	6	rs3130523	31,229,297	T	C	0.356266	-0.012041	0.002231	9.3E-09
HCG27 *	6	rs28397288	31,229,366	C	A	0.305880	0.014577	0.002279	4.1E-11
HCG27 *	6	rs3134783	31,229,486	A	G	0.358752	-0.011912	0.002222	9.7E-09
HCG27 *	6	rs3130942	31,229,516	T	C	0.358763	-0.011906	0.002222	9.8E-09
HCG27 *	6	rs3130470	31,229,751	G	A	0.358749	-0.011903	0.002222	9.9E-09
HCG27 *	6	rs3130471	31,229,919	T	G	0.357995	-0.012099	0.002225	6.3E-09
HCG27 *	6	rs3130524	31,229,952	C	T	0.357995	-0.012099	0.002225	6.3E-09
HCG27 *	6	rs3130940	31,230,436	G	T	0.358726	-0.011840	0.002222	1.1E-08
HCG27 *	6	rs5875298	31,230,498	A	AAGG	0.357536	-0.012005	0.002229	1.1E-08
HCG27 *	6	rs3130938	31,230,855	G	T	0.358726	-0.011840	0.002222	1.1E-08
HCG27 *	6	rs3134779	31,231,120	A	G	0.359224	-0.011815	0.002224	1.3E-08
HCG27 *	6	chr6:31231160_CAAAG_C	31,231,160	C	CAAAG	0.305884	0.014606	0.002279	3.8E-11
HCG27 *	6	rs11967684	31,231,989	A	G	0.306845	0.014554	0.002270	4.8E-11
HCG27 *	6	rs3130529	31,232,656	C	T	0.348619	-0.012826	0.002237	8.9E-10
HCG27 *	6	rs7757622	31,232,987	T	C	0.434013	0.015345	0.002246	5.0E-13
HCG27 *	6	rs3134776	31,233,037	A	G	0.353255	-0.012494	0.002230	2.3E-09
HCG27 *	6	rs3134775	31,233,580	C	A	0.353281	-0.012506	0.002230	2.2E-09
HCG27 *	6	rs3134774	31,233,747	C	T	0.353281	-0.012506	0.002230	2.2E-09
HCG27 *	6	rs9264086	31,233,907	A	G	0.432820	0.014836	0.002246	4.9E-12
HLA-C *	6	rs28397298	31,239,909	G	A	0.292375	0.013321	0.002316	3.1E-09
HLA-C *	6	rs113075583	31,254,848	T	C	0.064025	0.021709	0.004199	3.1E-08
HLA-C *	6	rs181793732	31,257,904	C	T	0.064111	0.021533	0.004197	3.8E-08
HLA-C *	6	rs112253861	31,258,519	T	C	0.063582	0.022504	0.004207	1.3E-08
HLA-C *	6	rs183076319	31,258,889	T	C	0.063542	0.022631	0.004209	1.0E-08
HLA-C *	6	rs112879586	31,260,662	CA	C	0.063561	0.022059	0.004208	2.4E-08
HLA-C *	6	rs17191797	31,260,763	G	T	0.063566	0.022026	0.004207	2.6E-08
HLA-C *	6	rs17191904	31,261,222	A	G	0.063569	0.022017	0.004207	2.6E-08
HLA-C *	6	rs72854960	31,261,346	T	A	0.063569	0.022017	0.004207	2.6E-08
HLA-C *	6	rs116556510	31,261,644	T	G	0.063570	0.022019	0.004207	2.6E-08
HLA-C *	6	rs113700423	31,261,720	T	C	0.065250	0.021137	0.004156	3.9E-08
HLA-C *	6	rs17192134	31,262,216	T	G	0.062362	0.023327	0.004219	5.2E-09
HLA-C *	6	rs112445341	31,264,169	T	C	0.062367	0.023375	0.004219	4.8E-09
HLA-C *	6	rs2853961	31,264,212	A	G	0.133035	0.017279	0.003277	1.1E-08
HLA-C *	6	rs112514637	31,264,420	T	TAA	0.062364	0.023366	0.004219	4.8E-09
HLA-C *	6	rs66509442	31,264,498	T	A	0.062365	0.023528	0.004219	3.8E-09
HLA-C *	6	rs67524139	31,266,505	C	T	0.062374	0.023535	0.004219	3.9E-09
HLA-C *	6	rs2524103	31,266,825	C	T	0.339247	-0.013179	0.002280	9.5E-11
HLA-C *	6	rs138428160	31,267,408	A	CAAGGT/	0.338076	-0.013224	0.002287	1.2E-10
HLA-C *	6	rs113509869	31,267,416	A	T	0.064632	0.021688	0.004159	4.5E-08
HLA-C *	6	rs112126458	31,267,423	T	C	0.063429	0.021617	0.004199	4.6E-08
HLA-C *	6	rs2524101	31,267,821	C	G	0.339037	-0.013131	0.002280	9.5E-11
HLA-C *	6	rs9264579	31,267,969	A	G	0.361707	-0.014380	0.002276	6.9E-12
HLA-C *	6	rs113792081	31,267,998	C	T	0.071858	0.022826	0.003946	1.4E-09
HLA-C *	6	rs2524096	31,268,690	T	G	0.433967	-0.013610	0.002223	1.6E-11
HLA-C	6	rs41553018	31,271,965	C	G	0.061821	0.023666	0.004240	4.7E-09
HLA-C	6	rs2074493	31,271,999	C	A	0.339191	0.016861	0.002459	9.1E-14
HLA-C *	6	rs2074489	31,272,351	T	C	0.329071	0.016340	0.002506	1.4E-12
HLA-C *	6	rs5010528	31,273,255	G	A	0.062436	0.022834	0.004227	1.3E-08
HLA-C *	6	rs58019823	31,273,438	G	A	0.063489	0.023606	0.004186	2.6E-09
HLA-C *	6	rs67058142	31,274,016	A	G	0.062162	0.023227	0.004229	6.6E-09
HLA-C *	6	rs3132482	31,275,643	A	G	0.480805	0.013084	0.002293	3.3E-09
HLA-C *	6	rs9378228	31,278,594	T	G	0.127078	-0.017523	0.003269	4.7E-08
HLA-C *	6	rs9468914	31,282,829	C	A	0.363015	0.013552	0.002393	7.4E-10
HLA-C *	6	rs9468915	31,283,024	C	A	0.303230	0.013059	0.002581	1.5E-08
HLA-C *	6	rs9468916	31,283,032	C	T	0.303316	0.012955	0.002581	1.9E-08
HLA-C *	6	rs9468917	31,283,141	T	C	0.303305	0.012958	0.002581	1.9E-08
HLA-C *	6	rs28367587	31,283,201	A	G	0.303325	0.012973	0.002580	1.8E-08
HLA-C *	6	rs28367588	31,283,226	A	G	0.303325	0.012973	0.002580	1.8E-08
HLA-C *	6	chr6:31283239_TA_T	31,283,239	T	TA	0.303325	0.012973	0.002580	1.8E-08
HLA-C *	6	rs28367589	31,283,255	A	C	0.363035	0.013550	0.002393	7.5E-10
HLA-C *	6	rs9461681	31,283,263	A	G	0.303325	0.012973	0.002580	1.8E-08
HLA-C *	6	rs3873374	31,283,534	C	T	0.303324	0.012959	0.002580	1.8E-08
HLA-C *	6	rs3873375	31,283,583	T	C	0.304205	0.012846	0.002570	2.0E-08
HLA-C *	6	rs2394963	31,283,685	T	C	0.303141	0.012880	0.002583	2.2E-08
HLA-C *	6	rs2394964	31,283,765	T	C	0.303152	0.012886	0.002583	2.2E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
HLA-C *	6	rs2894206	31,283,781	T	A	0.303152	0.012886	0.002583	2.2E-08
HLA-C *	6	rs2394965	31,283,804	T	G	0.303152	0.012886	0.002583	2.2E-08
HLA-C *	6	rs6910962	31,285,332	T	C	0.303147	0.012898	0.002583	2.1E-08
HLA-C *	6	rs7754443	31,286,486	A	G	0.303159	0.012884	0.002583	2.2E-08
HLA-C *	6	rs9468920	31,287,159	A	G	0.303322	0.012937	0.002583	1.9E-08
HLA-C *	6	rs9468921	31,287,304	G	A	0.303152	0.012886	0.002583	2.2E-08
HLA-C *	6	rs9468922	31,287,509	A	G	0.304348	0.012966	0.002581	1.7E-08
HLA-C *	6	rs9468923	31,287,745	C	T	0.303152	0.012886	0.002583	2.2E-08
HLA-C *	6	rs4628144	31,289,327	C	T	0.303668	0.013216	0.002576	9.4E-09
HLA-C *	6	rs9468925	31,291,060	A	G	0.357132	0.013097	0.002409	3.4E-09
HLA-C *	6	rs3906269	31,291,191	A	G	0.303158	0.012873	0.002583	2.2E-08
HLA-C *	6	rs28367595	31,291,610	A	G	0.304409	0.012903	0.002580	2.0E-08
HLA-C *	6	rs9468926	31,292,441	T	C	0.304498	0.012985	0.002579	1.6E-08
HLA-C *	6	rs3906276	31,293,307	A	T	0.303147	0.012886	0.002583	2.2E-08
HLA-C *	6	rs3873379	31,294,392	C	T	0.303156	0.012898	0.002583	2.1E-08
HLA-C *	6	rs3873380	31,294,661	T	C	0.318121	0.012593	0.002506	3.3E-08
HLA-C *	6	rs3909124	31,295,880	T	G	0.303092	0.012622	0.002584	3.9E-08
HLA-C *	6	rs28367684	31,303,287	C	G	0.323431	0.012476	0.002483	3.9E-08
HLA-C *	6	rs3873386	31,305,968	C	T	0.324822	0.012498	0.002480	3.6E-08
HLA-C *	6	rs2853916	31,307,469	A	G	0.322430	-0.011858	0.002322	3.4E-08
HLA-C *	6	rs13194791	31,307,500	G	A	0.341439	-0.012503	0.002351	2.1E-08
HLA-B *	6	rs9265461	31,328,942	A	G	0.264899	0.013812	0.002734	9.5E-09
HLA-B *	6	rs9265516	31,329,993	T	C	0.263852	0.013831	0.002743	8.5E-09
HLA-B *	6	rs200358110	31,330,110	A	AT	0.263132	0.014258	0.002746	4.2E-09
HLA-B *	6	rs9265525	31,330,131	T	C	0.261917	0.014236	0.002753	5.5E-09
HLA-B *	6	rs9265540	31,330,387	T	C	0.267098	0.012916	0.002724	4.7E-08
HLA-B *	6	rs28752849	31,330,400	C	A	0.263912	0.013900	0.002744	8.9E-09
HLA-B *	6	rs9265543	31,330,408	A	G	0.261596	0.013721	0.002763	1.8E-08
HLA-B *	6	rs9265545	31,330,420	C	T	0.262424	0.013902	0.002755	1.2E-08
HLA-B *	6	rs9265546	31,330,425	A	G	0.262424	0.013902	0.002755	1.2E-08
HLA-B *	6	rs9265547	31,330,433	C	G	0.262424	0.013902	0.002755	1.2E-08
HLA-B *	6	rs9265548	31,330,441	C	T	0.264827	0.013799	0.002735	9.2E-09
HLA-B *	6	rs9265549	31,330,463	A	G	0.265082	0.013693	0.002732	1.2E-08
HLA-B *	6	rs9265552	31,330,519	G	C	0.262631	0.014463	0.002741	3.3E-09
HLA-B *	6	rs9265554	31,330,535	G	A	0.263536	0.014254	0.002743	4.3E-09
HLA-B *	6	rs9265559	31,330,589	G	C	0.264538	0.013922	0.002737	7.9E-09
HLA-B *	6	rs9265560	31,330,617	G	C	0.264643	0.013655	0.002736	1.3E-08
HLA-B *	6	rs9265561	31,330,649	G	A	0.263369	0.014045	0.002744	5.8E-09
HLA-B *	6	rs9265562	31,330,662	A	G	0.264791	0.013784	0.002735	9.9E-09
HLA-B *	6	rs9265566	31,330,743	T	A	0.264789	0.013790	0.002735	9.8E-09
HLA-B *	6	rs9265568	31,330,790	T	C	0.265065	0.013814	0.002733	9.8E-09
HLA-B *	6	rs9265569	31,330,813	A	G	0.265061	0.013797	0.002733	1.0E-08
HLA-B *	6	rs6938680	31,331,524	A	G	0.264185	0.013866	0.002739	9.8E-09
HLA-B *	6	rs6938855	31,331,573	C	A	0.264318	0.013670	0.002739	1.4E-08
HLA-B *	6	rs9265614	31,331,831	A	T	0.264778	0.013728	0.002736	1.0E-08
HLA-B *	6	rs9265618	31,331,893	T	C	0.264696	0.013723	0.002737	1.0E-08
HLA-B *	6	rs9265620	31,331,908	C	T	0.271360	0.014268	0.002699	1.6E-09
HLA-B *	6	rs9265624	31,332,007	A	C	0.263738	0.013912	0.002742	8.1E-09
HLA-B *	6	rs9265627	31,332,082	C	T	0.264258	0.013999	0.002739	6.3E-09
HLA-B *	6	rs9265644	31,332,404	C	T	0.264552	0.013653	0.002739	1.5E-08
HLA-B *	6	rs6902116	31,332,509	G	A	0.258888	0.014213	0.002769	7.7E-09
HLA-B *	6	rs142459005	31,361,146	T	A	0.138736	-0.017455	0.003160	1.1E-08
MICA *	6	rs117884751	31,434,029	A	T	0.132161	-0.017126	0.003215	4.2E-08
GRM4 *	6	rs141604279	34,186,105	A	G	0.080089	-0.020502	0.003832	2.2E-08
GRM4 *	6	rs117658820	34,186,528	T	A	0.080118	-0.020549	0.003832	2.1E-08
GRM4 *	6	rs148061387	34,189,310	A	G	0.080464	-0.020422	0.003828	2.7E-08
GRM4 *	6	rs79658451	34,195,307	C	G	0.092884	-0.020017	0.003517	1.7E-09
HMGAI *	6	rs111643014	34,197,531	A	G	0.082880	-0.020483	0.003694	3.6E-09
HMGAI *	6	rs141574601	34,199,567	G	T	0.082238	-0.021048	0.003712	1.8E-09
HMGAI *	6	rs1187118	34,201,243	A	T	0.107237	-0.018381	0.003298	7.7E-09
HMGAI *	6	rs35310095	34,203,190	GC	G	0.108301	-0.018074	0.003281	1.0E-08
HMGAI *	6	rs1187115	34,204,278	C	A	0.110968	-0.017812	0.003257	1.7E-08
HMGAI *	6	rs10807136	34,210,781	T	C	0.096344	-0.018844	0.003457	1.1E-08
HMGAI *	6	rs138997002	34,210,816	T	C	0.082573	-0.021079	0.003704	1.6E-09
HMGAI *	6	rs6913361	34,211,613	A	G	0.096279	-0.018675	0.003461	1.5E-08
HMGAI *	6	rs7751671	34,211,979	A	G	0.080921	-0.020739	0.003770	1.1E-08
HMGAI *	6	rs139173280	34,212,499	T	C	0.082510	-0.020845	0.003706	2.3E-09
HMGAI *	6	rs9357174	34,214,218	C	T	0.112922	-0.017063	0.003222	3.9E-08
HMGAI *	6	rs10807137	34,215,249	C	T	0.112788	-0.017051	0.003224	4.5E-08
HMGAI *	6	rs1592269	34,215,280	G	A	0.094792	-0.018947	0.003483	8.3E-09
HMGAI *	6	rs1776901	34,215,317	A	G	0.092733	-0.019356	0.003514	4.8E-09
HMGAI *	6	rs6911780	34,216,690	T	C	0.085890	-0.020385	0.003638	3.0E-09
HMGAI *	6	rs10807138	34,217,161	G	A	0.116752	-0.017166	0.003177	3.1E-08
HMGAI *	6	rs10807139	34,217,235	T	C	0.093012	-0.020187	0.003505	1.6E-09
HMGAI *	6	rs151044302	34,217,884	T	C	0.085791	-0.020640	0.003638	2.1E-09
HMGAI *	6	rs2797963	34,217,972	C	T	0.104788	-0.019657	0.003333	9.3E-10
HMGAI *	6	rs2797964	34,217,978	C	T	0.109912	-0.018179	0.003264	9.9E-09
HMGAI *	6	rs147929923	34,217,995	C	T	0.083869	-0.020710	0.003682	4.2E-09
HMGAI *	6	rs9469745	34,220,690	G	A	0.110032	-0.018163	0.003252	8.6E-09
HMGAI *	6	rs12214804	34,221,089	C	T	0.108650	-0.018976	0.003288	2.3E-09
HMGAI *	6	rs10947487	34,221,835	A	G	0.093389	-0.020102	0.003495	1.6E-09
HMGAI *	6	rs77510989	34,223,158	G	A	0.088795	-0.019584	0.003581	9.2E-09
HMGAI *	6	rs7753429	34,224,101	C	G	0.093322	-0.020095	0.003497	1.6E-09
HMGAI *	6	rs117525671	34,224,197	T	C	0.086107	-0.020444	0.003629	2.6E-09
HMGAI *	6	rs1776899	34,225,453	G	A	0.093322	-0.020095	0.003497	1.6E-09
HMGAI *	6	rs1776898	34,226,315	C	T	0.110002	-0.018014	0.003253	1.2E-08
HMGAI *	6	rs1759645	34,227,089	C	T	0.113722	-0.017470	0.003204	2.4E-08
HMGAI *	6	rs1776897	34,227,234	G	T	0.111197	-0.017679	0.003234	1.6E-08
HMGAI *	6	rs1759646	34,227,670	C	T	0.110399	-0.017940	0.003247	1.3E-08
HMGAI *	6	rs148811065	34,228,788	T	C	0.086122	-0.020393	0.003628	2.9E-09
HMGAI *	6	rs1759627	34,229,328	C	T	0.113091	-0.017572	0.003214	2.5E-08
HMGAI *	6	rs1759628	34,229,411	T	C	0.093805	-0.019896	0.003488	2.0E-09
HMGAI *	6	rs5875500	34,229,442	G	GT	0.113086	-0.017598	0.003214	2.4E-08
HMGAI *	6	rs2780226	34,231,315	C	T	0.109976	-0.017895	0.003250	1.3E-08
HMGAI	6	rs116882763	34,237,755	T	G	0.096985	-0.020046	0.003439	1.1E-09
HMGAI	6	rs117741261	34,238,268	G	C	0.096985	-0.020039	0.003439	1.1E-09
HMGAI	6	rs59329931	34,239,697	T	TAA	0.109814	-0.017996	0.003253	1.2E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
HMGA1	6	rs4713761	34,241,504	A	T	0.097002	-0.020073	0.003439	1.0E-09
HMGA1	6	rs139876191	34,242,693	AC	A	0.097319	-0.020244	0.003434	6.9E-10
HMGA1	6	rs35381162	34,243,564	GT	G	0.104644	-0.019565	0.003323	8.1E-10
HMGA1	6	rs56657958	34,243,987	T	C	0.095856	-0.019749	0.003461	2.2E-09
C6orf1	6	rs4711389	34,246,893	G	A	0.098927	-0.018484	0.003413	1.3E-08
C6orf1	6	rs928482	34,247,444	A	G	0.104929	-0.019862	0.003323	4.9E-10
C6orf1	6	rs1150779	34,248,142	C	T	0.106954	-0.018556	0.003293	5.3E-09
C6orf1 *	6	rs1150777	34,249,404	C	A	0.111612	-0.018560	0.003236	4.8E-09
C6orf1 *	6	rs10080749	34,250,388	G	A	0.109039	-0.019327	0.003268	1.3E-09
C6orf1 *	6	rs59412811	34,250,798	C	A	0.108336	-0.018975	0.003276	2.3E-09
C6orf1 *	6	rs9394200	34,250,941	T	C	0.106370	-0.019245	0.003301	1.4E-09
C6orf1 *	6	rs6909732	34,251,233	T	C	0.103675	-0.020388	0.003339	2.0E-10
C6orf1 *	6	rs6932690	34,251,383	G	T	0.104011	-0.019965	0.003333	4.1E-10
C6orf1 *	6	rs149066177	34,251,783	A	T	0.109158	-0.018900	0.003270	2.9E-09
C6orf1 *	6	rs57026767	34,251,921	C	T	0.112021	-0.018080	0.003230	1.2E-08
C6orf1 *	6	rs7753987	34,252,903	A	C	0.103995	-0.019889	0.003334	4.9E-10
C6orf1 *	6	rs150005915	34,253,481	AAAAAA	A	0.110203	-0.018610	0.003303	1.3E-08
C6orf1 *	6	rs147736074	34,254,817	C	G	0.092965	-0.019898	0.003506	2.4E-09
C6orf1 *	6	rs9366846	34,255,162	A	G	0.111989	-0.018051	0.003231	1.3E-08
C6orf1 *	6	rs9348936	34,255,453	T	C	0.095255	-0.019213	0.003470	7.7E-09
C6orf1 *	6	chr6:34256162_TA_T	34,256,162	TA	T	0.112014	-0.018087	0.003231	1.2E-08
C6orf1 *	6	rs9394202	34,256,234	A	G	0.093546	-0.020173	0.003503	1.4E-09
C6orf1 *	6	rs9469750	34,256,257	T	C	0.092931	-0.020053	0.003507	1.9E-09
C6orf1 *	6	rs9461968	34,256,389	T	G	0.092849	-0.020231	0.003510	1.5E-09
C6orf1 *	6	rs9461969	34,256,491	A	C	0.093138	-0.020050	0.003504	1.8E-09
C6orf1 *	6	rs9368804	34,256,532	C	A	0.112413	-0.018303	0.003232	7.6E-09
C6orf1 *	6	rs2780216	34,256,769	G	A	0.093220	-0.020018	0.003505	1.9E-09
C6orf1 *	6	rs60311905	34,256,858	TAGC	T	0.112368	-0.018105	0.003231	1.1E-08
C6orf1 *	6	rs2797967	34,257,060	G	C	0.112211	-0.018070	0.003229	1.2E-08
C6orf1 *	6	rs9368805	34,257,298	T	C	0.094853	-0.020760	0.003490	4.7E-10
C6orf1 *	6	rs9394204	34,257,492	C	T	0.112207	-0.018048	0.003229	1.2E-08
C6orf1 *	6	rs13201774	34,257,707	G	C	0.093165	-0.020072	0.003504	1.8E-09
C6orf1 *	6	rs13217823	34,257,826	T	A	0.107490	-0.018162	0.003300	8.6E-09
C6orf1 *	6	rs200036606	34,257,827	AAT	A	0.093349	-0.019875	0.003504	2.3E-09
C6orf1 *	6	rs10947491	34,257,829	T	A	0.093349	-0.019875	0.003504	2.3E-09
C6orf1 *	6	rs2483211	34,258,154	T	C	0.112194	-0.018033	0.003229	1.3E-08
C6orf1 *	6	rs7761883	34,259,149	T	C	0.093131	-0.020119	0.003504	1.6E-09
C6orf1 *	6	rs73419191	34,259,832	C	T	0.093132	-0.020124	0.003504	1.6E-09
C6orf1 *	6	rs3997803	34,260,907	G	A	0.096325	-0.020070	0.003454	1.7E-09
C6orf1 *	6	rs7768482	34,260,983	T	A	0.096325	-0.020070	0.003454	1.7E-09
C6orf1 *	6	rs9394205	34,262,254	C	G	0.096748	-0.020377	0.003451	9.1E-10
C6orf1 *	6	rs7740907	34,262,666	C	G	0.093030	-0.020266	0.003506	1.2E-09
C6orf1 *	6	rs6457769	34,263,793	C	T	0.096312	-0.019993	0.003455	2.0E-09
C6orf1 *	6	rs4713762	34,263,884	A	G	0.093022	-0.020133	0.003506	1.6E-09
C6orf1 *	6	rs4713763	34,263,887	A	G	0.096312	-0.019993	0.003455	2.0E-09
C6orf1 *	6	rs4713764	34,264,114	C	T	0.096312	-0.019993	0.003455	2.0E-09
C6orf1 *	6	rs4713765	34,264,346	T	C	0.096317	-0.019986	0.003455	2.0E-09
C6orf1 *	6	rs148899910	34,264,482	C	G	0.093027	-0.020133	0.003506	1.6E-09
C6orf1 *	6	rs12530053	34,264,564	C	T	0.096323	-0.019983	0.003455	2.0E-09
C6orf1 *	6	rs35904412	34,264,883	TCTC	T	0.112764	-0.018281	0.003222	7.6E-09
C6orf1 *	6	rs7765484	34,265,150	T	A	0.093988	-0.019747	0.003502	3.9E-09
C6orf1 *	6	rs1573905	34,265,675	G	A	0.093133	-0.020042	0.003505	1.9E-09
C6orf1 *	6	rs9469758	34,265,986	C	A	0.093131	-0.020049	0.003505	1.9E-09
C6orf1 *	6	chr6:34266192_C_CA	34,266,192	CA	C	0.092837	-0.020409	0.003513	1.0E-09
C6orf1 *	6	rs73420913	34,266,243	A	C	0.093130	-0.020048	0.003505	1.9E-09
C6orf1 *	6	chr6:34266804_C_CA	34,266,804	CA	C	0.085527	-0.020312	0.003702	7.1E-09
C6orf1 *	6	rs6900030	34,267,462	T	C	0.096573	-0.020068	0.003450	1.7E-09
C6orf1 *	6	rs6899897	34,267,480	C	A	0.096573	-0.020068	0.003450	1.7E-09
C6orf1 *	6	rs6922851	34,267,515	C	T	0.096573	-0.020070	0.003450	1.7E-09
C6orf1 *	6	rs6900387	34,267,630	T	C	0.096366	-0.020033	0.003455	2.0E-09
NUDT3 *	6	rs144929479	34,268,357	AAAAAA	A	0.095539	-0.020346	0.003473	1.4E-09
NUDT3 *	6	rs9469761	34,268,652	A	G	0.096566	-0.020089	0.003451	1.7E-09
NUDT3 *	6	rs9469762	34,268,653	A	G	0.084796	-0.020902	0.003664	1.9E-09
NUDT3 *	6	rs9461975	34,268,682	T	C	0.096566	-0.020089	0.003451	1.7E-09
NUDT3 *	6	rs2780215	34,269,196	G	A	0.082726	-0.020993	0.003719	2.6E-09
NUDT3 *	6	rs186766320	34,269,213	A	G	0.082162	-0.020422	0.003722	6.6E-09
NUDT3 *	6	rs1759637	34,269,353	C	T	0.111166	-0.019990	0.003248	2.5E-10
NUDT3 *	6	rs1690799	34,269,619	T	C	0.097896	-0.020209	0.003428	1.1E-09
NUDT3 *	6	rs1776891	34,269,844	A	G	0.085155	-0.020732	0.003651	2.2E-09
NUDT3 *	6	rs1776890	34,269,970	G	A	0.097923	-0.020273	0.003428	9.4E-10
NUDT3 *	6	rs2797961	34,270,020	G	A	0.115341	-0.019200	0.003190	9.3E-10
NUDT3 *	6	rs6918981	34,270,737	G	A	0.118243	-0.018288	0.003151	4.2E-09
NUDT3 *	6	rs13207853	34,271,169	C	T	0.110449	-0.018694	0.003251	6.0E-09
NUDT3 *	6	rs60952447	34,271,383	A	G	0.085741	-0.020104	0.003638	7.0E-09
NUDT3 *	6	rs1187130	34,271,696	G	A	0.104948	-0.018413	0.003329	1.9E-08
NUDT3 *	6	rs1187129	34,272,212	A	G	0.084322	-0.019415	0.003681	2.9E-08
NUDT3 *	6	rs1307274	34,272,799	T	G	0.101464	-0.018236	0.003396	3.1E-08
NUDT3 *	6	rs1307273	34,273,109	G	A	0.119212	-0.017937	0.003171	1.0E-08
NUDT3 *	6	rs745630955	34,275,875	TTC	T	0.102103	-0.018072	0.003399	4.4E-08
NUDT3 *	6	rs34118277	34,275,876	TC	T	0.102103	-0.018069	0.003399	4.5E-08
VEGFA *	6	rs79469752	43,770,044	T	C	0.059193	-0.024285	0.004368	2.3E-08
VEGFA *	6	rs4711750	43,789,345	T	A	0.437178	-0.019321	0.002032	1.3E-22
VEGFA *	6	rs998584	43,790,159	C	A	0.443724	-0.019214	0.002031	2.6E-22
VEGFA *	6	rs6905288	43,791,136	G	A	0.298998	-0.020197	0.002205	4.2E-20
VEGFA *	6	rs6458349	43,792,052	G	A	0.214083	-0.020847	0.002492	8.2E-17
VEGFA *	6	rs11967262	43,792,590	C	G	0.431447	-0.019217	0.002042	1.9E-22
VEGFA *	6	rs1358980	43,796,814	C	T	0.449197	-0.018939	0.002028	3.3E-22
VEGFA *	6	rs1885659	43,797,796	A	G	0.159881	-0.018245	0.002830	3.0E-11
GSTA2 *	6	rs2748999	52,747,870	T	A	0.093909	-0.019893	0.003476	1.7E-08
GSTA2	6	rs2749005	52,756,635	T	G	0.110402	0.017738	0.003221	3.5E-08
GSTA2	6	rs2254050	52,758,016	C	T	0.110406	0.017724	0.003221	3.6E-08
GSTA2	6	rs2608625	52,758,297	C	T	0.110406	0.017724	0.003221	3.6E-08
GSTA2	6	rs1009064	52,758,692	G	C	0.110406	0.017724	0.003221	3.6E-08
GSTA2	6	rs1009063	52,758,707	T	A	0.110406	0.017724	0.003221	3.6E-08
GSTA2	6	rs2608627	52,760,243	C	T	0.110378	0.017779	0.003222	3.2E-08
GSTA2	6	rs2608629	52,760,996	G	A	0.110376	0.017764	0.003222	3.3E-08
GSTA2	6	rs2608630	52,761,115	T	A	0.110376	0.017764	0.003222	3.3E-08

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
GSTA2	6	rs2749007	52,761,165	A	T	0.110376	0.017764	0.003222	3.3E-08
GSTA2	6	rs2749008	52,761,322	C	T	0.110376	0.017764	0.003222	3.3E-08
GSTA2	6	rs2608631	52,761,471	G	A	0.110381	0.017762	0.003221	3.3E-08
GSTA2	6	rs2749010	52,761,774	C	T	0.112291	0.017828	0.003215	2.5E-08
GSTA2	6	rs2749012	52,762,252	C	G	0.110378	0.017774	0.003221	3.2E-08
GSTA2	6	rs2749013	52,762,367	A	G	0.110378	0.017774	0.003221	3.2E-08
GSTA2	6	rs2749014	52,762,524	G	A	0.110378	0.017774	0.003221	3.2E-08
GSTA2	6	rs2070774	52,763,237	C	T	0.110378	0.017774	0.003221	3.2E-08
GSTA2 *	6	rs2749019	52,763,753	A	G	0.110385	0.017793	0.003221	3.1E-08
GSTA2 *	6	rs4715316	52,764,200	C	T	0.110630	0.017845	0.003221	2.8E-08
GSTA2 *	6	rs4715317	52,764,212	T	G	0.110385	0.017793	0.003221	3.1E-08
GSTA2 *	6	rs6458868	52,765,355	C	T	0.110392	0.017838	0.003221	2.8E-08
GSTA2 *	6	rs6458869	52,765,471	C	A	0.110392	0.017838	0.003221	2.8E-08
GSTA2 *	6	rs2749024	52,765,789	T	A	0.110395	0.017840	0.003221	2.8E-08
GSTA2 *	6	rs2749026	52,765,837	A	G	0.110395	0.017840	0.003221	2.8E-08
GSTA2 *	6	rs2749029	52,766,390	A	G	0.110403	0.017828	0.003221	2.9E-08
GSTA2 *	6	rs2608639	52,767,415	C	T	0.110469	0.017915	0.003221	2.5E-08
GSTA2 *	6	rs2749035	52,769,135	G	A	0.110363	0.017835	0.003221	2.9E-08
GSTA2 *	6	rs4715318	52,770,533	T	C	0.110377	0.017774	0.003221	3.2E-08
GSTA2 *	6	rs9395816	52,772,796	A	G	0.110415	0.017832	0.003221	3.0E-08
GSTA2 *	6	rs2608644	52,775,315	A	C	0.110484	0.017740	0.003219	3.3E-08
GSTA2 *	6	rs9357746	52,776,573	T	C	0.110400	0.017911	0.003221	2.5E-08
GSTA2 *	6	rs9395817	52,777,044	C	T	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs2608652	52,777,970	C	T	0.110408	0.017817	0.003221	3.0E-08
GSTA1 *	6	rs9395819	52,779,189	G	C	0.109828	0.017845	0.003230	3.0E-08
GSTA1 *	6	rs2608653	52,779,558	A	T	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs9382138	52,781,312	A	T	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs9382139	52,782,746	G	A	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs2608659	52,782,862	T	G	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs9367495	52,783,308	G	A	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs9474321	52,783,479	C	T	0.110375	0.017774	0.003221	3.2E-08
GSTA1 *	6	rs1072340	52,783,930	C	T	0.110010	0.017561	0.003227	4.9E-08
GSTA1 *	6	rs34319590	52,784,038	TG	T	0.110002	0.017594	0.003228	4.6E-08
GSTA1 *	6	rs1075181	52,784,046	A	G	0.110036	0.017555	0.003228	4.9E-08
GSTA1 *	6	rs1072341	52,784,108	T	A	0.109982	0.017564	0.003228	4.9E-08
GSTA1 *	6	rs2608664	52,784,186	C	A	0.109982	0.017564	0.003228	4.9E-08
GSTA1 *	6	rs9395820	52,784,209	A	T	0.109982	0.017564	0.003228	4.9E-08
GSTA1 *	6	rs4715322	52,784,411	C	G	0.109979	0.017584	0.003228	4.7E-08
GSTA1 *	6	rs4715325	52,785,466	A	T	0.109973	0.017583	0.003228	4.7E-08
GSTA1 *	6	rs2608668	52,785,724	A	G	0.109973	0.017583	0.003228	4.7E-08
GSTA1 *	6	rs62407587	52,787,305	T	C	0.109966	0.017574	0.003228	4.8E-08
GSTA1 *	6	rs6458870	52,787,363	T	A	0.109966	0.017574	0.003228	4.8E-08
GSTA1 *	6	rs1986661	52,787,542	C	T	0.109966	0.017574	0.003228	4.8E-08
GSTA1 *	6	rs2397104	52,787,795	A	C	0.109966	0.017574	0.003228	4.8E-08
GSTA1 *	6	rs2397105	52,788,526	G	A	0.109963	0.017558	0.003228	4.9E-08
GSTA1 *	6	rs4715332	52,804,387	C	A	0.110275	0.017520	0.003222	4.3E-08
RGS17	6	rs3910736	153,091,341	C	T	0.324224	-0.011123	0.002151	2.8E-08
RGS17	6	rs3910737	153,091,342	A	G	0.323318	-0.011217	0.002152	2.1E-08
RGS17	6	rs9371672	153,101,005	C	G	0.320653	-0.011355	0.002162	1.5E-08
RGS17	6	rs6557271	153,116,600	T	C	0.315520	-0.010989	0.002170	4.6E-08
MIR148A *	7	rs12672425	25,900,103	G	T	0.423497	-0.011937	0.002075	8.9E-09
MIR148A *	7	rs4722555	25,973,632	C	T	0.442848	0.011180	0.002031	3.1E-08
MIR148A *	7	rs6970673	25,975,022	T	C	0.440496	0.011157	0.002032	2.7E-08
MIR148A *	7	rs28537499	25,975,772	C	A	0.440959	0.011193	0.002032	2.4E-08
MIR148A *	7	rs2893237	25,998,964	G	A	0.462307	0.011439	0.002035	2.4E-08
MIR148A *	7	rs4722562	25,999,068	T	C	0.462308	0.011439	0.002035	2.4E-08
MIR148A *	7	rs6461905	26,000,782	T	C	0.461985	0.011471	0.002033	2.0E-08
MIR148A *	7	rs58292232	26,001,109	G	T	0.462016	0.011455	0.002033	2.1E-08
MIR148A *	7	rs12112544	26,002,259	G	A	0.462952	0.011383	0.002032	2.7E-08
MIR148A *	7	rs12112549	26,002,308	G	A	0.462952	0.011383	0.002032	2.7E-08
MIR148A *	7	rs6979761	26,002,804	C	T	0.464711	0.011529	0.002032	1.8E-08
MIR148A *	7	rs6959733	26,002,919	T	C	0.464063	0.011551	0.002031	1.8E-08
MIR148A *	7	rs11367100	26,003,929	A	AC	0.464039	0.011506	0.002030	2.1E-08
MIR148A *	7	rs12111617	26,004,119	A	G	0.463870	0.011461	0.002031	2.5E-08
MIR148A *	7	rs7781851	26,004,501	A	T	0.462116	0.011705	0.002039	1.4E-08
MIR148A *	7	rs7798823	26,004,532	T	C	0.464038	0.011510	0.002030	2.1E-08
MIR148A *	7	rs11378017	26,005,456	GT	G	0.465746	0.011701	0.002030	1.2E-08
MIR148A *	7	rs4722564	26,007,843	T	G	0.465539	0.011757	0.002031	1.1E-08
MIR148A *	7	rs55995006	26,008,392	T	A	0.465254	0.011732	0.002033	1.1E-08
MIR148A *	7	rs2391217	26,008,798	A	C	0.465293	0.011783	0.002033	9.9E-09
MIR148A *	7	rs6968895	26,009,860	A	G	0.465273	0.011755	0.002037	1.2E-08
MIR148A *	7	rs6969557	26,010,228	A	G	0.465276	0.011732	0.002038	1.2E-08
MIR148A *	7	rs66561076	26,010,419	G	A	0.464277	0.011321	0.002039	3.7E-08
MIR148A *	7	rs6979884	26,012,069	G	C	0.465002	0.011657	0.002041	1.6E-08
MIR148A *	7	rs2391220	26,013,147	A	G	0.465366	0.011557	0.002041	2.1E-08
MIR148A *	7	rs2391221	26,013,318	A	G	0.465523	0.011565	0.002041	2.0E-08
MIR148A *	7	rs1016913	26,013,647	G	A	0.455021	0.011777	0.002051	1.1E-08
MIR148A *	7	chr7:26036104_T_TTTTGT	26,036,104	TTTTGT	T	0.455055	0.011781	0.002054	6.4E-09
MIR148A *	7	rs56056224	26,044,015	T	A	0.461361	0.011617	0.002041	1.4E-08
MIR148A *	7	rs7796594	26,046,376	C	T	0.454590	-0.011956	0.002057	9.9E-09
NFE2L3 *	7	rs10435096	26,060,150	C	T	0.458336	0.011865	0.002056	1.2E-08
NFE2L3 *	7	rs551101475	26,073,577	CACAT	C	0.496995	0.012032	0.002036	5.9E-09
NFE2L3 *	7	rs11978583	26,075,769	G	A	0.492263	0.011902	0.002046	1.4E-08
NFE2L3 *	7	chr7:26075774_GA_G	26,075,774	G	GA	0.486785	0.012277	0.002058	5.8E-09
NFE2L3 *	7	rs4722566	26,080,075	C	T	0.497124	0.012685	0.002034	7.2E-10
NFE2L3 *	7	rs11434047	26,080,151	GT	G	0.497109	0.012680	0.002034	7.2E-10
NFE2L3 *	7	rs9639528	26,080,958	T	C	0.496588	0.012755	0.002033	5.5E-10
NFE2L3 *	7	rs7805293	26,081,178	C	A	0.496227	0.012626	0.002034	7.2E-10
NFE2L3 *	7	rs2391223	26,082,321	A	G	0.495666	0.012473	0.002031	1.1E-09
POLD2	7	rs2075070	44,115,653	G	A	0.261616	-0.013482	0.002348	4.7E-09
POLD2	7	rs3087367	44,116,547	A	G	0.261401	-0.013233	0.002348	1.0E-08
POLD2	7	rs3217964	44,118,226	C	T	0.238828	-0.014765	0.002406	3.7E-10
POLD2	7	rs3217962	44,118,379	G	A	0.262303	-0.013306	0.002340	6.7E-09
POLD2	7	rs3087370	44,122,210	G	A	0.234617	-0.014681	0.002409	4.7E-10
POLD2 *	7	rs3217944	44,124,463	A	C	0.234787	-0.014842	0.002405	2.9E-10
POLD2 *	7	rs3217943	44,124,492	C	T	0.235238	-0.014830	0.002403	2.8E-10
POLD2 *	7	rs113784062	44,126,070	T	C	0.235192	-0.014899	0.002403	2.4E-10

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
POLD2 *	7	rs12538223	44,127,298	G	A	0.235420	-0.014406	0.002399	7.1E-10
POLD2 *	7	chr7:44127645_A_AT	44,127,645	AT	A	0.242163	-0.013803	0.002387	2.4E-09
POLD2 *	7	rs12535289	44,129,230	G	A	0.235909	-0.014259	0.002392	8.6E-10
POLD2 *	7	rs55907525	44,129,790	C	G	0.232452	-0.014697	0.002407	3.5E-10
POLD2 *	7	rs17769566	44,129,973	C	A	0.235980	-0.014388	0.002391	6.2E-10
POLD2 *	7	rs56902462	44,130,156	A	G	0.235366	-0.014340	0.002393	8.1E-10
POLD2 *	7	rs12531534	44,130,798	T	C	0.236125	-0.014315	0.002390	7.6E-10
MYL7 *	7	rs17831589	44,133,526	A	G	0.236098	-0.014001	0.002388	1.5E-09
MYL7 *	7	rs62460070	44,134,541	T	C	0.236447	-0.014312	0.002384	5.9E-10
MYL7 *	7	rs4397301	44,135,828	G	C	0.237991	-0.014177	0.002376	6.6E-10
MYL7 *	7	rs9791709	44,136,188	T	C	0.238322	-0.014476	0.002374	2.6E-10
MYL7 *	7	rs17136076	44,137,592	G	A	0.240101	-0.014509	0.002369	2.5E-10
MYL7 *	7	rs17769733	44,137,813	T	C	0.239837	-0.014586	0.002370	2.1E-10
MYL7 *	7	rs882021	44,138,273	C	T	0.242142	-0.014278	0.002364	4.3E-10
MYL7	7	rs1008384	44,139,027	G	A	0.257063	-0.013340	0.002343	3.3E-09
MYL7	7	rs741033	44,140,166	G	C	0.254830	-0.014795	0.002375	1.5E-10
GCK	7	rs2070971	44,157,984	T	G	0.256031	0.014952	0.002362	3.7E-10
GCK	7	rs1799831	44,159,543	T	C	0.256496	0.014705	0.002358	6.6E-10
GCK	7	rs79079664	44,161,116	TTAATTA	C	0.262558	0.014346	0.002334	1.3E-09
GCK	7	rs62460075	44,161,550	T	C	0.211907	-0.018048	0.002526	2.2E-13
GCK	7	rs12540369	44,165,915	T	A	0.233610	-0.018507	0.002387	1.1E-15
GCK	7	rs12535229	44,166,006	A	G	0.233614	-0.018499	0.002387	1.2E-15
GCK	7	rs2971672	44,166,307	C	A	0.458761	0.014597	0.002025	6.3E-13
GCK	7	rs77851840	44,166,756	G	GAT	0.233621	-0.018491	0.002387	1.2E-15
GCK	7	rs62460076	44,166,795	A	T	0.233496	-0.018402	0.002389	1.6E-15
GCK	7	rs62460077	44,167,083	T	C	0.233621	-0.018491	0.002387	1.2E-15
GCK	7	rs73112269	44,168,408	A	G	0.233789	-0.018480	0.002386	1.2E-15
GCK	7	rs16881016	44,171,808	C	T	0.235174	-0.018444	0.002380	1.5E-15
GCK	7	rs112745774	44,172,019	T	C	0.234796	-0.018418	0.002382	1.8E-15
GCK	7	rs60275913	44,172,686	T	G	0.234998	-0.018329	0.002381	2.4E-15
GCK	7	rs59419319	44,174,275	T	C	0.235942	-0.018834	0.002378	4.8E-16
GCK	7	rs3779606	44,175,415	C	T	0.236071	-0.018868	0.002377	4.1E-16
GCK	7	rs62460080	44,176,272	A	G	0.236077	-0.018876	0.002377	3.9E-16
GCK	7	rs17172566	44,176,513	A	G	0.236078	-0.018875	0.002377	3.9E-16
GCK	7	rs2908290	44,176,538	A	G	0.458149	0.015161	0.002024	6.9E-14
GCK	7	rs62459064	44,176,698	T	C	0.236066	-0.018902	0.002377	3.6E-16
GCK	7	rs2284777	44,176,999	C	T	0.235786	-0.018767	0.002379	5.4E-16
GCK	7	rs2284775	44,177,762	G	A	0.236200	-0.018887	0.002377	4.0E-16
GCK	7	rs2284774	44,178,742	A	G	0.236171	-0.018843	0.002377	4.7E-16
GCK	7	rs2300587	44,179,195	C	T	0.236176	-0.018836	0.002377	4.8E-16
GCK	7	rs12534104	44,180,143	A	C	0.226616	-0.019493	0.002448	2.5E-16
GCK	7	rs1990458	44,183,203	T	C	0.320284	-0.013247	0.002201	2.5E-09
GCK	7	rs34380942	44,183,693	TA	T	0.094168	-0.023160	0.003456	3.3E-11
GCK	7	rs34780996	44,183,696	A	G	0.094142	-0.023126	0.003456	3.5E-11
GCK	7	rs59727929	44,183,959	T	C	0.094067	-0.023359	0.003458	2.2E-11
GCK	7	rs730497	44,184,122	A	G	0.196928	0.021810	0.002538	1.2E-17
GCK	7	rs2908289	44,184,343	A	G	0.196908	0.021777	0.002539	1.4E-17
GCK	7	rs67253402	44,184,933	G	GAT	0.089880	-0.022197	0.003545	7.2E-10
GCK	7	rs201139382	44,185,031	C	CAG	0.088748	-0.022052	0.003567	5.0E-10
GCK	7	rs3808319	44,185,252	A	G	0.358800	-0.013749	0.002108	4.0E-11
GCK	7	rs34859037	44,185,887	C	G	0.094206	-0.023375	0.003456	2.3E-11
GCK	7	rs34807880	44,186,230	G	A	0.094209	-0.023375	0.003456	2.3E-11
GCK	7	rs2268570	44,186,491	G	C	0.370187	-0.013555	0.002093	5.1E-11
GCK	7	rs2971670	44,186,502	T	C	0.194510	0.021891	0.002557	1.7E-17
GCK	7	rs13239289	44,187,089	G	C	0.094208	-0.023351	0.003456	2.4E-11
GCK	7	rs41314139	44,187,345	A	G	0.094208	-0.023351	0.003456	2.4E-11
GCK	7	rs35276355	44,187,357	G	T	0.094208	-0.023351	0.003456	2.4E-11
GCK	7	rs34976798	44,187,686	C	A	0.094146	-0.023363	0.003457	2.2E-11
GCK	7	rs35079658	44,188,298	T	C	0.094208	-0.023372	0.003456	2.3E-11
GCK	7	rs34672149	44,188,548	G	GC	0.094208	-0.023372	0.003456	2.3E-11
GCK	7	rs13306391	44,189,037	C	G	0.094242	-0.023304	0.003455	2.5E-11
GCK *	7	rs1799884	44,189,469	T	C	0.194943	0.021869	0.002550	1.3E-17
GCK *	7	rs12702070	44,189,633	C	T	0.094237	-0.023317	0.003455	2.4E-11
GCK *	7	rs35670475	44,189,721	A	G	0.094237	-0.023317	0.003455	2.4E-11
GCK *	7	rs3757840	44,191,617	G	T	0.465437	-0.020591	0.002024	1.2E-24
GCK *	7	rs3757839	44,191,638	G	T	0.093257	-0.023378	0.003471	2.8E-11
GCK *	7	rs3757838	44,191,711	T	A	0.093266	-0.023355	0.003470	2.9E-11
GCK *	7	rs62459076	44,191,993	G	T	0.093400	-0.023403	0.003468	2.5E-11
GCK *	7	rs2971669	44,192,179	T	C	0.353985	0.019203	0.002109	2.0E-19
GCK *	7	rs6975024	44,192,287	C	T	0.204780	0.020442	0.002501	6.0E-16
GCK *	7	rs34443021	44,192,533	T	C	0.092892	-0.023312	0.003479	2.8E-11
GCK *	7	rs62459077	44,192,990	T	C	0.093477	-0.023206	0.003466	3.4E-11
GCK *	7	rs7789273	44,193,006	T	C	0.370625	-0.013515	0.002093	4.4E-11
GCK *	7	rs58053084	44,193,014	G	T	0.093513	-0.023144	0.003465	3.8E-11
GCK *	7	rs741037	44,193,234	A	G	0.198166	0.021923	0.002538	1.1E-17
GCK *	7	rs62459079	44,193,279	T	C	0.093477	-0.023206	0.003466	3.4E-11
GCK *	7	rs62459080	44,193,319	A	G	0.093477	-0.023206	0.003466	3.4E-11
GCK *	7	rs735670	44,193,746	T	A	0.093477	-0.023206	0.003466	3.4E-11
GCK *	7	rs35902302	44,194,829	A	C	0.093363	-0.023106	0.003468	3.9E-11
GCK *	7	rs741036	44,195,114	A	G	0.093360	-0.023092	0.003469	4.0E-11
GCK *	7	rs2908286	44,195,138	T	C	0.197834	0.021881	0.002537	1.0E-17
YKT6 *	7	rs741034	44,195,261	C	T	0.093360	-0.023092	0.003469	4.0E-11
YKT6 *	7	rs71533226	44,195,594	T	A	0.092416	-0.023333	0.003487	2.8E-11
YKT6 *	7	rs4607517	44,196,069	A	G	0.197949	0.021786	0.002533	1.1E-17
YKT6 *	7	rs55794846	44,196,764	G	C	0.093345	-0.023078	0.003469	4.1E-11
YKT6 *	7	rs150486663	44,200,116	A	G	0.093329	-0.023142	0.003470	3.8E-11
YKT6 *	7	rs71563938	44,200,289	T	TTC	0.093329	-0.023142	0.003470	3.8E-11
YKT6 *	7	rs1985469	44,200,725	T	A	0.191710	0.021294	0.002589	2.3E-16
YKT6 *	7	rs1004558	44,200,808	T	C	0.197721	0.021729	0.002538	1.6E-17
YKT6 *	7	rs35832856	44,200,964	T	C	0.093172	-0.023038	0.003472	4.8E-11
YKT6	7	rs11540050	44,201,065	T	G	0.092432	-0.022761	0.003488	8.0E-11
YKT6	7	rs61324019	44,201,373	A	G	0.093331	-0.023144	0.003470	3.8E-11
YKT6	7	rs34110131	44,202,297	C	T	0.093341	-0.023087	0.003470	4.2E-11
YKT6	7	rs2971668	44,203,839	C	G	0.206760	0.020951	0.002495	9.3E-17
YKT6	7	rs2072440	44,204,895	C	G	0.093319	-0.023128	0.003470	3.8E-11
YKT6	7	rs2971667	44,205,461	C	T	0.198013	0.021737	0.002535	1.5E-17
YKT6	7	rs10278336	44,205,764	G	A	0.368917	-0.013458	0.002093	6.3E-11

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
YKT6	7	rs917793	44,206,254	T	A	0.198039	0.021751	0.002534	1.5E-17
YKT6	7	rs2075068	44,206,935	G	A	0.093414	-0.022906	0.003468	5.9E-11
YKT6	7	rs41279621	44,207,134	C	A	0.093414	-0.022906	0.003468	5.9E-11
YKT6	7	rs3824065	44,207,659	T	C	0.369402	-0.013614	0.002088	3.3E-11
YKT6	7	rs34256495	44,209,029	T	C	0.093393	-0.022929	0.003468	5.5E-11
YKT6	7	rs57597270	44,209,121	C	T	0.093394	-0.022929	0.003468	5.5E-11
YKT6	7	rs2908282	44,209,229	A	G	0.197895	0.021733	0.002536	1.6E-17
YKT6	7	chr7:44210714_A_ATG	44,210,714	ATG	A	0.076984	-0.021643	0.003833	1.5E-08
YKT6	7	chr7:44210722_G_GTA	44,210,722	GTA	G	0.093047	-0.022732	0.003477	1.0E-10
YKT6	7	rs12670584	44,212,419	G	C	0.093296	-0.022723	0.003472	8.2E-11
YKT6	7	rs3840674	44,212,591	C	CTG	0.198538	0.021684	0.002543	1.9E-17
YKT6	7	rs3840673	44,212,709	T	TG	0.093293	-0.022689	0.003472	8.9E-11
YKT6	7	rs11540051	44,213,422	T	G	0.093260	-0.022747	0.003472	7.8E-11
YKT6	7	rs1045776	44,213,786	C	T	0.093257	-0.022780	0.003472	7.4E-11
YKT6 *	7	rs62459085	44,215,304	G	C	0.093339	-0.022801	0.003471	7.0E-11
YKT6 *	7	rs62459086	44,215,515	C	T	0.093336	-0.022828	0.003472	6.6E-11
YKT6 *	7	rs62459087	44,215,516	T	G	0.093336	-0.022828	0.003472	6.6E-11
CAMK2B *	7	rs35197372	44,215,937	G	A	0.093303	-0.022895	0.003473	5.6E-11
CAMK2B *	7	rs878521	44,216,044	A	G	0.354908	0.019189	0.002107	2.2E-19
CAMK2B	7	rs78359497	44,217,896	A	G	0.172006	0.020722	0.002709	1.7E-14
CAMK2B	7	rs758982	44,218,344	T	C	0.173119	0.020217	0.002704	5.0E-14
CAMK2B	7	rs35148004	44,219,975	T	C	0.092920	-0.022901	0.003483	6.2E-11
CAMK2B	7	rs1065359	44,220,107	A	G	0.355896	-0.013791	0.002115	2.3E-11
CAMK2B	7	rs1127065	44,220,272	T	C	0.370488	-0.013611	0.002094	3.7E-11
CAMK2B	7	rs34775092	44,221,182	A	G	0.097772	-0.021856	0.003406	2.3E-10
CAMK2B	7	rs58958064	44,221,545	GCAGCA	A	0.096548	-0.021200	0.003427	9.6E-10
CAMK2B	7	rs59877240	44,221,670	A	G	0.098037	-0.021554	0.003403	3.6E-10
CAMK2B	7	rs56958012	44,221,683	T	C	0.097665	-0.021768	0.003408	2.8E-10
CAMK2B	7	rs57522294	44,221,720	GC	G	0.097658	-0.021713	0.003408	3.1E-10
CAMK2B	7	rs62459090	44,222,066	A	G	0.097678	-0.021890	0.003410	2.2E-10
CAMK2B	7	rs62459091	44,222,249	A	G	0.097591	-0.021832	0.003410	2.4E-10
CAMK2B	7	rs732360	44,222,379	A	G	0.197583	0.020320	0.002568	3.9E-15
CAMK2B	7	rs2003563	44,222,454	G	T	0.095715	-0.021615	0.003446	5.2E-10
CAMK2B	7	rs75929284	44,222,646	G	A	0.097124	-0.022035	0.003421	1.9E-10
CAMK2B	7	rs62459093	44,224,074	A	G	0.094683	-0.022287	0.003479	2.3E-10
CAMK2B	7	rs149144486	44,224,253	A	GCTCAA	0.093982	-0.022516	0.003493	1.7E-10
CAMK2B	7	rs2877285	44,226,036	A	G	0.094853	-0.022254	0.003492	3.9E-10
CAMK2B	7	rs917792	44,226,380	T	C	0.096655	-0.021374	0.003470	1.4E-09
CAMK2B	7	rs117998298	44,229,771	T	C	0.082031	-0.021147	0.003739	1.9E-08
CAMK2B	7	rs79282401	44,231,427	T	C	0.088522	-0.020606	0.003597	1.5E-08
CAMK2B	7	rs2075075	44,235,097	T	C	0.080902	-0.021064	0.003741	3.5E-08
CAMK2B	7	rs79495881	44,235,964	T	C	0.088118	-0.020356	0.003582	3.0E-08
CAMK2B	7	rs78185111	44,236,885	T	C	0.088222	-0.020302	0.003580	3.2E-08
CAMK2B	7	rs75831906	44,237,177	G	T	0.088218	-0.020336	0.003580	3.0E-08
CAMK2B	7	rs76624683	44,237,572	G	C	0.088211	-0.020302	0.003579	3.1E-08
CAMK2B	7	rs79349916	44,237,881	A	G	0.088232	-0.020390	0.003579	2.7E-08
CAMK2B	7	rs75079129	44,239,085	A	G	0.087922	-0.021122	0.003586	9.6E-09
CAMK2B	7	rs76144629	44,240,596	T	G	0.084159	-0.021028	0.003654	1.9E-08
CAMK2B	7	rs116841749	44,241,434	A	G	0.084063	-0.021264	0.003658	1.4E-08
CAMK2B	7	rs74790674	44,243,161	T	C	0.083593	-0.021251	0.003670	1.7E-08
CAMK2B	7	rs17172630	44,243,329	A	G	0.084147	-0.021363	0.003660	1.3E-08
CAMK2B	7	rs141234985	44,247,783	A	T	0.083022	-0.021545	0.003683	1.4E-08
CAMK2B	7	rs10441113	44,249,066	A	G	0.113088	-0.017468	0.003225	4.1E-08
CAMK2B	7	rs77715675	44,249,899	C	G	0.084073	-0.020756	0.003661	2.9E-08
AUTS2	7	rs66936223	70,283,639	G	A	0.250060	0.012350	0.002330	2.6E-08
POM121	7	rs117135057	72,938,316	T	G	0.012017	-0.047979	0.009324	1.8E-08
NSUN5	7	rs3750074	73,308,628	T	C	0.016005	-0.064540	0.008075	1.1E-17
FKBP6 *	7	rs200456061	73,371,588	T	C	0.015965	-0.064047	0.008084	1.6E-17
FKBP6 *	7	rs186391487	73,384,030	A	G	0.015912	-0.064820	0.008101	9.2E-18
FZD9 *	7	rs42123	73,425,622	G	T	0.109503	-0.050235	0.003273	7.0E-58
FZD9 *	7	rs42122	73,427,493	A	G	0.092473	-0.058285	0.003497	8.1E-67
FZD9 *	7	chr7:73428127_GAC_G	73,428,127	G	GAC	0.086721	-0.056859	0.003615	3.8E-60
FZD9 *	7	rs140439318	73,428,135	C	CAT	0.087353	-0.059782	0.003606	2.9E-66
FZD9 *	7	chr7:73428147_GAC_G	73,428,147	G	GAC	0.089915	-0.059051	0.003560	3.0E-66
FZD9 *	7	chr7:73428394_GAC_G	73,428,394	G	GAC	0.092725	-0.054727	0.003559	1.3E-57
FZD9 *	7	rs200948285	73,429,969	AC	A	0.011905	-0.080803	0.009318	6.9E-20
FZD9 *	7	rs200392099	73,432,411	CTTT	C	0.086663	-0.058795	0.003597	1.1E-64
FZD9 *	7	rs868953856	73,432,413	T	A	0.074758	-0.061720	0.003886	4.7E-60
FZD9 *	7	rs782289776	73,432,414	T	C	0.074758	-0.061720	0.003886	4.7E-60
FZD9	7	rs138414411	73,434,563	T	C	0.020952	-0.055613	0.007068	1.7E-15
FZD9	7	rs1178947	73,435,848	C	T	0.090607	-0.059405	0.003520	5.8E-69
BAZ1B	7	rs2240466	73,441,939	A	G	0.091864	-0.059653	0.003492	1.7E-70
BAZ1B	7	rs1178979	73,442,100	C	T	0.091315	-0.059725	0.003502	2.4E-70
BAZ1B	7	rs1178977	73,442,719	G	A	0.091258	-0.059711	0.003503	2.7E-70
BAZ1B	7	rs34604283	73,443,383	C	CA	0.091260	-0.059868	0.003503	1.3E-70
BAZ1B	7	rs113452856	73,444,805	A	G	0.021269	-0.053147	0.007018	1.8E-14
BAZ1B	7	rs146626977	73,448,166	C	T	0.011930	-0.080484	0.009309	7.3E-20
BAZ1B	7	rs13231516	73,448,919	G	T	0.096065	-0.057974	0.003422	1.3E-69
BAZ1B	7	rs2074756	73,449,425	C	T	0.011937	-0.080118	0.009306	9.5E-20
BAZ1B	7	rs714052	73,450,539	G	A	0.096449	-0.057571	0.003418	5.8E-69
BAZ1B	7	rs34763247	73,452,286	T	A	0.095995	-0.058097	0.003424	8.2E-70
BAZ1B	7	rs1306476	73,454,192	G	A	0.095997	-0.058050	0.003424	1.1E-69
BAZ1B	7	rs71071936	73,455,536	CT	C	0.091968	-0.059388	0.003494	8.2E-70
BAZ1B	7	rs35330527	73,455,877	G	A	0.097482	-0.056962	0.003406	7.5E-68
BAZ1B	7	rs60982449	73,459,090	G	A	0.090003	-0.060183	0.003528	3.1E-70
BAZ1B	7	rs2074755	73,462,836	C	T	0.095254	-0.058385	0.003436	6.0E-70
BAZ1B	7	rs35797675	73,463,714	G	T	0.097445	-0.057476	0.003406	2.9E-69
BAZ1B	7	rs12056034	73,464,315	G	A	0.096607	-0.057463	0.003416	1.3E-68
BAZ1B	7	rs71556715	73,467,477	T	C	0.095238	-0.058516	0.003436	3.0E-70
BAZ1B	7	rs62465144	73,468,776	C	T	0.095893	-0.058168	0.003426	7.2E-70
BAZ1B	7	rs6976930	73,471,480	A	G	0.090629	-0.060326	0.003515	3.8E-71
BAZ1B	7	rs141027825	73,471,893	C	G	0.013927	-0.073732	0.008662	3.5E-19
BAZ1B	7	rs139267697	73,475,356	A	G	0.011941	-0.080174	0.009305	9.1E-20
BAZ1B	7	rs35695283	73,479,073	G	A	0.091146	-0.059969	0.003505	9.5E-71
BAZ1B	7	rs75229905	73,481,616	C	T	0.095889	-0.058078	0.003426	1.1E-69
BAZ1B	7	rs7797566	73,482,065	C	A	0.095889	-0.058078	0.003426	1.1E-69
BAZ1B	7	rs17145713	73,490,480	T	C	0.095283	-0.058410	0.003436	4.9E-70

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BAZ1B	7	rs111837003	73,493,129	T	C	0.090481	-0.060610	0.003518	1.2E-71
BAZ1B	7	rs118023175	73,494,447	G	C	0.011974	-0.079982	0.009292	9.4E-20
BAZ1B	7	rs117830225	73,494,457	C	G	0.011941	-0.080177	0.009305	9.1E-20
BAZ1B	7	rs13244268	73,497,513	C	T	0.095925	-0.058887	0.003433	4.0E-71
BAZ1B	7	rs67243124	73,497,702	A	AAAAAAC	0.094930	-0.058626	0.003442	2.5E-70
BAZ1B	7	rs201533187	73,497,710	A	AAAAAG	0.086585	-0.055160	0.003611	1.3E-56
BAZ1B	7	rs34482346	73,501,191	C	G	0.095232	-0.058609	0.003436	1.9E-70
BAZ1B	7	chr7:73505631_GA_G	73,505,631	G	GA	0.089726	-0.058625	0.003563	8.6E-66
BAZ1B	7	rs79862839	73,507,279	C	T	0.095235	-0.058621	0.003436	1.8E-70
BAZ1B	7	rs13221253	73,507,903	G	A	0.095124	-0.058524	0.003439	2.9E-70
BAZ1B	7	rs34437827	73,509,008	G	A	0.095225	-0.058608	0.003437	1.9E-70
BAZ1B	7	rs7811265	73,520,180	G	A	0.086719	-0.059516	0.003599	3.9E-66
BAZ1B *	7	rs62466264	73,524,388	C	T	0.095469	-0.058627	0.003434	1.6E-70
BAZ1B *	7	rs11983997	73,524,914	C	G	0.095120	-0.058485	0.003439	4.3E-70
BAZ1B *	7	rs80189144	73,525,609	C	T	0.095120	-0.058485	0.003439	4.3E-70
BCL7B *	7	rs66579735	73,530,040	T	C	0.382466	0.010730	0.002103	4.2E-08
BCL7B *	7	rs143934761	73,533,607	G	A	0.020926	-0.054445	0.007066	3.9E-15
BCL7B *	7	rs4717094	73,535,752	T	C	0.436521	0.011307	0.002047	3.9E-08
BCL7B	7	rs142030730	73,542,085	T	C	0.012995	-0.054383	0.008921	2.7E-11
BCL7B	7	rs17145732	73,555,938	G	T	0.099289	-0.061430	0.003376	2.9E-79
BCL7B	7	rs13233571	73,556,901	T	C	0.095250	-0.064374	0.003435	1.2E-83
BCL7B	7	rs7793710	73,557,201	G	C	0.095197	-0.064425	0.003437	1.1E-83
BCL7B	7	rs13234157	73,557,398	A	C	0.094234	-0.063773	0.003463	4.7E-81
BCL7B *	7	rs13244614	73,559,524	A	C	0.095179	-0.064458	0.003437	9.0E-84
BCL7B *	7	rs140173690	73,560,328	A	C	0.017140	-0.062896	0.007777	7.7E-18
BCL7B *	7	rs111269058	73,561,372	T	C	0.095187	-0.064471	0.003437	8.6E-84
BCL7B *	7	rs13225333	73,561,688	T	C	0.095160	-0.064491	0.003438	8.1E-84
BCL7B *	7	rs13225347	73,561,718	T	C	0.095185	-0.064496	0.003437	7.4E-84
BCL7B *	7	rs13225450	73,561,793	T	C	0.095060	-0.064364	0.003440	1.6E-83
BCL7B *	7	rs34594435	73,562,919	T	C	0.095188	-0.064491	0.003437	7.6E-84
BCL7B *	7	rs6946689	73,563,307	A	T	0.095256	-0.064441	0.003437	1.1E-83
TBL2 *	7	rs12539316	73,563,568	G	A	0.096271	-0.063545	0.003425	1.6E-81
TBL2 *	7	rs12539351	73,563,782	G	A	0.090413	-0.066834	0.003519	1.4E-85
TBL2 *	7	rs147472118	73,563,984	T	C	0.019156	-0.069670	0.007348	2.7E-21
TBL2 *	7	rs12531884	73,567,553	C	A	0.384784	0.011047	0.002082	2.0E-08
TBL2 *	7	rs17145738	73,568,544	T	C	0.095327	-0.064514	0.003435	5.6E-84
TBL2	7	rs13232120	73,568,980	T	A	0.095337	-0.064506	0.003435	5.7E-84
TBL2	7	rs14415	73,570,450	C	T	0.095337	-0.064506	0.003435	5.7E-84
TBL2	7	rs190174185	73,572,316	C	G	0.011465	-0.074014	0.009475	3.4E-15
TBL2	7	rs2286276	73,573,024	T	C	0.095451	-0.064240	0.003433	2.2E-83
TBL2	7	rs35659126	73,573,739	T	C	0.095074	-0.064619	0.003439	4.4E-84
TBL2	7	chr7:73574811_C_CA	73,574,811	CA	C	0.095837	-0.064135	0.003432	3.4E-83
TBL2	7	rs11974409	73,575,060	G	A	0.095146	-0.064537	0.003439	6.5E-84
TBL2	7	rs12540011	73,577,374	A	G	0.095215	-0.064696	0.003438	3.2E-84
TBL2	7	rs4717779	73,577,795	T	A	0.436099	0.011428	0.002061	3.5E-08
TBL2	7	rs13246490	73,578,020	T	C	0.095198	-0.064739	0.003438	2.6E-84
TBL2 *	7	rs66553475	73,579,219	CTGCTGC	T	0.094559	-0.064874	0.003450	3.6E-84
TBL2 *	7	chr7:73581580_C_CA	73,581,580	CA	C	0.083416	-0.062573	0.003700	1.5E-69
TBL2 *	7	rs66506038	73,581,613	C	T	0.095229	-0.064672	0.003437	3.3E-84
TBL2 *	7	rs67644909	73,581,624	T	C	0.093823	-0.064400	0.003465	2.5E-82
TBL2 *	7	rs9638180	73,584,622	G	A	0.095265	-0.064719	0.003438	2.8E-84
TBL2 *	7	rs9638181	73,584,713	G	A	0.095265	-0.064719	0.003438	2.8E-84
TBL2 *	7	rs9638182	73,584,775	G	T	0.095265	-0.064719	0.003438	2.8E-84
MLXIPL *	7	rs35173225	73,586,691	T	C	0.095301	-0.064709	0.003438	3.4E-84
MLXIPL *	7	rs187404224	73,588,697	G	A	0.095201	-0.064733	0.003438	2.7E-84
MLXIPL *	7	rs185081604	73,588,973	C	A	0.095201	-0.064733	0.003438	2.7E-84
MLXIPL *	7	rs145099458	73,589,985	T	C	0.090722	-0.063483	0.003529	4.1E-77
MLXIPL *	7	rs35866503	73,591,446	T	C	0.095200	-0.064736	0.003438	2.7E-84
MLXIPL *	7	rs13225660	73,592,058	T	C	0.095200	-0.064736	0.003438	2.7E-84
MLXIPL *	7	chr7:73592757_C_CA	73,592,757	CA	C	0.088332	-0.064597	0.003584	6.7E-78
MLXIPL	7	rs1051921	73,593,613	A	G	0.095200	-0.064732	0.003438	2.7E-84
MLXIPL	7	rs13247874	73,596,112	T	C	0.097106	-0.066142	0.003410	7.7E-89
MLXIPL	7	rs35332062	73,597,712	A	G	0.097901	-0.066035	0.003395	2.3E-89
MLXIPL	7	rs79624003	73,598,455	G	A	0.097818	-0.066411	0.003398	3.3E-90
MLXIPL	7	rs35732917	73,598,939	C	T	0.097717	-0.066648	0.003400	1.1E-90
MLXIPL	7	rs13235543	73,599,571	T	C	0.097652	-0.066735	0.003401	7.9E-91
MLXIPL	7	rs13240065	73,601,039	A	G	0.096609	-0.066667	0.003423	1.7E-89
MLXIPL	7	rs34346326	73,601,851	C	T	0.097470	-0.066570	0.003405	2.9E-90
MLXIPL	7	rs879969597	73,602,094	G	GCCTT	0.010612	-0.066994	0.010035	9.8E-12
MLXIPL	7	rs13240994	73,602,532	C	T	0.088210	-0.071826	0.003577	3.5E-95
MLXIPL	7	rs13226650	73,602,675	G	A	0.097600	-0.066567	0.003405	2.8E-90
MLXIPL	7	rs35368205	73,603,327	T	C	0.088513	-0.071256	0.003553	5.6E-95
MLXIPL	7	rs34166762	73,604,194	C	T	0.088981	-0.074196	0.003552	2.3E-102
MLXIPL	7	rs61010704	73,605,645	G	A	0.086336	-0.075735	0.003591	2.8E-104
MLXIPL	7	rs3812316	73,606,007	G	C	0.086346	-0.075923	0.003591	8.5E-105
MLXIPL	7	rs6968170	73,606,346	A	G	0.086384	-0.075757	0.003590	2.1E-104
MLXIPL	7	rs77048596	73,607,881	A	G	0.086376	-0.075780	0.003590	2.0E-104
MLXIPL	7	rs13246993	73,608,416	A	G	0.086377	-0.075773	0.003590	2.1E-104
MLXIPL	7	rs141854486	73,608,603	A	AAG	0.078138	-0.074549	0.003783	9.2E-93
MLXIPL	7	rs12531645	73,609,551	A	G	0.086298	-0.075734	0.003592	3.2E-104
MLXIPL	7	rs35512732	73,610,432	T	TC	0.086377	-0.075770	0.003590	2.2E-104
MLXIPL	7	rs13234131	73,611,645	G	A	0.099476	-0.069383	0.003363	1.6E-98
MLXIPL	7	rs13234378	73,611,821	T	A	0.099940	-0.069188	0.003360	2.4E-98
MLXIPL	7	rs17145750	73,612,048	T	C	0.099850	-0.069474	0.003358	4.2E-99
MLXIPL	7	rs7808877	73,613,120	G	C	0.099680	-0.069216	0.003361	3.3E-98
MLXIPL	7	rs139002804	73,613,553	A	G	0.011682	-0.083105	0.009420	1.0E-20
MLXIPL	7	rs33951980	73,615,107	T	C	0.099681	-0.069213	0.003361	3.3E-98
MLXIPL	7	rs2074768	73,615,773	C	A	0.099674	-0.069149	0.003361	4.4E-98
MLXIPL	7	rs13229619	73,615,845	A	G	0.099674	-0.069149	0.003361	4.4E-98
MLXIPL	7	rs7798357	73,617,935	C	G	0.099620	-0.069041	0.003363	1.0E-97
MLXIPL	7	rs7785479	73,618,505	C	T	0.099619	-0.069057	0.003363	9.3E-98
MLXIPL	7	rs34062580	73,619,229	A	G	0.099619	-0.069050	0.003363	9.6E-98
MLXIPL	7	rs6975495	73,619,700	G	A	0.099619	-0.069107	0.003363	6.9E-98
MLXIPL	7	rs71556736	73,620,599	T	C	0.099688	-0.069059	0.003362	9.2E-98
MLXIPL	7	rs7800944	73,621,527	C	T	0.100045	-0.068135	0.003358	2.2E-95
MLXIPL	7	rs1207541622	73,621,799	C	T	0.012049	-0.090142	0.009363	3.6E-23
MLXIPL	7	rs2736909	73,621,803	G	C	0.012049	-0.090142	0.009363	3.6E-23

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
MLXIPL	7	rs55747707	73,623,036	A	G	0.099585	-0.069141	0.003365	5.8E-98
MLXIPL	7	rs34060476	73,623,626	G	A	0.099558	-0.069122	0.003365	6.0E-98
MLXIPL *	7	rs35493868	73,625,076	G	C	0.099564	-0.069173	0.003365	4.1E-98
MLXIPL *	7	rs34121855	73,626,484	G	T	0.097506	-0.069290	0.003403	1.1E-96
MLXIPL *	7	rs62466318	73,627,755	T	C	0.107917	-0.063248	0.003248	2.7E-88
MLXIPL *	7	chr7:73627972_GCTTT_G	73,627,972	G	GCTTT	0.108203	-0.062734	0.003246	5.9E-87
MLXIPL *	7	rs117739002	73,628,073	T	C	0.017739	-0.066662	0.007642	4.7E-18
MLXIPL *	7	rs6460047	73,628,113	C	T	0.109403	-0.062212	0.003232	5.0E-86
MLXIPL *	7	rs7805504	73,628,255	C	T	0.109294	-0.062331	0.003233	2.9E-86
MLXIPL *	7	rs7786376	73,628,284	G	A	0.110626	-0.061877	0.003218	8.0E-86
MLXIPL *	7	rs35340690	73,628,738	C	G	0.152235	-0.042298	0.002836	3.2E-53
MLXIPL *	7	rs34958196	73,628,771	A	G	0.139737	-0.049131	0.002931	2.3E-66
MLXIPL *	7	rs34430945	73,629,335	C	T	0.139253	-0.048829	0.002934	1.9E-65
MLXIPL *	7	rs34321592	73,630,874	A	G	0.167343	-0.042378	0.002724	1.7E-57
MLXIPL *	7	rs7784668	73,631,153	C	T	0.138753	-0.048953	0.002941	1.9E-65
MLXIPL *	7	rs78815801	73,631,608	C	T	0.129390	-0.050584	0.003061	1.4E-64
MLXIPL *	7	rs1412452301	73,631,935	TTTCCTT	C	0.165871	-0.042427	0.002742	8.4E-57
MLXIPL *	7	rs17145813	73,632,428	A	C	0.165548	-0.042183	0.002747	6.3E-56
MLXIPL *	7	rs17145817	73,632,449	G	A	0.165550	-0.042191	0.002747	6.1E-56
MLXIPL *	7	rs36091304	73,633,181	C	T	0.163817	-0.042631	0.002765	3.3E-56
MLXIPL *	7	rs34899589	73,633,190	C	T	0.162355	-0.042217	0.002781	1.0E-54
MLXIPL *	7	rs35855035	73,633,221	T	C	0.162200	-0.041785	0.002781	1.9E-53
MLXIPL *	7	rs35703204	73,633,518	T	C	0.165284	-0.042238	0.002753	8.4E-56
MLXIPL *	7	rs13230514	73,633,765	G	A	0.165079	-0.042216	0.002753	8.8E-56
MLXIPL *	7	rs62466323	73,634,348	A	G	0.165052	-0.041908	0.002754	4.8E-55
MLXIPL *	7	rs13234805	73,634,852	A	G	0.134928	-0.048968	0.002997	3.7E-63
MLXIPL *	7	rs13222090	73,635,057	C	T	0.165253	-0.041633	0.002753	1.5E-54
VPS37D *	7	rs371515311	73,660,465	A	G	0.017282	-0.058604	0.007751	6.1E-16
DNAJC30	7	rs3828973	73,682,169	A	G	0.027147	-0.034389	0.006235	1.3E-09
ABHD11 *	7	rs10226706	73,751,424	A	C	0.476279	0.010737	0.002042	3.6E-08
CLDN3 *	7	rs11764572	73,764,105	G	A	0.474886	0.010693	0.002025	2.9E-08
CLDN3 *	7	rs11979807	73,768,611	G	T	0.475437	0.010681	0.002026	2.9E-08
CLDN3	7	rs7084	73,770,105	G	C	0.475846	0.010632	0.002027	3.2E-08
CLDN3	7	rs6460054	73,770,204	T	C	0.475026	0.010679	0.002026	3.0E-08
CLDN3 *	7	rs28408072	73,771,842	G	A	0.475441	0.010687	0.002026	2.8E-08
CLDN3 *	7	rs10558095	73,772,006	CTT	C	0.475369	0.010726	0.002026	2.5E-08
CLDN3 *	7	rs4484568	73,773,321	A	G	0.475345	0.010711	0.002025	2.6E-08
CLDN3 *	7	rs4131376	73,773,988	T	C	0.474784	0.010729	0.002025	2.6E-08
WBSCR28 *	7	rs1435702538	73,892,484	T	CTTTCTT	0.012187	-0.051698	0.009224	6.8E-10
WBSCR28 *	7	rs6964590	73,894,020	A	G	0.031951	-0.032865	0.005765	9.9E-10
WBSCR28 *	7	rs13241670	73,903,956	C	T	0.032313	-0.031934	0.005731	2.4E-09
WBSCR28 *	7	rs73144858	73,922,565	G	C	0.019937	-0.049304	0.007247	2.7E-13
ELN *	7	rs188072556	73,999,294	T	C	0.016791	-0.058560	0.007864	1.3E-15
ELN *	7	rs576957617	74,071,436	T	TAA	0.012272	-0.050016	0.009198	1.4E-09
RFC2	7	rs148741166	74,252,973	A	C	0.012912	-0.051692	0.008983	1.2E-10
CLIP2	7	rs151126504	74,392,493	T	C	0.020739	-0.049500	0.007133	1.0E-13
GTF2IRD1 *	7	rs145049525	74,440,602	G	C	0.015991	-0.042391	0.008123	9.0E-09
GNAT3 *	7	rs142895840	80,521,969	T	C	0.020002	-0.042658	0.007229	7.9E-10
GNAT3 *	7	rs145638771	80,550,968	G	A	0.020689	-0.043460	0.007097	2.4E-10
CD36 *	7	rs182480663	80,567,623	G	A	0.020685	-0.043413	0.007098	2.5E-10
CD36 *	7	rs531971155	80,601,582	T	G	0.020132	-0.045429	0.007194	9.7E-11
CD36	7	rs577611417	80,651,863	A	C	0.019981	-0.044908	0.007226	1.1E-10
CD36	7	rs572295823	80,661,109	A	AAC	0.019906	-0.045219	0.007240	8.8E-11
SEMA3C *	7	rs186972232	80,740,942	G	C	0.034220	-0.031444	0.005615	1.4E-08
CDK6	7	rs2282987	92,683,489	C	G	0.353802	0.011710	0.002122	4.7E-08
KLF14 *	7	rs6973807	130,739,211	G	A	0.308867	-0.015572	0.002223	2.1E-12
KLF14 *	7	rs6974400	130,739,314	A	G	0.308854	-0.015558	0.002222	2.1E-12
KLF14 *	7	rs6974288	130,739,451	G	A	0.308986	-0.015572	0.002221	1.8E-12
KLF14 *	7	rs11762784	130,739,885	A	G	0.309065	-0.015415	0.002218	3.0E-12
KLF14 *	7	rs39963350	130,742,296	C	G	0.310062	-0.015738	0.002204	8.4E-13
KLF14 *	7	rs13234269	130,744,427	A	T	0.311045	-0.016054	0.002194	2.0E-13
KLF14 *	7	rs4731701	130,746,171	T	C	0.309862	-0.015570	0.002203	1.4E-12
KLF14 *	7	rs10260148	130,746,210	T	C	0.399232	0.014631	0.002096	1.6E-12
KLF14 *	7	rs34072724	130,747,710	A	G	0.311787	-0.015820	0.002182	3.4E-13
KLF14 *	7	rs6971365	130,747,722	C	T	0.401573	0.014493	0.002088	2.9E-12
KLF14 *	7	rs13241165	130,747,779	T	A	0.311839	-0.015806	0.002182	3.5E-13
KLF14 *	7	rs4731702	130,748,625	T	C	0.311632	-0.015959	0.002180	2.1E-13
KLF14 *	7	rs11976955	130,748,835	G	C	0.403049	0.013946	0.002089	1.7E-11
KLF14 *	7	rs6961342	130,749,185	A	C	0.403034	0.013998	0.002088	1.5E-11
KLF14 *	7	rs35722851	130,749,741	C	T	0.310709	-0.015981	0.002189	2.4E-13
KLF14 *	7	rs35057928	130,749,767	C	T	0.310329	-0.016055	0.002190	1.9E-13
KLF14 *	7	rs34282904	130,749,770	A	G	0.310576	-0.015982	0.002190	2.4E-13
KLF14 *	7	rs287621	130,750,422	T	C	0.401548	0.014286	0.002087	6.2E-12
KLF14 *	7	chr7:130751316_A_AAT	130,751,316	AAT	A	0.311374	-0.016162	0.002186	1.2E-13
KLF14 *	7	rs34084575	130,751,643	TA	T	0.312243	-0.016089	0.002183	1.5E-13
KLF14 *	7	rs11979110	130,751,700	T	C	0.312163	-0.016013	0.002183	1.8E-13
KLF14 *	7	rs13230111	130,752,365	G	A	0.311492	-0.016111	0.002183	1.2E-13
KLF14 *	7	rs7810507	130,752,717	A	G	0.402124	0.014330	0.002085	4.7E-12
KLF14 *	7	rs13233731	130,752,930	A	G	0.311443	-0.016025	0.002183	1.6E-13
KLF14 *	7	rs13234407	130,753,455	A	G	0.311451	-0.016016	0.002183	1.6E-13
KLF14 *	7	rs7783857	130,754,299	G	C	0.421540	0.014942	0.002053	2.2E-13
KLF14 *	7	rs13241538	130,755,103	C	G	0.312222	-0.016225	0.002179	6.9E-14
KLF14 *	7	rs13228906	130,757,125	A	G	0.311881	-0.016045	0.002183	1.3E-13
KLF14 *	7	rs6467314	130,757,382	G	C	0.420416	0.015079	0.002051	1.2E-13
KLF14 *	7	rs17185445	130,757,868	T	C	0.312185	-0.016096	0.002184	1.2E-13
KLF14 *	7	rs3996352	130,760,175	G	A	0.309873	-0.015983	0.002191	1.7E-13
KLF14 *	7	rs13240528	130,760,369	A	C	0.309778	-0.016078	0.002192	1.3E-13
KLF14 *	7	chr7:130760669_C_CT	130,760,669	CT	C	0.302026	-0.015495	0.002229	2.4E-12
KLF14 *	7	rs17789506	130,760,815	A	G	0.310208	-0.015933	0.002192	2.0E-13
KLF14 *	7	rs35712907	130,761,088	T	TA	0.310183	-0.015932	0.002192	2.0E-13
KLF14 *	7	rs11765979	130,761,118	C	A	0.310186	-0.015934	0.002192	2.0E-13
KLF14 *	7	rs1364422	130,761,222	T	C	0.422063	0.014936	0.002043	1.3E-13
KLF14 *	7	rs59326756	130,762,371	G	A	0.423991	0.014553	0.002046	7.5E-13
KLF14 *	7	rs12667251	130,764,699	G	A	0.344348	-0.013236	0.002153	3.7E-10
KLF14 *	7	rs185963	130,765,392	C	T	0.342509	-0.012760	0.002155	1.5E-09
KLF14 *	7	rs288484	130,765,438	A	G	0.342437	-0.012739	0.002155	1.6E-09
KLF14 *	7	rs172306	130,765,628	G	A	0.344364	-0.013121	0.002152	5.3E-10

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
KLF14 *	7	rs577195	130,765,902	C	G	0.342455	-0.012708	0.002155	1.7E-09
KLF14 *	7	rs1665759	130,766,738	T	C	0.342506	-0.012745	0.002154	1.5E-09
KLF14 *	7	rs1646629	130,766,864	C	T	0.342342	-0.012698	0.002155	1.7E-09
KLF14 *	7	rs1646631	130,766,912	G	A	0.342454	-0.012782	0.002154	1.3E-09
KLF14 *	7	rs56258902	130,767,225	C	CTTTA	0.314849	-0.013026	0.002203	2.3E-09
KLF14 *	7	rs10238574	130,767,468	T	C	0.342452	-0.012764	0.002154	1.4E-09
KLF14 *	7	rs1596972	130,768,623	A	G	0.342589	-0.012698	0.002152	1.7E-09
KLF14 *	7	rs1562398	130,773,172	C	G	0.340242	-0.012296	0.002161	6.1E-09
KLF14 *	7	rs34748838	130,774,483	T	C	0.316327	-0.012600	0.002192	5.4E-09
KLF14 *	7	rs6968740	130,775,517	G	T	0.343142	-0.012586	0.002147	2.2E-09
KLF14 *	7	rs6951054	130,775,721	T	G	0.343143	-0.012571	0.002147	2.2E-09
KLF14 *	7	rs35964477	130,777,099	A	AT	0.316608	-0.012620	0.002191	5.3E-09
KLF14 *	7	rs4425698	130,777,483	T	C	0.343193	-0.012590	0.002146	2.1E-09
KLF14 *	7	rs1596973	130,777,524	G	A	0.343198	-0.012541	0.002146	2.4E-09
KLF14 *	7	rs6467315	130,778,433	C	G	0.319027	-0.012602	0.002198	6.1E-09
KLF14 *	7	rs6949956	130,778,566	T	G	0.342723	-0.012325	0.002143	4.5E-09
KLF14 *	7	rs6968233	130,778,697	G	A	0.342852	-0.012375	0.002142	3.7E-09
KLF14 *	7	rs10954284	130,778,999	A	T	0.316280	-0.012199	0.002186	1.7E-08
KLF14 *	7	rs10245520	130,779,072	T	C	0.342788	-0.012226	0.002141	6.0E-09
KLF14 *	7	rs6972634	130,779,366	A	G	0.343064	-0.012183	0.002141	6.7E-09
KLF14 *	7	rs6467316	130,779,837	C	T	0.342742	-0.012029	0.002142	9.9E-09
KLF14 *	7	rs6467317	130,779,901	A	G	0.343708	-0.012239	0.002141	6.3E-09
KLF14 *	7	rs9641894	130,780,295	T	G	0.342997	-0.012184	0.002139	6.6E-09
KLF14 *	7	rs34188023	130,780,856	G	GT	0.343718	-0.012063	0.002138	8.2E-09
KLF14 *	7	rs1447059	130,780,895	A	G	0.343252	-0.012092	0.002138	8.4E-09
KLF14 *	7	rs1447060	130,781,332	A	G	0.340905	-0.012185	0.002139	7.8E-09
KLF14 *	7	rs972283	130,782,095	A	G	0.314356	-0.012428	0.002173	1.0E-08
KLF14 *	7	rs972284	130,782,207	C	T	0.342061	-0.012257	0.002134	5.0E-09
NAT2 *	8	rs35548819	18,371,107	C	T	0.472483	0.017945	0.002035	2.6E-19
NAT2 *	8	rs2172426	18,371,511	C	T	0.441761	-0.018506	0.002036	3.6E-21
NAT2 *	8	rs28504072	18,372,368	T	A	0.293520	-0.013192	0.002247	3.5E-10
NAT2 *	8	rs1845736	18,372,655	T	C	0.439113	-0.018166	0.002035	1.8E-20
NAT2 *	8	rs12156288	18,373,470	T	A	0.295668	-0.012854	0.002239	7.1E-10
NAT2 *	8	rs77971624	18,373,672	G	GTA	0.293653	-0.013128	0.002245	4.1E-10
NAT2 *	8	rs28556847	18,374,233	G	A	0.299489	-0.012694	0.002228	8.4E-10
NAT2 *	8	rs13267304	18,374,424	T	C	0.490549	0.018024	0.002013	5.1E-20
NAT2 *	8	rs7818089	18,375,037	C	T	0.300165	-0.012617	0.002226	1.0E-09
NAT2 *	8	rs7835476	18,375,604	A	C	0.490641	0.017909	0.002013	8.1E-20
NAT2 *	8	rs10090387	18,375,924	C	T	0.299584	-0.012932	0.002226	4.5E-10
NAT2 *	8	rs7006687	18,376,073	C	T	0.463162	-0.018518	0.002018	2.4E-21
NAT2 *	8	rs4481648	18,378,050	G	T	0.461898	-0.018321	0.002031	1.4E-20
NAT2 *	8	rs2047252	18,380,477	T	C	0.486994	0.017978	0.002049	1.8E-19
NAT2 *	8	rs7010068	18,381,888	C	G	0.226966	-0.014109	0.002436	1.2E-08
NAT2 *	8	rs10448136	18,382,184	A	C	0.174534	-0.016374	0.002671	9.7E-10
NAT2 *	8	rs13266992	18,382,187	C	T	0.476963	0.018042	0.002048	1.6E-19
NAT2 *	8	rs62492994	18,382,666	T	A	0.266063	-0.012903	0.002300	2.0E-09
NAT2 *	8	rs28417619	18,383,255	A	G	0.272963	-0.011866	0.002282	3.2E-08
NAT2 *	8	rs28638278	18,383,265	A	G	0.222047	-0.013569	0.002447	3.8E-08
NAT2 *	8	rs59416053	18,383,290	C	G	0.474683	0.017512	0.002038	1.1E-18
NAT2 *	8	rs28670948	18,383,662	T	A	0.276594	-0.011473	0.002258	4.8E-08
NAT2 *	8	rs35354956	18,383,809	C	T	0.476815	0.017943	0.002031	1.2E-19
NAT2 *	8	rs13277738	18,383,997	T	C	0.473967	0.017663	0.002033	4.2E-19
NAT2 *	8	rs73666635	18,384,071	C	T	0.277444	-0.011550	0.002255	3.9E-08
NAT2 *	8	rs17642674	18,384,245	C	T	0.178353	-0.015485	0.002644	3.7E-09
NAT2 *	8	rs4921906	18,385,268	A	T	0.218563	-0.013867	0.002448	2.3E-08
NAT2 *	8	rs13262341	18,385,587	G	A	0.478329	0.017957	0.002029	1.3E-19
NAT2 *	8	rs7016785	18,385,603	C	T	0.278041	-0.011536	0.002255	4.0E-08
NAT2 *	8	rs6992093	18,385,683	A	G	0.277317	-0.011613	0.002256	3.6E-08
NAT2 *	8	rs10109286	18,386,093	C	T	0.475586	0.018000	0.002029	7.8E-20
NAT2 *	8	rs10095072	18,387,152	T	G	0.499421	0.018117	0.002025	3.3E-20
NAT2 *	8	rs10095159	18,387,174	G	A	0.500320	-0.018082	0.002029	4.8E-20
NAT2 *	8	rs75501607	18,387,243	T	C	0.499077	0.017945	0.002024	5.0E-20
NAT2 *	8	rs11783019	18,387,343	T	G	0.174877	-0.015361	0.002661	6.4E-09
NAT2 *	8	rs13282367	18,387,476	G	T	0.480134	0.017814	0.002028	2.3E-19
NAT2 *	8	rs10085931	18,387,939	A	G	0.500318	-0.018568	0.002032	3.1E-21
NAT2 *	8	rs11780884	18,388,543	A	G	0.491481	0.018031	0.002031	3.8E-20
NAT2 *	8	rs11992530	18,388,623	C	A	0.291720	-0.011514	0.002223	2.1E-08
NAT2 *	8	rs4646241	18,389,186	C	T	0.272518	-0.012447	0.002262	3.2E-09
NAT2 *	8	rs4646242	18,389,939	G	A	0.272494	-0.012588	0.002262	2.2E-09
NAT2 *	8	rs4646243	18,390,099	C	T	0.475573	0.018394	0.002018	6.6E-21
NAT2 *	8	rs4646244	18,390,208	A	T	0.272931	-0.012517	0.002259	2.4E-09
NAT2 *	8	rs4646267	18,390,403	G	A	0.475561	0.018354	0.002018	7.2E-21
NAT2 *	8	rs4345600	18,390,698	G	A	0.175505	-0.015554	0.002651	3.4E-09
NAT2 *	8	rs4345601	18,390,703	T	A	0.174262	-0.015231	0.002665	7.8E-09
NAT2 *	8	rs4271002	18,390,758	C	G	0.176505	-0.014737	0.002641	1.7E-08
NAT2 *	8	rs4646246	18,391,151	G	A	0.473439	0.018272	0.002020	1.2E-20
NAT2	8	rs6984200	18,392,807	T	A	0.272838	-0.011856	0.002265	1.3E-08
NAT2	8	rs55686478	18,392,865	A	G	0.472149	0.018115	0.002024	2.3E-20
NAT2	8	rs2087852	18,394,416	G	A	0.273064	-0.011819	0.002264	1.4E-08
NAT2	8	rs79533018	18,395,972	A	G	0.172733	-0.015713	0.002669	4.0E-09
NAT2	8	rs35583283	18,396,999	C	G	0.478011	0.018257	0.002025	1.8E-20
NAT2	8	rs11996129	18,397,065	C	T	0.271699	-0.011673	0.002269	2.5E-08
NAT2	8	rs62492997	18,398,274	A	G	0.170512	-0.015811	0.002684	3.9E-09
NAT2	8	rs1112005	18,398,366	T	C	0.263982	-0.012983	0.002288	1.7E-09
NAT2	8	rs1041983	18,400,285	T	C	0.432191	-0.019220	0.002030	9.2E-23
NAT2	8	rs1799930	18,400,593	A	G	0.265967	-0.012380	0.002278	6.8E-09
NAT2	8	rs1799931	18,400,860	A	G	0.158639	-0.018470	0.002755	2.6E-11
NAT2 *	8	rs4646247	18,401,398	A	G	0.265932	-0.012388	0.002278	6.6E-09
NAT2 *	8	rs971473	18,401,450	T	C	0.166250	-0.016623	0.002706	6.0E-10
NAT2 *	8	rs721398	18,401,795	G	A	0.273487	-0.011595	0.002258	3.0E-08
NAT2 *	8	rs11780610	18,402,366	T	C	0.306437	-0.011606	0.002183	2.5E-08
NAT2 *	8	rs11787313	18,402,516	C	G	0.306434	-0.011603	0.002183	2.5E-08
NAT2 *	8	rs45605031	18,402,729	T	G	0.266054	-0.012380	0.002278	7.4E-09
NAT2 *	8	rs4646248	18,402,845	T	C	0.306633	-0.011570	0.002183	2.8E-08
NAT2 *	8	rs4646249	18,402,921	G	T	0.306960	-0.011602	0.002183	2.2E-08
NAT2 *	8	rs4646250	18,403,088	A	G	0.306440	-0.011589	0.002183	2.6E-08
NAT2 *	8	rs79409592	18,403,606	T	C	0.165868	-0.016497	0.002710	9.0E-10

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
NAT2 *	8	rs1390360	18,403,983	A	G	0.306469	-0.011607	0.002183	2.5E-08
NAT2 *	8	rs115942586	18,404,518	C	T	0.166209	-0.016573	0.002707	7.3E-10
NAT2 *	8	rs4646254	18,404,549	G	A	0.480615	0.017970	0.002021	5.0E-20
NAT2 *	8	rs4921909	18,404,610	C	T	0.306209	-0.011674	0.002184	2.0E-08
NAT2 *	8	rs4646256	18,404,921	C	T	0.306343	-0.011613	0.002184	2.4E-08
NAT2 *	8	rs4244446	18,405,008	T	C	0.306330	-0.011581	0.002185	2.6E-08
NAT2 *	8	rs4646257	18,405,036	T	C	0.479892	0.018081	0.002020	3.2E-20
NAT2 *	8	rs1495745	18,405,213	G	T	0.306322	-0.011575	0.002185	2.6E-08
NAT2 *	8	rs1495746	18,405,332	T	C	0.305402	-0.011678	0.002187	2.1E-08
NAT2 *	8	rs1495747	18,405,351	C	T	0.306305	-0.011576	0.002185	2.7E-08
NAT2 *	8	rs12674710	18,406,153	C	A	0.480406	0.018070	0.002021	3.4E-20
NAT2 *	8	rs2088200	18,407,894	G	C	0.169183	-0.015839	0.002691	2.6E-09
NAT2 *	8	rs74303991	18,408,156	A	G	0.161652	-0.017417	0.002739	1.9E-10
NAT2 *	8	rs12676857	18,409,062	C	T	0.473057	0.017975	0.002027	6.8E-20
NAT2 *	8	rs2898475	18,409,186	C	T	0.428934	-0.014303	0.002046	3.6E-13
NAT2 *	8	rs2410561	18,409,264	A	G	0.473011	0.018028	0.002027	5.1E-20
NAT2 *	8	rs2410562	18,409,322	C	T	0.428932	-0.014302	0.002046	3.6E-13
NAT2 *	8	rs7837608	18,409,337	A	G	0.428932	-0.014302	0.002046	3.6E-13
NAT2 *	8	rs2898476	18,409,414	A	G	0.472484	0.018085	0.002028	4.1E-20
NAT2 *	8	rs7460653	18,409,473	C	G	0.474253	0.017895	0.002029	9.8E-20
NAT2 *	8	rs10103029	18,409,828	G	A	0.474848	0.017869	0.002027	1.1E-19
NAT2 *	8	rs10103148	18,409,919	C	A	0.476236	0.017733	0.002028	2.1E-19
NAT2 *	8	rs10087857	18,409,951	C	G	0.474820	0.017828	0.002027	1.3E-19
NAT2 *	8	rs10103281	18,410,032	A	G	0.426664	-0.014228	0.002047	5.2E-13
NAT2 *	8	rs10088333	18,410,368	A	G	0.474804	0.017810	0.002027	1.5E-19
NAT2 *	8	rs1603290	18,411,760	G	A	0.424523	-0.014500	0.002049	2.2E-13
NAT2 *	8	rs10089958	18,411,833	G	A	0.477333	0.017988	0.002027	7.1E-20
NAT2 *	8	rs57180587	18,412,071	T	A	0.476879	0.018096	0.002028	4.4E-20
NAT2 *	8	rs1845735	18,413,520	T	C	0.427204	-0.014023	0.002049	1.2E-12
NAT2 *	8	rs12543818	18,414,402	G	T	0.433968	-0.013687	0.002042	5.2E-12
NAT2 *	8	rs12545528	18,414,438	T	G	0.433639	-0.013779	0.002041	3.9E-12
NAT2 *	8	chr8:18414568_A_AT	18,414,568	AT	A	0.381070	-0.014936	0.002093	2.0E-13
NAT2 *	8	rs4921911	18,414,597	T	C	0.387914	-0.015108	0.002067	5.1E-14
NAT2 *	8	rs4921912	18,414,623	G	A	0.388244	-0.015206	0.002065	3.2E-14
NAT2 *	8	rs4921913	18,414,867	T	C	0.480682	-0.017988	0.002012	4.7E-20
NAT2 *	8	rs4921914	18,414,928	T	C	0.484704	-0.017970	0.002018	7.3E-20
NAT2 *	8	rs4921915	18,414,956	A	G	0.481874	-0.018365	0.002012	1.2E-20
NAT2 *	8	rs11267998	18,414,993	GAGCTG	C	0.484798	-0.018143	0.002013	3.0E-20
NAT2 *	8	rs35246381	18,415,025	T	C	0.484730	-0.018049	0.002012	4.2E-20
NAT2 *	8	rs35570672	18,415,125	C	T	0.484407	-0.018117	0.002013	3.3E-20
NAT2 *	8	rs1495741	18,415,371	A	G	0.483585	-0.018065	0.002012	3.9E-20
NAT2 *	8	rs1495742	18,415,391	T	C	0.267596	-0.016006	0.002278	2.5E-12
NAT2 *	8	rs13254811	18,415,508	G	A	0.468668	0.017078	0.002027	5.5E-18
NAT2 *	8	rs1495743	18,415,790	C	G	0.484327	-0.017961	0.002015	6.9E-20
NAT2 *	8	rs6998188	18,416,466	T	C	0.314036	-0.013473	0.002183	7.9E-10
NAT2 *	8	rs6998197	18,416,486	T	C	0.313825	-0.013437	0.002184	9.5E-10
NAT2 *	8	rs7815666	18,416,695	T	C	0.313549	-0.013536	0.002185	7.3E-10
NAT2 *	8	rs7828813	18,416,714	C	G	0.313966	-0.013498	0.002183	7.8E-10
NAT2 *	8	rs7815686	18,416,734	T	C	0.313928	-0.013471	0.002184	8.5E-10
NAT2 *	8	rs7815698	18,416,746	T	A	0.314090	-0.013512	0.002184	7.4E-10
NAT2 *	8	rs35942058	18,416,888	A	G	0.469139	0.017134	0.002028	7.1E-18
NAT2 *	8	rs34987019	18,416,933	C	T	0.469159	0.017122	0.002028	7.4E-18
NAT2 *	8	rs7812546	18,417,104	A	T	0.468453	0.017014	0.002032	1.7E-17
NAT2 *	8	rs34537991	18,417,174	C	G	0.470283	0.017219	0.002031	6.5E-18
NAT2 *	8	rs7828489	18,417,249	G	T	0.478724	0.017340	0.002032	3.0E-18
NAT2 *	8	rs12545875	18,417,281	C	T	0.170673	-0.015926	0.002690	3.7E-09
NAT2 *	8	rs7816847	18,417,679	C	A	0.470713	0.017186	0.002028	4.6E-18
NAT2 *	8	rs8180964	18,417,979	T	C	0.151523	-0.017259	0.002830	2.9E-09
NAT2 *	8	rs4560828	18,418,784	T	A	0.470730	0.017253	0.002034	6.4E-18
NAT2 *	8	rs13255048	18,419,130	A	G	0.468679	0.017582	0.002032	1.1E-18
NAT2 *	8	rs35492904	18,419,249	A	G	0.242001	-0.016983	0.002375	2.9E-12
NAT2 *	8	chr8:18419370_AAACAAC_A	18,419,370	AAACAAC	A	0.466619	0.017034	0.002036	2.0E-17
NAT2 *	8	rs1466753	18,419,609	T	C	0.262845	-0.016333	0.002302	1.7E-12
NAT2 *	8	rs983776	18,420,448	C	T	0.267258	-0.015892	0.002293	4.9E-12
NAT2 *	8	rs983777	18,420,469	G	A	0.251600	-0.016660	0.002342	2.7E-12
NAT2 *	8	rs7005648	18,420,698	T	A	0.473182	0.017396	0.002031	1.9E-18
NAT2 *	8	rs150364778	18,421,641	T	CACAAGT	0.150058	-0.017628	0.002857	1.5E-09
NAT2 *	8	rs17642824	18,421,743	A	G	0.146786	-0.018254	0.002884	5.8E-10
CSGALNACT1	8	rs140603833	19,757,757	G	T	0.010217	-0.050716	0.010032	4.9E-08
INTS10 *	8	rs142950473	19,771,660	C	T	0.011966	-0.053991	0.009313	5.1E-10
INTS10 *	8	rs74549553	19,874,863	C	G	0.075910	-0.027388	0.003856	6.8E-13
INTS10 *	8	rs28625109	19,875,076	C	T	0.157130	-0.014041	0.002768	4.7E-08
INTS10 *	8	rs7818070	19,877,405	A	G	0.153598	-0.014292	0.002803	4.1E-08
INTS10 *	8	rs4922113	19,877,440	A	G	0.120597	-0.024930	0.003141	9.2E-16
INTS10 *	8	rs75070501	19,880,081	G	A	0.118178	-0.027906	0.003160	3.0E-19
INTS10 *	8	rs17410407	19,881,732	T	G	0.116367	-0.027774	0.003174	5.2E-19
INTS10 *	8	rs77829308	19,883,675	T	C	0.114259	-0.027713	0.003202	1.0E-18
INTS10 *	8	chr8:19884251_C_CA	19,884,251	CA	C	0.111913	-0.029368	0.003243	2.5E-20
INTS10 *	8	rs73607783	19,884,693	A	T	0.123593	-0.027282	0.003107	2.4E-19
INTS10 *	8	rs79341217	19,885,706	T	C	0.100810	-0.031561	0.003375	9.6E-22
INTS10 *	8	rs74974359	19,885,743	C	T	0.068890	-0.030740	0.004020	7.5E-15
INTS10 *	8	rs10503666	19,887,085	C	G	0.086965	-0.037380	0.003581	6.5E-27
INTS10 *	8	rs17482310	19,889,365	T	G	0.096787	-0.032614	0.003418	1.5E-22
INTS10 *	8	rs79396901	19,890,937	C	T	0.087314	-0.037227	0.003571	8.3E-27
INTS10 *	8	rs78222518	19,891,345	C	T	0.490140	0.011188	0.002023	2.1E-08
INTS10 *	8	rs138094414	19,892,729	C	G	0.083911	-0.037516	0.003633	1.5E-26
INTS10 *	8	rs112861901	19,893,440	C	T	0.087139	-0.037379	0.003573	3.5E-27
INTS10 *	8	rs12550077	19,893,888	A	G	0.082608	-0.037630	0.003659	1.8E-26
INTS10 *	8	rs1441776	19,894,049	G	C	0.481220	0.011560	0.002039	9.8E-09
LPL *	8	rs17482386	19,896,010	G	A	0.098585	-0.034367	0.003393	2.6E-25
LPL *	8	chr8:19896793_C_CT	19,896,793	CT	C	0.103873	-0.034396	0.003328	9.5E-27
LPL *	8	rs1919482	19,897,207	T	A	0.099864	-0.032798	0.003375	3.2E-24
LPL *	8	rs76085257	19,897,616	A	C	0.082679	-0.037545	0.003654	1.7E-26
LPL *	8	rs73597688	19,897,664	A	C	0.096895	-0.035311	0.003420	7.7E-27
LPL *	8	rs73597690	19,898,115	A	C	0.088664	-0.036540	0.003554	7.4E-27
LPL *	8	rs12543154	19,898,466	T	G	0.087688	-0.037060	0.003569	3.2E-27
LPL *	8	rs10091649	19,898,910	G	T	0.092088	-0.037768	0.003508	1.5E-29

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
LPL *	8	rs73597699	19,899,081	T	C	0.078715	-0.037295	0.003770	8.8E-25
LPL *	8	rs10102717	19,899,302	T	C	0.089707	-0.037803	0.003548	4.3E-29
LPL *	8	rs1441771	19,899,789	T	C	0.089440	-0.038629	0.003555	3.5E-30
LPL *	8	rs1441770	19,899,808	A	G	0.089602	-0.038425	0.003552	6.3E-30
LPL *	8	rs183801835	19,904,479	C	T	0.020348	-0.066302	0.007152	8.3E-23
LPL *	8	rs77032723	19,906,481	T	C	0.128694	-0.039951	0.003044	2.3E-42
LPL *	8	rs192423215	19,907,403	C	G	0.019474	-0.068910	0.007302	1.3E-23
LPL *	8	rs60526148	19,909,692	T	C	0.153415	-0.043566	0.002814	1.2E-57
LPL *	8	rs3988301	19,912,868	G	T	0.157988	-0.043955	0.002784	5.1E-60
LPL *	8	rs28834434	19,917,379	A	C	0.151077	-0.044710	0.002810	4.5E-61
LPL *	8	rs4466415	19,919,470	C	A	0.162359	-0.043754	0.002743	7.7E-61
LPL *	8	rs77899453	19,922,799	A	G	0.150649	-0.045029	0.002818	2.0E-61
LPL *	8	rs2119692	19,922,946	C	G	0.151708	-0.044463	0.002811	2.3E-60
LPL *	8	rs3866470	19,927,611	A	G	0.016467	-0.072601	0.007919	1.8E-22
LPL *	8	rs7816032	19,929,380	T	C	0.156964	-0.043776	0.002765	3.6E-60
LPL *	8	rs139001474	19,931,094	A	T	0.160841	-0.043765	0.002747	8.0E-61
LPL *	8	rs149764042	19,931,164	C	G	0.068047	-0.070477	0.004209	3.6E-73
LPL *	8	rs4592053	19,931,255	G	A	0.161242	-0.043754	0.002745	6.2E-61
LPL *	8	rs150331294	19,932,487	A	T	0.156390	-0.043754	0.002773	5.8E-60
LPL *	8	rs182893294	19,933,207	C	T	0.013494	-0.067966	0.008755	9.1E-16
LPL *	8	rs9694336	19,933,560	T	C	0.149634	-0.044919	0.002831	4.8E-61
LPL *	8	rs145353248	19,933,835	T	C	0.149554	-0.045056	0.002831	2.2E-61
LPL	8	rs3779787	19,940,405	T	G	0.157065	-0.042562	0.002778	4.1E-57
LPL	8	rs1534649	19,942,130	T	G	0.157083	-0.043796	0.002775	1.9E-60
LPL	8	rs112127208	19,944,019	G	T	0.155681	-0.044189	0.002782	5.5E-61
LPL	8	rs10104051	19,944,891	T	C	0.155869	-0.044167	0.002781	5.7E-61
LPL	8	rs3779788	19,945,582	T	C	0.154965	-0.044371	0.002787	4.9E-61
LPL	8	rs56321069	19,946,485	A	T	0.154313	-0.044989	0.002799	3.0E-62
LPL	8	rs8176337	19,949,160	G	C	0.153680	-0.046001	0.002818	5.8E-64
LPL	8	rs74304285	19,950,519	A	G	0.152242	-0.046685	0.002849	8.1E-65
LPL	8	rs113023641	19,950,620	A	G	0.152173	-0.046745	0.002850	6.1E-65
LPL	8	rs73667472	19,952,184	C	T	0.059887	-0.074930	0.004285	1.3E-73
LPL	8	rs343	19,953,276	A	C	0.150343	-0.019359	0.002870	2.4E-12
LPL	8	rs249	19,953,495	C	T	0.060341	-0.078746	0.004264	3.4E-81
LPL	8	rs250	19,953,512	ATG	A	0.153791	-0.019015	0.002846	2.5E-12
LPL	8	rs254	19,954,386	G	C	0.218289	-0.041038	0.002469	1.0E-66
LPL	8	rs255	19,954,390	C	T	0.218293	-0.041066	0.002469	8.3E-67
LPL	8	rs256	19,954,456	T	C	0.218869	-0.041480	0.002464	2.5E-68
LPL	8	rs263	19,955,301	T	C	0.220321	-0.041762	0.002439	2.4E-70
LPL	8	rs264	19,955,669	A	G	0.210153	-0.037944	0.002474	2.4E-56
LPL	8	rs269	19,956,156	G	T	0.219606	-0.042822	0.002455	1.3E-72
LPL	8	rs271	19,956,191	A	G	0.218975	-0.042747	0.002457	3.0E-72
LPL	8	chr8:19956458_G_GT	19,956,458	GT	G	0.215596	-0.043128	0.002486	1.3E-71
LPL	8	rs285	19,957,678	T	C	0.352508	-0.037142	0.002153	8.9E-72
LPL	8	rs287	19,958,045	G	A	0.204168	-0.056081	0.002500	4.0E-118
LPL	8	rs289	19,958,108	C	T	0.203997	-0.056386	0.002498	1.4E-119
LPL	8	rs291	19,958,341	C	T	0.204884	-0.056507	0.002494	8.3E-121
LPL	8	chr8:19958567_T_TA	19,958,567	TA	T	0.204061	-0.055909	0.002500	1.5E-117
LPL	8	rs295	19,958,727	C	A	0.205167	-0.056362	0.002491	1.6E-120
LPL	8	rs297	19,958,860	C	T	0.203993	-0.056394	0.002498	1.3E-119
LPL	8	rs301	19,959,423	C	T	0.203802	-0.056851	0.002501	4.1E-121
LPL	8	rs304	19,959,850	G	T	0.198401	-0.055928	0.002543	6.1E-113
LPL	8	rs305	19,959,890	G	A	0.203033	-0.056757	0.002506	3.6E-120
LPL	8	rs308	19,959,965	G	T	0.079863	-0.081538	0.003720	6.9E-115
LPL	8	rs314	19,960,531	A	G	0.203930	-0.056710	0.002500	1.5E-120
LPL	8	rs117026536	19,961,262	T	G	0.103995	-0.082705	0.003302	3.9E-149
LPL	8	rs320	19,961,566	G	T	0.204337	-0.056779	0.002496	4.6E-121
LPL	8	rs322	19,961,706	C	A	0.204584	-0.056614	0.002499	5.7E-120
LPL	8	rs325	19,961,817	C	T	0.103364	-0.084065	0.003306	3.3E-153
LPL	8	rs326	19,961,928	G	A	0.204417	-0.056984	0.002495	5.7E-122
LPL	8	rs327	19,962,025	G	T	0.204665	-0.056816	0.002496	4.8E-121
LPL	8	rs328	19,962,213	G	C	0.103353	-0.083914	0.003306	1.1E-152
LPL	8	rs331	19,962,894	A	G	0.202854	-0.057014	0.002501	2.2E-121
LPL	8	rs12679834	19,962,922	C	T	0.103326	-0.084120	0.003306	2.2E-153
LPL	8	rs117199990	19,963,405	T	C	0.101117	-0.084522	0.003344	2.7E-151
LPL	8	rs145391587	19,963,422	C	A	0.100168	-0.085100	0.003359	3.7E-152
LPL	8	rs75278536	19,963,914	G	T	0.103029	-0.084222	0.003311	2.0E-153
LPL	8	rs146265243	19,963,956	G	GT	0.103053	-0.084229	0.003311	2.3E-153
LPL	8	rs77069344	19,964,271	G	T	0.103029	-0.084221	0.003311	2.0E-153
LPL	8	rs11570891	19,965,299	T	C	0.103244	-0.084058	0.003308	5.1E-153
LPL	8	rs3208305	19,966,137	T	A	0.196939	-0.057392	0.002536	1.7E-119
LPL	8	rs1803924	19,966,163	T	C	0.103246	-0.084065	0.003308	4.9E-153
LPL	8	rs3735964	19,966,534	A	C	0.103293	-0.084048	0.003306	3.7E-153
LPL	8	rs13702	19,966,981	C	T	0.200863	-0.057504	0.002511	3.4E-122
LPL	8	rs1059611	19,967,052	C	T	0.103324	-0.083980	0.003306	5.8E-153
LPL	8	rs10645926	19,967,115	CTT	C	0.103282	-0.084049	0.003307	3.6E-153
LPL	8	rs15285	19,967,156	T	C	0.200380	-0.057608	0.002512	2.9E-122
LPL *	8	rs3916027	19,967,357	A	G	0.200329	-0.057606	0.002513	3.8E-122
LPL *	8	rs77150190	19,968,791	C	G	0.094687	-0.082536	0.003439	2.5E-136
LPL *	8	rs77729186	19,968,807	G	A	0.094687	-0.082536	0.003439	2.5E-136
LPL *	8	rs2197089	19,968,862	A	G	0.346001	-0.036331	0.002116	7.9E-70
LPL *	8	rs79108221	19,969,190	T	C	0.094642	-0.082500	0.003439	3.6E-136
LPL *	8	rs1563590475	19,969,589	A	ACTT	0.080227	-0.079159	0.003745	2.0E-106
LPL *	8	rs10105606	19,970,337	A	C	0.200062	-0.057706	0.002514	1.7E-122
LPL *	8	rs1569209	19,972,659	G	T	0.021651	-0.077068	0.006919	4.7E-30
LPL *	8	rs1011685	19,973,258	T	C	0.102385	-0.083903	0.003319	2.9E-151
LPL *	8	rs10096633	19,973,410	T	C	0.102498	-0.083785	0.003318	4.7E-151
LPL *	8	rs17482753	19,975,135	T	G	0.101912	-0.083894	0.003326	1.5E-150
LPL *	8	rs78963197	19,979,135	C	T	0.098808	-0.081979	0.003386	4.3E-139
LPL *	8	rs74855321	19,979,473	T	C	0.100972	-0.083421	0.003342	3.9E-148
LPL *	8	rs4464984	19,980,958	T	C	0.196084	-0.057358	0.002541	8.2E-119
LPL *	8	rs58946909	19,982,830	A	G	0.101778	-0.083522	0.003331	1.0E-148
LPL *	8	rs75551077	19,982,897	C	G	0.101823	-0.083509	0.003330	9.8E-149
LPL *	8	rs1554519534	19,985,625	CA	C	0.056126	-0.083769	0.004466	9.0E-83
LPL *	8	rs17091891	19,985,660	C	T	0.092029	-0.083944	0.003507	2.1E-135
LPL *	8	rs17410914	19,985,951	A	C	0.099091	-0.084654	0.003371	1.5E-149
LPL *	8	rs117227752	19,986,350	A	G	0.101941	-0.084115	0.003326	1.6E-151

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
LPL *	8	rs59147390	19,986,368	C	T	0.101938	-0.084118	0.003326	1.5E-151
LPL *	8	rs184371102	19,986,419	T	G	0.078423	-0.081439	0.003749	5.6E-113
LPL *	8	rs12678919	19,986,711	G	A	0.102220	-0.083665	0.003322	2.0E-150
LPL *	8	rs7819706	19,986,904	G	A	0.101764	-0.084043	0.003330	5.3E-151
LPL *	8	rs115129770	19,986,928	G	C	0.101764	-0.084043	0.003330	5.3E-151
LPL *	8	rs149670831	19,986,936	C	CT	0.101764	-0.084043	0.003330	5.3E-151
LPL *	8	rs7841189	19,987,865	T	C	0.102238	-0.083845	0.003325	2.1E-150
LPL *	8	rs78458743	19,988,803	G	T	0.101872	-0.084123	0.003328	2.4E-151
LPL *	8	rs114566157	19,988,978	G	C	0.101872	-0.084123	0.003328	2.4E-151
LPL *	8	rs139894713	19,989,069	A	C	0.021639	-0.077640	0.006920	2.0E-30
LPL *	8	rs12682115	19,989,549	A	G	0.101872	-0.084123	0.003328	2.4E-151
LPL *	8	rs78013771	19,989,712	C	T	0.101871	-0.084121	0.003328	2.4E-151
LPL *	8	rs76496571	19,989,930	A	C	0.101914	-0.084155	0.003327	1.6E-151
LPL *	8	rs10503669	19,990,179	A	C	0.102015	-0.084005	0.003322	2.2E-151
LPL *	8	rs17410962	19,990,569	A	G	0.101938	-0.084175	0.003327	1.2E-151
LPL *	8	rs117604010	19,990,885	A	G	0.078798	-0.081575	0.003740	7.4E-114
LPL *	8	rs17489185	19,990,988	C	G	0.101939	-0.084178	0.003327	1.2E-151
LPL *	8	rs17410983	19,991,182	T	C	0.101940	-0.084175	0.003327	1.3E-151
LPL *	8	rs17489226	19,991,367	T	A	0.101940	-0.084173	0.003327	1.3E-151
LPL *	8	rs17410996	19,991,761	G	T	0.101863	-0.084116	0.003328	2.9E-151
LPL *	8	rs75801420	19,992,159	G	T	0.101937	-0.084001	0.003328	7.0E-151
LPL *	8	rs17091905	19,992,246	A	G	0.101960	-0.084192	0.003326	1.2E-151
LPL *	8	rs114964604	19,992,478	G	A	0.101105	-0.083955	0.003343	9.3E-150
LPL *	8	rs73600084	19,992,481	C	T	0.101105	-0.083955	0.003343	9.3E-150
LPL *	8	rs76975037	19,993,997	A	C	0.101899	-0.084274	0.003328	7.1E-152
LPL *	8	rs17489268	19,994,534	A	T	0.199910	-0.057275	0.002520	2.0E-120
LPL *	8	rs174111024	19,994,623	A	G	0.101719	-0.084165	0.003331	2.1E-151
LPL *	8	rs17091909	19,994,645	T	G	0.101876	-0.084262	0.003329	8.0E-152
LPL *	8	rs147729680	19,994,665	T	TTC	0.200022	-0.057399	0.002519	5.3E-121
LPL *	8	rs17411031	19,994,799	G	C	0.199946	-0.057348	0.002519	8.3E-121
LPL *	8	rs17411045	19,994,851	C	T	0.199817	-0.057436	0.002521	5.9E-121
LPL *	8	rs17489282	19,995,007	T	C	0.199988	-0.057389	0.002520	6.9E-121
LPL *	8	rs4922117	19,995,075	C	T	0.199944	-0.057351	0.002519	8.2E-121
LPL *	8	rs1822200	19,995,318	T	G	0.199944	-0.057351	0.002519	8.2E-121
LPL *	8	rs1372344	19,995,428	T	A	0.199944	-0.057351	0.002519	8.2E-121
LPL *	8	rs1992442	19,995,878	C	A	0.200101	-0.057199	0.002520	3.3E-120
LPL *	8	rs2410618	19,995,989	A	G	0.199952	-0.057386	0.002519	6.1E-121
LPL *	8	rs1992443	19,996,076	A	G	0.199952	-0.057386	0.002519	6.1E-121
LPL *	8	rs920588	19,996,756	T	C	0.199979	-0.057372	0.002519	7.1E-121
LPL *	8	rs920589	19,996,850	T	G	0.199951	-0.057395	0.002519	5.7E-121
LPL *	8	rs4425772	19,996,989	T	C	0.199458	-0.057360	0.002522	1.6E-120
LPL *	8	rs4628269	19,996,998	T	C	0.199458	-0.057360	0.002522	1.6E-120
LPL *	8	rs2410619	19,997,042	A	C	0.199951	-0.057395	0.002519	5.7E-121
LPL *	8	rs4320561	19,997,126	A	C	0.199778	-0.057221	0.002521	3.4E-120
LPL *	8	rs2410620	19,997,149	T	C	0.199778	-0.057221	0.002521	3.4E-120
LPL *	8	rs2410621	19,997,171	C	T	0.199778	-0.057221	0.002521	3.4E-120
LPL *	8	rs2410623	19,997,378	G	A	0.199960	-0.057394	0.002519	5.7E-121
LPL *	8	rs17411113	19,997,495	G	C	0.101950	-0.084131	0.003329	2.5E-151
LPL *	8	rs79734126	19,997,519	T	C	0.078227	-0.081380	0.003754	1.2E-112
LPL *	8	rs34564316	19,997,710	T	C	0.200026	-0.057275	0.002521	1.8E-120
LPL *	8	rs17411126	19,997,761	C	T	0.199964	-0.057404	0.002519	5.1E-121
LPL *	8	rs17411133	19,997,820	A	T	0.199992	-0.057362	0.002519	7.2E-121
LPL *	8	rs17489373	19,997,833	A	G	0.199998	-0.057364	0.002519	7.4E-121
LPL *	8	rs17411168	19,998,089	C	T	0.200228	-0.057238	0.002516	1.0E-120
LPL *	8	rs34932218	19,998,150	G	A	0.200286	-0.057222	0.002516	9.8E-121
LPL *	8	rs140426714	19,998,333	G	GTATTTT	0.198689	-0.057074	0.002528	4.3E-119
LPL *	8	rs2165558	19,998,749	G	T	0.220103	-0.052009	0.002467	1.5E-103
LPL *	8	rs4523270	19,999,028	C	T	0.200332	-0.057152	0.002515	1.4E-120
LPL *	8	rs2103325	20,000,832	T	C	0.200023	-0.057311	0.002516	3.1E-121
LPL *	8	rs1581675	20,000,988	A	T	0.200030	-0.057320	0.002516	2.9E-121
LPL *	8	rs4490856	20,001,609	C	T	0.353766	-0.039750	0.002120	3.4E-83
LPL *	8	rs2119690	20,002,028	A	G	0.200114	-0.057306	0.002515	2.9E-121
LPL *	8	rs2165556	20,002,116	T	C	0.200113	-0.057303	0.002515	3.1E-121
LPL *	8	rs12541912	20,002,280	C	G	0.200491	-0.057107	0.002513	1.3E-120
LPL *	8	rs74869266	20,002,686	C	A	0.021754	-0.078593	0.006901	2.6E-31
LPL *	8	rs79236614	20,002,949	G	C	0.101753	-0.084054	0.003330	4.1E-151
LPL *	8	rs34818360	20,003,236	A	G	0.199846	-0.057146	0.002516	2.0E-120
LPL *	8	rs4083261	20,003,715	C	T	0.200500	-0.057233	0.002513	4.0E-121
LPL *	8	rs38444510	20,003,850	C	A	0.200180	-0.057476	0.002515	6.7E-122
LPL *	8	rs2410625	20,004,709	T	C	0.200160	-0.057474	0.002515	6.4E-122
LPL *	8	rs46444277	20,005,059	C	T	0.200160	-0.057474	0.002515	6.4E-122
LPL *	8	rs4389957	20,005,235	A	G	0.354414	-0.038669	0.002116	2.5E-79
LPL *	8	rs1441766	20,005,277	T	A	0.201923	-0.057150	0.002512	4.6E-121
LPL *	8	rs1441764	20,005,513	T	C	0.200506	-0.057240	0.002513	3.7E-121
LPL *	8	rs6586884	20,005,847	C	T	0.101882	-0.084554	0.003328	6.9E-153
LPL *	8	rs6999813	20,005,960	A	T	0.101882	-0.084554	0.003328	6.9E-153
LPL *	8	rs2119689	20,005,996	T	C	0.200160	-0.057474	0.002515	6.4E-122
LPL *	8	chr8:20006328_G_GA	20,006,328	GA	G	0.197671	-0.058310	0.002533	1.6E-123
LPL *	8	rs1441763	20,007,045	C	T	0.200166	-0.057474	0.002515	6.0E-122
LPL *	8	rs1441762	20,007,176	A	G	0.200327	-0.057544	0.002516	4.1E-122
LPL *	8	rs1441761	20,007,237	C	G	0.199509	-0.057340	0.002519	6.3E-121
LPL *	8	rs1441760	20,007,238	T	C	0.199509	-0.057340	0.002519	6.3E-121
LPL *	8	chr8:20007371_T_TAAA	20,007,371	TAAA	T	0.193155	-0.057568	0.002566	8.2E-119
LPL *	8	rs2083637	20,007,664	G	A	0.200128	-0.057434	0.002514	7.5E-122
LPL *	8	rs2083636	20,007,752	G	T	0.200595	-0.057292	0.002512	2.0E-121
LPL *	8	rs77237194	20,007,944	T	A	0.101922	-0.084523	0.003327	7.7E-153
LPL *	8	rs35495249	20,007,998	A	C	0.199024	-0.057829	0.002522	1.3E-122
LPL *	8	rs894211	20,008,236	T	C	0.199095	-0.057838	0.002522	1.1E-122
LPL *	8	rs894210	20,008,332	A	G	0.355683	-0.039194	0.002113	1.4E-81
LPL *	8	rs765547	20,008,763	A	G	0.200236	-0.057506	0.002514	4.5E-122
LPL *	8	rs765548	20,009,083	T	C	0.200225	-0.057511	0.002514	4.2E-122
LPL *	8	rs765549	20,009,120	G	A	0.200535	-0.057262	0.002513	3.0E-121
LPL *	8	rs1441758	20,009,367	T	A	0.200225	-0.057511	0.002514	4.2E-122
LPL *	8	rs139547332	20,009,665	CT	C	0.078743	-0.081764	0.003741	2.5E-114
LPL *	8	rs9644637	20,009,709	C	T	0.200225	-0.057511	0.002514	4.2E-122
LPL *	8	rs9644638	20,009,889	T	C	0.199804	-0.057398	0.002517	2.4E-121
LPL *	8	rs11986942	20,009,934	G	C	0.200535	-0.057262	0.002513	3.0E-121

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
LPL *	8	rs34327087	20,009,983	T	G	0.200157	-0.057449	0.002514	7.4E-122
LPL *	8	rs34345068	20,010,025	T	G	0.200158	-0.057408	0.002514	1.1E-121
LPL *	8	rs2009493	20,010,342	A	G	0.200227	-0.057504	0.002514	4.7E-122
LPL *	8	rs1837843	20,010,591	T	C	0.196350	-0.056604	0.002534	8.3E-117
LPL *	8	rs1837842	20,010,779	C	T	0.200227	-0.057504	0.002514	4.7E-122
LPL *	8	rs1441757	20,010,866	C	G	0.200227	-0.057504	0.002514	4.7E-122
LPL *	8	rs1441755	20,011,377	C	T	0.200227	-0.057504	0.002514	4.7E-122
LPL *	8	rs1441754	20,011,428	A	G	0.199451	-0.057769	0.002520	1.5E-122
LPL *	8	rs4406409	20,011,460	C	T	0.199259	-0.057116	0.002523	1.2E-119
LPL *	8	rs1441753	20,011,553	A	G	0.200227	-0.057504	0.002514	4.7E-122
LPL *	8	rs4126104	20,011,855	T	G	0.200227	-0.057504	0.002514	4.7E-122
LPL *	8	rs1919484	20,012,165	A	G	0.200211	-0.057464	0.002514	7.2E-122
LPL *	8	rs35687633	20,012,476	G	A	0.199809	-0.057471	0.002519	2.4E-121
LPL *	8	rs34942551	20,012,504	G	T	0.199816	-0.057478	0.002519	2.3E-121
LPL *	8	rs34499461	20,012,516	C	G	0.199688	-0.057484	0.002521	2.9E-121
LPL *	8	rs35369244	20,012,533	C	G	0.199690	-0.057481	0.002521	3.0E-121
LPL *	8	rs35739466	20,012,576	A	G	0.196654	-0.056023	0.002538	3.1E-114
LPL *	8	rs35617716	20,012,752	A	T	0.197233	-0.056311	0.002530	9.7E-116
LPL *	8	rs35237252	20,012,760	A	C	0.197273	-0.056208	0.002530	2.9E-115
LPL *	8	rs1569213	20,013,224	A	G	0.177774	-0.052082	0.002684	3.1E-89
LPL *	8	rs78810414	20,013,602	T	C	0.084320	-0.080910	0.003634	4.1E-119
LPL *	8	rs1372343	20,013,809	T	C	0.185167	-0.053337	0.002600	8.7E-99
LPL *	8	rs1372342	20,013,820	A	T	0.185172	-0.053342	0.002600	8.2E-99
LPL *	8	rs1372341	20,013,821	A	T	0.185172	-0.053342	0.002600	8.2E-99
LPL *	8	rs1372340	20,013,861	A	G	0.181955	-0.052255	0.002619	5.0E-94
LPL *	8	rs2410627	20,014,002	C	T	0.185551	-0.053167	0.002597	1.4E-98
LPL *	8	rs7461115	20,014,029	G	C	0.185552	-0.053160	0.002597	1.6E-98
LPL *	8	rs2410628	20,014,118	T	C	0.185544	-0.053115	0.002597	2.2E-98
LPL *	8	rs2410629	20,014,126	C	T	0.185628	-0.053133	0.002596	1.6E-98
LPL *	8	rs2898495	20,014,381	G	A	0.185626	-0.053139	0.002596	1.5E-98
LPL *	8	rs4593558	20,014,497	G	A	0.185638	-0.053133	0.002596	1.5E-98
LPL *	8	rs6986010	20,015,269	C	T	0.185627	-0.053140	0.002596	1.5E-98
LPL *	8	rs35465966	20,016,045	A	C	0.185276	-0.053171	0.002598	1.4E-98
LPL *	8	rs34693282	20,016,055	G	A	0.185540	-0.053112	0.002596	2.0E-98
LPL *	8	rs17489539	20,016,071	A	T	0.185364	-0.053112	0.002598	2.9E-98
LPL *	8	rs4922118	20,016,634	T	C	0.185330	-0.053328	0.002602	9.7E-99
LPL *	8	rs4922119	20,016,642	T	C	0.185330	-0.053328	0.002602	9.7E-99
LPL *	8	rs4375019	20,016,987	A	T	0.181686	-0.052174	0.002619	6.6E-94
LPL *	8	rs141287949	20,017,421	A	AAGAC	0.084766	-0.080827	0.003620	6.9E-120
LPL *	8	rs4333617	20,017,493	G	A	0.182267	-0.051806	0.002616	5.8E-93
LPL *	8	rs2410630	20,017,589	T	C	0.182328	-0.051693	0.002616	1.4E-92
LPL *	8	rs6586886	20,017,897	A	G	0.182440	-0.051804	0.002614	5.5E-93
LPL *	8	rs73208815	20,018,604	C	G	0.182249	-0.052023	0.002614	1.3E-93
LPL *	8	rs28675909	20,018,723	T	A	0.084719	-0.081396	0.003621	4.1E-121
LPL *	8	rs79198716	20,018,753	T	C	0.084920	-0.081332	0.003616	2.0E-121
LPL *	8	chr8:20018790_G_GA	20,018,790	GA	G	0.183604	-0.052014	0.002614	2.7E-93
LPL *	8	rs78300069	20,019,013	T	C	0.085383	-0.081144	0.003606	1.8E-121
LPL *	8	rs76737188	20,019,083	C	G	0.089079	-0.081468	0.003534	9.3E-127
LPL *	8	rs7016880	20,019,235	C	G	0.089140	-0.081226	0.003533	3.1E-126
LPL *	8	rs7007609	20,019,286	C	T	0.089079	-0.081468	0.003534	9.3E-127
LPL *	8	rs7007797	20,019,459	G	T	0.089080	-0.081467	0.003534	9.4E-127
LPL *	8	rs7004149	20,019,697	G	A	0.089080	-0.081467	0.003534	9.4E-127
LPL *	8	rs7004158	20,019,722	G	A	0.089080	-0.081467	0.003534	9.4E-127
LPL *	8	rs6983430	20,019,742	C	G	0.089080	-0.081467	0.003534	9.4E-127
LPL *	8	rs77219697	20,019,950	C	T	0.089084	-0.081450	0.003535	1.1E-126
LPL *	8	rs12678603	20,020,221	T	C	0.085396	-0.081194	0.003607	1.1E-121
LPL *	8	rs12678604	20,020,262	G	C	0.085367	-0.081258	0.003607	8.3E-122
LPL *	8	rs1534650	20,020,643	C	T	0.350198	-0.036845	0.002127	2.0E-72
LPL *	8	rs7013777	20,020,845	C	T	0.186824	-0.052750	0.002590	1.0E-97
LPL *	8	rs4922120	20,021,087	G	A	0.349569	-0.036479	0.002126	3.7E-71
LPL *	8	rs112994260	20,021,193	A	T	0.089037	-0.081558	0.003536	6.3E-127
LPL *	8	rs142117848	20,021,359	A	C	0.089040	-0.081568	0.003536	5.9E-127
LPL *	8	rs4335137	20,021,363	T	A	0.187819	-0.052447	0.002585	5.0E-97
LPL *	8	rs1819092	20,021,566	C	T	0.186809	-0.052845	0.002590	4.5E-98
LPL *	8	rs1819094	20,021,804	G	C	0.183423	-0.051609	0.002610	1.1E-92
LPL *	8	rs75082673	20,022,298	A	G	0.085310	-0.081285	0.003608	7.6E-122
LPL *	8	rs11989309	20,022,819	T	C	0.088986	-0.081542	0.003537	6.4E-127
LPL *	8	rs75675187	20,023,215	T	C	0.088970	-0.081571	0.003537	5.3E-127
LPL *	8	rs74511360	20,023,529	A	G	0.085285	-0.081214	0.003609	1.2E-121
LPL *	8	rs78404258	20,023,547	G	A	0.089037	-0.081414	0.003536	1.5E-126
LPL *	8	rs74615535	20,023,725	A	G	0.088961	-0.081574	0.003537	5.3E-127
LPL *	8	rs60223219	20,024,290	G	A	0.089004	-0.081535	0.003537	7.3E-127
LPL *	8	rs35048052	20,024,541	AT	A	0.350748	-0.036427	0.002122	4.4E-71
LPL *	8	rs7816447	20,025,439	C	T	0.087661	-0.081641	0.003567	2.8E-125
LPL *	8	rs1919487	20,026,019	A	T	0.182834	-0.051958	0.002612	1.1E-93
LPL *	8	rs73208819	20,026,413	C	T	0.223915	0.016449	0.002421	4.3E-13
LPL *	8	rs114650503	20,026,746	A	G	0.085261	-0.081194	0.003609	1.2E-121
LPL *	8	rs9644639	20,027,436	G	C	0.085230	-0.081290	0.003611	8.6E-122
LPL *	8	rs2410631	20,028,057	T	A	0.184202	-0.051679	0.002604	4.2E-93
LPL *	8	rs2410632	20,028,146	A	G	0.184074	-0.051693	0.002605	4.3E-93
LPL *	8	rs11984636	20,028,215	C	T	0.085806	-0.081203	0.003602	9.2E-122
LPL *	8	rs11984698	20,028,423	C	T	0.085773	-0.081194	0.003604	1.1E-121
LPL *	8	rs35147888	20,028,593	T	TG	0.184156	-0.051728	0.002604	2.9E-93
LPL *	8	rs11995475	20,029,177	T	C	0.085746	-0.081244	0.003604	9.0E-122
LPL *	8	rs75469215	20,029,651	T	A	0.085201	-0.080746	0.003622	3.8E-119
LPL *	8	rs4543558	20,030,818	G	C	0.184108	-0.051745	0.002607	1.9E-93
LPL *	8	rs2178296	20,031,614	T	G	0.167223	-0.052240	0.002699	6.6E-89
LPL *	8	rs78358410	20,031,888	G	T	0.099437	-0.078933	0.003395	6.5E-129
LPL *	8	rs10103634	20,033,101	A	G	0.249959	-0.035419	0.002334	5.5E-57
LPL *	8	rs139315015	20,035,786	G	A	0.113525	-0.062781	0.003184	4.8E-95
LPL *	8	rs28841897	20,036,993	C	T	0.338206	-0.035847	0.002144	1.7E-67
LPL *	8	rs149001621	20,039,893	T	C	0.010900	0.070217	0.009784	3.2E-14
LPL *	8	rs4244457	20,041,535	T	C	0.327945	-0.036399	0.002144	2.3E-69
LPL *	8	rs76259755	20,041,650	C	T	0.113086	-0.062878	0.003185	1.1E-95
LPL *	8	rs78263306	20,043,160	C	G	0.330271	-0.035298	0.002143	1.5E-65
LPL *	8	rs6993414	20,045,407	G	A	0.113942	-0.063255	0.003174	1.9E-97
LPL *	8	rs74983646	20,045,739	A	G	0.097771	-0.060035	0.003404	6.5E-77

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
LPL *	8	rs78299715	20,048,393	G	C	0.048831	-0.031365	0.004682	5.3E-13
LPL *	8	rs118099376	20,048,449	A	G	0.016771	-0.077255	0.007864	5.5E-24
LPL *	8	rs11991231	20,050,401	C	T	0.113763	-0.063170	0.003178	7.3E-97
LPL *	8	rs66462329	20,054,549	A	G	0.242254	-0.037504	0.002359	2.0E-62
LPL *	8	rs115849089	20,054,859	A	G	0.110328	-0.061102	0.003220	4.6E-89
LPL *	8	rs4585763	20,055,743	T	A	0.327743	-0.036422	0.002155	2.6E-69
SLC18A1 *	8	rs6586891	20,057,087	A	C	0.323519	-0.035352	0.002164	1.5E-64
SLC18A1 *	8	rs10104610	20,058,043	C	G	0.242644	-0.037647	0.002358	5.1E-63
SLC18A1 *	8	rs66778572	20,058,609	A	G	0.241668	-0.037404	0.002363	4.5E-62
SLC18A1 *	8	rs4128744	20,062,144	T	C	0.111488	-0.061175	0.003207	7.0E-90
SLC18A1 *	8	rs4637851	20,065,099	A	G	0.342776	-0.036267	0.002154	2.8E-68
SLC18A1 *	8	rs6999158	20,070,502	A	T	0.264676	-0.038006	0.002316	4.3E-66
SLC18A1 *	8	rs10106652	20,070,649	A	G	0.263216	-0.038215	0.002321	1.1E-66
SLC18A1 *	8	rs9644568	20,071,071	A	G	0.112729	-0.060751	0.003184	2.8E-90
SLC18A1 *	8	rs34351848	20,071,686	T	TC	0.262265	-0.038399	0.002338	2.3E-66
SLC18A1 *	8	rs76722925	20,073,987	G	A	0.045851	-0.028333	0.004845	6.9E-11
SLC18A1 *	8	rs80026582	20,075,352	T	C	0.042844	-0.027368	0.005023	1.8E-09
SLC18A1 *	8	rs79445051	20,075,578	G	C	0.042592	-0.026601	0.005039	4.6E-09
SLC18A1 *	8	rs80302977	20,076,828	C	T	0.041479	-0.027240	0.005117	5.1E-09
SLC18A1 *	8	rs13281248	20,077,573	A	G	0.055547	-0.077829	0.004463	1.0E-74
SLC18A1 *	8	rs13257289	20,077,715	C	T	0.056893	-0.075915	0.004427	3.8E-72
SLC18A1 *	8	rs28597716	20,079,176	G	A	0.120839	-0.018639	0.003316	4.5E-10
SLC18A1 *	8	chr8:20081391_CAAAT_C	20,081,391	C	CAAAT	0.118258	-0.019845	0.003128	2.9E-11
SLC18A1 *	8	rs7001307	20,081,435	C	T	0.116693	-0.020788	0.003155	6.2E-12
SLC18A1 *	8	rs12542766	20,082,161	G	A	0.215280	-0.015573	0.002450	1.4E-10
SLC18A1 *	8	rs111648692	20,082,711	CTT	C	0.215484	-0.015465	0.002448	2.0E-10
SLC18A1 *	8	rs35094081	20,082,955	AT	A	0.216022	-0.015231	0.002447	3.9E-10
SLC18A1 *	8	rs11204085	20,083,285	C	T	0.120561	-0.020125	0.003093	1.1E-11
SLC18A1 *	8	rs11204086	20,083,434	G	T	0.120561	-0.020125	0.003093	1.1E-11
SLC18A1 *	8	rs11204087	20,083,516	T	C	0.120679	-0.020050	0.003091	1.2E-11
SLC18A1 *	8	rs6586892	20,083,634	A	C	0.212093	-0.015806	0.002460	8.6E-11
SLC18A1 *	8	rs12544702	20,083,748	C	T	0.120477	-0.020243	0.003094	8.8E-12
SLC18A1 *	8	rs6989064	20,083,937	T	C	0.204205	-0.016346	0.002497	4.1E-11
SLC18A1 *	8	rs4543559	20,084,343	G	A	0.216195	-0.015589	0.002443	1.2E-10
SLC18A1 *	8	rs34095314	20,084,640	TA	T	0.120483	-0.020192	0.003094	9.9E-12
SLC18A1 *	8	rs13263508	20,084,670	T	G	0.200635	-0.016124	0.002516	9.9E-11
SLC18A1 *	8	rs34758843	20,085,184	T	C	0.120437	-0.020252	0.003095	9.2E-12
SLC18A1 *	8	rs35005862	20,085,189	C	T	0.120437	-0.020252	0.003095	9.2E-12
SLC18A1 *	8	rs73210856	20,085,295	G	A	0.120283	-0.020362	0.003097	7.5E-12
SLC18A1 *	8	rs73210858	20,085,296	A	T	0.120283	-0.020362	0.003097	7.5E-12
SLC18A1 *	8	rs11986461	20,085,397	A	C	0.210195	-0.016187	0.002473	3.1E-11
SLC18A1 *	8	rs28475019	20,085,440	A	T	0.120330	-0.020145	0.003097	1.2E-11
SLC18A1 *	8	rs13265868	20,085,516	A	G	0.120171	-0.020043	0.003099	1.5E-11
SLC18A1 *	8	rs28450859	20,085,556	C	G	0.120004	-0.020124	0.003102	1.3E-11
SLC18A1 *	8	rs13273470	20,085,675	C	G	0.118761	-0.019912	0.003122	3.3E-11
SLC18A1 *	8	rs13275622	20,085,708	A	C	0.118255	-0.019976	0.003131	3.3E-11
SLC18A1 *	8	rs13276972	20,085,797	G	A	0.139059	-0.017724	0.002951	4.4E-10
SLC18A1 *	8	rs12676079	20,085,853	T	C	0.115912	-0.019486	0.003172	1.3E-10
KCNU1 *	8	rs56687477	36,974,792	A	G	0.320123	0.012683	0.002181	7.5E-09
KCNU1 *	8	chr8:36977582_G_GA	36,977,582	GA	G	0.327711	0.011980	0.002165	3.8E-08
KCNU1 *	8	rs7816345	36,988,591	T	C	0.335909	0.011849	0.002134	3.0E-08
KCNU1 *	8	rs75772194	36,988,917	G	A	0.335792	0.011832	0.002134	3.1E-08
KCNU1 *	8	rs10086016	36,990,191	C	T	0.335776	0.011835	0.002134	3.0E-08
KCNU1 *	8	rs28735403	36,990,520	C	T	0.335775	0.011838	0.002134	3.0E-08
KCNU1 *	8	rs16885613	36,990,839	C	T	0.335778	0.011836	0.002134	3.0E-08
KCNU1 *	8	rs4286946	36,992,428	G	C	0.335768	0.011890	0.002134	2.6E-08
KCNU1 *	8	rs10955009	36,994,383	A	C	0.335775	0.011826	0.002134	3.1E-08
KCNU1 *	8	rs10096213	36,995,695	T	C	0.335385	0.011965	0.002135	2.0E-08
KCNU1 *	8	rs10095380	36,995,699	C	G	0.335385	0.011965	0.002135	2.0E-08
KCNU1 *	8	rs10092900	36,997,193	G	T	0.335441	0.011953	0.002135	2.2E-08
KCNU1 *	8	rs10087804	37,000,622	G	C	0.335333	0.011938	0.002135	2.3E-08
KCNU1 *	8	rs13365225	37,000,965	G	A	0.335345	0.011945	0.002135	2.3E-08
CYP7A1 *	8	rs28483956	58,492,900	A	G	0.257562	-0.012357	0.002326	7.6E-09
CYP7A1 *	8	rs6997473	58,493,664	G	A	0.256527	-0.012191	0.002327	1.2E-08
CYP7A1 *	8	rs112784971	58,493,931	T	C	0.230694	-0.013876	0.002404	6.9E-10
CYP7A1 *	8	rs16923530	58,506,936	T	C	0.214288	-0.014183	0.002458	5.2E-09
CYP7A1 *	8	rs200378757	58,506,959	G	A	0.210967	-0.013578	0.002479	3.5E-08
CYP7A1 *	8	rs202181871	58,506,961	A	G	0.213888	-0.014242	0.002460	4.9E-09
CYP7A1 *	8	rs76133469	58,508,253	A	T	0.215707	-0.013947	0.002451	9.0E-09
CYP7A1 *	8	rs58021454	58,509,233	A	C	0.215705	-0.013958	0.002451	8.7E-09
CYP7A1 *	8	rs57586133	58,510,150	G	C	0.215940	-0.013893	0.002451	1.0E-08
CYP7A1 *	8	rs79242462	58,513,517	T	C	0.215655	-0.013946	0.002451	8.5E-09
CYP7A1 *	8	rs4738689	58,518,054	C	A	0.215733	-0.013893	0.002451	1.0E-08
CYP7A1 *	8	rs41428647	58,518,544	G	T	0.215782	-0.013968	0.002450	8.3E-09
CYP7A1 *	8	rs56743550	58,518,727	C	T	0.215739	-0.013968	0.002450	8.1E-09
CYP7A1 *	8	rs141308993	58,518,938	C	T	0.215782	-0.013968	0.002450	8.3E-09
CYP7A1 *	8	rs77520539	58,519,538	T	G	0.215780	-0.013961	0.002450	8.4E-09
CYP7A1 *	8	rs75304727	58,519,780	A	G	0.215832	-0.013889	0.002449	9.8E-09
CYP7A1 *	8	rs200528271	58,520,001	T	C	0.189316	-0.015210	0.002633	6.8E-09
CYP7A1 *	8	rs34726782	58,520,942	G	A	0.215913	-0.013966	0.002450	8.7E-09
CYP7A1 *	8	rs76658138	58,521,491	G	A	0.215141	-0.013970	0.002454	9.2E-09
CYP7A1 *	8	chr8:58521995_AT_A	58,521,995	A	AT	0.221876	-0.013101	0.002435	4.0E-08
CYP7A1 *	8	rs74984505	58,522,596	G	A	0.215799	-0.013934	0.002450	9.0E-09
CYP7A1 *	8	rs138570001	58,522,842	G	C	0.215805	-0.013937	0.002450	9.0E-09
CYP7A1 *	8	rs75797469	58,523,084	A	G	0.215987	-0.013949	0.002449	8.3E-09
CYP7A1 *	8	rs75441763	58,525,293	A	G	0.215805	-0.013937	0.002450	9.0E-09
CYP7A1 *	8	rs78463309	58,525,673	A	G	0.215805	-0.013937	0.002450	9.0E-09
CYP7A1 *	8	rs7846047	58,525,702	T	A	0.215805	-0.013937	0.002450	9.0E-09
SDCBP *	8	rs76304302	58,527,230	A	G	0.215805	-0.013937	0.002450	9.0E-09
SDCBP *	8	chr8:58532491_T_TA	58,532,491	TA	T	0.201464	-0.013929	0.002545	2.7E-08
SDCBP *	8	rs79719702	58,535,541	G	C	0.215025	-0.013887	0.002456	9.1E-09
SDCBP *	8	rs57119091	58,537,720	C	T	0.213745	-0.014096	0.002464	5.9E-09
SDCBP *	8	rs16923547	58,537,806	T	C	0.214918	-0.013953	0.002455	7.4E-09
SDCBP *	8	rs75022950	58,538,575	G	C	0.214918	-0.013953	0.002455	7.4E-09
SDCBP *	8	rs60163136	58,542,629	G	A	0.214275	-0.013780	0.002457	1.0E-08
SDCBP *	8	rs78897568	58,550,819	G	C	0.214091	-0.013755	0.002460	1.1E-08
SDCBP *	8	rs74407357	58,550,842	C	A	0.213839	-0.013776	0.002461	1.1E-08

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SDCBP	8	rs77121175	58,554,876	G	T	0.227648	-0.013813	0.002401	6.6E-09
SDCBP	8	rs58586560	58,555,472	G	A	0.227644	-0.013828	0.002401	6.3E-09
SDCBP	8	rs58276148	58,557,610	G	T	0.227648	-0.013810	0.002401	6.6E-09
SDCBP	8	rs75120937	58,561,531	A	C	0.227650	-0.013812	0.002401	6.6E-09
SDCBP	8	chr8:585632074_T_TA	58,562,074	TA	T	0.324101	-0.012184	0.002162	4.8E-09
SDCBP	8	chr8:58563572_T_TA	58,563,572	TA	T	0.226470	-0.013655	0.002409	1.2E-08
SDCBP	8	rs77422315	58,565,102	T	C	0.227541	-0.013866	0.002402	5.9E-09
SDCBP	8	chr8:58569239_T_TTGCCATGTTGGCCATGACAAACATGACAACA	58,569,239	CATGAC/	T	0.222219	-0.014303	0.002432	2.0E-09
SDCBP	8	rs79273134	58,571,506	A	G	0.227653	-0.013748	0.002401	7.9E-09
SDCBP	8	rs57137362	58,573,770	G	A	0.227651	-0.013746	0.002401	7.9E-09
SDCBP	8	rs16923573	58,573,961	T	C	0.227651	-0.013746	0.002401	7.9E-09
SDCBP	8	rs77342596	58,574,294	A	C	0.226781	-0.013946	0.002407	5.0E-09
SDCBP	8	rs80072390	58,574,300	T	A	0.226781	-0.013946	0.002407	5.0E-09
SDCBP	8	rs7833413	58,575,730	G	A	0.227722	-0.013687	0.002401	9.0E-09
SDCBP	8	rs60600243	58,580,172	T	A	0.227570	-0.013815	0.002402	6.5E-09
SDCBP	8	rs3739326	58,582,153	A	T	0.227500	-0.013737	0.002402	8.1E-09
NSMAF	8	rs59644857	58,584,375	T	C	0.227453	-0.013430	0.002403	1.7E-08
NSMAF	8	rs76354168	58,585,855	T	A	0.226851	-0.013600	0.002410	1.5E-08
TRPS1	8	rs727582	115,638,241	G	A	0.346398	-0.011191	0.002126	4.6E-08
TRPS1	8	rs727581	115,638,264	C	T	0.346457	-0.011187	0.002126	4.5E-08
TRPS1	8	rs2178950	115,640,791	C	G	0.345141	-0.011294	0.002127	3.7E-08
TRPS1	8	rs2721956	115,641,429	A	G	0.344153	-0.011341	0.002128	3.3E-08
TRPS1	8	rs1983541	115,642,330	T	C	0.343532	-0.011214	0.002131	4.5E-08
TRPS1	8	rs2721959	115,643,980	G	T	0.344967	-0.011334	0.002125	3.0E-08
TRPS1	8	rs2721960	115,644,502	A	G	0.344432	-0.011356	0.002124	3.0E-08
TRPS1	8	rs2737239	115,644,722	G	A	0.344430	-0.011356	0.002124	3.0E-08
TRPS1	8	rs2737241	115,645,229	A	G	0.344414	-0.011366	0.002124	2.9E-08
TRPS1	8	rs2737242	115,645,500	C	T	0.344396	-0.011378	0.002124	2.8E-08
TRPS1	8	rs2737243	115,645,654	C	G	0.344465	-0.011467	0.002127	2.3E-08
TRPS1	8	rs2737244	115,646,004	T	A	0.344070	-0.011571	0.002128	1.7E-08
TRPS1	8	rs3808478	115,666,050	C	T	0.365840	-0.011237	0.002097	4.3E-08
TRPS1 *	8	rs179456	115,682,885	A	G	0.353251	-0.011900	0.002127	1.5E-08
TRPS1 *	8	rs17729317	115,683,666	A	G	0.353154	-0.011849	0.002128	1.7E-08
TRPS1 *	8	rs110505262	115,685,625	T	A	0.354241	-0.011549	0.002129	4.2E-08
TRPS1 *	8	rs4876612	115,686,812	T	C	0.352905	-0.011855	0.002129	1.7E-08
TRPS1 *	8	rs12682033	115,688,903	T	C	0.355269	-0.011703	0.002124	2.2E-08
TRPS1 *	8	rs751078958	115,690,717	A	C	0.353450	-0.011951	0.002128	1.2E-08
TRPS1 *	8	rs9297543	115,692,754	C	T	0.419607	-0.011453	0.002066	6.5E-09
TRPS1 *	8	rs800562	115,696,794	C	T	0.355683	-0.011651	0.002124	2.6E-08
TRPS1 *	8	rs800566	115,697,608	A	G	0.353198	-0.011967	0.002128	1.2E-08
TRPS1 *	8	rs11337200	115,701,567	AT	A	0.355684	-0.011606	0.002123	3.1E-08
TRPS1 *	8	rs800575	115,703,162	C	T	0.353964	-0.011773	0.002126	2.0E-08
TRPS1 *	8	rs800574	115,705,224	A	C	0.343102	-0.012188	0.002138	6.6E-09
TRPS1 *	8	rs800572	115,706,211	A	G	0.344979	-0.011871	0.002134	1.4E-08
TRPS1 *	8	rs2960151	115,706,393	C	A	0.343085	-0.012166	0.002138	7.0E-09
TRPS1 *	8	rs800534	115,707,671	C	T	0.402230	-0.011293	0.002073	1.3E-08
TRPS1 *	8	rs800535	115,708,163	T	G	0.401699	-0.011310	0.002073	1.2E-08
TRPS1 *	8	rs800536	115,708,179	A	T	0.401725	-0.011301	0.002073	1.3E-08
TRPS1 *	8	rs800537	115,709,757	C	T	0.357338	-0.011503	0.002117	3.2E-08
TRPS1 *	8	rs800538	115,710,763	A	G	0.326460	-0.012776	0.002162	2.1E-09
TRPS1 *	8	rs2736231	115,711,170	C	T	0.404254	-0.011122	0.002076	2.3E-08
TRPS1 *	8	rs2694027	115,711,171	T	G	0.404294	-0.011297	0.002074	1.4E-08
TRPS1 *	8	rs800539	115,712,972	G	A	0.325695	-0.012924	0.002166	1.4E-09
TRPS1 *	8	rs800541	115,717,911	G	T	0.328517	-0.012340	0.002159	6.6E-09
TRPS1 *	8	rs800542	115,719,218	C	T	0.326741	-0.012728	0.002162	2.5E-09
TRPS1 *	8	rs800571	115,720,681	T	C	0.326468	-0.012687	0.002162	2.8E-09
TRPS1 *	8	chr8:115722505_TAC_T	115,722,505	TAC	T	0.332570	-0.013373	0.002162	4.2E-10
TRPS1 *	8	rs2694034	115,728,597	A	G	0.404072	-0.011190	0.002064	1.5E-08
TRPS1 *	8	rs7834801	115,731,575	T	C	0.332101	-0.011757	0.002133	2.0E-08
TRPS1 *	8	rs139674239	115,731,796	TG	T	0.327289	-0.012439	0.002144	3.6E-09
TRPS1 *	8	rs800521	115,732,282	A	C	0.329909	-0.012071	0.002138	9.6E-09
TRPS1 *	8	rs800520	115,732,360	G	T	0.329912	-0.012074	0.002138	9.5E-09
TRPS1 *	8	rs71287295	115,733,764	C	CT	0.331796	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs1880816	115,733,959	T	G	0.331796	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs1880815	115,734,059	G	A	0.331866	-0.011769	0.002133	1.9E-08
TRPS1 *	8	rs1880814	115,734,251	C	T	0.332086	-0.011733	0.002133	2.2E-08
TRPS1 *	8	rs2205265	115,734,520	G	T	0.331798	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs2205266	115,734,673	G	A	0.331796	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs149197697	115,735,087	T	TTCTC	0.334208	-0.011821	0.002140	1.8E-08
TRPS1 *	8	rs2736233	115,735,138	G	T	0.332476	-0.011487	0.002136	4.1E-08
TRPS1 *	8	rs1405297	115,735,275	G	T	0.331796	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs1830141	115,735,511	A	G	0.332282	-0.011637	0.002135	3.1E-08
TRPS1 *	8	rs1405296	115,735,525	C	A	0.332033	-0.011841	0.002134	1.7E-08
TRPS1 *	8	rs2960148	115,735,563	C	T	0.331796	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs2736234	115,735,598	G	T	0.331796	-0.011754	0.002133	2.1E-08
TRPS1 *	8	rs2694049	115,735,831	T	C	0.332144	-0.011508	0.002133	3.8E-08
TRPS1 *	8	rs2694048	115,735,937	C	T	0.331777	-0.011759	0.002134	2.0E-08
TRPS1 *	8	rs2254555	115,741,374	T	G	0.331358	-0.011732	0.002134	2.4E-08
TRPS1 *	8	rs5894291	115,741,527	A	AT	0.331912	-0.011761	0.002137	2.4E-08
TRPS1 *	8	rs985161	115,741,917	C	T	0.331478	-0.011717	0.002135	2.5E-08
TRPS1 *	8	rs11040331	115,742,981	T	C	0.329097	-0.011986	0.002139	1.3E-08
TRPS1 *	8	rs2975510	115,742,985	T	C	0.332062	-0.011777	0.002135	2.1E-08
TRPS1 *	8	rs2960146	115,743,211	A	G	0.331387	-0.011751	0.002135	2.3E-08
TRPS1 *	8	rs2223058	115,744,962	G	A	0.332980	-0.011558	0.002132	3.6E-08
TRPS1 *	8	rs800505	115,750,077	G	C	0.331079	-0.011544	0.002147	4.3E-08
TRPS1 *	8	rs800540	115,779,523	A	C	0.362830	-0.011483	0.002096	4.6E-08
TRPS1 *	8	rs2736202	115,780,200	C	T	0.417381	-0.011255	0.002038	9.0E-09
TRPS1 *	8	chr8:115780370_TTGTG_T	115,780,370	TTGTG	T	0.386496	-0.011598	0.002064	7.2E-09
TRPS1 *	8	rs2736203	115,781,341	T	C	0.386246	-0.011623	0.002064	6.9E-09
TRPS1 *	8	rs2694037	115,782,005	G	A	0.386170	-0.011641	0.002064	6.8E-09
TRPS1 *	8	rs2694036	115,782,050	G	T	0.386246	-0.011623	0.002064	6.9E-09
TRPS1 *	8	rs2694035	115,782,367	G	C	0.436509	-0.010968	0.002027	1.4E-08
TRPS1 *	8	rs2960157	115,783,315	T	G	0.436679	-0.011045	0.002027	1.2E-08
TRPS1 *	8	rs2960156	115,783,651	A	G	0.386362	-0.011539	0.002066	9.3E-09
TRPS1 *	8	rs800507	115,784,313	G	T	0.386800	-0.011748	0.002067	4.8E-09
TRPS1 *	8	rs800508	115,784,686	C	A	0.417292	-0.011262	0.002037	9.1E-09
TRPS1 *	8	rs800509	115,785,304	A	C	0.417292	-0.011262	0.002037	9.1E-09

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
TRPS1 *	8	rs35940052	115,785,590	T	TA	0.387634	-0.011551	0.002064	1.0E-08
TRPS1 *	8	rs800510	115,786,001	G	A	0.417293	-0.011263	0.002037	9.1E-09
TRPS1 *	8	rs813889	115,786,626	C	T	0.436511	-0.010962	0.002027	1.5E-08
TRPS1 *	8	rs800511	115,786,942	C	A	0.386240	-0.011620	0.002064	7.1E-09
TRPS1 *	8	rs800512	115,787,367	C	T	0.386240	-0.011620	0.002064	7.1E-09
TRPS1 *	8	rs808982	115,788,025	T	G	0.417261	-0.011266	0.002038	9.1E-09
TRPS1 *	8	rs800514	115,788,658	T	A	0.386558	-0.011736	0.002065	5.3E-09
TRPS1 *	8	rs800516	115,789,141	A	G	0.386321	-0.011696	0.002063	5.3E-09
TRPS1 *	8	rs800517	115,789,263	G	A	0.417306	-0.011404	0.002037	5.6E-09
TRPS1 *	8	rs800518	115,789,554	C	T	0.416921	-0.011276	0.002038	8.3E-09
TRPS1 *	8	rs1065806	115,790,856	A	G	0.387382	-0.011941	0.002065	3.0E-09
TRPS1 *	8	rs1065805	115,790,904	C	T	0.417319	-0.011459	0.002037	4.9E-09
TRPS1 *	8	rs1089116	115,792,232	C	A	0.386899	-0.011698	0.002062	5.2E-09
TRPS1 *	8	rs1089117	115,793,066	T	C	0.417323	-0.011455	0.002037	5.0E-09
TRPS1 *	8	rs800519	115,793,803	A	G	0.436966	-0.011183	0.002027	7.6E-09
TRPS1 *	8	rs702775	115,794,278	G	A	0.386308	-0.011752	0.002063	4.6E-09
TRPS1 *	8	rs702774	115,794,425	G	A	0.387067	-0.011672	0.002065	5.6E-09
TRPS1 *	8	rs702773	115,794,432	C	A	0.437388	-0.011151	0.002029	8.1E-09
TRPS1 *	8	rs702772	115,794,691	G	A	0.386891	-0.011685	0.002062	5.4E-09
TRPS1 *	8	chr8:115795930_CT_C	115,795,930	CT	C	0.386649	-0.011699	0.002064	5.1E-09
TRPS1 *	8	rs10566864	115,796,972	CTTTAG	C	0.417433	-0.011288	0.002039	8.6E-09
TRPS1 *	8	rs2736207	115,797,429	C	T	0.436378	-0.011101	0.002027	1.0E-08
TRPS1 *	8	rs2694033	115,797,806	G	A	0.437137	-0.011079	0.002026	9.8E-09
TRPS1 *	8	rs800591	115,799,160	T	C	0.410273	-0.010831	0.002043	3.2E-08
TRPS1 *	8	rs800590	115,800,352	C	T	0.412674	-0.010755	0.002049	4.8E-08
TRPS1 *	8	rs3036187	115,800,358	T	TGAA	0.381471	-0.011115	0.002077	3.7E-08
TRPS1 *	8	rs800589	115,800,477	T	C	0.379433	-0.011129	0.002071	3.2E-08
TRPS1 *	8	rs800588	115,800,917	T	G	0.410579	-0.010704	0.002041	4.8E-08
TRPS1 *	8	rs800587	115,801,052	T	G	0.379433	-0.011129	0.002071	3.2E-08
TRPS1 *	8	rs800586	115,801,679	G	A	0.439023	-0.010704	0.002025	3.0E-08
TRPS1 *	8	rs800585	115,801,697	T	A	0.379432	-0.011126	0.002071	3.2E-08
TRPS1 *	8	rs10636176	115,803,173	A	AAC	0.379388	-0.011141	0.002072	3.2E-08
TRPS1 *	8	rs800553	115,804,366	T	C	0.379205	-0.011333	0.002077	1.9E-08
TRPS1 *	8	rs800552	115,804,530	G	T	0.379805	-0.011253	0.002077	2.4E-08
TRPS1 *	8	rs800551	115,807,041	C	G	0.408204	-0.011044	0.002054	2.2E-08
TRPS1 *	8	rs702771	115,807,640	C	T	0.380075	-0.011176	0.002080	3.3E-08
TRPS1 *	8	rs800547	115,807,948	T	G	0.379687	-0.011292	0.002078	2.2E-08
TRPS1 *	8	rs800546	115,808,960	C	A	0.408194	-0.011127	0.002055	1.8E-08
TRPS1 *	8	rs800545	115,810,420	A	G	0.407570	-0.011155	0.002055	1.6E-08
TRPS1 *	8	rs800544	115,811,384	A	G	0.379160	-0.011452	0.002079	1.4E-08
TRPS1 *	8	rs2694045	115,811,975	G	A	0.378661	-0.011704	0.002086	7.6E-09
TRPS1 *	8	rs2254401	115,812,474	C	T	0.365667	-0.011733	0.002101	8.4E-09
TRPS1 *	8	rs1040333	115,813,123	T	C	0.415853	-0.010982	0.002048	1.8E-08
TRPS1 *	8	rs1474517	115,813,316	C	T	0.365129	-0.011545	0.002091	1.5E-08
TRPS1 *	8	rs1474518	115,813,464	C	T	0.365352	-0.011577	0.002091	1.4E-08
TRPS1 *	8	rs2736208	115,814,018	T	C	0.396761	-0.010892	0.002064	3.7E-08
TRPS1 *	8	rs2694043	115,814,036	A	G	0.365536	-0.011582	0.002095	1.3E-08
TRPS1 *	8	rs2694042	115,814,038	C	A	0.365530	-0.011570	0.002095	1.3E-08
TRPS1 *	8	rs2736209	115,814,130	C	T	0.365255	-0.011622	0.002094	1.1E-08
TRPS1 *	8	rs2736212	115,815,002	T	C	0.364692	-0.011687	0.002095	9.7E-09
TRPS1 *	8	rs2694041	115,815,047	G	A	0.364694	-0.011678	0.002095	1.0E-08
TRPS1 *	8	rs2736213	115,815,632	G	A	0.364696	-0.011681	0.002095	9.9E-09
TRPS1 *	8	rs2736215	115,816,495	T	C	0.364709	-0.011614	0.002096	1.2E-08
TRPS1 *	8	rs2736216	115,817,111	T	C	0.364704	-0.011610	0.002096	1.2E-08
TRPS1 *	8	rs2736217	115,817,243	G	A	0.364711	-0.011627	0.002096	1.2E-08
TRPS1 *	8	rs2736219	115,817,495	T	C	0.396417	-0.010865	0.002063	4.6E-08
TRPS1 *	8	rs2960153	115,819,348	T	C	0.417837	-0.011243	0.002049	1.0E-08
TRPS1 *	8	rs2736222	115,819,542	G	A	0.395947	-0.011100	0.002059	2.5E-08
TRPS1 *	8	rs2960155	115,819,606	G	A	0.396053	-0.010993	0.002059	3.3E-08
TRPS1 *	8	rs2975506	115,819,720	T	C	0.365910	-0.011609	0.002091	1.2E-08
TRPS1 *	8	rs2736223	115,820,066	A	G	0.366396	-0.011659	0.002092	1.1E-08
TRPS1 *	8	rs2736224	115,820,106	G	A	0.395945	-0.011175	0.002060	2.1E-08
TRPS1 *	8	rs2694039	115,820,120	C	T	0.395945	-0.011175	0.002060	2.1E-08
TRPS1 *	8	rs2736225	115,820,121	A	G	0.395945	-0.011175	0.002060	2.1E-08
TRPS1 *	8	rs71508456	115,820,588	C	T	0.415218	-0.011470	0.002046	5.8E-09
TRPS1 *	8	rs2975507	115,820,984	T	C	0.415535	-0.011400	0.002045	6.3E-09
TRPS1 *	8	chr8:115822230_C_CT	115,822,230	C	CT	0.418935	-0.011491	0.002060	6.4E-09
TRPS1 *	8	rs800555	115,822,721	G	C	0.415644	-0.011400	0.002044	6.5E-09
TRPS1 *	8	rs800556	115,823,198	A	G	0.415645	-0.011392	0.002044	6.6E-09
TRPS1 *	8	rs800557	115,823,633	G	T	0.395849	-0.011129	0.002060	2.4E-08
TRPS1 *	8	rs60591294	115,824,044	T	TTG	0.395994	-0.011089	0.002060	2.8E-08
TRPS1 *	8	rs800558	115,824,362	C	T	0.368630	-0.011634	0.002090	1.1E-08
TRPS1 *	8	rs800559	115,824,846	A	C	0.416077	-0.011306	0.002044	8.3E-09
TRPS1 *	8	rs800560	115,825,661	C	G	0.368492	-0.011844	0.002090	6.0E-09
TRPS1 *	8	rs3036205	115,826,036	C	CTCTT	0.368874	-0.011911	0.002090	5.3E-09
TRPS1 *	8	rs1014180	115,827,487	A	T	0.395876	-0.011048	0.002060	3.0E-08
TRPS1 *	8	rs2358065	115,827,713	T	C	0.415647	-0.011296	0.002044	8.7E-09
TRPS1 *	8	rs2960152	115,828,444	C	T	0.395881	-0.011119	0.002060	2.6E-08
TRPS1 *	8	rs2975508	115,828,544	A	G	0.365612	-0.011561	0.002093	1.5E-08
TRPS1 *	8	rs800533	115,828,760	C	T	0.415595	-0.011340	0.002045	8.0E-09
TRPS1 *	8	rs800532	115,829,884	A	G	0.429937	-0.011646	0.002042	2.3E-09
TRPS1 *	8	rs800531	115,831,047	T	C	0.359803	-0.011282	0.002128	3.0E-08
TRPS1 *	8	rs800530	115,831,666	C	T	0.389662	-0.010927	0.002103	4.0E-08
SLC30A8	8	rs11558471	117,173,494	G	A	0.467177	-0.010948	0.002014	3.7E-08
SLC30A8 *	8	rs11774700	117,208,031	C	T	0.470860	-0.010836	0.002018	4.3E-08
TRIB1 *	8	rs2003370	125,456,589	C	A	0.125647	0.017800	0.003094	3.7E-09
TRIB1 *	8	rs12678799	125,458,589	T	C	0.127608	0.018410	0.003065	9.4E-10
TRIB1 *	8	rs68089270	125,460,482	G	A	0.128827	0.018673	0.003048	4.3E-10
TRIB1 *	8	rs6983834	125,460,570	A	G	0.128860	0.018713	0.003047	3.9E-10
TRIB1 *	8	rs10956249	125,461,257	T	C	0.129184	0.018465	0.003038	5.8E-10
TRIB1 *	8	rs12679189	125,461,323	C	T	0.129442	0.018250	0.003034	9.1E-10
TRIB1 *	8	rs6999569	125,463,528	G	A	0.144804	-0.023183	0.002888	2.4E-16
TRIB1 *	8	rs2980856	125,464,137	G	C	0.144535	-0.023017	0.002887	4.1E-16
TRIB1 *	8	rs2954017	125,464,631	T	C	0.434925	0.031515	0.002030	2.8E-56
TRIB1 *	8	rs2954018	125,464,911	C	T	0.297002	0.026942	0.002203	1.5E-35
TRIB1 *	8	rs2980855	125,465,234	C	T	0.144540	-0.023043	0.002887	3.8E-16
TRIB1 *	8	rs2980854	125,465,255	T	C	0.144546	-0.023053	0.002887	3.7E-16

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
TRIB1 *	8	rs2954019	125,465,517	A	G	0.144398	-0.023104	0.002889	3.4E-16
TRIB1 *	8	rs2001945	125,465,736	G	C	0.434991	0.031533	0.002030	2.4E-56
TRIB1 *	8	rs2980853	125,466,108	A	C	0.441586	0.031022	0.002028	1.4E-54
TRIB1 *	8	rs2001846	125,466,208	T	C	0.435015	0.031526	0.002031	2.5E-56
TRIB1 *	8	rs2001845	125,466,402	A	G	0.297036	0.026942	0.002204	1.5E-35
TRIB1 *	8	rs2001844	125,466,503	A	G	0.441656	0.031078	0.002028	9.4E-55
TRIB1 *	8	rs7015677	125,466,516	G	A	0.137529	0.017831	0.002927	4.7E-10
TRIB1 *	8	rs6982636	125,467,073	G	A	0.441773	0.031067	0.002028	9.5E-55
TRIB1 *	8	rs6982502	125,467,120	C	T	0.435024	0.031481	0.002030	3.3E-56
TRIB1 *	8	rs2980886	125,467,846	G	A	0.441827	0.031032	0.002027	1.2E-54
TRIB1 *	8	rs4871603	125,468,125	C	T	0.303941	0.026084	0.002188	8.5E-34
TRIB1 *	8	rs2980882	125,468,458	A	G	0.441857	0.031026	0.002028	1.3E-54
TRIB1 *	8	rs2980880	125,468,730	G	A	0.297232	0.026899	0.002202	1.7E-35
TRIB1 *	8	rs2980879	125,469,233	A	T	0.297038	0.026619	0.002200	7.1E-35
TRIB1 *	8	rs2980876	125,469,452	C	T	0.297310	0.026848	0.002202	2.3E-35
TRIB1 *	8	chr8:125469461_C_CTT	125,469,461	CTT	C	0.135987	0.018122	0.002944	3.3E-10
TRIB1 *	8	rs2980875	125,469,505	A	G	0.448751	0.031260	0.002027	1.3E-55
TRIB1 *	8	rs2954020	125,469,710	A	G	0.297396	0.026964	0.002201	1.3E-35
TRIB1 *	8	rs2954021	125,469,835	A	G	0.440838	0.031964	0.002028	4.4E-58
TRIB1 *	8	rs2954022	125,470,379	C	A	0.447474	0.031482	0.002025	1.8E-56
TRIB1 *	8	rs79658059	125,470,680	T	TA	0.297434	0.026893	0.002202	1.9E-35
TRIB1 *	8	rs28495284	125,470,681	G	A	0.310176	0.025035	0.002218	1.3E-30
TRIB1 *	8	rs2954024	125,470,688	A	G	0.297434	0.026893	0.002202	1.9E-35
TRIB1 *	8	rs17406109	125,470,898	T	C	0.143327	0.018635	0.002875	3.2E-11
TRIB1 *	8	rs71576787	125,471,148	AT	A	0.143350	0.018541	0.002876	4.2E-11
TRIB1 *	8	rs12544593	125,471,585	A	G	0.142902	0.018582	0.002879	3.8E-11
TRIB1 *	8	rs2980870	125,471,598	A	G	0.311505	0.025835	0.002202	5.1E-33
TRIB1 *	8	chr8:125471601_TAA_T	125,471,601	TAA	T	0.302739	0.026215	0.002195	4.2E-34
TRIB1 *	8	rs148664420	125,471,740	T	TAATAA	0.143356	0.018648	0.002875	3.2E-11
TRIB1 *	8	rs4336630	125,472,034	T	G	0.304586	0.025752	0.002186	3.7E-33
TRIB1 *	8	rs2954025	125,472,221	C	T	0.304593	0.025763	0.002186	3.5E-33
TRIB1 *	8	rs2954026	125,472,284	T	G	0.297802	0.026577	0.002200	8.2E-35
TRIB1 *	8	rs2980862	125,472,396	G	C	0.297787	0.026619	0.002200	6.5E-35
TRIB1 *	8	rs13265432	125,472,467	A	G	0.143324	0.018656	0.002875	3.1E-11
TRIB1 *	8	rs35575186	125,472,985	A	AT	0.304595	0.025762	0.002186	3.5E-33
TRIB1 *	8	rs7828194	125,473,041	A	G	0.143321	0.018658	0.002875	3.1E-11
TRIB1 *	8	rs2954027	125,473,052	T	A	0.447952	0.031368	0.002025	3.5E-56
TRIB1 *	8	rs2954028	125,473,054	T	C	0.297789	0.026618	0.002200	6.5E-35
TRIB1 *	8	rs2980860	125,473,095	A	G	0.448049	0.031372	0.002026	3.5E-56
TRIB1 *	8	rs7828113	125,473,225	A	G	0.304661	0.025874	0.002186	1.8E-33
TRIB1 *	8	rs7846466	125,473,289	T	C	0.297912	0.026704	0.002201	4.6E-35
TRIB1 *	8	rs7828701	125,473,531	G	C	0.143416	0.018678	0.002874	2.9E-11
TRIB1 *	8	rs12545963	125,473,875	T	C	0.143416	0.018674	0.002874	2.9E-11
TRIB1 *	8	rs4592055	125,473,903	C	T	0.143413	0.018675	0.002874	2.9E-11
TRIB1 *	8	chr8:125473988_G_GT	125,473,988	G	GT	0.303124	0.026359	0.002205	4.0E-34
TRIB1 *	8	rs4567059	125,474,045	G	T	0.139840	0.018561	0.002910	7.5E-11
TRIB1 *	8	rs17321515	125,474,167	A	G	0.448126	0.031426	0.002025	2.0E-56
TRIB1 *	8	rs4567057	125,474,664	G	A	0.143305	0.018682	0.002876	3.1E-11
TRIB1 *	8	rs12679184	125,475,269	T	C	0.142938	0.018762	0.002879	2.4E-11
TRIB1 *	8	rs2980867	125,475,449	T	G	0.297856	0.026657	0.002201	4.8E-35
TRIB1 *	8	rs34604874	125,475,615	A	G	0.143307	0.018679	0.002876	3.1E-11
TRIB1 *	8	rs2980868	125,475,993	C	T	0.448248	0.031450	0.002026	2.2E-56
TRIB1 *	8	rs2980869	125,476,008	C	T	0.448435	0.031516	0.002026	1.5E-56
TRIB1 *	8	rs34417638	125,476,332	C	T	0.143307	0.018679	0.002876	3.1E-11
TRIB1 *	8	rs59871348	125,476,465	ATTG	A	0.305289	0.025913	0.002187	1.3E-33
TRIB1 *	8	rs2980871	125,476,688	G	A	0.126351	-0.024881	0.003044	1.5E-16
TRIB1 *	8	rs2954029	125,478,730	A	T	0.447994	0.031576	0.002024	7.2E-57
TRIB1 *	8	rs5894757	125,478,769	T	TG	0.304891	0.025781	0.002187	2.8E-33
TRIB1 *	8	rs2954030	125,479,062	T	C	0.318156	0.023818	0.002163	6.0E-29
TRIB1 *	8	rs2954031	125,479,491	G	T	0.461806	0.030228	0.002021	3.2E-52
TRIB1 *	8	rs13258507	125,480,355	G	T	0.143071	0.018811	0.002877	2.4E-11
TRIB1 *	8	rs35017684	125,480,557	A	AT	0.142886	0.018748	0.002880	2.5E-11
TRIB1 *	8	rs56116731	125,480,684	C	CT	0.301867	0.026564	0.002208	1.0E-34
TRIB1 *	8	rs12679547	125,480,843	A	G	0.142902	0.018815	0.002880	2.3E-11
TRIB1 *	8	rs2954032	125,481,150	A	G	0.297539	0.026821	0.002203	1.6E-35
TRIB1 *	8	rs2954033	125,481,504	A	G	0.298259	0.026801	0.002200	1.8E-35
TRIB1 *	8	rs4457349	125,482,075	G	A	0.418962	-0.020180	0.002041	7.3E-24
TRIB1 *	8	rs12680798	125,483,251	G	C	0.097882	-0.027728	0.003425	5.2E-16
TRIB1 *	8	rs10808546	125,483,576	T	C	0.125904	-0.024735	0.003036	1.4E-16
TRIB1 *	8	rs6470358	125,483,683	G	A	0.436916	0.010953	0.002034	4.5E-08
TRIB1 *	8	rs35309034	125,486,023	A	C	0.152451	0.019618	0.002803	7.5E-13
TRIB1 *	8	rs4870941	125,486,586	C	G	0.160584	0.016816	0.002751	2.5E-10
TRIB1 *	8	rs4870942	125,486,661	C	T	0.440193	0.011169	0.002041	2.3E-08
TRIB1 *	8	rs72442317	125,486,996	CCAGT	C	0.436734	0.010978	0.002036	4.2E-08
TRIB1 *	8	rs1055748815	125,486,998	AGTCG	A	0.436734	0.010978	0.002036	4.2E-08
TRIB1 *	8	rs2980859	125,487,187	C	G	0.283268	0.029053	0.002239	5.6E-40
TRIB1 *	8	rs4351435	125,487,636	G	A	0.283267	0.029043	0.002239	5.9E-40
TRIB1 *	8	rs28601761	125,487,789	G	C	0.150973	-0.024590	0.002821	3.0E-19
TRIB1 *	8	rs8180991	125,488,108	G	C	0.154942	0.019201	0.002779	1.5E-12
TRIB1 *	8	rs2980858	125,488,935	T	C	0.283746	0.028911	0.002238	1.2E-39
TRIB1 *	8	rs11320307	125,489,095	CA	C	0.436146	0.010990	0.002038	4.9E-08
TRIB1 *	8	rs12677676	125,490,284	G	A	0.154696	0.019125	0.002782	1.9E-12
TRIB1 *	8	rs55921265	125,491,673	A	G	0.154698	0.019123	0.002782	2.0E-12
TRIB1 *	8	rs71940472	125,492,114	C	ACCACC	0.153384	0.019384	0.002795	1.5E-12
TRIB1 *	8	rs13252684	125,492,119	A	G	0.140935	0.020676	0.002927	6.4E-13
TRIB1 *	8	rs13252187	125,492,126	T	C	0.137388	0.021430	0.002969	2.9E-13
TRIB1 *	8	rs13252202	125,492,129	T	C	0.137388	0.021430	0.002969	2.9E-13
TRIB1 *	8	rs6987702	125,492,484	T	C	0.434318	0.011243	0.002035	2.2E-08
TRIB1 *	8	rs34087092	125,492,520	A	G	0.154689	0.019058	0.002782	2.4E-12
TRIB1 *	8	rs75998532	125,493,463	C	T	0.403623	-0.021042	0.002057	1.6E-25
TRIB1 *	8	rs13271368	125,493,898	T	C	0.160337	0.017966	0.002749	2.1E-11
TRIB1 *	8	rs112875651	125,494,452	A	G	0.130443	-0.024420	0.002998	2.2E-16
TRIB1 *	8	rs2980888	125,495,066	T	C	0.281184	0.029603	0.002241	1.4E-41
TRIB1 *	8	rs2954038	125,495,147	C	A	0.281354	0.029721	0.002240	6.6E-42
TRIB1 *	8	rs6987904	125,495,783	T	C	0.402681	-0.020764	0.002070	1.4E-24
TRIB1 *	8	rs6989280	125,496,504	G	A	0.439109	0.011321	0.002063	2.1E-08
DMRT2 *	9	rs10958983	1,035,081	C	T	0.371824	0.012174	0.002098	1.5E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
DMRT2 *	9	rs150549203	1,035,756	AAAAAAC	A	0.368830	0.012156	0.002107	1.8E-08
DMRT2 *	9	rs4741016	1,036,132	C	T	0.371603	0.012236	0.002097	1.3E-08
DMRT2 *	9	rs12001314	1,038,063	C	A	0.373980	0.012277	0.002093	1.0E-08
DMRT2 *	9	rs10959032	1,038,666	T	C	0.372216	0.012376	0.002097	8.4E-09
ABCA1	9	rs2740488	104,899,461	C	A	0.230758	-0.016678	0.002395	6.3E-13
ABCA1	9	rs1883025	104,902,020	T	C	0.233430	-0.017287	0.002379	1.1E-13
ABCA1	9	rs2575876	104,903,458	A	G	0.231243	-0.017501	0.002387	5.4E-14
ABCA1	9	rs1800978	104,903,697	G	C	0.165987	-0.014393	0.002712	3.4E-08
ABCA1	9	rs1799777	104,903,754	GC	G	0.164736	-0.015149	0.002719	7.2E-09
ABCA1	9	rs2254708	104,904,866	C	T	0.164030	-0.015091	0.002737	1.0E-08
PTPN3	9	rs149557654	109,434,560	A	G	0.201425	-0.017610	0.002534	8.7E-13
PTPN3	9	rs61543659	109,434,691	G	A	0.266156	-0.014337	0.002302	7.7E-11
PTPN3	9	rs17201500	109,434,773	A	G	0.201584	-0.017755	0.002532	5.3E-13
PTPN3	9	rs75992442	109,434,977	G	A	0.201600	-0.017795	0.002532	4.7E-13
PTPN3	9	rs16914135	109,435,232	C	A	0.266318	-0.014449	0.002301	5.6E-11
PTPN3	9	rs75714696	109,435,291	C	G	0.201696	-0.017711	0.002532	6.0E-13
PTPN3	9	rs7044766	109,435,739	T	C	0.266392	-0.014420	0.002301	5.8E-11
PTPN3	9	rs56208012	109,436,498	T	A	0.266397	-0.014408	0.002301	6.0E-11
PTPN3	9	rs112194983	109,437,194	T	C	0.201976	-0.017672	0.002530	6.1E-13
PTPN3	9	rs17793718	109,437,226	A	G	0.201904	-0.017661	0.002531	6.4E-13
PTPN3	9	rs17201542	109,437,914	C	T	0.202121	-0.017635	0.002530	6.3E-13
PTPN3	9	rs79420384	109,441,288	T	TTA	0.282741	-0.013103	0.002243	1.6E-09
PTPN3	9	rs17793748	109,441,345	T	C	0.283027	-0.013058	0.002241	1.9E-09
PTPN3	9	rs3793527	109,443,174	A	C	0.283084	-0.013053	0.002241	2.0E-09
PTPN3	9	rs45581632	109,445,147	T	A	0.283091	-0.013082	0.002241	1.8E-09
PTPN3	9	rs3835284	109,445,599	AG	A	0.283179	-0.013113	0.002241	1.8E-09
PTPN3	9	rs76329186	109,446,543	A	G	0.283125	-0.013094	0.002240	1.8E-09
PTPN3	9	rs17793778	109,446,759	G	A	0.283125	-0.013094	0.002240	1.8E-09
PTPN3	9	rs146084146	109,446,922	C	3CTACCA'	0.281282	-0.013143	0.002250	1.7E-09
PTPN3	9	rs17201598	109,448,583	A	T	0.289477	-0.012676	0.002226	7.1E-09
PTPN3	9	rs1541090	109,451,227	T	A	0.309265	-0.012860	0.002188	1.4E-09
PTPN3	9	rs1541091	109,451,408	A	G	0.311178	-0.013068	0.002180	8.6E-10
PTPN3	9	rs1970940	109,451,966	T	A	0.353128	-0.011252	0.002113	4.1E-08
PTPN3	9	rs1970941	109,452,200	A	C	0.350678	-0.011352	0.002126	3.4E-08
PTPN3	9	rs78978964	109,452,807	T	C	0.289274	-0.012764	0.002227	5.9E-09
PTPN3	9	rs3838721	109,453,324	T	TG	0.289285	-0.012753	0.002227	6.1E-09
PTPN3	9	rs3793526	109,453,595	T	C	0.300476	-0.012285	0.002206	1.5E-08
PTPN3	9	rs76520773	109,456,424	T	C	0.289413	-0.012881	0.002226	4.2E-09
PTPN3	9	rs74742845	109,456,548	A	G	0.289373	-0.012877	0.002226	4.2E-09
PTPN3	9	rs3793524	109,457,194	G	C	0.352389	-0.011538	0.002116	2.0E-08
PTPN3	9	rs79566734	109,458,062	A	G	0.289302	-0.012874	0.002227	4.4E-09
PTPN3	9	rs148093522	109,458,493	C	CTTTT	0.289221	-0.012859	0.002227	4.7E-09
PTPN3	9	rs79587374	109,458,949	T	C	0.289295	-0.012914	0.002227	4.0E-09
PTPN3	9	rs12000215	109,460,779	G	A	0.351862	-0.011768	0.002125	1.6E-08
PTPN3	9	rs12006266	109,460,804	C	T	0.351862	-0.011766	0.002125	1.6E-08
PTPN3	9	rs2274786	109,463,494	C	T	0.353753	-0.011847	0.002123	1.2E-08
PTPN3	9	rs3808877	109,463,552	G	C	0.353711	-0.011869	0.002123	1.1E-08
PTPN3	9	rs74479508	109,464,472	C	G	0.309846	-0.013675	0.002195	2.4E-10
PTPN3	9	rs111960097	109,468,618	A	G	0.314349	-0.013892	0.002190	1.5E-10
PTPN3	9	rs57707037	109,473,833	C	T	0.244730	-0.018071	0.002383	1.6E-15
PTPN3	9	rs60227798	109,473,873	T	C	0.244780	-0.018133	0.002382	1.2E-15
PTPN3	9	rs76298084	109,474,452	T	G	0.243929	-0.018162	0.002388	1.3E-15
PTPN3	9	rs7046039	109,474,599	C	T	0.295024	-0.014564	0.002248	8.7E-12
PTPN3	9	rs58272963	109,474,628	A	G	0.244719	-0.018293	0.002383	7.0E-16
PTPN3	9	rs59668107	109,474,718	A	G	0.244715	-0.018292	0.002383	7.0E-16
PTPN3	9	rs78579422	109,475,873	T	C	0.243884	-0.018485	0.002389	5.2E-16
PTPN3	9	rs75862441	109,477,363	T	C	0.229238	-0.018757	0.002444	4.7E-16
PTPN3	9	rs41529151	109,478,114	G	C	0.229196	-0.019588	0.002442	3.0E-17
PTPN3	9	rs56279802	109,478,850	T	C	0.254937	-0.016869	0.002354	2.1E-14
PTPN3	9	rs77824033	109,478,856	C	T	0.229591	-0.019518	0.002439	3.2E-17
PTPN3	9	rs796238584	109,479,010	TGTC	T	0.255665	-0.016883	0.002356	2.0E-14
PTPN3	9	rs55727942	109,479,011	G	T	0.254677	-0.016649	0.002363	5.6E-14
PTPN3	9	rs55824262	109,479,013	C	T	0.254791	-0.016603	0.002362	6.4E-14
PTPN3	9	rs12376215	109,479,090	A	T	0.254658	-0.016984	0.002355	1.5E-14
PTPN3	9	rs117969049	109,480,282	T	C	0.229773	-0.019235	0.002436	8.4E-17
PTPN3	9	rs17793873	109,482,041	T	C	0.230194	-0.018838	0.002434	3.1E-16
PTPN3	9	rs10816818	109,482,093	G	A	0.382466	-0.012767	0.002116	4.6E-10
PTPN3	9	rs74928072	109,482,095	A	G	0.230208	-0.018862	0.002433	3.0E-16
PTPN3	9	rs75024825	109,482,136	T	C	0.229982	-0.018857	0.002432	3.3E-16
PTPN3	9	rs10816819	109,482,961	T	C	0.382590	-0.012917	0.002112	2.7E-10
PTPN3	9	rs75113691	109,483,493	C	G	0.231021	-0.018683	0.002426	4.6E-16
PTPN3	9	rs78919659	109,483,714	T	C	0.230746	-0.018634	0.002427	6.0E-16
PTPN3	9	rs57906233	109,485,510	GA	G	0.231793	-0.017800	0.002424	8.8E-15
PTPN3	9	rs10816820	109,485,747	G	A	0.383991	-0.012410	0.002108	1.2E-09
PTPN3	9	rs78424787	109,485,849	A	C	0.232217	-0.017849	0.002419	6.0E-15
PTPN3	9	rs1541088	109,486,171	C	A	0.383276	-0.012584	0.002106	7.5E-10
PTPN3	9	rs944359	109,487,352	C	T	0.388661	-0.011704	0.002073	6.9E-09
PTPN3	9	rs944358	109,487,414	A	G	0.388674	-0.011705	0.002073	6.8E-09
PTPN3	9	rs7860448	109,487,631	G	T	0.388673	-0.011715	0.002073	6.5E-09
PTPN3	9	rs59380239	109,488,319	T	C	0.249815	-0.016919	0.002332	2.6E-14
PTPN3	9	rs12002395	109,488,846	T	A	0.388478	-0.011757	0.002073	6.0E-09
PTPN3	9	rs4978392	109,489,512	C	A	0.388533	-0.011793	0.002073	5.4E-09
PTPN3	9	rs139465238	109,494,073	A	AAGG	0.249874	-0.017194	0.002330	9.8E-15
PTPN3	9	rs75577555	109,495,675	T	C	0.250075	-0.017236	0.002329	8.4E-15
PTPN3	9	rs184172568	109,497,966	T	C	0.249803	-0.016897	0.002335	2.4E-14
PTPN3	9	rs117533884	109,499,788	G	C	0.250091	-0.017184	0.002328	9.2E-15
PTPN3	9	rs10979893	109,499,895	C	A	0.387798	-0.011968	0.002070	2.8E-09
PTPN3	9	rs12685453	109,500,599	G	C	0.391866	-0.012310	0.002080	1.0E-09
PTPN3	9	rs78042633	109,502,844	T	C	0.250048	-0.017142	0.002328	9.8E-15
PTPN3	9	rs17793891	109,502,949	G	A	0.250437	-0.017075	0.002326	1.4E-14
PTPN3	9	rs7847913	109,505,698	T	G	0.387770	-0.011916	0.002070	3.4E-09
PTPN3	9	chr9:109506470_C_CCCTT	109,506,470	C	CCCTT	0.382488	-0.011929	0.002093	6.1E-09
PTPN3	9	rs140269699	109,506,584	C	CTCTT	0.244579	-0.018070	0.002357	8.8E-16
PTPN3	9	rs10123707	109,508,041	C	G	0.275322	-0.015167	0.002258	9.8E-13
PTPN3	9	rs4978816	109,509,115	C	T	0.387556	-0.011690	0.002071	6.6E-09
PTPN3	9	rs61358126	109,511,453	G	A	0.249963	-0.017111	0.002329	1.3E-14
PTPN3	9	rs2150260	109,511,914	G	A	0.281790	-0.014739	0.002240	5.4E-12

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
PTPN3	9	rs79437785	109,512,085	C	T	0.249929	-0.017065	0.002330	1.4E-14
PTPN3	9	rs6477708	109,513,462	G	A	0.281643	-0.014703	0.002242	6.4E-12
PTPN3	9	rs7341726	109,513,495	G	C	0.281632	-0.014723	0.002242	6.0E-12
PTPN3	9	rs1411682	109,514,077	T	C	0.281634	-0.014731	0.002242	5.8E-12
PTPN3	9	rs10124300	109,515,460	C	A	0.281569	-0.014586	0.002241	8.8E-12
PTPN3	9	rs10759346	109,516,959	A	C	0.368186	-0.011364	0.002102	1.6E-08
PTPN3	9	rs77218860	109,517,046	A	G	0.246912	-0.016741	0.002342	6.5E-14
PTPN3	9	rs76636909	109,518,424	T	C	0.249241	-0.016614	0.002331	7.6E-14
PTPN3	9	rs3061727	109,519,749	CCAGGA	G	0.386548	-0.011198	0.002071	3.1E-08
PTPN3	9	rs139346903	109,520,059	A	T	0.249244	-0.016610	0.002331	7.8E-14
PTPN3	9	rs80070092	109,521,917	T	C	0.249244	-0.016610	0.002331	7.8E-14
PTPN3	9	rs9696316	109,524,019	G	A	0.386642	-0.011259	0.002071	2.2E-08
PTPN3	9	rs117827315	109,532,784	G	T	0.250261	-0.016669	0.002332	6.4E-14
PTPN3	9	rs117527665	109,533,559	A	C	0.249045	-0.016731	0.002333	5.4E-14
PTPN3	9	chr9:109535507_C_CT	109,535,507	CT	C	0.245876	-0.016574	0.002367	2.0E-13
PTPN3	9	rs77274786	109,536,366	G	A	0.249184	-0.017037	0.002342	2.1E-14
PTPN3	9	rs7849787	109,538,090	A	T	0.385916	-0.011619	0.002080	8.8E-09
PTPN3	9	rs1831446	109,539,055	G	A	0.370032	-0.011274	0.002133	2.2E-08
PTPN3 *	9	rs1541087	109,541,250	A	G	0.386973	-0.011369	0.002081	1.2E-08
PTPN3 *	9	rs17201835	109,541,578	G	A	0.252289	-0.016380	0.002336	8.1E-14
PTPN3 *	9	chr9:109544207_GT_G	109,544,207	G	GT	0.276457	-0.014180	0.002284	3.8E-11
PTPN3 *	9	chr9:109545280_CT_C	109,545,280	CT	C	0.388667	-0.011434	0.002117	1.7E-08
PTPN3 *	9	rs1571642	109,548,492	A	G	0.255793	-0.015978	0.002326	5.6E-13
PTPN3 *	9	rs1330850	109,549,386	A	C	0.386263	-0.011243	0.002084	1.9E-08
PTPN3 *	9	rs17201954	109,556,943	G	A	0.387120	-0.011458	0.002089	1.3E-08
PTPN3 *	9	rs75803161	109,558,741	A	T	0.247407	-0.016457	0.002355	1.3E-13
PTPN3 *	9	rs1571640	109,560,075	G	A	0.387500	-0.011227	0.002090	2.3E-08
PTPN3 *	9	rs139221760	109,560,788	CT	C	0.249513	-0.016609	0.002352	1.0E-13
PTPN3 *	9	rs7858161	109,562,771	A	G	0.254587	-0.016086	0.002333	4.7E-13
PTPN3 *	9	rs75001090	109,565,034	C	A	0.250000	-0.016567	0.002352	1.1E-13
PTPN3 *	9	rs7849221	109,567,429	A	G	0.248163	-0.016709	0.002358	6.2E-14
PTPN3 *	9	rs7037432	109,567,677	T	C	0.385195	-0.011162	0.002097	3.0E-08
PTPN3 *	9	rs7861875	109,570,956	G	A	0.217327	-0.014301	0.002470	3.2E-10
PTPN3 *	9	rs150040590	109,573,935	T	C	0.191366	-0.017135	0.002586	1.9E-12
PTPN3 *	9	rs117103218	109,574,154	A	G	0.188947	-0.017450	0.002596	9.2E-13
PALM2 *	9	rs200290358	109,577,536	A	AT	0.191469	-0.017386	0.002581	9.3E-13
PALM2 *	9	rs200745414	109,577,539	C	A	0.192492	-0.017358	0.002573	7.4E-13
PALM2 *	9	chr9:109578848_A_AT	109,578,848	AT	A	0.220946	-0.014276	0.002444	7.3E-10
PALM2 *	9	rs76508340	109,580,420	T	C	0.178599	-0.016581	0.002661	1.3E-11
PALM2 *	9	rs78815286	109,582,984	T	G	0.192950	-0.017004	0.002567	1.9E-12
PALM2 *	9	rs78864591	109,583,284	T	C	0.192951	-0.017002	0.002567	1.9E-12
PALM2 *	9	rs5899855	109,586,400	CTTAGCA	C	0.221008	-0.014278	0.002440	4.8E-10
PALM2 *	9	rs1330845	109,587,240	T	A	0.308857	-0.011675	0.002183	3.8E-08
PALM2 *	9	rs10979952	109,587,348	C	A	0.221012	-0.014477	0.002439	3.0E-10
PALM2 *	9	rs10979955	109,587,981	C	T	0.306245	-0.011768	0.002186	2.9E-08
PALM2 *	9	rs17202062	109,591,436	C	G	0.191045	-0.017614	0.002577	3.6E-13
PALM2 *	9	rs17794184	109,592,937	C	A	0.190847	-0.017754	0.002576	2.5E-13
PALM2 *	9	rs10125565	109,593,113	T	G	0.218055	-0.015041	0.002449	7.6E-11
PALM2 *	9	rs58105812	109,593,130	A	T	0.190845	-0.017763	0.002577	2.4E-13
PALM2 *	9	rs78927344	109,593,586	G	A	0.190860	-0.017774	0.002577	2.4E-13
PALM2 *	9	rs10979958	109,595,732	A	G	0.194580	-0.017269	0.002565	1.1E-12
PALM2 *	9	rs75235286	109,596,281	T	C	0.195780	-0.017456	0.002555	4.9E-13
PALM2 *	9	rs10979959	109,597,137	A	G	0.306261	-0.011717	0.002184	3.1E-08
PALM2 *	9	rs12238594	109,598,183	C	T	0.306087	-0.011824	0.002186	2.4E-08
PALM2 *	9	rs137989413	109,598,306	A	C	0.195548	-0.017348	0.002556	6.5E-13
PALM2 *	9	rs1169625	109,600,193	A	G	0.305504	-0.011873	0.002189	2.1E-08
AKRIC4	10	rs74827952	5,203,233	A	G	0.089524	-0.021258	0.003568	1.1E-09
AKRIC4	10	rs76669111	5,203,817	T	G	0.100877	-0.019242	0.003354	3.6E-09
AKRIC4	10	rs17134531	5,204,122	A	G	0.100984	-0.019277	0.003350	3.0E-09
AKRIC4	10	rs77697233	5,204,162	T	C	0.100983	-0.019277	0.003350	3.0E-09
AKRIC4	10	rs3039101	5,204,214	TGTA	T	0.101021	-0.019352	0.003350	2.6E-09
AKRIC4	10	rs3039099	5,204,247	A	AAAAC	0.101014	-0.019317	0.003350	2.7E-09
AKRIC4	10	rs10600924	5,204,790	C	CACAGA1	0.100870	-0.019288	0.003352	2.8E-09
AKRIC4	10	rs17134533	5,205,135	A	G	0.101026	-0.019365	0.003349	2.5E-09
AKRIC4	10	rs113775538	5,205,155	CT	C	0.100846	-0.019350	0.003352	2.6E-09
AKRIC4	10	rs6601924	5,205,339	T	C	0.101036	-0.019306	0.003348	2.7E-09
AKRIC4	10	rs3750572	5,205,413	C	T	0.101036	-0.019306	0.003348	2.7E-09
AKRIC4	10	rs3750571	5,205,471	A	C	0.101036	-0.019306	0.003348	2.7E-09
AKRIC4	10	rs3750569	5,205,567	G	A	0.101036	-0.019306	0.003348	2.7E-09
AKRIC4	10	rs3750568	5,205,668	A	G	0.101036	-0.019306	0.003348	2.7E-09
AKRIC4	10	rs3750567	5,205,671	A	G	0.101036	-0.019306	0.003348	2.7E-09
AKRIC4	10	rs7921838	5,205,738	A	G	0.101043	-0.019305	0.003348	2.7E-09
AKRIC4	10	rs3829125	5,205,821	G	C	0.101176	-0.019341	0.003346	2.4E-09
AKRIC4	10	rs1931679	5,208,490	T	C	0.099698	-0.018858	0.003370	6.5E-09
AKRIC4	10	rs7908297	5,209,739	A	G	0.101078	-0.019229	0.003348	3.0E-09
AKRIC4	10	rs7909379	5,209,851	A	C	0.101033	-0.019376	0.003349	2.2E-09
AKRIC4	10	rs7909380	5,209,852	T	C	0.101033	-0.019376	0.003349	2.2E-09
AKRIC4	10	rs117310669	5,210,050	G	C	0.101015	-0.019297	0.003349	2.8E-09
AKRIC4	10	rs4424574	5,210,114	T	G	0.101018	-0.019291	0.003349	2.9E-09
AKRIC4	10	rs7477230	5,210,768	T	C	0.101160	-0.019498	0.003348	1.9E-09
AKRIC4	10	rs7477114	5,210,875	T	G	0.101018	-0.019291	0.003349	2.9E-09
AKRIC4	10	rs7475279	5,210,903	C	A	0.101080	-0.019222	0.003348	3.0E-09
AKRIC4	10	rs7475281	5,210,939	C	A	0.101080	-0.019222	0.003348	3.0E-09
AKRIC4	10	rs117071142	5,211,396	G	T	0.100912	-0.019347	0.003350	2.4E-09
AKRIC4	10	rs111481000	5,211,476	GTCA	G	0.101083	-0.019211	0.003348	3.1E-09
AKRIC4	10	rs7078211	5,211,675	G	A	0.101086	-0.019205	0.003348	3.1E-09
AKRIC4	10	rs6601927	5,212,183	G	A	0.101103	-0.019208	0.003347	3.2E-09
AKRIC4	10	rs7897431	5,212,225	A	G	0.101103	-0.019208	0.003347	3.2E-09
AKRIC4	10	rs4098025	5,212,857	C	A	0.100665	-0.019310	0.003355	2.8E-09
AKRIC4	10	rs1831977	5,212,858	G	C	0.100665	-0.019310	0.003355	2.8E-09
AKRIC4	10	rs1832007	5,212,884	G	A	0.101085	-0.018979	0.003348	4.7E-09
AKRIC4	10	rs111648698	5,213,372	T	TCA	0.101102	-0.019217	0.003347	3.1E-09
AKRIC4	10	rs148205663	5,214,017	A	ATATAT	0.100999	-0.019140	0.003350	3.6E-09
AKRIC4	10	rs17134585	5,214,309	C	T	0.102362	-0.019287	0.003334	2.8E-09
AKRIC4	10	rs59582332	5,214,373	TC	T	0.101345	-0.019103	0.003349	3.4E-09
AKRIC4	10	rs56068105	5,214,375	T	A	0.109158	-0.017308	0.003293	4.2E-08
AKRIC4	10	rs17134588	5,214,534	A	G	0.101274	-0.019315	0.003348	2.6E-09

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
AKRIC4	10	chr10:5214682_CTTT_C	5,214,682	C	CTTT	0.101258	-0.018930	0.003346	5.5E-09
AKRIC4	10	rs148929884	5,214,779	TTC	T	0.101103	-0.019181	0.003348	3.3E-09
AKRIC4	10	rs77503049	5,214,795	T	C	0.101291	-0.019321	0.003347	2.5E-09
AKRIC4	10	rs76551580	5,214,871	C	T	0.101103	-0.019181	0.003348	3.3E-09
AKRIC4	10	rs78585347	5,215,134	T	G	0.101038	-0.019229	0.003349	3.2E-09
AKRIC4	10	rs75406471	5,215,684	A	G	0.101041	-0.019271	0.003349	3.0E-09
AKRIC4	10	rs78686304	5,215,834	T	C	0.101038	-0.019229	0.003349	3.2E-09
AKRIC4	10	rs7912751	5,215,978	T	C	0.101038	-0.019229	0.003349	3.2E-09
AKRIC4	10	rs10586998	5,216,482	A	ATCTTT	0.100713	-0.019266	0.003355	2.8E-09
AKRIC4	10	rs4881413	5,216,487	T	G	0.100713	-0.019266	0.003355	2.8E-09
AKRIC4	10	rs17134589	5,217,078	C	G	0.100854	-0.019327	0.003351	2.8E-09
AKRIC4	10	rs141745211	5,218,585	CAT	C	0.101031	-0.019187	0.003349	3.6E-09
AKRIC4	10	rs17134592	5,218,719	G	C	0.101031	-0.019187	0.003349	3.6E-09
AKRIC4	10	rs141695403	5,218,823	G	GTC	0.101028	-0.019201	0.003349	3.5E-09
AKRIC4 *	10	rs75811842	5,219,138	G	A	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs76494948	5,219,148	T	C	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs11253048	5,219,196	G	A	0.101165	-0.019351	0.003348	2.8E-09
AKRIC4 *	10	rs17134601	5,219,212	G	A	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs77353068	5,219,263	C	G	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs17134604	5,219,293	A	T	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs77896903	5,219,528	T	C	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs80264034	5,219,613	A	T	0.101026	-0.019228	0.003349	3.3E-09
AKRIC4 *	10	rs74404998	5,219,720	G	A	0.101026	-0.019225	0.003349	3.3E-09
AKRIC4 *	10	rs117849125	5,219,866	T	C	0.100627	-0.019169	0.003356	3.9E-09
AKRIC4 *	10	rs117146235	5,219,867	G	A	0.100627	-0.019169	0.003356	3.9E-09
AKRIC4 *	10	rs117488242	5,219,869	G	A	0.100627	-0.019169	0.003356	3.9E-09
AKRIC4 *	10	rs17134607	5,219,947	A	G	0.101028	-0.019219	0.003349	3.4E-09
AKRIC4 *	10	rs17134608	5,220,056	A	G	0.101028	-0.019219	0.003349	3.4E-09
AKRIC4 *	10	rs79849481	5,220,133	A	G	0.101028	-0.019219	0.003349	3.4E-09
AKRIC4 *	10	rs77355283	5,220,173	T	C	0.101028	-0.019219	0.003349	3.4E-09
AKRIC4 *	10	rs79717793	5,220,304	A	G	0.101029	-0.019221	0.003349	3.4E-09
AKRIC4 *	10	chr10:5220490_G_GT	5,220,490	GT	G	0.100857	-0.019358	0.003351	2.7E-09
AKRIC4 *	10	rs78231592	5,220,527	C	G	0.101029	-0.019221	0.003349	3.4E-09
AKRIC4 *	10	rs75529951	5,220,549	A	G	0.101029	-0.019221	0.003349	3.4E-09
AKRIC4 *	10	rs140168704	5,220,815	T	C	0.101029	-0.019225	0.003349	3.4E-09
AKRIC4 *	10	rs151163925	5,220,847	T	C	0.101051	-0.019200	0.003349	3.5E-09
AKRIC4 *	10	rs143690051	5,220,859	T	C	0.101051	-0.019200	0.003349	3.5E-09
AKRIC4 *	10	rs112455458	5,220,920	C	G	0.101029	-0.019225	0.003349	3.4E-09
AKRIC4 *	10	rs111932715	5,220,978	C	G	0.101029	-0.019225	0.003349	3.4E-09
AKRIC4 *	10	rs2151901	5,221,002	C	A	0.101029	-0.019225	0.003349	3.4E-09
AKRIC4 *	10	rs17134610	5,221,060	T	G	0.101030	-0.019218	0.003349	3.4E-09
AKRIC4 *	10	rs142122182	5,221,378	G	A	0.097567	-0.020097	0.003410	1.3E-09
AKRIC4 *	10	rs17134616	5,221,498	T	A	0.099820	-0.018676	0.003371	1.2E-08
AKRIC4 *	10	rs75413156	5,221,531	A	C	0.100316	-0.019475	0.003364	2.7E-09
AKRIC4 *	10	rs80011059	5,221,553	T	A	0.101030	-0.019218	0.003349	3.4E-09
AKRIC4 *	10	rs17134617	5,221,739	A	C	0.101030	-0.019218	0.003349	3.4E-09
AKRIC4 *	10	rs145211548	5,221,893	CA	C	0.101028	-0.019206	0.003349	3.5E-09
AKRIC4 *	10	rs149977283	5,223,568	A	C	0.100564	-0.019207	0.003362	3.4E-09
AKRIC4 *	10	rs138695384	5,223,859	G	A	0.101258	-0.019101	0.003348	4.1E-09
AKRIC4 *	10	rs150754448	5,224,911	A	G	0.101026	-0.019190	0.003349	3.7E-09
AKRIC4 *	10	rs140107293	5,225,228	G	A	0.101052	-0.019263	0.003350	3.2E-09
AKRIC4 *	10	rs143431627	5,228,338	T	C	0.101117	-0.019220	0.003351	3.5E-09
AKRIC4 *	10	rs7897822	5,242,594	A	G	0.100730	-0.019048	0.003364	6.4E-09
AKRIC4 *	10	rs151227875	5,255,358	G	C	0.095813	-0.018529	0.003443	1.8E-08
AKRIC4 *	10	rs143119289	5,255,430	G	T	0.093519	-0.018522	0.003487	2.6E-08
AKRIC4 *	10	rs80079690	5,258,474	T	C	0.094464	-0.018490	0.003463	2.1E-08
AKRIC4 *	10	rs12415198	5,262,828	T	C	0.092387	-0.018604	0.003506	2.7E-08
AKRIC4 *	10	rs77714023	5,263,928	A	G	0.094021	-0.018717	0.003474	1.6E-08
AKRIC4 *	10	rs117600605	5,263,996	T	C	0.094510	-0.018360	0.003465	2.5E-08
AKRIC4 *	10	rs4339945	5,264,435	G	A	0.094551	-0.018401	0.003465	2.3E-08
AKRIC4 *	10	rs117292237	5,265,566	C	T	0.094583	-0.018275	0.003465	2.8E-08
AKRIC4 *	10	rs77364195	5,266,772	A	T	0.094821	-0.018392	0.003461	2.2E-08
AKRIC4 *	10	rs1574227	5,270,304	A	G	0.096361	-0.018213	0.003439	2.8E-08
AKRIC4 *	10	rs1574228	5,270,347	G	A	0.096373	-0.018220	0.003438	2.8E-08
AKRIC4 *	10	rs1574351	5,270,402	A	G	0.096375	-0.018251	0.003438	2.6E-08
AKRIC4 *	10	rs1574352	5,270,475	C	T	0.096378	-0.018233	0.003438	2.7E-08
AKRIC4 *	10	rs869009	5,271,066	C	T	0.096418	-0.018266	0.003437	2.6E-08
AKRIC4 *	10	rs12763722	5,271,530	C	T	0.096468	-0.018321	0.003437	2.3E-08
AKRIC4 *	10	rs35383392	5,271,569	CAG	C	0.096468	-0.018321	0.003437	2.3E-08
AKRIC4 *	10	rs1889460	5,272,032	T	C	0.096496	-0.018402	0.003437	2.0E-08
AKRIC4 *	10	rs1889459	5,272,080	C	G	0.095287	-0.018475	0.003454	1.9E-08
AKRIC4 *	10	rs11815997	5,272,373	T	G	0.096496	-0.018402	0.003437	2.0E-08
AKRIC4 *	10	rs17307911	5,272,389	C	T	0.096496	-0.018402	0.003437	2.0E-08
AKRIC4 *	10	rs17399127	5,272,661	C	A	0.096500	-0.018384	0.003437	2.1E-08
AKRIC4 *	10	rs12413267	5,273,161	G	A	0.096601	-0.018521	0.003436	1.5E-08
AKRIC4 *	10	rs17399232	5,273,898	G	C	0.096560	-0.018538	0.003437	1.6E-08
AKRIC4 *	10	rs79504871	5,273,912	T	A	0.096516	-0.018414	0.003437	2.0E-08
AKRIC4 *	10	rs7082291	5,275,907	C	A	0.096937	-0.018493	0.003427	1.8E-08
AKRIC4 *	10	rs17134724	5,276,549	A	G	0.095747	-0.018553	0.003444	1.7E-08
AKRIC4 *	10	rs75857264	5,283,345	T	C	0.095629	-0.018806	0.003445	1.0E-08
AKRIC4 *	10	rs17134733	5,283,400	A	G	0.093100	-0.018595	0.003494	2.2E-08
NRBF2 *	10	rs10822118	63,068,681	T	C	0.288667	0.012698	0.002264	5.6E-09
NRBF2 *	10	rs67460150	63,114,009	G	GA	0.243259	-0.015623	0.002394	4.6E-11
NRBF2 *	10	rs10995445	63,114,994	T	A	0.317362	-0.013932	0.002184	3.6E-11
NRBF2 *	10	rs7903602	63,115,551	A	G	0.384640	0.021174	0.002098	5.5E-26
NRBF2 *	10	rs4414112	63,115,786	A	G	0.384229	0.021424	0.002091	8.5E-27
NRBF2 *	10	rs4545434	63,115,985	C	T	0.375188	0.020949	0.002099	1.0E-25
NRBF2 *	10	rs7084569	63,116,794	A	G	0.316356	-0.013957	0.002184	3.1E-11
NRBF2 *	10	rs7084396	63,116,965	A	G	0.384060	0.021303	0.002087	1.3E-26
NRBF2 *	10	rs35248047	63,117,160	A	AC	0.387355	0.020935	0.002090	1.1E-25
NRBF2 *	10	rs10822138	63,117,400	G	A	0.389711	0.021299	0.002099	3.6E-26
NRBF2 *	10	rs6479877	63,118,358	G	C	0.317069	-0.013538	0.002167	1.1E-10
NRBF2 *	10	rs1396964	63,118,538	G	A	0.387284	0.021391	0.002075	7.0E-27
NRBF2 *	10	rs6479878	63,118,657	A	G	0.387833	0.021301	0.002076	1.0E-26
NRBF2 *	10	rs6479879	63,118,669	G	T	0.387831	0.021314	0.002076	9.5E-27
NRBF2 *	10	rs6479880	63,118,671	A	T	0.387831	0.021314	0.002076	9.5E-27
NRBF2 *	10	rs6479881	63,118,802	T	C	0.387211	0.021343	0.002075	8.6E-27

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
NRBF2 *	10	rs1553789	63,119,469	T	C	0.336416	-0.012840	0.002140	6.6E-10
NRBF2 *	10	rs10995447	63,119,761	A	G	0.378227	0.020788	0.002087	1.6E-25
NRBF2 *	10	rs4601646	63,120,520	A	G	0.336437	-0.012920	0.002141	5.2E-10
NRBF2 *	10	rs10761716	63,122,540	G	C	0.318348	-0.013881	0.002169	3.7E-11
NRBF2 *	10	rs10822140	63,123,267	T	C	0.336328	-0.012889	0.002141	5.7E-10
NRBF2 *	10	rs2896496	63,123,622	A	G	0.335044	-0.012899	0.002145	5.6E-10
NRBF2 *	10	rs2896495	63,123,644	C	G	0.333571	-0.013007	0.002149	4.6E-10
NRBF2 *	10	rs4746951	63,123,839	G	A	0.378265	0.020850	0.002087	1.1E-25
NRBF2 *	10	rs61853335	63,124,977	T	C	0.378242	0.020844	0.002087	1.1E-25
NRBF2 *	10	rs72824948	63,126,343	G	A	0.378299	0.020838	0.002087	1.1E-25
NRBF2 *	10	rs10761717	63,126,354	C	T	0.335997	-0.012890	0.002141	5.7E-10
NRBF2 *	10	rs10995448	63,127,299	G	A	0.336064	-0.012888	0.002141	5.5E-10
NRBF2 *	10	rs12771984	63,127,434	A	T	0.336212	-0.012934	0.002142	5.0E-10
NRBF2 *	10	rs10995449	63,127,712	A	G	0.336529	-0.012989	0.002143	4.3E-10
NRBF2 *	10	rs10822143	63,128,096	T	C	0.318046	-0.014108	0.002176	2.2E-11
NRBF2 *	10	rs10761718	63,128,127	T	C	0.335789	-0.012627	0.002146	1.5E-09
NRBF2 *	10	rs7082200	63,128,561	G	C	0.335903	-0.012724	0.002143	1.0E-09
NRBF2 *	10	rs10995450	63,129,151	C	T	0.336059	-0.012881	0.002141	5.6E-10
NRBF2 *	10	rs10740105	63,129,957	T	C	0.336054	-0.012880	0.002141	5.5E-10
NRBF2 *	10	rs10761719	63,130,337	G	A	0.335457	-0.012685	0.002143	1.0E-09
NRBF2 *	10	rs7923014	63,130,405	T	C	0.336065	-0.012862	0.002141	5.8E-10
NRBF2 *	10	rs7908990	63,130,890	A	T	0.336070	-0.012852	0.002141	5.9E-10
NRBF2 *	10	rs4746974	63,132,292	T	G	0.378453	0.020699	0.002083	1.9E-25
NRBF2 *	10	rs1533068	63,132,407	C	A	0.336119	-0.012811	0.002140	6.6E-10
NRBF2 *	10	rs1533069	63,132,408	A	C	0.336119	-0.012811	0.002140	6.6E-10
NRBF2	10	rs871690	63,134,299	G	A	0.335499	-0.012928	0.002141	5.3E-10
NRBF2	10	rs868798	63,135,250	G	A	0.378823	0.020655	0.002081	2.2E-25
NRBF2	10	rs12416113	63,136,717	A	T	0.378648	0.020678	0.002082	2.0E-25
NRBF2	10	rs10761720	63,139,023	A	G	0.333595	-0.012760	0.002143	8.9E-10
NRBF2	10	rs61853336	63,140,115	A	G	0.378808	0.020732	0.002081	1.6E-25
NRBF2	10	rs80082080	63,142,032	AT	A	0.248937	-0.015759	0.002342	9.1E-12
NRBF2	10	rs7070052	63,144,054	A	G	0.378833	0.020685	0.002081	1.9E-25
NRBF2	10	rs7073746	63,144,311	G	A	0.315950	-0.013801	0.002172	5.6E-11
NRBF2	10	rs7916224	63,144,843	T	C	0.387862	0.012128	0.002072	1.1E-26
NRBF2	10	rs4746994	63,145,564	A	T	0.378912	0.020633	0.002079	2.2E-25
NRBF2	10	rs10733787	63,147,078	T	A	0.387956	0.021196	0.002071	1.1E-26
NRBF2	10	chr10:63147321_AT_A	63,147,321	A	AT	0.379977	0.020809	0.002092	1.9E-25
NRBF2	10	rs12240740	63,147,478	C	A	0.387955	0.021193	0.002071	1.1E-26
NRBF2	10	rs11278263	63,147,821	T	GCTGTAC	0.314337	-0.013533	0.002175	1.2E-10
NRBF2	10	rs931972	63,150,467	C	G	0.333128	-0.012445	0.002142	2.4E-09
NRBF2	10	rs12415984	63,150,528	A	G	0.378921	0.020609	0.002079	2.3E-25
NRBF2	10	rs35751397	63,154,256	TA	T	0.315792	-0.013675	0.002168	7.1E-11
NRBF2	10	rs13095	63,154,612	C	G	0.315794	-0.013677	0.002168	7.1E-11
NRBF2	10	rs1160843	63,154,758	C	CATA	0.315707	-0.013630	0.002170	8.1E-11
NRBF2 *	10	rs7897470	63,156,304	G	T	0.365628	0.019520	0.002111	1.7E-22
NRBF2 *	10	rs1009984	63,156,709	T	G	0.387644	0.021076	0.002072	2.0E-26
NRBF2 *	10	rs11814792	63,157,799	T	C	0.377611	0.020729	0.002080	1.7E-25
NRBF2 *	10	rs10733788	63,158,105	T	C	0.387588	0.021143	0.002072	1.5E-26
NRBF2 *	10	rs61853339	63,158,919	C	T	0.378023	0.020713	0.002079	1.8E-25
NRBF2 *	10	rs12413415	63,159,751	C	T	0.375092	0.020559	0.002084	4.6E-25
NRBF2 *	10	rs34132715	63,160,401	C	CTAAA	0.377218	0.020724	0.002082	2.3E-25
JMJD1C *	10	rs11817689	63,164,457	C	T	0.379445	0.020668	0.002078	1.9E-25
JMJD1C *	10	rs3072249	63,165,570	CCAT	C	0.388110	0.021332	0.002071	5.4E-27
JMJD1C *	10	rs57618271	63,165,939	C	CTAAAG	0.354904	-0.012803	0.002134	5.8E-10
JMJD1C *	10	rs4747045	63,166,722	T	C	0.378325	0.020741	0.002079	1.3E-25
JMJD1C	10	rs1935	63,168,063	G	C	0.312463	-0.013819	0.002176	3.8E-11
JMJD1C	10	rs57138498	63,171,287	G	GA	0.330594	-0.012806	0.002145	5.7E-10
JMJD1C	10	rs1904296	63,173,019	C	G	0.387688	0.020804	0.002075	6.8E-26
JMJD1C	10	rs4466712	63,173,508	C	G	0.376858	0.020684	0.002080	1.6E-25
JMJD1C	10	chr10:63173739_G_GA	63,173,739	GA	G	0.371076	0.020767	0.002099	2.5E-25
JMJD1C	10	rs35447916	63,173,832	CA	C	0.314641	-0.013526	0.002172	7.8E-11
JMJD1C	10	rs10995453	63,174,571	T	C	0.386111	0.021103	0.002073	1.7E-26
JMJD1C	10	rs10822145	63,174,788	T	C	0.314433	-0.013520	0.002172	8.1E-11
JMJD1C	10	rs10995455	63,176,601	A	G	0.244485	-0.015565	0.002352	1.3E-11
JMJD1C	10	rs907	63,176,919	A	G	0.386553	0.021078	0.002076	1.7E-26
JMJD1C	10	rs10761721	63,178,644	T	G	0.386112	0.021100	0.002073	1.7E-26
JMJD1C	10	rs72829170	63,180,529	G	A	0.376550	0.020638	0.002080	2.5E-25
JMJD1C	10	rs10995459	63,183,050	A	G	0.385965	0.021008	0.002073	3.0E-26
JMJD1C	10	rs56369591	63,184,054	A	AG	0.385281	0.021022	0.002075	3.9E-26
JMJD1C	10	rs61853340	63,184,415	C	G	0.371879	0.020449	0.002096	1.5E-24
JMJD1C	10	rs10740107	63,184,557	T	A	0.376366	0.020420	0.002082	9.9E-25
JMJD1C	10	rs3211105	63,185,604	G	A	0.386251	0.021115	0.002072	1.6E-26
JMJD1C	10	rs10733789	63,188,924	C	T	0.244806	-0.015964	0.002352	5.2E-12
JMJD1C	10	rs10822146	63,191,707	A	G	0.332428	-0.012641	0.002142	8.4E-10
JMJD1C	10	rs10761722	63,195,287	C	G	0.386096	0.021176	0.002074	1.3E-26
JMJD1C	10	rs10761723	63,195,821	T	C	0.314325	-0.013588	0.002172	6.9E-11
JMJD1C	10	rs61855465	63,196,847	T	A	0.377150	0.020620	0.002078	2.3E-25
JMJD1C	10	rs10465990	63,200,776	A	G	0.330739	-0.012760	0.002145	6.3E-10
JMJD1C	10	rs7099425	63,200,957	C	T	0.377573	0.020592	0.002079	3.0E-25
JMJD1C	10	rs7895472	63,201,652	A	G	0.312627	-0.013762	0.002176	4.5E-11
JMJD1C	10	rs7895610	63,201,899	T	C	0.310258	-0.013628	0.002186	7.5E-11
JMJD1C	10	rs4379723	63,203,689	C	T	0.313925	-0.013573	0.002174	7.4E-11
JMJD1C	10	rs12413730	63,204,388	T	C	0.377128	0.020621	0.002078	2.3E-25
JMJD1C	10	rs1579045	63,210,688	G	A	0.386886	0.021156	0.002070	1.2E-26
JMJD1C	10	chr10:63211997_TAAG_T	63,211,997	T	TAAG	0.314233	-0.013702	0.002173	5.0E-11
JMJD1C	10	rs7920159	63,212,416	C	G	0.386886	0.021156	0.002070	1.2E-26
JMJD1C	10	rs10761725	63,214,777	T	A	0.332785	-0.012597	0.002144	9.7E-10
JMJD1C	10	rs11819167	63,216,409	A	G	0.377186	0.020684	0.002077	1.7E-25
JMJD1C	10	rs10822147	63,216,537	C	T	0.386841	0.021174	0.002069	1.1E-26
JMJD1C	10	rs10822148	63,219,487	A	G	0.386996	0.021048	0.002070	2.1E-26
JMJD1C	10	rs10761726	63,220,958	A	C	0.386778	0.021131	0.002070	1.4E-26
JMJD1C	10	rs1904295	63,223,116	G	A	0.387294	0.019589	0.002102	8.6E-23
JMJD1C	10	rs4335432	63,226,057	T	C	0.332436	-0.012644	0.002142	7.8E-10
JMJD1C	10	rs6415875	63,226,657	A	G	0.378246	0.020567	0.002077	3.6E-25
JMJD1C	10	rs10822149	63,227,652	A	G	0.314342	-0.013627	0.002172	5.7E-11
JMJD1C	10	rs4281380	63,227,938	C	A	0.377248	0.020716	0.002077	1.5E-25
JMJD1C	10	rs6479889	63,228,867	A	C	0.331602	-0.012795	0.002146	6.1E-10

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
JMJD1C	10	rs7916868	63,229,171	A	T	0.337664	0.019881	0.002173	4.3E-21
JMJD1C	10	rs10761727	63,235,733	T	C	0.314289	-0.013678	0.002173	5.1E-11
JMJD1C	10	rs10761728	63,235,808	C	T	0.386827	0.021158	0.002069	1.2E-26
JMJD1C	10	rs10761729	63,235,844	C	G	0.314289	-0.013678	0.002173	5.1E-11
JMJD1C	10	chr10:63237348_T_TAAA	63,237,348	T	TAAA	0.377553	0.020582	0.002078	3.0E-25
JMJD1C	10	rs4439410	63,239,012	C	G	0.377168	0.020675	0.002077	1.7E-25
JMJD1C	10	rs7082066	63,239,211	A	G	0.386760	0.021123	0.002070	1.4E-26
JMJD1C	10	rs7082090	63,239,252	A	G	0.377168	0.020675	0.002077	1.7E-25
JMJD1C	10	rs4399232	63,239,730	T	C	0.314323	-0.013657	0.002172	5.3E-11
JMJD1C	10	rs9414780	63,241,673	A	C	0.377168	0.020675	0.002077	1.7E-25
JMJD1C	10	rs7902343	63,245,639	T	C	0.285398	-0.014842	0.002239	1.2E-11
JMJD1C	10	rs6479891	63,246,696	T	C	0.376988	0.020618	0.002077	2.5E-25
JMJD1C	10	chr10:63247839_TAAAACAAAAC_T	63,247,839	AAACAA	T	0.391810	0.020731	0.002076	2.3E-25
JMJD1C	10	rs10995477	63,250,912	C	T	0.285933	-0.014565	0.002233	2.2E-11
JMJD1C	10	rs7081614	63,252,088	C	T	0.386534	0.021147	0.002071	1.4E-26
JMJD1C	10	rs4400684	63,252,927	G	A	0.285483	-0.014370	0.002236	4.0E-11
JMJD1C	10	rs4454603	63,252,990	T	C	0.285949	-0.014545	0.002233	2.5E-11
JMJD1C	10	rs4403688	63,253,156	G	A	0.386525	0.021137	0.002071	1.4E-26
JMJD1C	10	rs4595427	63,253,184	C	A	0.285941	-0.014538	0.002233	2.5E-11
JMJD1C	10	rs4450077	63,253,976	G	C	0.304125	-0.013365	0.002195	4.8E-10
JMJD1C	10	rs4469770	63,254,152	G	A	0.304032	-0.013418	0.002195	4.2E-10
JMJD1C	10	rs4405189	63,254,175	G	A	0.285773	-0.014466	0.002234	3.0E-11
JMJD1C	10	rs71025138	63,254,706	G	GT	0.300913	-0.012992	0.002210	1.8E-09
JMJD1C	10	rs1904297	63,255,428	G	A	0.386456	0.021197	0.002071	1.1E-26
JMJD1C	10	rs7070693	63,256,402	A	G	0.386464	0.021165	0.002071	1.3E-26
JMJD1C	10	rs7088799	63,256,414	G	T	0.285800	-0.014605	0.002232	2.0E-11
JMJD1C	10	rs7896910	63,256,961	A	G	0.246182	-0.015898	0.002343	4.1E-12
JMJD1C	10	rs10761730	63,257,293	C	T	0.377359	0.020668	0.002082	2.6E-25
JMJD1C	10	rs10822150	63,257,736	G	A	0.386435	0.021088	0.002071	2.0E-26
JMJD1C	10	rs11370668	63,260,747	G	GC	0.382211	0.019925	0.002088	7.7E-24
JMJD1C	10	rs35843321	63,260,755	A	AT	0.391730	0.020328	0.002081	8.5E-25
JMJD1C	10	rs9415680	63,261,130	A	G	0.376210	0.020394	0.002080	5.1E-25
JMJD1C	10	chr10:63262822_AC_A	63,262,822	AC	A	0.377348	0.020523	0.002079	3.3E-25
JMJD1C	10	rs7098181	63,267,383	T	G	0.286104	-0.014055	0.002230	7.3E-11
JMJD1C	10	rs10761731	63,267,850	T	A	0.286083	-0.014071	0.002230	7.0E-11
JMJD1C	10	rs10761732	63,268,497	C	T	0.385896	0.020893	0.002072	3.5E-26
JMJD1C	10	rs7916282	63,272,051	A	T	0.389165	0.020389	0.002115	3.7E-24
JMJD1C	10	rs7909555	63,273,348	T	C	0.387977	0.020310	0.002070	8.2E-25
JMJD1C	10	rs9415682	63,274,057	G	T	0.376740	0.020637	0.002079	2.4E-25
JMJD1C	10	rs10761733	63,275,024	T	C	0.404064	0.019895	0.002075	1.3E-23
JMJD1C	10	rs10822151	63,276,907	G	C	0.375624	0.020475	0.002080	4.2E-25
JMJD1C	10	rs9787438	63,278,270	C	G	0.286588	-0.014131	0.002229	6.8E-11
JMJD1C	10	rs10740109	63,280,379	A	C	0.302162	-0.012970	0.002201	1.7E-09
JMJD1C	10	rs10995489	63,281,085	A	G	0.303985	-0.013356	0.002204	6.2E-10
JMJD1C	10	rs10761734	63,281,453	C	T	0.385292	0.021027	0.002072	2.2E-26
JMJD1C	10	rs10740110	63,283,461	A	G	0.375653	0.020512	0.002080	3.7E-25
JMJD1C	10	rs10761735	63,284,158	A	G	0.379157	0.020275	0.002083	1.2E-24
JMJD1C	10	rs9414786	63,284,562	T	A	0.375653	0.020512	0.002080	3.7E-25
JMJD1C	10	rs4417159	63,285,938	T	A	0.385289	0.021023	0.002072	2.3E-26
JMJD1C	10	rs67907125	63,286,034	GA	G	0.375653	0.020512	0.002080	3.7E-25
JMJD1C	10	rs10995493	63,287,266	C	T	0.385291	0.021023	0.002072	2.3E-26
JMJD1C	10	rs10761736	63,288,009	A	T	0.385332	0.021050	0.002072	2.0E-26
JMJD1C	10	rs7080386	63,288,546	A	C	0.286588	-0.014131	0.002229	6.8E-11
JMJD1C	10	rs67135607	63,289,318	CAT	C	0.385378	0.020987	0.002072	2.7E-26
JMJD1C	10	rs7074351	63,290,343	A	T	0.375698	0.020511	0.002080	3.6E-25
JMJD1C	10	rs7075195	63,290,899	G	A	0.287063	-0.014414	0.002228	2.9E-11
JMJD1C	10	rs4486510	63,291,134	C	G	0.375141	0.020493	0.002081	4.0E-25
JMJD1C	10	rs10761737	63,292,445	C	T	0.286924	-0.014521	0.002229	2.2E-11
JMJD1C	10	rs6479892	63,292,472	A	G	0.375660	0.020513	0.002080	3.7E-25
JMJD1C	10	rs7084707	63,292,782	T	C	0.287090	-0.014435	0.002228	2.8E-11
JMJD1C	10	rs11408050	63,293,789	A	AT	0.386292	0.020650	0.002075	1.9E-25
JMJD1C	10	rs7913332	63,293,890	A	T	0.385297	0.021022	0.002072	2.3E-26
JMJD1C	10	rs7093899	63,294,576	A	G	0.385293	0.021014	0.002072	2.4E-26
JMJD1C	10	rs5785566	63,295,026	TA	T	0.286994	-0.014498	0.002228	2.1E-11
JMJD1C	10	rs7907462	63,295,773	T	C	0.385807	0.021059	0.002073	2.0E-26
JMJD1C	10	rs9414788	63,296,952	A	G	0.375644	0.020536	0.002080	3.4E-25
JMJD1C	10	rs10822153	63,297,053	A	C	0.287218	-0.014393	0.002227	3.0E-11
JMJD1C	10	rs12773283	63,298,464	C	T	0.375649	0.020528	0.002080	3.5E-25
JMJD1C	10	rs10822154	63,299,284	C	T	0.385299	0.021048	0.002072	2.1E-26
JMJD1C	10	rs7920768	63,300,754	C	T	0.375663	0.020531	0.002080	3.5E-25
JMJD1C	10	chr10:63300891_C_CA	63,300,891	C	CA	0.390232	0.021207	0.002083	1.7E-26
JMJD1C	10	rs10761739	63,302,248	C	G	0.286980	-0.014339	0.002228	3.7E-11
JMJD1C	10	rs7073753	63,303,060	T	C	0.286992	-0.014280	0.002228	4.2E-11
JMJD1C	10	rs10761740	63,303,503	G	A	0.385321	0.021060	0.002072	2.0E-26
JMJD1C	10	rs74506613	63,304,076	A	ACTTTGCT	0.286781	-0.014373	0.002230	3.4E-11
JMJD1C	10	rs61855497	63,304,084	A	T	0.285917	-0.014234	0.002232	5.0E-11
JMJD1C	10	rs7100372	63,304,484	T	C	0.375674	0.020534	0.002080	3.4E-25
JMJD1C	10	rs7896676	63,305,542	T	C	0.357959	0.020413	0.002131	5.9E-24
JMJD1C	10	rs7896677	63,305,545	T	G	0.358718	0.020217	0.002133	1.8E-23
JMJD1C	10	rs7897326	63,306,059	T	C	0.385291	0.021029	0.002072	2.3E-26
JMJD1C	10	rs10761741	63,306,426	T	G	0.286900	-0.014340	0.002228	3.4E-11
JMJD1C	10	rs7092139	63,306,540	A	C	0.385327	0.021048	0.002072	2.1E-26
JMJD1C	10	rs7092539	63,306,749	C	T	0.385657	0.020866	0.002074	7.3E-26
JMJD1C	10	rs7922587	63,309,854	C	T	0.286740	-0.014128	0.002229	6.3E-11
JMJD1C	10	rs7085869	63,310,403	C	T	0.375652	0.020527	0.002080	3.6E-25
JMJD1C	10	rs7070296	63,310,678	A	T	0.287159	-0.014263	0.002227	4.4E-11
JMJD1C	10	rs10822155	63,311,455	A	C	0.286975	-0.014263	0.002228	4.6E-11
JMJD1C	10	rs67173357	63,312,116	TG	T	0.419292	0.019256	0.002054	4.9E-23
JMJD1C	10	rs9299455	63,313,841	A	G	0.374725	0.020449	0.002082	5.3E-25
JMJD1C	10	chr10:63314548_A_AAC	63,314,548	AAC	A	0.287081	-0.014265	0.002228	4.3E-11
JMJD1C	10	rs9733126	63,314,727	C	A	0.385039	0.020915	0.002074	4.8E-26
JMJD1C	10	rs9414793	63,315,349	G	A	0.375653	0.020543	0.002081	3.3E-25
JMJD1C	10	rs7090111	63,318,234	G	C	0.287005	-0.014286	0.002228	4.2E-11
JMJD1C	10	rs7899715	63,318,695	T	C	0.375718	0.020489	0.002081	4.4E-25
JMJD1C	10	rs4518976	63,319,017	C	T	0.380359	0.020935	0.002086	6.7E-26
JMJD1C	10	rs7088045	63,319,637	A	T	0.305138	-0.013249	0.002190	5.5E-10
JMJD1C	10	rs10822156	63,320,967	C	T	0.287154	-0.014293	0.002227	4.0E-11

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
JMJD1C	10	rs10740112	63,322,315	G	A	0.385310	0.021021	0.002072	2.5E-26
JMJD1C	10	rs10740113	63,322,516	T	C	0.385310	0.021021	0.002072	2.5E-26
JMJD1C	10	rs10740114	63,322,659	A	G	0.385310	0.021021	0.002072	2.5E-26
JMJD1C	10	rs34979184	63,323,439	GA	G	0.385309	0.021028	0.002072	2.4E-26
JMJD1C	10	rs10761742	63,325,288	G	A	0.287261	-0.014331	0.002227	3.6E-11
JMJD1C	10	rs4525102	63,326,513	C	T	0.375647	0.020581	0.002081	2.8E-25
JMJD1C	10	rs7899503	63,327,708	C	G	0.375642	0.020577	0.002081	2.8E-25
JMJD1C	10	rs12767177	63,327,882	C	G	0.386159	0.020870	0.002074	6.4E-26
JMJD1C	10	chr10:63329478_GA_G	63,329,478	GA	G	0.377607	0.020005	0.002100	2.7E-23
JMJD1C	10	rs7092504	63,329,679	A	G	0.375645	0.020564	0.002081	3.0E-25
JMJD1C	10	rs10822157	63,329,720	A	G	0.385299	0.021040	0.002072	2.2E-26
JMJD1C	10	rs10995505	63,331,399	G	A	0.305245	-0.013234	0.002190	5.6E-10
JMJD1C	10	rs4133250	63,332,645	G	A	0.375642	0.020552	0.002081	3.2E-25
JMJD1C	10	rs7918743	63,333,302	T	C	0.385276	0.021052	0.002072	2.1E-26
JMJD1C	10	rs7902187	63,333,375	C	T	0.385276	0.021052	0.002072	2.1E-26
JMJD1C	10	rs10822158	63,334,623	G	A	0.287066	-0.014241	0.002228	4.8E-11
JMJD1C	10	rs10995506	63,334,706	A	G	0.375644	0.020553	0.002081	3.2E-25
JMJD1C	10	rs10740115	63,335,230	A	G	0.286679	-0.014384	0.002230	3.3E-11
JMJD1C	10	rs10740116	63,335,232	C	T	0.286679	-0.014384	0.002230	3.3E-11
JMJD1C	10	rs12219332	63,335,932	G	C	0.375681	0.020524	0.002081	3.6E-25
JMJD1C	10	rs10761743	63,336,258	C	T	0.385386	0.020956	0.002073	3.6E-26
JMJD1C	10	rs10822159	63,336,490	T	C	0.286946	-0.014245	0.002228	4.8E-11
JMJD1C	10	rs10740117	63,338,517	G	A	0.375630	0.020548	0.002081	3.4E-25
JMJD1C	10	rs6479894	63,338,981	T	C	0.375631	0.020548	0.002081	3.4E-25
JMJD1C	10	rs56674933	63,339,623	T	TAA	0.384473	0.020899	0.002074	4.4E-26
JMJD1C	10	rs71025161	63,340,059	C	CAATA	0.382354	0.021230	0.002085	1.7E-26
JMJD1C	10	rs10733790	63,340,574	G	C	0.372021	0.020650	0.002089	2.9E-25
JMJD1C	10	rs10761744	63,341,266	C	G	0.375630	0.020553	0.002081	3.4E-25
JMJD1C	10	rs10761745	63,341,311	G	C	0.375834	0.020307	0.002083	1.5E-24
JMJD1C	10	rs10740118	63,341,447	C	G	0.287150	-0.014276	0.002228	4.5E-11
JMJD1C	10	rs7091664	63,342,040	G	A	0.375630	0.020553	0.002081	3.4E-25
JMJD1C	10	rs7896518	63,344,740	G	A	0.286969	-0.014295	0.002228	4.2E-11
JMJD1C	10	rs10761746	63,345,134	A	G	0.385265	0.021057	0.002072	2.1E-26
JMJD1C	10	rs7081275	63,346,791	G	T	0.375704	0.020512	0.002081	4.2E-25
JMJD1C	10	chr10:63348205_CAA_C	63,348,205	CAA	C	0.372081	0.020721	0.002089	2.7E-25
JMJD1C	10	rs10761747	63,348,396	C	G	0.305241	-0.013285	0.002190	5.0E-10
JMJD1C	10	rs7895348	63,349,781	C	A	0.375644	0.020575	0.002081	2.9E-25
JMJD1C	10	rs7073932	63,350,160	C	T	0.385274	0.021074	0.002072	1.9E-26
JMJD1C	10	rs10761748	63,350,216	T	G	0.385274	0.021074	0.002072	1.9E-26
JMJD1C	10	rs10822160	63,353,036	G	T	0.282360	-0.014159	0.002248	1.1E-10
JMJD1C	10	rs7912797	63,353,620	G	A	0.305242	-0.013288	0.002190	4.8E-10
JMJD1C	10	rs7913278	63,353,774	G	A	0.386125	0.021110	0.002072	1.6E-26
JMJD1C	10	rs10761749	63,354,049	C	T	0.418590	0.018909	0.002061	1.3E-21
JMJD1C	10	rs200427687	63,354,672	G	GCTT	0.375170	0.020634	0.002085	2.9E-25
JMJD1C	10	rs149520237	63,354,674	T	TTTTG	0.384822	0.021129	0.002076	1.9E-26
JMJD1C	10	rs9415692	63,355,392	A	G	0.374543	0.020625	0.002083	2.6E-25
JMJD1C	10	rs7098614	63,355,667	T	C	0.304997	-0.013194	0.002191	6.1E-10
JMJD1C	10	rs7082926	63,355,771	T	G	0.384565	0.021131	0.002074	1.9E-26
JMJD1C	10	rs7083356	63,356,028	T	A	0.384339	0.021210	0.002074	1.1E-26
JMJD1C	10	rs35971912	63,357,004	C	CA	0.384390	0.020976	0.002076	4.1E-26
JMJD1C	10	rs10822161	63,358,443	A	G	0.287071	-0.014284	0.002228	4.3E-11
JMJD1C	10	rs9415693	63,360,127	C	T	0.375865	0.020569	0.002081	3.3E-25
JMJD1C	10	rs12355784	63,361,805	A	C	0.274842	-0.013151	0.002267	5.5E-09
JMJD1C	10	rs144958118	63,362,473	TTATATA	T	0.386027	0.020964	0.002075	3.7E-26
JMJD1C	10	rs9629895	63,363,027	A	C	0.385324	0.020975	0.002072	3.1E-26
JMJD1C	10	rs10822162	63,364,320	A	G	0.385323	0.020959	0.002072	3.4E-26
JMJD1C	10	rs10822163	63,364,338	G	C	0.287421	-0.014179	0.002228	6.1E-11
JMJD1C	10	rs10740119	63,365,477	T	G	0.384448	0.021125	0.002074	1.7E-26
JMJD1C	10	rs6479896	63,367,072	C	T	0.287088	-0.014314	0.002228	4.0E-11
JMJD1C	10	rs10822164	63,367,498	A	G	0.287088	-0.014314	0.002228	4.0E-11
JMJD1C	10	rs7909692	63,368,517	T	A	0.384662	0.021156	0.002074	1.6E-26
JMJD1C	10	rs10761750	63,368,859	A	G	0.287091	-0.014306	0.002228	4.1E-11
JMJD1C	10	rs9414799	63,369,842	C	T	0.373727	0.020774	0.002086	1.2E-25
JMJD1C	10	rs4746119	63,370,157	C	T	0.375671	0.020470	0.002081	4.9E-25
JMJD1C	10	rs9414800	63,371,522	A	T	0.374819	0.020621	0.002082	2.6E-25
JMJD1C	10	rs10546984	63,371,680	C	CATA	0.287103	-0.014329	0.002228	3.8E-11
JMJD1C	10	rs2393967	63,373,396	C	A	0.248144	-0.015746	0.002333	4.8E-12
JMJD1C	10	rs7923609	63,374,062	G	A	0.287564	-0.014267	0.002227	4.5E-11
JMJD1C	10	rs9415696	63,374,588	T	A	0.374802	0.020643	0.002082	2.2E-25
JMJD1C	10	rs2893919	63,375,018	A	G	0.287218	-0.014286	0.002228	4.2E-11
JMJD1C	10	rs2393966	63,375,054	G	T	0.287218	-0.014286	0.002228	4.2E-11
JMJD1C	10	rs9415697	63,375,377	C	T	0.374816	0.020627	0.002082	2.5E-25
JMJD1C	10	rs7076310	63,375,912	A	C	0.287218	-0.014286	0.002228	4.2E-11
JMJD1C	10	rs6479897	63,376,868	C	T	0.384459	0.021141	0.002073	1.5E-26
JMJD1C	10	rs4310508	63,378,813	G	A	0.287218	-0.014286	0.002228	4.2E-11
JMJD1C	10	rs7910927	63,379,150	G	T	0.287768	-0.014510	0.002228	1.8E-11
JMJD1C	10	rs6479899	63,379,287	T	A	0.375751	0.020558	0.002085	5.3E-25
JMJD1C	10	rs724553	63,380,624	C	G	0.374816	0.020627	0.002082	2.5E-25
JMJD1C	10	rs2393969	63,380,680	C	A	0.287298	-0.014270	0.002228	4.4E-11
JMJD1C	10	rs9415699	63,383,798	C	T	0.375663	0.020487	0.002080	4.2E-25
JMJD1C	10	rs9415700	63,385,805	T	C	0.303647	0.018087	0.002195	4.7E-19
JMJD1C	10	rs10822165	63,387,199	T	C	0.385309	0.020988	0.002072	2.7E-26
JMJD1C	10	rs71025168	63,387,563	GA	G	0.386206	0.020828	0.002073	6.0E-26
JMJD1C	10	rs10995527	63,387,659	A	G	0.294799	-0.014451	0.002221	2.2E-11
JMJD1C	10	chr10:63390573_TACA_T	63,390,573	TACA	T	0.386531	0.020910	0.002078	7.6E-26
JMJD1C	10	rs9414802	63,391,622	C	T	0.312448	0.018716	0.002179	2.7E-20
JMJD1C	10	rs9415701	63,391,749	C	T	0.302801	0.018236	0.002197	3.0E-19
JMJD1C	10	rs4746125	63,393,125	A	G	0.306156	0.018357	0.002194	2.1E-19
JMJD1C	10	rs10740122	63,395,451	C	A	0.384017	0.021096	0.002075	2.0E-26
JMJD1C	10	rs10822167	63,398,991	C	T	0.385840	0.021095	0.002073	1.7E-26
JMJD1C	10	rs67434572	63,399,012	A	AAAG	0.287223	-0.014244	0.002228	5.1E-11
JMJD1C	10	rs4745706	63,399,820	C	T	0.370986	0.020711	0.002098	4.3E-25
JMJD1C	10	rs12415038	63,401,098	G	A	0.376284	0.020612	0.002081	2.4E-25
JMJD1C	10	rs9415705	63,401,790	G	T	0.375194	0.020695	0.002080	1.7E-25
JMJD1C	10	rs10740123	63,404,755	A	G	0.313560	0.018799	0.002175	1.4E-20
JMJD1C	10	rs10822168	63,405,424	A	G	0.286482	-0.014309	0.002231	3.9E-11
JMJD1C	10	chr10:63407820_CA_C	63,407,820	C	CA	0.305950	0.018109	0.002199	3.9E-19

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
JMJD1C	10	rs10822170	63,411,395	G	T	0.386688	0.020971	0.002076	4.8E-26
JMJD1C	10	rs10761755	63,412,212	G	A	0.386149	0.021126	0.002071	1.4E-26
JMJD1C	10	rs10761756	63,412,568	T	C	0.287061	-0.014208	0.002228	5.4E-11
JMJD1C	10	rs10761757	63,412,790	C	G	0.386148	0.021127	0.002071	1.4E-26
JMJD1C	10	rs10761758	63,412,987	T	A	0.286346	-0.014364	0.002232	3.2E-11
JMJD1C	10	rs71837985	63,413,039	A	AAAC	0.287310	-0.014266	0.002228	4.9E-11
JMJD1C	10	rs10761759	63,414,032	G	T	0.314112	0.018986	0.002180	7.3E-21
JMJD1C	10	rs61853587	63,414,817	C	G	0.303618	0.018576	0.002194	6.7E-20
JMJD1C	10	rs7909269	63,418,006	A	G	0.287054	-0.014295	0.002228	4.3E-11
JMJD1C	10	rs35999426	63,418,722	T	TG	0.375547	0.020774	0.002081	1.4E-25
JMJD1C	10	rs10761760	63,419,392	C	A	0.284230	-0.014065	0.002244	8.4E-11
JMJD1C	10	rs10761761	63,419,398	T	A	0.389550	0.021006	0.002076	3.6E-26
JMJD1C	10	rs10995530	63,419,654	G	A	0.313316	0.019000	0.002177	6.8E-21
JMJD1C	10	rs11818194	63,420,692	A	G	0.364685	0.020359	0.002145	1.1E-23
JMJD1C	10	rs6479901	63,421,016	C	A	0.385363	0.021234	0.002073	9.3E-27
JMJD1C	10	rs7077580	63,421,125	A	G	0.287052	-0.014290	0.002228	4.3E-11
JMJD1C	10	rs35654741	63,425,460	CAT	C	0.303535	0.018513	0.002195	8.7E-20
JMJD1C	10	rs10740124	63,426,034	C	T	0.313227	0.019015	0.002177	6.8E-21
JMJD1C	10	rs9415706	63,426,587	T	C	0.303630	0.018579	0.002194	6.7E-20
JMJD1C	10	rs72837019	63,427,258	C	T	0.313227	0.019015	0.002177	6.8E-21
JMJD1C	10	rs61853589	63,427,351	A	T	0.304181	0.018601	0.002195	5.1E-20
JMJD1C	10	rs9414803	63,428,309	A	G	0.303627	0.018576	0.002194	6.8E-20
JMJD1C	10	rs9415707	63,428,530	C	T	0.304458	0.018455	0.002192	9.6E-20
JMJD1C	10	rs10761764	63,429,143	C	G	0.313375	0.018966	0.002178	8.4E-21
JMJD1C	10	rs10761765	63,429,213	A	G	0.313227	0.019009	0.002177	6.9E-21
JMJD1C	10	rs12413029	63,429,366	C	T	0.303629	0.018574	0.002194	6.8E-20
JMJD1C	10	rs9415708	63,430,282	C	G	0.303629	0.018574	0.002194	6.8E-20
JMJD1C	10	rs7924036	63,431,885	G	T	0.332597	0.019054	0.002144	1.1E-21
JMJD1C	10	rs10761767	63,432,671	T	C	0.312746	0.018993	0.002177	7.1E-21
JMJD1C	10	rs7917169	63,433,181	T	C	0.313731	0.018810	0.002176	1.3E-20
JMJD1C	10	rs10761768	63,434,369	C	A	0.313817	0.018878	0.002175	1.0E-20
JMJD1C	10	rs72837025	63,434,731	C	A	0.304502	0.018471	0.002192	8.8E-20
JMJD1C	10	rs12784772	63,435,695	A	T	0.304456	0.018511	0.002192	7.5E-20
JMJD1C	10	rs77494594	63,437,549	C	A	0.303649	0.018638	0.002194	5.0E-20
JMJD1C	10	rs10437345	63,443,186	C	T	0.303644	0.018642	0.002194	4.9E-20
JMJD1C	10	rs2616631	63,448,154	A	T	0.303178	0.018569	0.002194	6.6E-20
JMJD1C	10	rs2466128	63,448,561	C	T	0.303178	0.018569	0.002194	6.6E-20
JMJD1C	10	rs2719815	63,450,534	C	G	0.303178	0.018569	0.002194	6.6E-20
JMJD1C	10	rs2616630	63,453,579	C	A	0.303178	0.018569	0.002194	6.6E-20
JMJD1C	10	rs2616629	63,454,056	C	T	0.303178	0.018569	0.002194	6.6E-20
JMJD1C	10	rs10822172	63,455,478	T	C	0.313077	0.019009	0.002178	6.9E-21
JMJD1C	10	rs12573212	63,458,665	A	C	0.312682	0.018978	0.002177	7.7E-21
JMJD1C	10	rs7074735	63,459,519	T	A	0.312922	0.019005	0.002177	7.0E-21
JMJD1C	10	rs7075205	63,459,834	T	C	0.312752	0.019031	0.002177	6.2E-21
JMJD1C	10	rs10995540	63,460,170	C	G	0.312752	0.019031	0.002177	6.2E-21
JMJD1C	10	rs2616628	63,460,197	C	G	0.303171	0.018601	0.002194	5.8E-20
JMJD1C	10	rs10159609	63,461,168	C	T	0.312752	0.019031	0.002177	6.2E-21
JMJD1C	10	chr10:63464698_CA_C	63,464,698	CA	C	0.330619	0.019259	0.002152	7.3E-22
JMJD1C	10	rs2393980	63,464,750	G	C	0.303171	0.018601	0.002194	5.8E-20
JMJD1C, JMJD1C-AS	10	rs1061259	63,465,484	G	C	0.313087	0.019037	0.002178	6.1E-21
JMJD1C *	10	rs58806797	63,466,790	A	AT	0.303171	0.018601	0.002194	5.8E-20
JMJD1C *	10	rs10995541	63,473,575	G	T	0.312498	0.019043	0.002178	5.7E-21
JMJD1C *	10	rs59215788	63,474,074	G	A	0.303171	0.018601	0.002194	5.8E-20
JMJD1C *	10	chr10:63474104_TAATA_T	63,474,104	T	TAATA	0.331982	0.014906	0.002147	1.7E-14
JMJD1C *	10	rs59246603	63,474,182	C	T	0.303171	0.018601	0.002194	5.8E-20
JMJD1C *	10	chr10:63474856_T_TA	63,474,856	TA	T	0.312934	0.018966	0.002178	8.4E-21
JMJD1C *	10	rs12414159	63,479,017	T	A	0.303171	0.018601	0.002194	5.8E-20
JMJD1C *	10	rs10995543	63,479,787	C	T	0.303171	0.018601	0.002194	5.8E-20
JMJD1C *	10	rs10761773	63,480,322	G	C	0.322525	0.018600	0.002191	4.8E-20
JMJD1C *	10	rs4746138	63,481,981	G	A	0.303023	0.018624	0.002195	4.9E-20
JMJD1C *	10	rs2393978	63,482,050	C	A	0.313621	0.019035	0.002176	6.9E-21
JMJD1C *	10	rs10822173	63,483,842	A	T	0.312742	0.019023	0.002177	6.3E-21
JMJD1C *	10	rs7915680	63,484,544	C	T	0.312742	0.019023	0.002177	6.3E-21
JMJD1C *	10	rs7085862	63,486,687	T	G	0.312742	0.019023	0.002177	6.3E-21
JMJD1C *	10	rs2893922	63,487,259	G	T	0.303203	0.018604	0.002194	5.8E-20
JMJD1C *	10	chr10:63488541_TA_T	63,488,541	TA	T	0.313161	0.019072	0.002178	5.6E-21
JMJD1C *	10	rs9919452	63,488,812	T	C	0.312737	0.019028	0.002177	6.2E-21
JMJD1C *	10	rs10740128	63,490,783	A	G	0.311019	0.019176	0.002184	3.5E-21
JMJD1C *	10	rs10761776	63,491,217	C	T	0.312644	0.019016	0.002177	7.3E-21
JMJD1C *	10	rs2393976	63,493,679	C	G	0.304255	0.018448	0.002193	9.9E-20
REEP3 *	10	rs7910662	63,493,940	C	T	0.312456	0.018998	0.002178	7.3E-21
REEP3 *	10	chr10:63495406_TA_T	63,495,406	T	TA	0.303101	0.018649	0.002194	4.7E-20
REEP3 *	10	rs10822175	63,495,414	A	T	0.307833	0.019168	0.002196	6.1E-21
REEP3 *	10	rs4746149	63,497,633	C	T	0.303180	0.018650	0.002194	4.8E-20
REEP3 *	10	rs72837056	63,500,718	G	T	0.302734	0.018681	0.002196	4.8E-20
REEP3 *	10	rs2893924	63,501,594	A	G	0.312757	0.019045	0.002177	5.8E-21
REEP3 *	10	rs2393981	63,501,605	A	G	0.312757	0.019045	0.002177	5.8E-21
REEP3 *	10	rs9971294	63,503,108	A	G	0.312757	0.019045	0.002177	5.8E-21
REEP3 *	10	rs76677248	63,503,505	C	CAT	0.303187	0.018619	0.002194	5.5E-20
REEP3 *	10	rs80026135	63,505,240	G	C	0.302698	0.018668	0.002198	5.1E-20
REEP3 *	10	rs11815969	63,506,095	T	C	0.303188	0.018616	0.002194	5.5E-20
REEP3 *	10	rs7078456	63,509,719	C	T	0.303353	0.018600	0.002194	6.1E-20
REEP3 *	10	rs7083823	63,510,912	G	C	0.313412	0.018855	0.002178	1.3E-20
REEP3 *	10	chr10:63512289_C_CT	63,512,289	CT	C	0.295281	0.018845	0.002228	1.3E-19
REEP3 *	10	rs7097698	63,513,635	G	A	0.312812	0.019130	0.002178	4.4E-21
REEP3 *	10	rs7068144	63,514,500	C	G	0.312809	0.019132	0.002178	4.4E-21
REEP3 *	10	rs72837070	63,514,919	C	T	0.303244	0.018690	0.002195	4.4E-20
REEP3 *	10	chr10:63514949_A_AT	63,514,949	AT	A	0.300668	0.018526	0.002206	1.1E-19
REEP3 *	10	rs35605123	63,516,140	GA	G	0.313232	0.018899	0.002178	1.2E-20
REEP3 *	10	rs61853635	63,516,750	G	T	0.303250	0.018687	0.002195	4.4E-20
REEP3 *	10	rs7082076	63,517,185	C	G	0.314280	0.019174	0.002180	4.6E-21
REEP3 *	10	rs4745729	63,517,323	G	A	0.303231	0.018675	0.002195	4.7E-20
REEP3 *	10	rs10740133	63,517,676	C	T	0.312798	0.019112	0.002178	4.7E-21
REEP3 *	10	rs12416349	63,517,783	T	C	0.300382	0.019220	0.002214	1.2E-20
REEP3 *	10	rs7358191	63,519,028	A	C	0.312798	0.019112	0.002178	4.7E-21
REEP3 *	10	rs7358152	63,519,138	T	C	0.312798	0.019112	0.002178	4.7E-21
REEP3 *	10	rs10822179	63,520,404	T	C	0.312798	0.019112	0.002178	4.7E-21

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
REEP3	10	rs10761780	63,524,272	C	T	0.303317	0.018719	0.002195	3.9E-20
REEP3	10	rs10761781	63,524,843	T	C	0.303231	0.018704	0.002195	4.2E-20
REEP3	10	rs12412946	63,529,792	G	T	0.295529	0.018355	0.002228	4.2E-19
REEP3	10	rs12414188	63,529,854	G	A	0.302540	0.018700	0.002198	5.1E-20
REEP3	10	rs11375382	63,530,178	A	AC	0.303189	0.018669	0.002195	4.9E-20
REEP3	10	rs5785580	63,530,494	AT	A	0.331154	0.019029	0.002146	1.5E-21
REEP3	10	rs7087279	63,532,176	T	A	0.303234	0.018667	0.002195	4.7E-20
REEP3	10	rs59035163	63,532,283	G	C	0.303234	0.018667	0.002195	4.7E-20
REEP3	10	rs12413081	63,533,959	T	C	0.303234	0.018667	0.002195	4.7E-20
REEP3	10	rs16918567	63,534,910	C	A	0.303091	0.018573	0.002195	6.5E-20
REEP3	10	rs16918573	63,541,045	A	T	0.300757	0.018618	0.002199	5.5E-20
REEP3	10	rs16918575	63,541,565	G	A	0.300757	0.018614	0.002199	5.6E-20
REEP3	10	rs147232123	63,541,637	G	GT	0.300757	0.018614	0.002199	5.6E-20
REEP3	10	rs12414796	63,543,327	A	G	0.300720	0.018620	0.002200	5.5E-20
REEP3	10	rs61853639	63,545,353	T	G	0.301286	0.018649	0.002198	5.0E-20
REEP3	10	rs4746195	63,547,893	G	A	0.301325	0.018654	0.002198	4.6E-20
REEP3	10	rs4469774	63,550,017	T	G	0.302383	0.018541	0.002198	1.1E-19
REEP3	10	rs61853642	63,554,019	A	G	0.285222	0.018181	0.002233	2.1E-18
REEP3	10	rs9919429	63,554,059	G	A	0.313114	0.018514	0.002176	7.9E-20
REEP3	10	rs2163188	63,554,951	C	G	0.313261	0.018432	0.002177	1.0E-19
REEP3	10	rs2393984	63,555,211	G	A	0.313115	0.018510	0.002176	8.0E-20
REEP3	10	rs6479905	63,555,471	G	A	0.311128	0.018762	0.002182	5.3E-20
REEP3	10	rs12411988	63,555,637	C	G	0.285410	0.018125	0.002232	2.6E-18
REEP3	10	rs12412012	63,556,003	T	C	0.285335	0.018157	0.002232	2.3E-18
REEP3	10	rs7919685	63,556,040	T	G	0.313232	0.018486	0.002176	8.6E-20
REEP3	10	rs61117531	63,556,475	T	TACTC	0.312813	0.018601	0.002182	5.5E-20
REEP3	10	rs12247907	63,557,285	C	G	0.313228	0.018507	0.002176	7.9E-20
REEP3	10	rs7070761	63,557,296	T	A	0.313228	0.018507	0.002176	7.9E-20
REEP3	10	rs10761785	63,559,006	G	T	0.314762	0.018506	0.002175	8.3E-20
REEP3	10	rs61579729	63,559,553	G	A	0.285333	0.018187	0.002232	2.0E-18
REEP3	10	rs7898861	63,559,918	C	T	0.312129	0.018533	0.002181	8.6E-20
REEP3	10	rs16918599	63,560,319	C	T	0.285308	0.018166	0.002232	2.2E-18
REEP3	10	rs16918600	63,560,690	A	C	0.285308	0.018166	0.002232	2.2E-18
REEP3	10	rs11812934	63,560,970	A	G	0.285312	0.018163	0.002232	2.2E-18
REEP3	10	rs16918601	63,561,291	A	C	0.285325	0.018205	0.002233	1.9E-18
REEP3	10	rs12245149	63,561,387	A	C	0.313210	0.018520	0.002177	7.9E-20
REEP3	10	rs12245367	63,561,704	T	C	0.312772	0.018594	0.002183	8.1E-20
REEP3	10	rs16918603	63,561,712	G	A	0.284863	0.018359	0.002240	1.4E-18
REEP3	10	rs4746201	63,562,621	T	G	0.284915	0.018377	0.002241	1.3E-18
REEP3	10	rs10666196	63,562,704	ATCAG	A	0.312849	0.018642	0.002184	6.3E-20
REEP3	10	rs7899657	63,563,505	A	G	0.312862	0.018599	0.002184	7.7E-20
REEP3	10	rs4746203	63,564,237	T	G	0.312345	0.018637	0.002187	7.4E-20
REEP3	10	rs10822181	63,565,366	A	G	0.313150	0.018465	0.002186	1.3E-19
REEP3	10	rs4746204	63,568,758	T	C	0.313032	0.018619	0.002187	8.1E-20
REEP3	10	rs7907451	63,568,980	A	T	0.313041	0.018628	0.002187	8.0E-20
REEP3	10	rs4746205	63,569,758	G	A	0.313053	0.018636	0.002187	8.2E-20
REEP3	10	rs7100409	63,570,435	A	T	0.313045	0.018629	0.002188	8.6E-20
REEP3	10	rs7100413	63,570,448	C	T	0.313047	0.018624	0.002188	8.8E-20
REEP3	10	rs61853655	63,570,645	G	A	0.284751	0.018247	0.002246	3.0E-18
REEP3	10	rs3847325	63,571,751	C	G	0.313475	0.018610	0.002187	9.9E-20
REEP3	10	rs3847326	63,572,099	G	A	0.315462	0.018402	0.002185	2.4E-19
REEP3	10	chr10:63572305_C_CT	63,572,305	CT	C	0.299130	0.017674	0.002225	1.2E-17
REEP3	10	rs6479908	63,573,888	G	C	0.305649	0.017872	0.002202	3.3E-18
REEP3	10	rs7090758	63,575,555	C	T	0.305659	0.017843	0.002202	3.7E-18
REEP3	10	rs7077256	63,576,425	G	A	0.305696	0.017912	0.002202	2.8E-18
REEP3	10	rs7902616	63,576,613	A	G	0.305696	0.017912	0.002202	2.8E-18
REEP3	10	rs10822183	63,577,381	C	T	0.305539	0.017990	0.002202	2.1E-18
REEP3	10	rs7910951	63,578,544	G	A	0.305694	0.017908	0.002202	2.9E-18
REEP3	10	rs7911761	63,578,993	G	C	0.305712	0.017896	0.002202	3.0E-18
REEP3	10	rs11817901	63,580,123	A	G	0.286856	0.018038	0.002243	7.4E-18
REEP3	10	rs12768534	63,581,137	A	G	0.305691	0.017899	0.002202	3.0E-18
REEP3	10	rs16918638	63,583,371	C	T	0.288030	0.018110	0.002241	6.1E-18
REEP3	10	rs61853658	63,590,037	T	C	0.282026	0.017247	0.002260	2.7E-16
REEP3	10	chr10:63590519_AT_A	63,590,519	AT	A	0.309910	0.017565	0.002204	1.6E-17
REEP3	10	rs11817169	63,596,549	G	A	0.283402	0.017348	0.002262	2.6E-16
REEP3	10	rs4746244	63,599,941	T	C	0.281532	0.017200	0.002269	4.9E-16
REEP3	10	rs11818738	63,604,971	C	A	0.285279	0.016969	0.002273	9.8E-16
REEP3 *	10	rs2565187	63,632,093	C	T	0.232748	0.015054	0.002399	3.7E-11
REEP3 *	10	rs2565186	63,632,270	A	G	0.232722	0.015044	0.002399	3.8E-11
REEP3 *	10	rs1268639	63,632,720	A	G	0.232879	0.015128	0.002398	3.1E-11
REEP3 *	10	rs1255495	63,634,690	G	A	0.233126	0.015003	0.002393	4.1E-11
IDE *	10	rs2798253	92,443,148	C	G	0.344555	0.011747	0.002129	2.5E-08
IDE *	10	rs6583813	92,450,182	C	T	0.342857	0.011577	0.002125	4.8E-08
IDE	10	rs3781241	92,456,753	T	C	0.346128	0.011851	0.002127	2.0E-08
IDE	10	rs2149632	92,472,490	T	C	0.342758	0.011732	0.002123	2.7E-08
IDE	10	chr10:92479610_AGT_A	92,479,610	AGT	A	0.346749	0.011611	0.002129	3.7E-08
IDE	10	rs10882067	92,484,511	T	C	0.341226	0.011759	0.002127	2.4E-08
IDE	10	rs11187022	92,495,286	T	C	0.340745	0.011821	0.002131	2.2E-08
IDE	10	rs34459034	92,499,489	G	A	0.437561	0.012424	0.002049	1.3E-09
IDE	10	rs10786048	92,500,211	C	T	0.342477	0.011877	0.002126	1.8E-08
IDE	10	rs10882071	92,500,348	T	C	0.343097	0.012119	0.002128	1.2E-08
IDE	10	rs10882072	92,500,955	C	A	0.343726	0.012020	0.002129	1.3E-08
IDE	10	rs11187030	92,501,246	C	T	0.343131	0.011769	0.002129	2.5E-08
IDE	10	rs11187033	92,502,602	T	A	0.342469	0.011886	0.002127	1.7E-08
IDE	10	chr10:92507108_CA_C	92,507,108	CA	C	0.340076	0.011668	0.002141	4.1E-08
IDE	10	rs11286004	92,508,474	GA	G	0.343357	0.011755	0.002130	2.8E-08
IDE	10	rs35831688	92,511,694	A	AT	0.342316	0.011676	0.002127	3.1E-08
IDE	10	rs10509645	92,518,109	C	A	0.343156	0.011724	0.002127	2.7E-08
IDE	10	rs10882074	92,521,928	T	G	0.339449	0.012591	0.002141	4.7E-09
IDE	10	rs7073833	92,526,663	T	C	0.344303	0.011946	0.002127	2.0E-08
IDE	10	rs12220493	92,551,152	C	T	0.344404	0.012074	0.002125	1.4E-08
IDE	10	rs2421943	92,552,058	G	A	0.344437	0.012044	0.002125	1.5E-08
IDE	10	rs7078418	92,560,777	C	T	0.347022	0.011966	0.002134	1.8E-08
IDE	10	rs10882083	92,562,216	C	G	0.344102	0.011974	0.002126	1.7E-08
IDE	10	rs11187072	92,564,652	C	T	0.344756	0.012653	0.002134	3.0E-09
IDE	10	rs7076966	92,565,754	C	T	0.344526	0.012194	0.002125	1.1E-08
IDE *	10	rs11187078	92,580,948	C	G	0.344603	0.012512	0.002123	3.9E-09

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
IDE *	10	rs2901597	92,582,906	C	T	0.344645	0.012466	0.002124	4.3E-09
KIF11 *	10	rs7921210	92,587,812	G	A	0.345009	0.012496	0.002121	4.3E-09
KIF11 *	10	rs7922041	92,588,443	G	A	0.437341	0.012340	0.002037	1.3E-09
KIF11 *	10	rs12355158	92,590,924	G	A	0.334702	0.013030	0.002147	1.4E-09
KIF11	10	rs3824735	92,594,447	T	G	0.336260	0.012973	0.002139	1.6E-09
KIF11	10	rs11187090	92,600,915	C	T	0.336294	0.012948	0.002138	1.6E-09
KIF11	10	rs10882085	92,605,125	C	T	0.336297	0.012952	0.002138	1.6E-09
KIF11	10	rs11187094	92,608,421	G	A	0.428200	0.012377	0.002043	1.2E-09
KIF11	10	rs11187096	92,609,831	G	T	0.336278	0.012939	0.002138	1.6E-09
KIF11	10	rs11187098	92,615,134	T	C	0.336601	0.012951	0.002138	1.5E-09
KIF11	10	rs11187099	92,615,240	C	T	0.336285	0.012959	0.002138	1.5E-09
KIF11	10	rs10882092	92,619,466	G	A	0.336489	0.013062	0.002139	1.1E-09
KIF11	10	rs11187105	92,624,670	C	T	0.428725	0.012281	0.002042	1.6E-09
KIF11	10	rs1573051	92,627,577	T	C	0.336277	0.012956	0.002138	1.5E-09
KIF11	10	rs11187107	92,631,940	G	A	0.336411	0.012858	0.002139	2.0E-09
KIF11	10	rs10882095	92,634,645	T	G	0.336228	0.012799	0.002139	2.4E-09
KIF11	10	rs1972360	92,636,831	C	T	0.337842	0.012842	0.002139	2.2E-09
KIF11	10	rs10882096	92,641,629	G	T	0.336465	0.012821	0.002139	2.3E-09
KIF11	10	rs11187114	92,646,480	A	T	0.336702	0.013162	0.002140	1.1E-09
KIF11	10	rs11187117	92,652,401	A	C	0.336340	0.012861	0.002139	2.4E-09
KIF11	10	rs1044153	92,655,321	A	C	0.335999	0.012838	0.002139	2.5E-09
KIF11 *	10	rs2153827	92,664,316	T	G	0.336141	0.013490	0.002146	4.6E-10
KIF11 *	10	rs35978445	92,664,665	G	A	0.336134	0.013494	0.002146	4.4E-10
KIF11 *	10	rs2185756	92,670,740	A	C	0.300588	0.012164	0.002203	2.7E-08
HHEX *	10	rs10882098	92,685,036	C	T	0.300484	0.012028	0.002201	3.1E-08
HHEX *	10	rs11187133	92,685,099	G	A	0.390344	0.011718	0.002081	1.8E-08
HHEX *	10	rs11187138	92,700,524	A	G	0.298582	0.012586	0.002204	9.9E-09
HHEX *	10	rs10882099	92,700,893	T	C	0.298828	0.012522	0.002202	1.1E-08
HHEX *	10	chr10:92701901_T_TA	92,701,901	T	TA	0.298853	0.012489	0.002203	1.3E-08
HHEX *	10	rs10882101	92,702,670	T	C	0.299991	0.012472	0.002196	1.2E-08
HHEX *	10	chr10:92702822_G_GA	92,702,822	G	GA	0.301964	0.012470	0.002204	1.5E-08
HHEX *	10	rs1111875	92,703,125	C	T	0.300541	0.012505	0.002195	1.0E-08
HHEX *	10	rs1977832	92,704,022	G	T	0.300240	0.012418	0.002197	1.3E-08
HHEX *	10	rs1977833	92,704,188	G	A	0.299792	0.012421	0.002198	1.4E-08
HHEX *	10	rs11309330	92,704,205	GT	G	0.299792	0.012421	0.002198	1.4E-08
EXOC6	10	rs11187236	92,986,483	G	A	0.290247	0.012364	0.002242	1.3E-08
CYP26A1 *	10	rs11812460	93,072,371	G	A	0.173702	0.015496	0.002730	8.7E-09
CYP26A1 *	10	rs61863116	93,078,631	G	A	0.126332	0.018551	0.003078	1.8E-09
CYP26A1 *	10	rs2068888	93,079,885	G	A	0.189842	0.020077	0.002576	1.3E-15
CYP26A1 *	10	rs4418728	93,079,967	G	T	0.189761	0.019863	0.002578	2.8E-15
CYP26A1 *	10	rs10882140	93,082,456	G	T	0.160964	0.017080	0.002760	1.3E-10
CYP26A1 *	10	rs10786068	93,082,720	C	G	0.160540	0.017156	0.002761	1.2E-10
CYP26A1 *	10	rs12359135	93,083,778	T	C	0.165962	0.016401	0.002730	8.1E-10
CYP26A1 *	10	rs10748591	93,084,109	C	G	0.153299	0.017110	0.002815	2.9E-10
CYP26A1 *	10	rs10882141	93,084,327	G	A	0.156300	0.016990	0.002790	3.2E-10
CYP26A1 *	10	rs913423	93,085,279	G	A	0.161200	0.016716	0.002748	2.1E-10
CYP26A1 *	10	rs10786069	93,085,789	C	T	0.162262	0.016136	0.002744	6.0E-10
CYP26A1 *	10	rs10610109	93,086,224	TCA	T	0.157012	0.015526	0.002797	3.9E-09
CYP26A1 *	10	rs7080494	93,086,336	G	A	0.150755	0.015689	0.002883	6.8E-09
WDR11 *	10	rs2246958	121,129,610	C	T	0.377593	-0.012378	0.002094	5.9E-09
WDR11 *	10	rs2246730	121,131,141	C	T	0.376110	-0.012773	0.002098	2.8E-09
WDR11 *	10	rs1873446	121,131,995	C	T	0.375804	-0.012729	0.002095	2.7E-09
WDR11 *	10	rs1907239	121,135,315	A	C	0.367314	0.013564	0.002092	4.6E-11
WDR11 *	10	rs2250266	121,138,399	A	G	0.365909	0.013540	0.002096	5.0E-11
WDR11 *	10	rs1907240	121,138,445	G	A	0.414321	-0.014861	0.002048	7.3E-13
WDR11 *	10	rs1907241	121,138,470	G	T	0.413810	-0.014996	0.002048	4.4E-13
WDR11 *	10	rs2257129	121,139,183	T	C	0.411379	-0.015291	0.002050	1.2E-13
WDR11 *	10	rs2263985	121,143,992	C	T	0.411401	-0.015451	0.002051	6.6E-14
WDR11 *	10	rs2451876	121,144,368	T	C	0.411309	-0.015420	0.002050	7.5E-14
WDR11 *	10	rs2263983	121,145,186	T	C	0.411304	-0.015404	0.002050	8.0E-14
WDR11 *	10	rs2220607	121,146,746	C	A	0.412846	-0.015443	0.002049	7.3E-14
WDR11 *	10	rs2172073	121,150,111	C	A	0.413019	-0.015392	0.002049	7.5E-14
WDR11 *	10	rs1907256	121,150,416	A	G	0.370804	0.013720	0.002089	1.4E-11
WDR11 *	10	rs2263997	121,151,174	A	C	0.367349	0.013522	0.002102	3.5E-11
WDR11 *	10	rs7098433	121,153,961	C	T	0.413124	-0.015398	0.002048	7.3E-14
WDR11 *	10	rs17101518	121,155,455	G	A	0.366237	-0.015318	0.002094	4.7E-13
WDR11 *	10	rs58846742	121,155,542	C	G	0.316950	-0.013711	0.002166	2.0E-10
WDR11 *	10	rs72631105	121,155,831	A	G	0.352253	0.013566	0.002112	4.8E-11
WDR11 *	10	rs56351107	121,155,983	G	C	0.366083	-0.015331	0.002093	4.0E-13
WDR11 *	10	rs17101521	121,156,039	C	T	0.365157	-0.015285	0.002097	5.3E-13
WDR11 *	10	rs56132357	121,156,071	A	T	0.315682	-0.013723	0.002172	2.2E-10
WDR11 *	10	rs59313277	121,156,141	T	G	0.365925	-0.015244	0.002094	5.6E-13
WDR11 *	10	chr10:121156208_T_TA	121,156,208	TA	T	0.358204	-0.015267	0.002127	9.2E-13
WDR11 *	10	rs73366917	121,156,240	A	G	0.365546	-0.015248	0.002094	5.7E-13
WDR11 *	10	rs17101524	121,156,265	A	C	0.366083	-0.015331	0.002093	4.0E-13
WDR11 *	10	rs59082214	121,156,440	A	CACACAC	0.359945	-0.014130	0.002118	2.8E-11
WDR11 *	10	rs4752500	121,156,448	T	A	0.368429	-0.015245	0.002097	5.6E-13
WDR11 *	10	rs1907266	121,156,628	T	C	0.412902	-0.015306	0.002048	1.0E-13
WDR11 *	10	rs7920116	121,156,957	C	T	0.366083	-0.015331	0.002093	4.0E-13
WDR11 *	10	rs7903585	121,157,114	G	A	0.364527	-0.015293	0.002097	5.7E-13
WDR11 *	10	rs7903948	121,157,125	A	G	0.365959	-0.015362	0.002094	3.6E-13
WDR11 *	10	rs7903733	121,157,208	G	A	0.316960	-0.013719	0.002166	2.0E-10
WDR11 *	10	rs10710843	121,157,294	C	CA	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs7904102	121,157,377	G	C	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs58960052	121,157,487	A	G	0.316960	-0.013719	0.002166	2.0E-10
WDR11 *	10	rs59754371	121,157,811	C	T	0.365384	-0.015176	0.002096	7.1E-13
WDR11 *	10	rs57615383	121,157,842	A	G	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs112209982	121,158,067	A	G	0.361999	-0.015050	0.002106	1.5E-12
WDR11 *	10	rs58324269	121,158,215	G	A	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs60089052	121,158,221	C	T	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs58217496	121,158,313	C	T	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs60711290	121,158,469	T	G	0.366077	-0.015336	0.002093	3.9E-13
WDR11 *	10	rs57142282	121,158,561	T	C	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs17101530	121,158,601	C	T	0.366124	-0.015333	0.002093	4.0E-13
WDR11 *	10	rs71945618	121,158,703	AG	A	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs73366943	121,158,995	G	A	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs17101534	121,159,361	C	T	0.366080	-0.015338	0.002093	3.8E-13

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
WDR11 *	10	rs11199803	121,159,565	G	A	0.366080	-0.015338	0.002093	3.8E-13
WDR11 *	10	rs11199804	121,159,660	G	C	0.366079	-0.015338	0.002093	3.9E-13
WDR11 *	10	rs11199805	121,159,692	T	C	0.366079	-0.015338	0.002093	3.9E-13
WDR11 *	10	rs11199806	121,159,795	A	G	0.366083	-0.015334	0.002093	3.9E-13
WDR11 *	10	rs7917346	121,160,328	G	A	0.366201	-0.015287	0.002093	4.5E-13
WDR11 *	10	rs7902796	121,160,495	C	T	0.316963	-0.013713	0.002166	2.0E-10
WDR11 *	10	rs7902919	121,160,588	C	T	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs7917833	121,160,641	A	C	0.366087	-0.015347	0.002093	3.7E-13
WDR11 *	10	rs7917847	121,160,676	A	C	0.317012	-0.013819	0.002166	1.4E-10
WDR11 *	10	rs2130786	121,161,069	C	T	0.412936	-0.015314	0.002048	9.9E-14
WDR11 *	10	rs1907267	121,161,442	T	C	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs1907268	121,161,733	C	T	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs1907269	121,161,835	C	A	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs6585696	121,162,049	G	A	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs6585697	121,162,083	T	C	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs6585698	121,162,088	G	T	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs6585699	121,162,146	C	T	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs6585700	121,162,243	C	G	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs6585701	121,162,277	C	T	0.366082	-0.015330	0.002093	4.0E-13
WDR11 *	10	rs7920041	121,162,857	C	T	0.366087	-0.015335	0.002093	3.9E-13
WDR11 *	10	rs7920045	121,162,867	C	T	0.316966	-0.013721	0.002166	2.0E-10
WDR11 *	10	rs7906567	121,162,944	C	A	0.366087	-0.015335	0.002093	3.9E-13
WDR11 *	10	rs59296617	121,163,320	A	T	0.366087	-0.015335	0.002093	3.9E-13
WDR11 *	10	rs11199810	121,164,064	C	T	0.366087	-0.015335	0.002093	3.9E-13
WDR11 *	10	rs60590589	121,164,227	AAAAC	A	0.366135	-0.015324	0.002093	4.0E-13
WDR11 *	10	rs7087606	121,164,303	T	C	0.366044	-0.015369	0.002093	3.4E-13
WDR11 *	10	rs6585702	121,164,396	T	G	0.366044	-0.015369	0.002093	3.4E-13
WDR11 *	10	rs6585703	121,164,626	A	G	0.366089	-0.015338	0.002093	3.9E-13
WDR11 *	10	rs7915733	121,165,125	A	C	0.366102	-0.015353	0.002093	3.7E-13
WDR11 *	10	rs10788141	121,165,340	G	T	0.412990	-0.015327	0.002048	9.4E-14
WDR11 *	10	rs1907272	121,165,648	A	G	0.316659	-0.013822	0.002168	1.5E-10
WDR11 *	10	rs1907273	121,165,771	C	T	0.316965	-0.013765	0.002166	1.7E-10
WDR11 *	10	rs1907274	121,165,824	T	G	0.366098	-0.015366	0.002093	3.5E-13
WDR11 *	10	rs7096589	121,165,945	G	A	0.316965	-0.013765	0.002166	1.7E-10
WDR11 *	10	rs7080940	121,166,105	A	T	0.316965	-0.013765	0.002166	1.7E-10
WDR11 *	10	rs6585704	121,166,509	G	A	0.317029	-0.013736	0.002167	1.9E-10
WDR11 *	10	rs7920839	121,166,658	T	C	0.317029	-0.013736	0.002167	1.9E-10
WDR11 *	10	rs7921081	121,166,703	T	G	0.316987	-0.013688	0.002167	2.1E-10
WDR11 *	10	rs17559591	121,166,830	G	A	0.316987	-0.013688	0.002167	2.1E-10
WDR11 *	10	rs7921353	121,166,901	A	G	0.318635	-0.013659	0.002168	2.1E-10
WDR11 *	10	rs7893136	121,166,946	T	C	0.316987	-0.013688	0.002167	2.1E-10
WDR11 *	10	rs6585705	121,167,044	C	T	0.316541	-0.013783	0.002168	1.6E-10
WDR11 *	10	rs6585706	121,167,075	G	A	0.316056	-0.013836	0.002170	1.5E-10
WDR11 *	10	rs6585707	121,167,285	G	C	0.316987	-0.013688	0.002167	2.1E-10
WDR11 *	10	rs6585708	121,167,429	T	C	0.366079	-0.015355	0.002094	3.6E-13
WDR11 *	10	rs7897890	121,168,240	T	C	0.316421	-0.013675	0.002168	2.2E-10
WDR11 *	10	rs11199811	121,169,559	A	C	0.316649	-0.013701	0.002168	2.0E-10
WDR11 *	10	rs10886862	121,169,894	C	T	0.412673	-0.015338	0.002049	8.5E-14
WDR11 *	10	rs35326857	121,169,898	G	T	0.370227	0.013933	0.002089	5.2E-12
WDR11 *	10	rs10886863	121,169,979	T	C	0.412673	-0.015338	0.002049	8.5E-14
WDR11 *	10	rs10886864	121,170,023	C	T	0.412673	-0.015338	0.002049	8.5E-14
WDR11 *	10	rs7071036	121,171,054	C	T	0.365856	-0.015349	0.002094	3.7E-13
WDR11 *	10	rs7071062	121,171,098	C	T	0.365856	-0.015349	0.002094	3.7E-13
WDR11 *	10	rs11199812	121,171,431	A	G	0.316321	-0.013986	0.002169	9.1E-11
WDR11 *	10	rs1873449	121,172,138	T	G	0.362501	-0.015457	0.002102	3.2E-13
WDR11 *	10	rs754227	121,172,490	C	T	0.368819	-0.015353	0.002096	3.4E-13
WDR11 *	10	rs74764497	121,173,614	A	G	0.235262	-0.013066	0.002397	4.4E-08
WDR11 *	10	rs3962120	121,177,844	A	C	0.362974	-0.015777	0.002127	1.1E-13
WDR11 *	10	rs191959515	121,178,085	T	C	0.324645	-0.015664	0.002186	6.1E-13
WDR11 *	10	rs200553592	121,178,117	ATAGAT^	A	0.324173	-0.015487	0.002185	1.1E-12
WDR11 *	10	rs12218818	121,178,570	T	G	0.232703	-0.013019	0.002406	4.4E-08
WDR11 *	10	rs7085142	121,179,860	C	T	0.421187	0.011083	0.002054	1.7E-08
WDR11 *	10	rs10788142	121,181,315	C	T	0.378037	0.012474	0.002086	5.9E-10
WDR11 *	10	rs1907279	121,181,633	C	G	0.423925	0.010688	0.002051	4.4E-08
WDR11 *	10	rs1907282	121,182,017	A	G	0.386105	0.012711	0.002074	1.9E-10
WDR11 *	10	rs1907284	121,182,265	G	T	0.386640	0.012705	0.002075	2.1E-10
WDR11 *	10	rs6585711	121,182,277	A	G	0.430483	0.011307	0.002041	6.8E-09
WDR11 *	10	rs3943077	121,185,572	G	A	0.387965	0.012762	0.002084	2.2E-10
WDR11 *	10	rs7088428	121,185,738	G	T	0.386523	0.012669	0.002076	2.3E-10
WDR11 *	10	rs17101591	121,187,689	T	C	0.226733	-0.013433	0.002411	2.7E-08
WDR11 *	10	rs12221113	121,187,774	G	T	0.226801	-0.013551	0.002410	1.9E-08
WDR11 *	10	rs35234305	121,188,328	C	CT	0.403375	0.010307	0.002061	4.6E-08
WDR11 *	10	rs10788144	121,188,708	T	C	0.402414	0.010360	0.002068	4.8E-08
WDR11 *	10	rs7089185	121,189,319	A	G	0.402107	0.010429	0.002060	3.6E-08
WDR11 *	10	rs1907287	121,189,936	A	G	0.401295	0.010462	0.002061	3.4E-08
WDR11 *	10	rs2901288	121,192,680	A	G	0.401824	0.010480	0.002060	3.5E-08
FGFR2 *	10	rs7077138	121,195,851	A	T	0.402355	0.010465	0.002061	3.5E-08
FGFR2 *	10	rs7067847	121,197,234	T	C	0.401856	0.010395	0.002061	4.5E-08
FGFR2 *	10	rs7082125	121,199,983	T	G	0.401870	0.010573	0.002062	2.9E-08
FGFR2 *	10	rs12358575	121,203,420	T	C	0.333027	0.011974	0.002142	1.5E-09
FGFR2 *	10	rs11199828	121,205,116	A	G	0.326972	0.011816	0.002200	4.7E-09
FGFR2 *	10	rs10788149	121,207,656	G	A	0.320097	0.012729	0.002162	4.1E-10
FGFR2 *	10	rs10749408	121,208,012	C	T	0.319561	0.012846	0.002165	2.7E-10
FGFR2 *	10	rs2172071	121,208,516	C	T	0.318456	0.012870	0.002169	2.9E-10
FGFR2 *	10	rs11199830	121,208,601	T	C	0.337058	-0.011887	0.002136	6.4E-09
FGFR2 *	10	rs11592107	121,209,450	A	G	0.318480	0.012841	0.002169	3.2E-10
FGFR2 *	10	rs1907218	121,210,702	T	C	0.318426	0.012896	0.002169	2.7E-10
FGFR2 *	10	rs1907219	121,210,790	A	G	0.337559	-0.011938	0.002133	5.4E-09
FGFR2 *	10	rs1907220	121,211,409	A	G	0.318302	0.012871	0.002169	2.9E-10
FGFR2 *	10	rs1994655	121,211,732	T	G	0.318311	0.012868	0.002169	3.0E-10
FGFR2 *	10	rs1907221	121,212,913	C	T	0.319297	0.012680	0.002164	4.8E-10
FGFR2 *	10	rs1907225	121,216,119	C	T	0.318752	0.012736	0.002168	5.0E-10
FGFR2 *	10	rs10749409	121,217,052	C	G	0.318797	0.012702	0.002168	6.0E-10
FGFR2 *	10	rs11199835	121,217,643	G	A	0.318848	0.012747	0.002169	5.3E-10
FGFR2 *	10	rs1907228	121,219,430	G	A	0.497302	-0.012818	0.002023	1.3E-10
FGFR2 *	10	rs7093348	121,221,734	C	T	0.495193	-0.012620	0.002027	2.1E-10
FGFR2 *	10	rs1907231	121,221,742	T	A	0.495193	-0.012620	0.002027	2.1E-10

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
FGFR2 *	10	rs10886871	121,222,283	A	C	0.335540	-0.012101	0.002139	5.2E-09
FGFR2 *	10	rs2420922	121,223,863	G	A	0.497212	-0.012593	0.002019	2.4E-10
FGFR2 *	10	rs7920546	121,224,230	G	A	0.497208	-0.012590	0.002019	2.4E-10
FGFR2 *	10	rs7921069	121,224,591	A	C	0.335638	-0.012024	0.002136	6.0E-09
FGFR2 *	10	rs7098079	121,224,699	G	C	0.493629	-0.012236	0.002021	6.8E-10
FGFR2 *	10	rs11595340	121,225,312	T	C	0.335638	-0.012024	0.002136	6.0E-09
FGFR2 *	10	rs10886873	121,225,604	T	C	0.335664	-0.012020	0.002136	6.0E-09
FGFR2 *	10	rs56124706	121,226,884	A	T	0.335583	-0.012005	0.002136	6.3E-09
FGFR2 *	10	rs11199837	121,227,134	A	T	0.497244	-0.012679	0.002019	1.9E-10
FGFR2 *	10	rs1907232	121,227,612	A	G	0.495890	-0.012451	0.002019	3.6E-10
FGFR2 *	10	rs1907233	121,227,775	T	C	0.336266	-0.012051	0.002137	5.6E-09
FGFR2 *	10	rs11199838	121,228,771	A	G	0.335557	-0.011969	0.002136	7.0E-09
FGFR2 *	10	rs4752518	121,229,421	T	C	0.300187	0.011296	0.002209	4.7E-08
FGFR2 *	10	rs11597855	121,229,534	T	C	0.497233	-0.012671	0.002019	2.0E-10
FGFR2 *	10	rs4500422	121,230,633	A	G	0.486826	-0.011866	0.002027	2.9E-09
FGFR2 *	10	rs11199840	121,230,824	G	A	0.486911	-0.011860	0.002027	3.0E-09
FGFR2 *	10	rs11199842	121,230,972	C	T	0.486499	-0.011850	0.002031	2.9E-09
FGFR2 *	10	rs11199843	121,230,977	C	T	0.487033	-0.011842	0.002033	3.2E-09
FGFR2 *	10	rs10886874	121,232,008	A	G	0.494283	-0.011936	0.002036	1.5E-09
FGFR2 *	10	rs4294510	121,232,748	A	G	0.485714	-0.011900	0.002027	2.7E-09
FGFR2 *	10	rs11199844	121,232,928	T	C	0.325298	-0.011522	0.002161	3.6E-08
FGFR2 *	10	rs11199845	121,232,961	T	C	0.325307	-0.011514	0.002161	3.7E-08
FGFR2 *	10	rs10886876	121,233,331	G	C	0.486790	-0.012133	0.002026	1.3E-09
FGFR2 *	10	rs60834189	121,233,878	A	AT	0.483265	-0.012407	0.002034	6.5E-10
FGFR2 *	10	rs11199848	121,235,094	G	A	0.486815	-0.011942	0.002029	2.4E-09
FGFR2 *	10	rs12217412	121,235,456	C	T	0.489431	-0.011968	0.002031	2.2E-09
FGFR2 *	10	rs12220647	121,235,627	A	C	0.324427	-0.011475	0.002165	4.0E-08
FGFR2 *	10	rs11199850	121,236,106	T	C	0.485005	-0.011821	0.002030	3.3E-09
FGFR2 *	10	rs878409	121,240,036	A	G	0.496526	-0.012597	0.002023	2.0E-10
FGFR2 *	10	rs12245393	121,240,386	T	C	0.496533	-0.012575	0.002024	2.1E-10
FGFR2 *	10	rs145325908	121,241,120	TG	T	0.494632	-0.012387	0.002057	5.3E-10
FGFR2 *	10	rs5016035	121,241,124	G	T	0.494008	-0.012048	0.002055	1.5E-09
ARNTL	11	rs7947951	13,334,483	G	A	0.364561	0.013195	0.002085	3.0E-10
ARNTL	11	rs10832027	13,335,636	A	G	0.363532	0.012943	0.002082	6.1E-10
ARNTL	11	rs2896635	13,338,198	A	T	0.363716	0.013249	0.002088	2.3E-10
ARNTL	11	rs1037169	13,339,458	C	T	0.359407	0.012875	0.002109	1.3E-09
ARNTL	11	rs6486122	13,339,977	T	C	0.367095	0.013310	0.002079	1.8E-10
ARNTL	11	rs10766078	13,341,701	G	A	0.391291	0.012363	0.002091	2.9E-09
ARNTL	11	rs3816360	13,346,203	C	T	0.367250	0.011416	0.002086	4.2E-08
DAGLA *	11	rs7925523	61,675,020	A	G	0.253680	-0.018955	0.002314	2.0E-16
DAGLA *	11	rs60399071	61,675,683	A	G	0.253810	-0.018948	0.002314	2.0E-16
DAGLA *	11	rs151242175	61,679,851	T	C	0.253266	-0.018954	0.002319	2.3E-16
DAGLA *	11	rs115702847	61,679,884	A	T	0.253270	-0.018953	0.002319	2.3E-16
DAGLA	11	rs11230779	61,682,061	A	G	0.491985	-0.011698	0.002039	1.6E-09
DAGLA	11	rs34700917	61,682,076	TG	T	0.491561	-0.011739	0.002041	1.5E-09
DAGLA	11	rs59200224	61,682,665	G	A	0.253782	-0.018925	0.002317	2.4E-16
DAGLA	11	rs59371352	61,682,823	A	G	0.253964	-0.018855	0.002320	3.5E-16
DAGLA	11	rs72918042	61,684,076	G	C	0.253791	-0.018923	0.002317	2.4E-16
DAGLA	11	rs61898525	61,686,132	G	A	0.492001	-0.011504	0.002038	2.6E-09
DAGLA	11	rs35404524	61,687,658	C	CTT	0.253796	-0.018861	0.002317	3.1E-16
DAGLA	11	rs4963308	61,688,954	A	G	0.253788	-0.018909	0.002317	2.6E-16
DAGLA	11	rs883724	61,690,385	T	C	0.253407	-0.018678	0.002319	6.2E-16
DAGLA	11	rs11827215	61,691,123	A	G	0.254143	-0.018652	0.002316	6.6E-16
DAGLA	11	rs72315101	61,695,289	C	CTCTG	0.253774	-0.018836	0.002318	3.6E-16
DAGLA	11	rs60507107	61,696,297	T	C	0.253738	-0.018779	0.002318	4.3E-16
DAGLA	11	rs17827816	61,697,053	T	C	0.440031	-0.012289	0.002057	5.4E-10
DAGLA	11	rs198453	61,697,078	C	T	0.492521	-0.011522	0.002035	2.6E-09
DAGLA	11	rs2097853	61,698,795	T	G	0.253895	-0.018736	0.002318	5.2E-16
DAGLA	11	rs81659	61,699,580	G	A	0.466171	-0.013097	0.002048	2.3E-11
DAGLA	11	rs58217294	61,702,031	A	T	0.253919	-0.018718	0.002318	5.6E-16
DAGLA	11	rs12274157	61,710,175	C	A	0.254064	-0.018733	0.002320	5.7E-16
DAGLA	11	rs731842	61,712,719	C	T	0.254175	-0.018721	0.002319	5.7E-16
DAGLA	11	rs2107617	61,714,167	G	C	0.304592	-0.016173	0.002206	9.4E-14
DAGLA	11	rs17156244	61,714,923	G	T	0.254257	-0.018728	0.002319	5.5E-16
DAGLA	11	rs198435	61,715,852	C	G	0.251225	-0.018412	0.002331	2.0E-15
DAGLA	11	rs2903825	61,721,496	T	C	0.261475	-0.019259	0.002300	5.5E-17
DAGLA	11	rs9735635	61,723,408	A	C	0.260873	-0.019369	0.002301	3.8E-17
DAGLA	11	rs4963243	61,726,855	A	G	0.261874	-0.019318	0.002297	3.4E-17
DAGLA	11	rs2240287	61,738,111	A	G	0.264282	-0.019152	0.002294	5.9E-17
DAGLA	11	rs2240286	61,738,982	C	T	0.264299	-0.019182	0.002294	5.5E-17
DAGLA	11	rs4963255	61,740,134	A	G	0.264323	-0.019231	0.002295	4.9E-17
DAGLA	11	rs3741252	61,744,026	T	C	0.261640	-0.019239	0.002308	6.5E-17
MYRF	11	rs174528	61,776,027	T	C	0.402265	-0.021355	0.002061	1.6E-25
MYRF	11	rs174529	61,776,489	T	C	0.402364	-0.021271	0.002062	2.7E-25
MYRF	11	rs174530	61,779,120	A	G	0.411776	-0.022240	0.002051	8.2E-28
MYRF	11	rs108499	61,779,765	C	T	0.415183	-0.022338	0.002049	4.9E-28
MYRF	11	rs509360	61,781,087	A	G	0.402310	-0.020917	0.002063	1.4E-24
MYRF	11	rs174533	61,781,553	G	A	0.414853	-0.022013	0.002051	2.7E-27
MYRF	11	rs174534	61,781,986	A	G	0.411584	-0.022101	0.002053	2.1E-27
MYRF	11	rs174535	61,783,884	T	C	0.410732	-0.022182	0.002052	1.4E-27
MYRF	11	rs174536	61,784,455	A	C	0.413300	-0.022521	0.002051	2.0E-28
MYRF	11	rs174537	61,785,208	G	T	0.414209	-0.022464	0.002049	2.7E-28
TMEM258	11	rs102275	61,790,331	T	C	0.413789	-0.022535	0.002049	1.5E-28
TMEM258	11	rs102274	61,790,354	T	C	0.413956	-0.022551	0.002049	1.5E-28
TMEM258	11	rs174538	61,792,609	G	A	0.416338	-0.022248	0.002047	7.9E-28
FEN1	11	rs4246215	61,796,827	G	T	0.414268	-0.022487	0.002049	2.4E-28
FADS1 *	11	rs174541	61,798,436	T	C	0.414078	-0.022713	0.002050	8.4E-29
FADS1	11	rs174544	61,800,281	C	A	0.423208	-0.022314	0.002049	6.1E-28
FADS1	11	rs174545	61,801,834	C	G	0.414510	-0.022521	0.002048	2.0E-28
FADS1	11	rs174546	61,802,358	C	T	0.414550	-0.022623	0.002049	1.2E-28
FADS1	11	rs174547	61,803,311	T	C	0.414437	-0.022392	0.002049	4.3E-28
FADS1	11	rs174548	61,803,876	C	G	0.422251	-0.022649	0.002044	7.7E-29
FADS1	11	rs174549	61,803,910	G	A	0.422738	-0.022561	0.002045	1.4E-28
FADS1	11	rs174550	61,804,006	T	C	0.414484	-0.022624	0.002048	1.1E-28
FADS1	11	rs174553	61,807,686	A	G	0.414810	-0.022755	0.002049	6.2E-29
FADS1	11	rs72643557	61,811,955	T	C	0.411304	-0.022877	0.002058	6.8E-29
FADS1	11	rs174554	61,811,991	A	G	0.414830	-0.022766	0.002048	5.8E-29

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
FADS1	11	rs174555	61,812,288	T	C	0.422113	-0.022810	0.002044	3.6E-29
FADS1	11	rs174556	61,813,163	C	T	0.422159	-0.022835	0.002044	3.1E-29
FADS1	11	rs174559	61,814,184	G	A	0.423855	-0.022676	0.002044	8.5E-29
FADS1	11	rs174560	61,814,292	T	C	0.422145	-0.022875	0.002045	2.6E-29
FADS1, MIR1908	11	rs174561	61,815,236	T	C	0.422119	-0.022866	0.002045	2.6E-29
FADS2	11	rs174562	61,817,672	A	G	0.414053	-0.022854	0.002051	4.5E-29
FADS2	11	rs35473591	61,818,856	C	CT	0.414270	-0.022735	0.002050	8.5E-29
FADS2	11	rs174564	61,820,833	A	G	0.413123	-0.022466	0.002053	4.1E-28
FADS2	11	rs28456	61,822,009	A	G	0.420836	-0.022439	0.002051	4.1E-28
FADS2	11	rs174565	61,824,164	C	G	0.415066	-0.022175	0.002052	2.0E-27
FADS2	11	chr11:61824525_A_AAG	61,824,525	A	AAG	0.417336	-0.022070	0.002058	4.5E-27
FADS2	11	rs174566	61,824,890	A	G	0.413124	-0.022458	0.002053	4.3E-28
FADS2	11	rs174567	61,825,533	A	G	0.416035	-0.022980	0.002050	2.4E-29
FADS2	11	rs174568	61,826,344	C	T	0.415059	-0.022792	0.002050	5.2E-29
FADS2	11	rs3834458	61,827,448	CT	C	0.414240	-0.022787	0.002051	6.5E-29
FADS2	11	rs5792235	61,828,850	CA	C	0.413186	-0.022665	0.002050	1.5E-28
FADS2	11	rs99780	61,829,161	C	T	0.413192	-0.022661	0.002050	1.6E-28
FADS2	11	rs174570	61,829,740	C	T	0.415197	-0.022426	0.002049	5.5E-28
FADS2	11	rs1535	61,830,500	A	G	0.413120	-0.022700	0.002050	1.3E-28
FADS2	11	rs174574	61,832,870	C	A	0.413183	-0.022574	0.002051	2.6E-28
FADS2	11	rs2524296	61,833,906	T	C	0.438675	0.019521	0.002036	5.5E-22
FADS2	11	rs2845574	61,834,400	T	C	0.443484	0.019984	0.002026	4.1E-23
FADS2	11	rs2845573	61,834,436	G	A	0.448876	0.019498	0.002026	6.2E-22
FADS2	11	rs199649489	61,834,989	A	C	0.431714	-0.021627	0.002083	3.0E-25
FADS2	11	rs2727270	61,835,765	T	C	0.445756	0.020377	0.002025	4.5E-24
FADS2	11	rs2727271	61,835,886	T	A	0.445796	0.020228	0.002025	1.0E-23
FADS2	11	rs174576	61,836,038	C	A	0.412736	-0.022529	0.002051	3.4E-28
FADS2	11	rs2524299	61,837,310	T	A	0.446028	0.020279	0.002024	6.2E-24
FADS2	11	rs174577	61,837,342	C	A	0.412863	-0.022540	0.002051	3.2E-28
FADS2	11	rs2072113	61,837,495	T	C	0.445745	0.020424	0.002025	3.1E-24
FADS2	11	rs2072114	61,837,743	G	A	0.445701	0.020243	0.002025	9.0E-24
FADS2	11	rs174578	61,838,027	T	A	0.413088	-0.022469	0.002051	4.7E-28
FADS2	11	rs174580	61,839,170	A	G	0.412469	-0.022497	0.002052	4.3E-28
FADS2	11	rs174581	61,839,211	G	A	0.412598	-0.022468	0.002053	5.0E-28
FADS2	11	rs2727265	61,841,532	A	C	0.446293	0.020549	0.002037	3.8E-24
FADS2	11	rs174583	61,842,278	C	T	0.412122	-0.022541	0.002051	3.7E-28
FADS2	11	rs174584	61,843,278	G	A	0.411812	-0.022568	0.002053	3.6E-28
FADS2	11	rs2526680	61,843,744	T	C	0.448202	0.020368	0.002028	5.8E-24
FADS2	11	rs2845572	61,847,123	A	G	0.444651	0.020390	0.002029	5.6E-24
FADS2	11	rs2851682	61,848,540	G	A	0.445080	0.020166	0.002026	1.4E-23
FADS2	11	rs2727263	61,850,540	T	C	0.446077	0.020325	0.002034	1.1E-23
FADS2	11	rs174592	61,851,136	A	G	0.409028	-0.022738	0.002052	1.0E-28
FADS2	11	rs174594	61,852,357	A	C	0.408949	-0.022980	0.002055	2.8E-29
FADS2	11	rs72643559	61,852,802	C	T	0.405256	-0.022672	0.002066	2.4E-28
FADS2	11	chr11:61853156_AAACAAC_A	61,853,156	AAACAAC	A	0.409032	-0.022222	0.002063	2.0E-27
FADS2	11	rs174598	61,853,722	G	A	0.410336	-0.022739	0.002053	1.1E-28
FADS2	11	rs174599	61,854,084	G	C	0.408190	-0.023001	0.002055	2.4E-29
FADS2	11	rs174600	61,854,755	T	C	0.409720	-0.022767	0.002056	1.1E-28
FADS2	11	rs174601	61,855,668	C	T	0.404479	-0.022591	0.002057	2.2E-28
FADS2 *	11	rs174626	61,869,585	G	A	0.318597	0.012161	0.002160	3.0E-08
FADS3	11	rs174453	61,878,495	G	C	0.300852	0.014160	0.002230	9.8E-11
FADS3	11	rs174634	61,879,915	G	C	0.308624	0.013824	0.002209	1.9E-10
FADS3	11	rs174635	61,879,955	T	G	0.308624	0.013817	0.002209	1.9E-10
FADS3	11	rs174454	61,883,275	G	A	0.311585	0.013355	0.002191	6.0E-10
FADS3	11	rs1000778	61,887,833	A	G	0.303024	0.013502	0.002183	4.7E-10
FADS3	11	rs174455	61,888,645	G	A	0.390260	0.013606	0.002062	5.6E-11
FADS3	11	rs174456	61,888,710	C	A	0.302641	0.013506	0.002185	4.8E-10
FADS3	11	rs36047269	61,888,782	T	TC	0.302635	0.013513	0.002185	4.7E-10
FADS3	11	rs5792240	61,889,069	A	AT	0.312823	0.013362	0.002177	3.9E-10
FADS3	11	rs1511144	61,889,113	T	C	0.313484	0.013170	0.002174	6.2E-10
FADS3	11	rs1295988	61,889,186	A	C	0.303237	0.013411	0.002187	6.5E-10
FADS3	11	rs174457	61,889,503	T	C	0.312571	0.013453	0.002176	2.8E-10
FADS3	11	rs174458	61,889,523	C	T	0.313342	0.013526	0.002175	2.4E-10
FADS3	11	rs174459	61,889,578	C	T	0.313049	0.013420	0.002175	3.0E-10
FADS3	11	rs174460	61,889,638	C	T	0.313558	0.013554	0.002175	2.4E-10
FADS3	11	rs174461	61,889,929	A	C	0.313746	0.014035	0.002180	5.9E-11
FADS3	11	rs174462	61,890,194	A	G	0.306791	0.014046	0.002207	9.9E-11
FADS3	11	rs174463	61,890,366	G	A	0.312606	0.013695	0.002196	2.5E-10
FADS3	11	rs174464	61,890,454	A	G	0.312634	0.013637	0.002198	3.2E-10
FADS3	11	rs693672	61,891,157	T	C	0.295506	0.014303	0.002232	1.2E-10
FADS3	11	rs174465	61,891,328	C	T	0.301594	0.014040	0.002219	2.6E-10
FADS3 *	11	rs35870730	61,891,648	A	AC	0.292899	0.015236	0.002258	1.5E-11
RAB31L1	11	rs174469	61,899,971	T	C	0.330439	0.013365	0.002179	8.1E-10
RAB31L1	11	rs174473	61,904,763	C	T	0.364677	0.012669	0.002129	1.6E-09
RAB31L1	11	rs174474	61,904,793	C	T	0.331780	0.013299	0.002176	8.7E-10
RAB31L1	11	rs174479	61,911,282	G	C	0.338242	0.012110	0.002117	6.0E-09
MTNR1B *	11	rs4331050	92,962,848	T	G	0.438187	0.011082	0.002041	2.4E-08
MTNR1B *	11	rs10466351	92,964,815	T	C	0.439258	0.011355	0.002017	9.9E-09
MTNR1B *	11	rs10830962	92,965,261	G	C	0.439800	0.011284	0.002018	1.2E-08
MTNR1B *	11	rs7941837	92,966,500	T	A	0.440235	0.011553	0.002023	6.1E-09
MTNR1B *	11	rs7945617	92,967,121	C	T	0.473221	0.011063	0.002015	3.0E-08
MTNR1B	11	rs10830963	92,975,544	G	C	0.433009	0.011228	0.002021	1.4E-08
BUD13 *	11	rs191081678	116,505,105	T	G	0.011733	0.067045	0.009378	4.3E-13
BUD13 *	11	rs79859462	116,509,279	A	G	0.022096	0.041627	0.006861	6.3E-10
BUD13 *	11	rs188115846	116,511,441	A	G	0.020428	0.045352	0.007149	8.8E-11
BUD13 *	11	rs140673349	116,525,979	A	G	0.015876	0.070755	0.008097	1.2E-18
BUD13 *	11	rs61904846	116,578,975	A	G	0.062763	-0.023472	0.004138	2.2E-08
BUD13 *	11	rs144641996	116,579,022	T	A	0.035715	0.039107	0.005469	1.2E-12
BUD13 *	11	rs61904847	116,583,168	C	T	0.059354	-0.023627	0.004245	3.4E-08
BUD13 *	11	rs7951761	116,597,136	A	G	0.462336	-0.011914	0.002047	1.8E-09
BUD13 *	11	rs114594921	116,602,565	C	T	0.050870	0.035141	0.004651	4.2E-14
BUD13 *	11	rs74733106	116,608,826	T	G	0.055847	0.033749	0.004371	3.0E-14
BUD13 *	11	rs116585768	116,615,113	A	G	0.058332	0.038901	0.004320	4.1E-19
BUD13 *	11	rs11216040	116,617,822	A	G	0.084316	0.023625	0.003610	1.5E-11
BUD13 *	11	rs10891999	116,618,165	T	A	0.146169	0.031653	0.002870	7.1E-29
BUD13 *	11	rs12365864	116,618,319	G	A	0.084762	0.023408	0.003599	2.1E-11
BUD13 *	11	rs11216043	116,619,262	C	T	0.144987	0.031383	0.002877	3.9E-28

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BUD13 *	11	rs148093284	116,620,192	C	T	0.030113	0.050089	0.005953	1.2E-11
BUD13 *	11	rs12365322	116,620,253	G	T	0.085740	0.023361	0.003580	2.0E-11
BUD13 *	11	rs182744169	116,620,615	C	T	0.012911	0.065367	0.008944	2.6E-13
BUD13 *	11	rs61904858	116,621,390	G	A	0.086701	0.023667	0.003558	8.4E-12
BUD13 *	11	rs11216045	116,621,694	C	T	0.146128	0.030893	0.002868	1.8E-27
BUD13 *	11	rs11216046	116,621,984	T	G	0.084395	0.023277	0.003614	3.5E-11
BUD13 *	11	rs79801428	116,623,547	A	G	0.083375	-0.030684	0.003707	7.8E-18
BUD13 *	11	rs11216048	116,624,342	G	A	0.087691	-0.029759	0.003597	1.1E-17
BUD13 *	11	rs11216049	116,624,458	C	T	0.087925	-0.029439	0.003592	2.2E-17
BUD13 *	11	rs11216050	116,624,597	T	C	0.088408	-0.029259	0.003580	2.4E-17
BUD13 *	11	rs112305884	116,625,067	T	C	0.089849	-0.027890	0.003544	3.2E-16
BUD13 *	11	rs112494128	116,625,184	T	C	0.089951	-0.027751	0.003540	4.2E-16
BUD13 *	11	rs7114844	116,625,470	A	G	0.142306	0.030543	0.002877	1.7E-26
BUD13 *	11	rs4340085	116,625,592	T	C	0.090370	-0.028166	0.003530	1.4E-16
BUD13 *	11	rs7114993	116,625,593	T	G	0.141913	0.030693	0.002880	1.2E-26
BUD13 *	11	rs2156122	116,625,906	A	C	0.142753	0.031567	0.002870	2.9E-28
BUD13 *	11	rs77984767	116,626,027	G	A	0.091242	-0.027047	0.003512	1.4E-15
BUD13 *	11	rs77623050	116,626,231	T	C	0.089209	-0.027516	0.003553	9.7E-16
BUD13 *	11	rs78485217	116,626,244	A	T	0.088343	-0.027123	0.003574	4.1E-15
BUD13 *	11	rs147788053	116,626,296	CAT	C	0.077815	-0.025782	0.003817	2.9E-12
BUD13 *	11	rs77966841	116,627,973	AC	A	0.092841	-0.028187	0.003470	4.7E-17
BUD13 *	11	rs10892000	116,628,145	G	T	0.147743	0.029775	0.002839	8.8E-26
BUD13 *	11	rs11216054	116,628,234	C	T	0.147757	0.029822	0.002839	7.5E-26
BUD13 *	11	rs61270867	116,628,783	G	A	0.173975	-0.014196	0.002677	2.0E-08
BUD13 *	11	rs11216055	116,629,871	T	C	0.093757	-0.027890	0.003447	6.6E-17
BUD13 *	11	rs11216056	116,629,912	A	C	0.093796	-0.027828	0.003446	7.4E-17
BUD13 *	11	rs11216057	116,630,051	T	C	0.093745	-0.027776	0.003445	7.9E-17
BUD13 *	11	rs77649044	116,630,336	C	T	0.093772	-0.027729	0.003443	8.6E-17
BUD13 *	11	rs76055915	116,630,355	T	C	0.093778	-0.027725	0.003443	8.6E-17
BUD13 *	11	rs74424292	116,630,372	T	A	0.093778	-0.027725	0.003443	8.6E-17
BUD13 *	11	rs76267862	116,630,652	C	CCCT	0.093955	-0.028045	0.003439	3.7E-17
BUD13 *	11	rs11216059	116,631,270	A	C	0.094112	-0.028604	0.003436	8.3E-18
BUD13 *	11	rs11216060	116,631,550	A	G	0.094719	-0.028628	0.003429	9.2E-18
BUD13 *	11	rs58675830	116,631,757	TATTG	T	0.094081	-0.029070	0.003436	2.5E-18
BUD13 *	11	rs11216061	116,632,035	C	T	0.094057	-0.029151	0.003436	2.1E-18
BUD13 *	11	rs11216062	116,632,051	A	C	0.094069	-0.029160	0.003436	2.0E-18
BUD13 *	11	rs11216063	116,632,059	A	T	0.094069	-0.029160	0.003436	2.0E-18
BUD13 *	11	rs11216064	116,632,106	C	G	0.094072	-0.029146	0.003436	2.1E-18
BUD13 *	11	rs4502019	116,632,117	G	C	0.143661	0.030053	0.002883	2.4E-25
BUD13 *	11	rs60952109	116,632,129	CT	C	0.094259	-0.028988	0.003433	3.0E-18
BUD13 *	11	rs7946423	116,632,686	T	A	0.145436	0.029732	0.002876	6.3E-25
BUD13 *	11	rs2096961	116,632,927	A	G	0.091973	-0.029345	0.003477	2.8E-18
BUD13 *	11	rs11216067	116,633,660	G	A	0.093562	-0.029292	0.003450	2.1E-18
BUD13 *	11	rs76801336	116,634,037	C	T	0.092849	-0.029385	0.003466	2.3E-18
BUD13 *	11	rs59232710	116,634,267	G	A	0.091817	-0.029301	0.003493	4.1E-18
BUD13 *	11	rs11216068	116,634,522	T	C	0.136433	0.032673	0.002978	5.9E-28
BUD13 *	11	rs10892001	116,634,723	A	G	0.140141	0.034390	0.002949	1.9E-31
BUD13 *	11	rs10892002	116,634,775	C	G	0.139997	0.034359	0.002951	2.4E-31
BUD13 *	11	rs2077334	116,635,693	A	C	0.089810	-0.031350	0.003551	5.2E-20
BUD13 *	11	rs77983701	116,636,339	C	T	0.090087	-0.031797	0.003552	1.5E-20
BUD13 *	11	rs74948313	116,636,865	G	A	0.095662	-0.035994	0.003490	4.6E-27
BUD13 *	11	rs76747451	116,638,116	G	T	0.083476	-0.037196	0.003673	1.4E-25
BUD13 *	11	rs725524	116,639,652	A	G	0.083726	-0.037661	0.003663	2.5E-26
BUD13 *	11	rs79315770	116,639,825	A	T	0.083806	-0.037468	0.003661	3.9E-26
BUD13 *	11	rs184616707	116,639,841	G	C	0.029358	0.076948	0.006006	3.1E-39
BUD13 *	11	rs117437529	116,641,735	T	C	0.087536	-0.037204	0.003566	7.4E-27
BUD13 *	11	rs116892227	116,642,030	A	G	0.088879	-0.037858	0.003532	6.3E-28
BUD13 *	11	rs1145184	116,642,465	A	G	0.137782	0.038777	0.002949	5.6E-41
BUD13 *	11	rs117239953	116,642,471	C	T	0.092413	-0.036699	0.003462	2.6E-27
BUD13 *	11	rs116859831	116,642,711	C	T	0.092593	-0.036894	0.003459	1.2E-27
BUD13 *	11	rs78642155	116,643,375	C	G	0.092071	-0.036888	0.003470	1.7E-27
BUD13 *	11	rs116948654	116,643,602	C	T	0.092151	-0.036958	0.003471	1.5E-27
BUD13 *	11	rs117689643	116,643,612	T	G	0.092152	-0.036942	0.003471	1.5E-27
BUD13 *	11	rs191049803	116,643,878	A	G	0.020271	-0.043066	0.007086	1.7E-09
BUD13 *	11	rs1145185	116,643,982	A	G	0.137591	0.039408	0.002927	7.0E-43
BUD13 *	11	rs78221557	116,644,811	A	G	0.213083	0.020975	0.002491	3.6E-18
BUD13 *	11	rs71480306	116,644,840	C	T	0.142479	0.040242	0.002871	1.6E-46
BUD13 *	11	rs11216072	116,645,635	C	T	0.026342	-0.046482	0.006278	1.1E-13
BUD13 *	11	chr11:116645661_CA_C	116,645,661	C	CA	0.098468	-0.034240	0.003431	2.5E-24
BUD13 *	11	rs139668970	116,645,673	T	TAAAAAC	0.141884	0.040081	0.002873	3.6E-46
BUD13 *	11	rs869271932	116,645,674	A	AAAAAC	0.142697	0.040288	0.002866	1.1E-46
BUD13 *	11	rs2212428	116,645,870	T	C	0.091969	-0.038609	0.003485	1.0E-29
BUD13 *	11	rs1002037	116,646,019	C	G	0.096533	-0.038849	0.003424	1.8E-31
BUD13 *	11	rs71480307	116,646,156	A	G	0.142197	0.040604	0.002869	2.6E-47
BUD13 *	11	rs35165288	116,646,608	C	T	0.142828	0.040256	0.002864	1.2E-46
BUD13 *	11	rs1124874	116,647,291	A	G	0.089403	-0.037843	0.003530	6.1E-28
BUD13 *	11	rs117338034	116,648,026	G	T	0.089375	-0.037898	0.003531	5.1E-28
BUD13 *	11	rs1240771	116,648,172	G	A	0.229039	0.020168	0.002382	2.9E-18
BUD13 *	11	rs73580632	116,648,184	T	C	0.089360	-0.037900	0.003531	5.4E-28
BUD13 *	11	rs1261672	116,648,243	G	A	0.228515	0.020454	0.002384	1.0E-18
BUD13 *	11	rs1240772	116,648,412	C	G	0.320621	0.022181	0.002180	4.7E-25
BUD13 *	11	rs513533	116,648,641	G	A	0.115595	0.050273	0.003143	3.5E-59
BUD13 *	11	rs516043	116,648,867	G	C	0.115658	0.050099	0.003142	8.0E-59
BUD13 *	11	rs516226	116,648,938	T	C	0.294324	0.015669	0.002244	3.1E-12
BUD13 *	11	rs499790	116,649,022	T	C	0.115640	0.050106	0.003142	7.9E-59
BUD13 *	11	rs504268	116,649,487	T	C	0.115643	0.050165	0.003142	5.7E-59
BUD13 *	11	rs544479	116,649,681	C	T	0.115647	0.050098	0.003142	8.0E-59
BUD13 *	11	rs506222	116,649,717	C	A	0.115649	0.050102	0.003142	7.9E-59
BUD13 *	11	rs1240773	116,649,810	T	G	0.229195	0.020549	0.002378	5.6E-19
BUD13 *	11	rs549125	116,650,209	G	C	0.119566	0.052693	0.003097	9.5E-67
BUD13 *	11	rs533668	116,650,418	G	T	0.119567	0.052734	0.003097	7.5E-67
BUD13 *	11	rs573985	116,650,599	A	G	0.119403	0.052820	0.003099	7.3E-67
BUD13 *	11	rs575906	116,650,841	G	A	0.119760	0.052755	0.003095	7.8E-67
BUD13 *	11	rs143762798	116,650,954	A	G	0.020602	-0.059091	0.007063	3.5E-17
BUD13 *	11	rs562756	116,651,258	C	G	0.119498	0.052619	0.003098	2.1E-66
BUD13 *	11	rs491022	116,651,271	C	T	0.137703	0.042459	0.002951	7.3E-48
BUD13 *	11	rs563796	116,651,394	G	A	0.120426	0.052890	0.003085	2.1E-67

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BUD13 *	11	rs563917	116,651,439	T	C	0.120453	0.052917	0.003085	1.7E-67
BUD13 *	11	rs492182	116,651,447	A	G	0.120478	0.052999	0.003084	9.9E-68
BUD13 *	11	rs5795043	116,651,516	T	TC	0.111438	0.050668	0.003216	4.0E-58
BUD13 *	11	rs565607	116,651,613	T	C	0.120405	0.053020	0.003085	8.4E-68
BUD13 *	11	rs567576	116,651,842	G	A	0.120325	0.053064	0.003083	5.5E-68
BUD13 *	11	rs567599	116,651,848	T	G	0.120344	0.053057	0.003082	5.7E-68
BUD13 *	11	rs3017237	116,651,908	C	G	0.120503	0.053001	0.003080	6.3E-68
BUD13 *	11	rs480028	116,652,053	G	C	0.120539	0.052992	0.003079	6.2E-68
BUD13 *	11	rs480878	116,652,137	A	G	0.121032	0.052671	0.003075	2.3E-67
BUD13 *	11	rs499563	116,652,244	T	C	0.120678	0.053169	0.003077	1.9E-68
BUD13 *	11	rs138535309	116,652,253	C	CTT	0.120456	0.053032	0.003079	4.4E-68
BUD13 *	11	rs202191031	116,652,259	A	AAGTGG	0.120456	0.053032	0.003079	4.4E-68
BUD13 *	11	rs79770434	116,652,448	T	C	0.086129	-0.039718	0.003597	1.6E-29
BUD13 *	11	rs483747	116,652,450	C	T	0.120572	0.052997	0.003078	5.6E-68
BUD13 *	11	rs141584077	116,652,587	T	A	0.112751	0.049626	0.003196	1.9E-55
BUD13 *	11	rs523980	116,652,589	T	A	0.107612	0.049013	0.003275	1.3E-51
BUD13 *	11	rs485638	116,652,656	C	G	0.120568	0.053000	0.003078	5.5E-68
BUD13 *	11	rs143547828	116,652,846	G	A	0.016874	-0.044090	0.007858	4.0E-08
BUD13 *	11	rs117742492	116,652,940	A	G	0.085981	-0.039827	0.003602	1.2E-29
BUD13 *	11	rs528647	116,653,104	T	C	0.120559	0.053022	0.003078	4.9E-68
BUD13 *	11	rs528732	116,653,127	A	G	0.120559	0.053022	0.003078	4.9E-68
BUD13 *	11	rs3017778	116,653,214	T	C	0.120521	0.052994	0.003079	6.1E-68
BUD13 *	11	rs3017779	116,653,271	T	C	0.120482	0.052966	0.003079	7.2E-68
BUD13 *	11	rs76860051	116,654,589	C	A	0.085624	-0.040704	0.003613	8.9E-31
BUD13 *	11	rs79862998	116,654,602	A	G	0.085461	-0.040956	0.003617	4.4E-31
BUD13 *	11	rs480823	116,655,013	C	T	0.115530	0.056867	0.003169	2.0E-73
BUD13 *	11	rs481843	116,655,150	T	C	0.114729	0.056428	0.003183	9.6E-72
BUD13 *	11	rs116857027	116,655,278	T	C	0.085393	-0.041126	0.003620	3.3E-31
BUD13 *	11	rs34485603	116,655,315	C	CCT	0.114713	0.056262	0.003185	3.0E-71
BUD13 *	11	rs486394	116,655,605	C	A	0.117993	0.058053	0.003152	5.7E-77
BUD13 *	11	rs34821424	116,657,330	A	T	0.096267	0.020967	0.003447	2.8E-09
BUD13 *	11	rs78347813	116,658,413	T	C	0.084762	-0.044184	0.003619	1.1E-35
BUD13 *	11	rs117935983	116,658,471	G	T	0.182311	0.021379	0.002639	1.4E-16
BUD13 *	11	rs71480309	116,659,239	T	C	0.098179	0.020350	0.003403	5.5E-09
BUD13 *	11	rs1892947	116,659,344	A	G	0.086960	-0.044892	0.003563	6.1E-38
BUD13 *	11	rs116905034	116,659,391	C	G	0.064624	0.039119	0.004152	2.0E-22
BUD13 *	11	rs11216080	116,660,281	T	G	0.097851	0.019824	0.003403	1.3E-08
BUD13 *	11	rs146893332	116,660,321	AGGGGG	T	0.064889	0.039132	0.004142	1.8E-22
BUD13 *	11	rs117889066	116,660,333	C	G	0.087718	-0.045276	0.003543	7.3E-39
BUD13 *	11	rs117293980	116,660,758	G	T	0.087712	-0.045260	0.003543	7.4E-39
BUD13 *	11	rs2155216	116,661,022	T	C	0.192054	0.018483	0.002548	5.5E-14
BUD13 *	11	rs2186670	116,661,233	T	C	0.192079	0.018513	0.002548	5.0E-14
BUD13 *	11	rs71117145	116,661,252	T	A	0.087883	-0.044845	0.003539	3.2E-38
BUD13 *	11	rs11944153	116,661,504	C	T	0.192100	0.018541	0.002548	4.4E-14
BUD13 *	11	rs78198334	116,661,566	C	G	0.087890	-0.044794	0.003539	3.7E-38
BUD13 *	11	rs118175510	116,661,831	C	T	0.082295	0.069136	0.003679	1.7E-80
BUD13 *	11	rs79291519	116,662,593	T	C	0.086556	-0.044939	0.003562	9.0E-38
BUD13 *	11	rs75942205	116,662,878	C	T	0.086822	-0.044791	0.003556	1.2E-37
BUD13 *	11	rs61659529	116,662,911	G	A	0.086809	-0.044772	0.003557	1.2E-37
BUD13 *	11	rs486915	116,663,571	T	A	0.368282	-0.045286	0.002128	9.4E-105
BUD13 *	11	rs146134775	116,663,577	C	CT	0.086769	-0.044466	0.003560	4.9E-37
BUD13 *	11	rs76547220	116,663,833	G	T	0.086847	-0.044807	0.003556	1.1E-37
BUD13 *	11	rs567209	116,664,111	T	C	0.167767	0.028697	0.002709	2.2E-27
BUD13 *	11	rs12802672	116,664,246	G	A	0.093193	0.022919	0.003472	1.3E-10
BUD13 *	11	rs2105609	116,664,370	A	G	0.086847	-0.044807	0.003556	1.1E-37
BUD13 *	11	rs2105610	116,664,409	C	T	0.086446	-0.044469	0.003565	4.1E-37
BUD13 *	11	rs77226464	116,664,718	T	C	0.086951	-0.044651	0.003555	1.6E-37
BUD13 *	11	rs190069353	116,664,907	A	C	0.086823	-0.044761	0.003557	1.3E-37
BUD13 *	11	rs117014628	116,664,914	T	C	0.086842	-0.044727	0.003557	1.4E-37
BUD13 *	11	rs1240776	116,665,564	T	C	0.374673	-0.046239	0.002077	1.9E-114
BUD13 *	11	rs12803249	116,665,701	G	A	0.167771	0.028689	0.002709	2.4E-27
BUD13 *	11	rs1240777	116,665,759	C	T	0.200308	0.018757	0.002505	1.2E-14
BUD13 *	11	rs1240778	116,665,773	C	A	0.370990	0.030684	0.002104	6.9E-51
BUD13 *	11	rs10892010	116,665,939	C	A	0.247870	0.020086	0.002354	7.2E-18
BUD13 *	11	rs79063991	116,666,103	T	C	0.086841	-0.044715	0.003557	1.5E-37
BUD13 *	11	rs61906081	116,666,342	A	G	0.167784	0.028643	0.002708	2.9E-27
BUD13 *	11	rs118103820	116,666,399	G	A	0.086841	-0.044715	0.003557	1.5E-37
BUD13 *	11	rs6589557	116,667,044	T	C	0.423955	0.031979	0.002032	1.0E-57
BUD13 *	11	rs140973748	116,667,081	C	T	0.086847	-0.044718	0.003557	1.5E-37
BUD13 *	11	rs35933073	116,667,129	A	C	0.167803	0.028638	0.002708	2.8E-27
BUD13 *	11	rs6589558	116,667,225	A	G	0.423956	0.031981	0.002032	1.0E-57
BUD13 *	11	rs1784125	116,667,245	C	G	0.200296	0.018829	0.002505	9.3E-15
BUD13 *	11	rs12787592	116,667,257	C	G	0.167815	0.028610	0.002708	3.2E-27
BUD13 *	11	rs143380339	116,667,386	A	C	0.086847	-0.044718	0.003557	1.5E-37
BUD13 *	11	rs1784126	116,667,498	T	G	0.372679	-0.045838	0.002078	1.6E-112
BUD13 *	11	rs57258844	116,667,690	C	G	0.093354	0.023254	0.003467	5.8E-11
BUD13 *	11	rs1784127	116,667,859	A	G	0.373001	-0.045854	0.002078	1.4E-112
BUD13 *	11	rs1784128	116,667,972	A	G	0.373009	-0.045873	0.002078	1.2E-112
BUD13 *	11	rs1632755	116,668,134	C	A	0.200355	0.018830	0.002505	9.2E-15
BUD13 *	11	rs112464350	116,668,341	A	C	0.093366	0.023277	0.003467	5.6E-11
BUD13 *	11	rs1787682	116,668,486	G	C	0.200298	0.018822	0.002505	9.5E-15
BUD13 *	11	rs150937658	116,668,605	G	A	0.099706	-0.040712	0.003385	1.1E-32
BUD13 *	11	rs9681206	116,668,801	T	C	0.249787	0.019396	0.002346	7.3E-17
BUD13 *	11	rs112550319	116,669,092	G	C	0.093391	0.023354	0.003466	4.8E-11
BUD13 *	11	rs1784131	116,669,151	C	T	0.200053	0.018775	0.002506	1.2E-14
BUD13 *	11	rs11216085	116,669,432	C	T	0.249832	0.019436	0.002346	6.8E-17
BUD13 *	11	rs2846015	116,669,722	T	C	0.200294	0.018828	0.002505	9.4E-15
BUD13 *	11	rs3016354	116,670,075	C	T	0.200299	0.018805	0.002504	9.9E-15
BUD13 *	11	rs3017337	116,670,090	T	C	0.200451	0.019006	0.002505	5.1E-15
BUD13 *	11	rs7925553	116,670,267	G	A	0.168007	0.028588	0.002706	3.0E-27
BUD13 *	11	rs144188664	116,670,317	T	A	0.086857	-0.044742	0.003557	1.4E-37
BUD13 *	11	rs1784133	116,670,700	T	C	0.200298	0.018801	0.002504	1.0E-14
BUD13 *	11	rs1787686	116,670,755	A	G	0.285803	-0.035278	0.002227	4.5E-59
BUD13 *	11	rs2846016	116,670,822	T	C	0.200028	0.018936	0.002506	6.9E-15
BUD13 *	11	rs36195057	116,671,530	A	G	0.249949	0.019460	0.002345	6.4E-17
BUD13 *	11	rs1787692	116,671,779	G	T	0.459499	0.014240	0.002039	4.1E-13
BUD13 *	11	rs148462279	116,672,020	G	A	0.086862	-0.044710	0.003557	1.6E-37

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
BUD13 *	11	rs75930640	116,672,095	T	G	0.200295	0.018786	0.002504	1.1E-14
BUD13 *	11	rs144256947	116,672,308	C	T	0.086781	-0.044836	0.003559	1.1E-37
BUD13 *	11	rs111446876	116,672,353	T	TA	0.249889	0.019508	0.002346	5.5E-17
BUD13 *	11	rs113264811	116,672,394	T	C	0.202092	0.018975	0.002498	5.2E-15
BUD13 *	11	rs12294322	116,672,835	G	A	0.200288	0.018784	0.002504	1.1E-14
BUD13 *	11	chr11:116672851_TA_T	116,672,851	TA	T	0.285804	-0.035277	0.002227	4.6E-59
BUD13 *	11	chr11:116673046_T_TA	116,673,046	TA	T	0.091873	0.024283	0.003496	9.4E-12
BUD13 *	11	rs74724948	116,673,298	T	A	0.197705	0.017277	0.002521	1.0E-12
BUD13 *	11	chr11:116674066_A_ATATT	116,674,066	ATATT	A	0.086443	-0.045066	0.003568	5.3E-38
BUD13 *	11	rs180815846	116,674,155	G	T	0.243784	0.019283	0.002372	3.3E-16
BUD13 *	11	rs559604795	116,674,196	T	A	0.093476	0.023363	0.003465	4.6E-11
BUD13 *	11	rs71466774	116,674,354	A	T	0.091129	0.022865	0.003511	2.0E-10
BUD13 *	11	rs117179746	116,674,534	A	G	0.086597	-0.044873	0.003565	1.1E-37
BUD13 *	11	rs3016355	116,674,778	T	A	0.200296	0.018742	0.002504	1.2E-14
BUD13 *	11	rs11530558	116,674,881	C	A	0.025296	0.056591	0.006415	4.5E-19
BUD13 *	11	rs1787688	116,675,006	C	T	0.285362	-0.035216	0.002229	9.4E-59
BUD13 *	11	rs78106248	116,675,263	CA	C	0.172187	0.028242	0.002687	3.9E-27
BUD13 *	11	rs61906102	116,675,786	C	T	0.172450	0.028055	0.002684	7.7E-27
BUD13 *	11	rs11694258	116,675,916	A	C	0.086993	-0.044745	0.003558	1.7E-37
BUD13 *	11	rs58672319	116,676,219	T	TG	0.284893	-0.035183	0.002230	1.2E-58
BUD13 *	11	rs1960036	116,676,692	A	C	0.172443	0.028030	0.002684	8.6E-27
BUD13 *	11	rs1614444	116,676,831	G	A	0.200546	0.018553	0.002506	2.1E-14
BUD13 *	11	rs59371082	116,677,028	G	A	0.093800	0.023611	0.003460	2.8E-11
BUD13 *	11	rs372407480	116,677,221	A	C	0.014115	0.076468	0.008542	5.2E-20
BUD13 *	11	rs868329903	116,677,410	C	A	0.067495	-0.045849	0.004060	1.2E-30
BUD13 *	11	rs12801136	116,677,632	A	G	0.172474	0.028023	0.002684	8.5E-27
BUD13 *	11	rs79678269	116,678,255	C	G	0.087094	-0.044797	0.003558	1.4E-37
BUD13 *	11	rs1005705	116,678,399	C	A	0.086976	-0.044852	0.003559	1.1E-37
BUD13 *	11	rs74792494	116,678,691	C	A	0.197707	0.017477	0.002518	5.3E-13
BUD13 *	11	chr11:116678728_T_TGA	116,678,728	TGA	T	0.086981	-0.044830	0.003559	1.2E-37
BUD13 *	11	chr11:116678738_A_AGAAT	116,678,738	AGAAT	A	0.198222	0.018910	0.002521	1.1E-14
BUD13 *	11	rs58060512	116,678,740	A	AAT	0.171092	0.027227	0.002709	6.9E-25
BUD13 *	11	rs1787687	116,679,179	G	A	0.200327	0.018702	0.002503	1.3E-14
BUD13 *	11	rs35963862	116,679,180	C	T	0.168425	0.028314	0.002702	7.0E-27
BUD13 *	11	rs117830617	116,679,254	A	G	0.086984	-0.044827	0.003559	1.2E-37
BUD13 *	11	rs61906104	116,679,398	G	A	0.172544	0.027914	0.002683	1.3E-26
BUD13 *	11	rs11216091	116,679,966	G	A	0.021647	-0.049180	0.006909	1.4E-12
BUD13 *	11	rs12417015	116,680,059	G	A	0.197485	0.017341	0.002519	8.1E-13
BUD13 *	11	chr11:116681564_G_GA	116,681,564	GA	G	0.172585	0.027910	0.002683	1.3E-26
BUD13 *	11	rs1787717	116,682,049	T	C	0.370368	-0.046005	0.002085	1.3E-112
BUD13 *	11	rs12806224	116,682,098	C	T	0.172344	0.027844	0.002685	1.8E-26
BUD13 *	11	rs113194822	116,682,143	A	G	0.092659	0.024964	0.003483	2.8E-12
BUD13 *	11	rs12805061	116,682,308	G	A	0.172636	0.027869	0.002682	1.6E-26
BUD13 *	11	rs5795046	116,682,757	T	TG	0.370345	-0.045851	0.002085	7.6E-112
BUD13 *	11	rs11826999	116,683,062	A	G	0.172746	0.027691	0.002682	3.5E-26
BUD13 *	11	rs71480312	116,683,372	T	C	0.098841	0.022904	0.003380	3.6E-11
BUD13 *	11	rs66560466	116,683,783	T	TG	0.283984	-0.034995	0.002228	3.9E-58
BUD13 *	11	rs35310854	116,684,317	TA	T	0.172764	0.027913	0.002682	1.4E-26
BUD13 *	11	rs117341026	116,684,410	A	G	0.085867	-0.046117	0.003588	3.9E-39
BUD13 *	11	rs7932330	116,684,491	G	A	0.246739	0.019103	0.002361	3.2E-16
BUD13 *	11	rs35681250	116,684,670	T	A	0.172969	0.027785	0.002684	2.6E-26
BUD13 *	11	rs3016357	116,684,699	T	C	0.291665	-0.036286	0.002239	6.8E-62
BUD13 *	11	rs1145213	116,684,706	G	A	0.294972	-0.034466	0.002238	5.1E-56
BUD13 *	11	rs77835865	116,684,713	G	A	0.172759	0.027863	0.002682	1.8E-26
BUD13 *	11	rs956832572	116,684,717	T	A	0.014421	0.076593	0.008452	1.7E-20
BUD13 *	11	rs71037408	116,684,780	C	CTG	0.091860	0.024561	0.003499	5.6E-12
BUD13 *	11	rs61906112	116,685,049	A	T	0.172696	0.027931	0.002683	1.4E-26
BUD13 *	11	rs17092638	116,685,520	G	C	0.172711	0.028169	0.002684	5.6E-27
BUD13 *	11	rs1145212	116,686,149	A	G	0.452218	0.028035	0.002046	2.1E-44
BUD13 *	11	rs2156120	116,686,439	G	A	0.249736	0.019987	0.002351	6.9E-18
BUD13 *	11	rs1145211	116,686,500	A	C	0.283594	-0.035657	0.002240	6.9E-60
BUD13 *	11	rs17092642	116,686,532	C	T	0.172644	0.028327	0.002686	3.2E-27
BUD13 *	11	rs947990	116,686,598	T	G	0.061881	-0.043759	0.004182	2.6E-25
BUD13 *	11	rs11216093	116,687,166	C	A	0.250409	0.020244	0.002352	3.0E-18
BUD13 *	11	rs61906115	116,687,529	A	T	0.168313	0.028847	0.002708	1.2E-27
BUD13 *	11	rs12799766	116,687,711	A	G	0.168341	0.028894	0.002708	9.7E-28
BUD13 *	11	rs12799441	116,687,799	T	A	0.168457	0.028936	0.002708	8.1E-28
BUD13 *	11	rs12799449	116,687,809	G	A	0.168489	0.029034	0.002708	5.8E-28
BUD13 *	11	rs1145210	116,688,286	T	C	0.202354	-0.014270	0.002543	1.4E-09
BUD13 *	11	rs80134543	116,688,524	C	CTT	0.080189	0.031686	0.003743	1.8E-16
BUD13 *	11	rs77277788	116,688,720	T	C	0.092413	0.024128	0.003480	1.2E-11
BUD13 *	11	rs11824135	116,688,837	T	G	0.201712	0.014496	0.002545	1.8E-09
BUD13 *	11	rs11828763	116,688,947	G	A	0.212414	0.016637	0.002479	3.7E-12
BUD13 *	11	rs3016360	116,689,027	C	T	0.212893	0.016804	0.002476	3.4E-12
BUD13 *	11	rs1787716	116,689,458	A	G	0.198765	0.020320	0.002519	1.4E-16
BUD13 *	11	rs1787715	116,689,609	T	C	0.198759	0.020311	0.002519	1.4E-16
BUD13 *	11	rs1623797	116,689,731	T	C	0.432325	-0.041455	0.002047	1.2E-96
BUD13 *	11	rs34937367	116,689,808	C	T	0.198884	0.020267	0.002519	1.6E-16
BUD13 *	11	rs74330350	116,689,812	G	A	0.198884	0.020267	0.002519	1.6E-16
BUD13 *	11	rs79280888	116,689,813	G	A	0.198884	0.020267	0.002519	1.6E-16
BUD13 *	11	rs1787714	116,689,894	A	G	0.246483	-0.046709	0.002367	2.0E-90
BUD13 *	11	rs1787713	116,689,895	G	C	0.246483	-0.046709	0.002367	2.0E-90
BUD13 *	11	rs12291024	116,689,951	G	T	0.365896	0.029873	0.002098	6.2E-49
BUD13 *	11	rs1787711	116,690,062	G	A	0.198800	0.020189	0.002518	2.0E-16
BUD13 *	11	rs3017232	116,690,167	T	C	0.199120	0.020365	0.002516	1.1E-16
BUD13 *	11	rs3017231	116,690,232	A	G	0.198807	0.020186	0.002518	2.0E-16
BUD13 *	11	rs3017230	116,690,245	C	G	0.198808	0.020183	0.002518	2.1E-16
BUD13 *	11	rs3017229	116,690,251	A	G	0.248185	-0.047109	0.002358	2.1E-92
BUD13 *	11	rs3017228	116,690,276	G	A	0.198808	0.020183	0.002518	2.1E-16
BUD13 *	11	rs1787710	116,690,486	A	G	0.198817	0.020133	0.002518	2.5E-16
BUD13 *	11	rs76483212	116,690,550	A	G	0.092287	0.025038	0.003474	1.7E-12
BUD13 *	11	rs1787709	116,690,612	G	C	0.198803	0.020111	0.002518	2.6E-16
BUD13 *	11	rs1784123	116,690,665	C	T	0.198802	0.020140	0.002518	2.4E-16
BUD13 *	11	rs1787708	116,690,677	A	G	0.198827	0.020150	0.002517	2.4E-16
BUD13 *	11	rs116505113	116,690,754	A	C	0.198296	0.019366	0.002522	3.0E-15
BUD13 *	11	rs116116656	116,690,755	A	T	0.198296	0.019366	0.002522	3.0E-15
BUD13 *	11	rs116365797	116,690,756	A	C	0.198295	0.019373	0.002522	2.9E-15

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
BUD13 *	11	rs118013839	116,690,798	A	G	0.083774	-0.048120	0.003641	1.7E-41
BUD13 *	11	rs1784122	116,690,985	A	T	0.198855	0.020196	0.002517	2.1E-16
BUD13 *	11	rs1784121	116,691,074	T	G	0.431595	-0.041386	0.002049	2.9E-96
BUD13 *	11	rs1784120	116,691,143	G	C	0.198857	0.020211	0.002517	2.0E-16
BUD13 *	11	rs1787706	116,691,212	A	G	0.198851	0.020246	0.002517	1.8E-16
BUD13 *	11	rs1787705	116,691,222	A	G	0.198853	0.020237	0.002517	1.8E-16
BUD13 *	11	rs1787704	116,691,280	T	C	0.432968	-0.041733	0.002047	5.1E-98
BUD13 *	11	rs1787703	116,691,550	T	C	0.198847	0.020220	0.002517	1.9E-16
BUD13 *	11	rs1787702	116,691,572	A	G	0.198847	0.020220	0.002517	1.9E-16
BUD13 *	11	rs11216096	116,691,864	A	C	0.366115	0.030021	0.002096	1.8E-49
BUD13 *	11	rs117393825	116,691,971	T	C	0.100256	-0.042224	0.003374	1.5E-35
BUD13 *	11	rs35256265	116,691,985	ACC	A	0.198860	0.020280	0.002517	1.6E-16
BUD13 *	11	rs1784119	116,692,089	T	C	0.248148	-0.047320	0.002358	3.1E-93
BUD13 *	11	rs12785772	116,692,892	A	G	0.366143	0.029947	0.002096	3.3E-49
BUD13 *	11	rs12785990	116,692,990	A	G	0.364158	0.030582	0.002099	4.7E-51
BUD13 *	11	rs79962987	116,693,078	T	G	0.039124	-0.053307	0.005174	2.3E-26
BUD13 *	11	rs12420888	116,693,106	G	C	0.364412	0.030597	0.002098	3.9E-51
BUD13 *	11	rs1787701	116,693,276	C	G	0.336204	-0.056918	0.002155	6.7E-160
BUD13 *	11	chr11:116693645_G_GCA	116,693,645	GCA	G	0.186494	0.019689	0.002605	7.3E-15
BUD13 *	11	rs117889337	116,693,777	T	C	0.083099	-0.048255	0.003654	2.2E-41
BUD13 *	11	rs1787699	116,693,837	G	A	0.247427	-0.047746	0.002362	1.3E-94
BUD13 *	11	rs1787698	116,693,846	T	C	0.247423	-0.047737	0.002362	1.3E-94
BUD13 *	11	rs1784118	116,694,339	T	C	0.250180	-0.048027	0.002351	1.7E-96
BUD13 *	11	rs12293222	116,694,593	A	G	0.286200	0.027336	0.002240	2.3E-34
BUD13 *	11	rs111226221	116,694,718	T	C	0.091990	0.024518	0.003481	5.1E-12
BUD13 *	11	rs117607796	116,694,887	A	C	0.083537	-0.048237	0.003646	1.4E-41
BUD13 *	11	rs16978945	116,694,974	T	C	0.090780	0.021894	0.003503	1.2E-09
BUD13 *	11	rs111218525	116,695,822	T	C	0.206192	0.029528	0.002505	1.8E-33
BUD13 *	11	rs59854309	116,696,047	T	C	0.255655	-0.049216	0.002359	1.5E-100
BUD13 *	11	rs60954647	116,696,217	T	C	0.409064	-0.029074	0.002086	7.4E-45
BUD13 *	11	rs1784106	116,696,733	A	C	0.252300	-0.048608	0.002347	7.2E-99
BUD13 *	11	rs78888567	116,696,897	A	G	0.095974	0.023701	0.003419	1.1E-11
BUD13 *	11	rs4938300	116,696,903	T	C	0.203052	0.032364	0.002509	1.0E-39
BUD13 *	11	rs10892017	116,697,165	C	G	0.359910	0.033280	0.002092	1.5E-60
BUD13 *	11	rs66473272	116,697,382	G	GT	0.352652	0.033863	0.002118	8.3E-61
BUD13 *	11	rs11605568	116,697,452	A	G	0.359857	0.033226	0.002092	2.2E-60
BUD13 *	11	rs11606013	116,697,509	T	G	0.359918	0.033202	0.002091	2.7E-60
BUD13 *	11	rs140078194	116,697,574	A	C	0.086781	-0.047121	0.003582	1.3E-40
BUD13 *	11	rs11608173	116,697,648	A	T	0.359919	0.033190	0.002091	2.9E-60
BUD13 *	11	rs1787689	116,697,666	G	A	0.442940	-0.043047	0.002032	1.5E-104
BUD13 *	11	rs1787690	116,697,800	T	G	0.252040	-0.048536	0.002343	6.5E-99
BUD13 *	11	rs1787691	116,697,997	A	G	0.442317	-0.042988	0.002032	2.2E-104
BUD13 *	11	rs947986	116,698,488	A	G	0.250751	-0.048508	0.002347	1.3E-98
BUD13 *	11	rs3017338	116,698,629	A	G	0.442256	-0.042330	0.002035	7.1E-101
BUD13 *	11	rs71037412	116,699,941	CA	C	0.444809	-0.042246	0.002028	3.4E-101
BUD13 *	11	rs1145191	116,700,002	G	C	0.444809	-0.042246	0.002028	3.4E-101
BUD13 *	11	rs200445365	116,700,100	A	AAAAAA	0.086619	-0.047155	0.003586	1.2E-40
BUD13 *	11	rs150808564	116,700,125	T	C	0.041694	-0.053439	0.005034	9.7E-27
BUD13 *	11	rs1145193	116,700,226	G	A	0.446025	-0.042602	0.002027	5.0E-103
BUD13 *	11	rs1145194	116,700,252	A	C	0.249592	-0.048825	0.002354	5.7E-99
BUD13 *	11	rs11601168	116,700,422	A	T	0.078200	-0.047151	0.003736	1.0E-36
BUD13 *	11	rs1145195	116,700,534	A	G	0.444967	-0.042229	0.002027	3.9E-101
BUD13 *	11	rs11601584	116,700,568	C	T	0.348663	0.034619	0.002097	3.9E-65
BUD13 *	11	rs61905066	116,700,892	G	A	0.206955	0.014072	0.002491	1.5E-08
BUD13 *	11	rs1892948	116,701,373	T	C	0.206218	0.014127	0.002495	1.4E-08
BUD13 *	11	rs1145196	116,701,489	T	C	0.445207	-0.042348	0.002028	1.1E-101
BUD13 *	11	rs1240783	116,701,809	C	T	0.445166	-0.042350	0.002028	1.0E-101
BUD13 *	11	rs11216100	116,701,814	G	C	0.344380	0.035430	0.002106	3.3E-67
BUD13 *	11	rs879858	116,702,404	A	G	0.206078	0.014268	0.002498	1.0E-08
BUD13 *	11	rs947989	116,702,805	A	C	0.451764	-0.042593	0.002060	7.5E-100
BUD13 *	11	rs882398	116,703,122	C	T	0.206833	0.014140	0.002497	1.4E-08
BUD13 *	11	rs77206548	116,703,747	A	G	0.086875	-0.047260	0.003582	7.5E-41
BUD13 *	11	rs11216103	116,703,772	A	G	0.203353	0.013741	0.002515	4.2E-08
BUD13 *	11	rs1240782	116,703,868	A	G	0.352128	-0.029015	0.002128	9.2E-45
BUD13 *	11	rs10617144	116,703,898	CTG	C	0.351946	-0.028911	0.002129	2.0E-44
BUD13 *	11	rs1240781	116,704,101	T	C	0.244663	-0.048004	0.002374	4.3E-94
BUD13 *	11	rs1268832	116,704,513	T	G	0.305170	-0.022316	0.002210	2.6E-25
BUD13 *	11	rs4938301	116,704,757	A	G	0.205953	0.030148	0.002497	1.2E-34
BUD13 *	11	rs1263058	116,704,839	A	G	0.306974	-0.020921	0.002203	1.3E-22
BUD13 *	11	rs76124005	116,704,898	G	T	0.087378	-0.047212	0.003573	5.1E-41
BUD13 *	11	rs12574790	116,704,971	T	C	0.016037	-0.051192	0.008081	3.5E-11
BUD13 *	11	rs74939223	116,705,164	G	A	0.087386	-0.047386	0.003574	3.0E-41
BUD13 *	11	rs59873384	116,705,494	T	C	0.087304	-0.047353	0.003575	3.2E-41
BUD13 *	11	rs12802944	116,705,684	C	T	0.204405	0.031761	0.002505	3.2E-38
BUD13 *	11	rs1263056	116,705,699	A	G	0.343391	-0.057338	0.002148	4.6E-162
BUD13 *	11	rs1263055	116,706,327	A	G	0.252239	-0.048448	0.002351	2.1E-97
BUD13 *	11	rs11216105	116,706,725	A	G	0.252338	-0.048474	0.002352	1.4E-97
BUD13 *	11	rs117684324	116,707,255	T	A	0.087374	-0.047198	0.003574	5.0E-41
BUD13 *	11	rs12221682	116,707,501	G	C	0.308209	-0.024538	0.002208	1.3E-28
BUD13 *	11	rs11216107	116,708,947	C	T	0.496205	0.031175	0.002020	6.6E-55
BUD13 *	11	rs148075162	116,709,936	C	G	0.015762	0.082408	0.008074	4.9E-26
BUD13 *	11	rs61346349	116,710,082	G	A	0.178437	-0.056817	0.002630	9.9E-107
BUD13 *	11	rs11216109	116,710,099	G	C	0.309918	0.076029	0.002170	1.9E-276
BUD13 *	11	rs75476300	116,710,153	C	G	0.054499	0.088797	0.004430	1.1E-90
BUD13 *	11	rs59620302	116,710,443	G	C	0.086347	-0.047869	0.003585	7.4E-42
BUD13 *	11	rs2367970	116,710,925	A	G	0.310079	0.076123	0.002170	4.1E-277
BUD13 *	11	rs77574778	116,711,084	T	C	0.086426	-0.047795	0.003582	8.7E-42
BUD13 *	11	rs77646493	116,711,464	A	C	0.086408	-0.047779	0.003583	1.0E-41
BUD13 *	11	rs74360954	116,711,826	T	C	0.086444	-0.047778	0.003582	1.1E-41
BUD13 *	11	rs7480302	116,712,301	G	A	0.494359	0.030963	0.002006	8.6E-55
BUD13 *	11	rs6589562	116,712,723	A	G	0.310658	0.075707	0.002169	3.8E-274
BUD13 *	11	rs886022	116,712,797	A	C	0.235062	-0.058263	0.002390	6.4E-136
BUD13 *	11	rs117450838	116,712,972	A	G	0.068341	-0.052376	0.003984	8.4E-42
BUD13 *	11	rs151007118	116,713,148	T	G	0.099789	0.083292	0.003377	6.5E-137
BUD13 *	11	rs1144035	116,713,601	C	T	0.236020	-0.058436	0.002387	5.6E-137
BUD13 *	11	rs117837319	116,713,731	C	A	0.084895	-0.047682	0.003615	7.0E-41
BUD13 *	11	rs4938302	116,713,788	C	T	0.494431	0.030870	0.002004	1.5E-54

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
BUD13 *	11	rs49383303	116,714,271	C	T	0.494376	0.031000	0.002003	4.6E-55
BUD13 *	11	rs79886324	116,714,728	A	G	0.086760	-0.048138	0.003576	2.0E-42
BUD13 *	11	rs2000571	116,714,817	A	G	0.309528	0.076480	0.002174	5.8E-279
BUD13 *	11	rs17119918	116,714,897	A	G	0.108109	-0.050076	0.003250	1.6E-54
BUD13 *	11	rs34100096	116,714,909	A	G	0.102854	0.023918	0.003302	3.2E-14
BUD13 *	11	rs117785509	116,715,515	A	G	0.086813	-0.048255	0.003577	1.2E-42
BUD13 *	11	rs7350481	116,715,567	T	C	0.235046	0.114039	0.002363	1.5E-520
BUD13 *	11	rs7926828	116,715,707	C	T	0.312870	0.080359	0.002166	8.9E-310
BUD13 *	11	rs5795050	116,716,065	T	TC	0.101170	0.023171	0.003324	3.2E-13
BUD13 *	11	rs151061355	116,716,138	A	G	0.087558	-0.048498	0.003562	2.1E-43
BUD13 *	11	rs555105607	116,716,397	CT	C	0.087781	-0.048494	0.003554	1.5E-43
BUD13 *	11	rs373804009	116,716,399	T	TG	0.087347	-0.048534	0.003563	2.2E-43
BUD13 *	11	rs142290703	116,716,430	A	G	0.087781	-0.048494	0.003554	1.5E-43
BUD13 *	11	rs17119920	116,717,173	G	C	0.100811	0.022453	0.003327	1.4E-12
BUD13 *	11	rs76542665	116,717,237	A	C	0.100822	0.022450	0.003326	1.4E-12
BUD13 *	11	rs49383304	116,717,709	T	C	0.079032	-0.049432	0.003708	8.3E-41
BUD13 *	11	rs79408961	116,717,877	T	C	0.054199	0.092107	0.004433	8.1E-98
BUD13 *	11	rs49383305	116,717,913	T	C	0.311380	0.082515	0.002177	1.6E-323
BUD13 *	11	rs1262892	116,718,188	A	G	0.101132	0.022425	0.003319	1.3E-12
BUD13 *	11	rs180378	116,718,193	A	G	0.312344	0.082302	0.002174	1.4E-322
BUD13 *	11	rs10711344	116,718,401	TA	T	0.311619	0.082452	0.002176	3.9E-323
BUD13 *	11	rs180377	116,718,411	T	C	0.312293	0.082382	0.002175	5.1E-323
BUD13 *	11	rs56881207	116,718,802	T	C	0.101503	0.022280	0.003311	1.5E-12
BUD13 *	11	rs10892020	116,718,936	G	C	0.311179	0.082429	0.002178	2.3E-322
BUD13 *	11	rs12419326	116,719,152	A	G	0.101589	0.022091	0.003309	2.2E-12
BUD13 *	11	rs180376	116,719,323	C	G	0.328725	-0.034774	0.002153	2.3E-60
BUD13 *	11	rs118046012	116,719,812	A	G	0.086170	-0.049043	0.003583	7.1E-44
BUD13 *	11	rs6589563	116,720,071	A	G	0.102721	0.021877	0.003291	3.1E-12
BUD13 *	11	rs180375	116,720,324	T	C	0.328837	-0.034786	0.002152	2.0E-60
BUD13 *	11	rs116962103	116,720,402	A	G	0.021708	-0.060662	0.006912	2.4E-18
BUD13 *	11	rs117305246	116,720,548	A	G	0.037117	0.030678	0.005335	9.0E-09
BUD13 *	11	rs12421490	116,720,725	G	T	0.101942	0.021802	0.003301	3.5E-12
BUD13 *	11	rs180373	116,720,837	A	C	0.166361	-0.059389	0.002706	7.7E-112
BUD13 *	11	rs147232672	116,721,147	A	C	0.011591	0.100011	0.009380	9.0E-27
BUD13 *	11	rs180372	116,721,218	A	G	0.327948	-0.034663	0.002153	7.2E-60
BUD13 *	11	rs180371	116,721,487	A	G	0.417373	-0.047287	0.002041	3.5E-122
BUD13 *	11	rs143315658	116,721,532	C	T	0.086597	-0.049058	0.003573	3.7E-44
BUD13 *	11	rs180370	116,721,649	T	C	0.327948	-0.034663	0.002153	7.2E-60
BUD13 *	11	rs74680844	116,721,744	C	G	0.164827	-0.059942	0.002715	7.0E-113
BUD13 *	11	rs79100692	116,722,391	A	G	0.164515	-0.060020	0.002718	5.1E-113
BUD13 *	11	rs79826170	116,723,038	C	T	0.101881	0.021779	0.003303	3.9E-12
BUD13 *	11	rs12420920	116,723,315	A	G	0.164519	-0.060021	0.002718	4.9E-113
BUD13 *	11	rs12421191	116,723,578	T	C	0.164519	-0.060021	0.002718	4.9E-113
BUD13 *	11	rs75779227	116,724,640	T	C	0.101878	0.021681	0.003303	4.8E-12
BUD13 *	11	rs180365	116,725,458	T	C	0.294316	-0.064884	0.002233	2.7E-191
BUD13 *	11	rs61905078	116,725,593	C	A	0.163696	-0.059222	0.002726	8.8E-110
BUD13 *	11	rs11216118	116,725,679	T	C	0.076683	0.120009	0.003787	4.2E-225
BUD13 *	11	rs180364	116,726,036	G	A	0.255941	-0.063216	0.002322	5.5E-170
BUD13 *	11	rs78347254	116,726,040	A	G	0.100877	0.022433	0.003323	1.4E-12
BUD13 *	11	rs146714678	116,726,114	G	T	0.092445	-0.056345	0.003485	1.2E-60
BUD13 *	11	rs75662937	116,726,178	T	C	0.034707	0.169538	0.005482	7.0E-217
BUD13 *	11	rs144027752	116,726,289	A	G	0.010044	0.100184	0.010034	7.5E-24
BUD13 *	11	rs180363	116,727,173	C	T	0.254360	-0.064507	0.002322	5.6E-177
BUD13 *	11	rs78484485	116,727,349	A	G	0.252718	-0.064819	0.002326	1.0E-177
BUD13 *	11	rs10892023	116,727,532	T	C	0.308705	0.084227	0.002183	4.5E-335
BUD13 *	11	rs180361	116,727,933	T	C	0.328489	-0.034512	0.002154	2.5E-59
BUD13 *	11	rs139628269	116,727,934	A	G	0.014219	-0.046737	0.008488	1.0E-08
BUD13 *	11	rs139283556	116,728,079	T	C	0.012975	0.087542	0.008847	2.6E-23
BUD13 *	11	rs180360	116,728,272	G	A	0.253689	-0.064743	0.002324	1.1E-177
BUD13 *	11	rs180357	116,728,788	C	T	0.102958	0.021618	0.003291	5.3E-12
BUD13 *	11	rs76240380	116,728,819	A	G	0.034881	0.169432	0.005468	1.1E-217
BUD13 *	11	rs76986530	116,728,870	A	G	0.101854	0.021552	0.003304	6.1E-12
BUD13 *	11	rs7123583	116,729,305	C	T	0.434208	-0.023006	0.002042	1.9E-29
BUD13 *	11	rs189131104	116,730,452	A	C	0.017081	-0.047504	0.007745	5.9E-10
BUD13 *	11	rs141882698	116,730,622	C	A	0.091891	-0.056336	0.003495	2.9E-60
BUD13 *	11	rs49383306	116,730,762	T	G	0.100155	0.021542	0.003332	1.0E-11
BUD13 *	11	rs108533	116,730,995	T	A	0.330755	-0.034535	0.002150	1.1E-59
BUD13 *	11	rs3212282	116,731,229	A	G	0.309791	0.083822	0.002178	3.7E-333
BUD13 *	11	rs75387300	116,731,683	A	G	0.164088	-0.060333	0.002720	5.6E-114
BUD13 *	11	rs2008915	116,732,418	C	G	0.308563	0.084397	0.002180	2.0E-337
BUD13 *	11	rs60273659	116,732,424	T	C	0.099210	0.022314	0.003346	2.4E-12
BUD13 *	11	rs74503308	116,732,841	A	G	0.099242	0.022123	0.003346	3.7E-12
BUD13 *	11	rs1893460	116,732,961	A	G	0.333920	-0.071831	0.002142	1.0E-254
BUD13 *	11	rs78192008	116,733,154	G	A	0.099171	0.022172	0.003348	3.6E-12
BUD13 *	11	rs49383307	116,733,798	A	G	0.243445	-0.064482	0.002343	2.5E-172
BUD13 *	11	rs117170971	116,734,549	A	G	0.088143	-0.048589	0.003544	5.7E-44
BUD13 *	11	rs79210888	116,734,607	T	C	0.098085	0.021687	0.003367	1.4E-11
BUD13 *	11	rs80022746	116,735,146	A	G	0.020009	-0.041213	0.007172	1.4E-08
BUD13 *	11	rs1013526	116,735,178	G	A	0.099896	0.021641	0.003337	9.3E-12
BUD13 *	11	chr11:116735204_C_CT	116,735,204	CT	C	0.013873	0.073816	0.008616	8.8E-19
BUD13 *	11	rs138202725	116,735,858	ATAGT	A	0.099923	0.021491	0.003337	1.3E-11
BUD13 *	11	rs1974718	116,736,050	G	A	0.204235	0.106542	0.002482	5.8E-413
BUD13 *	11	rs68149171	116,736,335	T	TTCTG	0.241684	-0.064321	0.002350	2.8E-170
BUD13 *	11	rs1558860	116,736,652	A	C	0.203988	0.106932	0.002482	6.7E-416
BUD13 *	11	rs1558861	116,736,721	C	T	0.204011	0.106781	0.002482	5.9E-415
BUD13 *	11	chr11:116736812_G_GA	116,736,812	GA	G	0.098051	0.020828	0.003371	7.4E-11
BUD13 *	11	rs180351	116,736,925	T	C	0.353005	-0.014470	0.002111	4.7E-12
BUD13 *	11	rs114554198	116,736,935	T	C	0.010498	0.072555	0.009873	4.9E-14
BUD13 *	11	rs77032561	116,738,180	C	T	0.100673	0.021486	0.003327	1.4E-11
BUD13 *	11	rs180350	116,739,332	T	C	0.279208	-0.069664	0.002253	7.5E-216
BUD13 *	11	rs10466588	116,739,533	G	A	0.100732	0.021417	0.003326	1.5E-11
BUD13 *	11	rs61905084	116,739,578	C	T	0.340718	-0.072263	0.002128	1.1E-261
BUD13 *	11	rs9326246	116,741,017	C	G	0.203904	0.107090	0.002485	2.4E-416
BUD13 *	11	rs180349	116,741,111	A	T	0.204400	0.107046	0.002483	1.4E-416
BUD13 *	11	rs17092646	116,741,248	C	G	0.100482	0.021065	0.003331	3.8E-11
BUD13 *	11	rs180348	116,741,279	A	G	0.067651	-0.045568	0.004004	5.1E-30
BUD13 *	11	rs10466533	116,741,412	G	A	0.101202	0.020682	0.003322	7.5E-11

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BUD13 *	11	rs11216125	116,741,558	A	G	0.259053	-0.062508	0.002287	8.0E-171
BUD13 *	11	chr11:116741689_AACACACACACACAC_A	116,741,689	A	ACACAC#	0.071046	0.153792	0.003930	1.4E-344
BUD13 *	11	rs180346	116,741,943	C	A	0.278643	-0.069343	0.002249	2.0E-214
BUD13 *	11	rs117788500	116,742,318	C	G	0.084100	-0.048860	0.003622	1.7E-42
BUD13 *	11	rs180344	116,742,468	C	T	0.355801	-0.014557	0.002103	2.8E-12
BUD13 *	11	rs17518841	116,744,528	A	G	0.084440	-0.048741	0.003613	1.5E-42
BUD13 *	11	rs4938308	116,745,386	T	C	0.098139	0.020533	0.003367	1.8E-10
BUD13 *	11	rs180340	116,745,686	C	T	0.357534	-0.015236	0.002102	2.3E-13
BUD13 *	11	rs75197796	116,746,360	C	A	0.098311	0.020234	0.003364	3.2E-10
BUD13 *	11	rs11216126	116,746,524	C	A	0.256185	-0.064978	0.002291	1.7E-183
BUD13 *	11	rs180339	116,747,066	T	C	0.440900	-0.058774	0.002028	9.7E-190
BUD13 *	11	rs45539536	116,747,179	T	C	0.084521	-0.048657	0.003612	2.1E-42
BUD13	11	rs11556024	116,748,335	A	G	0.097253	0.020003	0.003389	5.0E-10
BUD13	11	rs34637368	116,748,889	A	G	0.249804	-0.063956	0.002332	3.1E-172
BUD13	11	rs141923916	116,749,021	GA	G	0.084617	-0.048715	0.003610	1.7E-42
BUD13	11	rs77684111	116,749,413	A	G	0.097128	0.019808	0.003392	8.1E-10
BUD13	11	rs11216129	116,749,540	A	C	0.251500	-0.065082	0.002314	1.1E-180
BUD13	11	rs57950207	116,749,954	C	T	0.084697	-0.048705	0.003610	1.9E-42
BUD13	11	rs2849179	116,750,080	T	C	0.353371	-0.015247	0.002104	2.1E-13
BUD13	11	rs17440396	116,751,054	A	G	0.083430	-0.048276	0.003637	3.4E-41
BUD13	11	rs74368849	116,751,583	A	G	0.066662	0.154432	0.004054	8.4E-328
BUD13	11	rs112064363	116,751,626	A	G	0.098154	0.019249	0.003374	1.9E-09
BUD13	11	rs180329	116,752,242	A	G	0.355089	-0.015190	0.002103	2.9E-13
BUD13	11	chr11:116752497_TA_T	116,752,497	TA	T	0.303816	0.092645	0.002184	1.7E-406
BUD13	11	rs180327	116,752,943	C	T	0.305067	0.092403	0.002181	9.0E-406
BUD13	11	rs6589564	116,753,437	C	G	0.201823	0.110152	0.002493	7.4E-438
BUD13	11	rs180326	116,753,987	G	T	0.203657	0.109370	0.002484	1.5E-434
BUD13	11	rs7930786	116,754,011	C	G	0.202038	0.110238	0.002494	2.0E-438
BUD13	11	rs117728849	116,754,200	T	C	0.100348	0.021555	0.003333	1.2E-11
BUD13	11	rs12421652	116,755,159	T	G	0.252849	-0.065229	0.002309	3.1E-182
BUD13	11	rs77112220	116,755,510	T	C	0.084450	-0.048711	0.003613	1.8E-42
BUD13	11	rs79869230	116,755,799	A	T	0.099580	0.020171	0.003354	2.9E-10
BUD13	11	rs182500870	116,755,846	A	T	0.011254	0.164775	0.009527	7.9E-71
BUD13	11	rs180322	116,756,019	C	T	0.357922	-0.045983	0.002089	2.0E-110
BUD13	11	rs4938309	116,756,339	T	C	0.253068	-0.065348	0.002309	6.5E-183
BUD13	11	rs117685786	116,756,907	C	T	0.043656	-0.054491	0.004916	7.1E-29
BUD13	11	rs2075295	116,757,685	C	T	0.441017	-0.058745	0.002028	1.3E-189
BUD13	11	rs17519093	116,759,189	A	G	0.084652	-0.048388	0.003609	5.1E-42
BUD13	11	rs75955612	116,759,802	T	A	0.042431	0.093782	0.004992	7.1E-82
BUD13	11	rs918143	116,759,884	T	C	0.354601	-0.014459	0.002103	3.5E-12
BUD13	11	rs3741301	116,760,675	C	T	0.281319	-0.069256	0.002242	2.8E-215
BUD13	11	rs3741300	116,760,974	A	G	0.357036	-0.014324	0.002099	5.6E-12
BUD13	11	rs3825041	116,760,991	T	C	0.200343	0.110418	0.002500	9.3E-438
BUD13	11	rs1205200881	116,761,069	T	TA	0.097859	0.020167	0.003382	4.5E-10
BUD13	11	rs189069311	116,761,070	T	A	0.098008	0.020112	0.003381	4.8E-10
BUD13	11	rs139872819	116,761,196	C	T	0.084485	-0.048421	0.003610	5.2E-42
BUD13	11	rs11602240	116,762,082	C	T	0.257028	-0.065456	0.002297	1.5E-185
BUD13	11	rs918144	116,763,109	T	C	0.441466	-0.058778	0.002029	7.7E-190
BUD13	11	rs10488698	116,763,231	A	G	0.083858	-0.048735	0.003622	2.7E-42
BUD13	11	rs17440824	116,763,457	T	C	0.086535	-0.045622	0.003573	2.0E-38
BUD13	11	rs116877083	116,763,581	C	A	0.086464	-0.045542	0.003574	2.8E-38
BUD13	11	rs17119975	116,763,841	C	T	0.254418	-0.065346	0.002309	5.8E-183
BUD13	11	rs2187126	116,765,068	G	A	0.040930	-0.037805	0.005064	2.8E-14
BUD13	11	rs75542782	116,766,286	A	G	0.040908	-0.038071	0.005066	1.8E-14
BUD13	11	rs141740187	116,766,961	T	G	0.106867	0.021924	0.003244	2.7E-12
BUD13	11	rs1145208	116,767,269	C	A	0.342881	-0.016317	0.002116	7.3E-15
BUD13	11	rs532088210	116,767,607	G	A	0.014419	-0.056333	0.008496	1.9E-11
BUD13	11	rs57643109	116,768,035	A	G	0.040958	-0.038223	0.005063	1.5E-14
BUD13	11	rs78908794	116,768,138	C	T	0.108710	0.021820	0.003217	1.9E-12
BUD13	11	rs10790162	116,768,388	A	G	0.200605	0.110848	0.002502	9.5E-441
BUD13	11	rs1268353	116,768,976	T	C	0.300406	-0.069976	0.002196	5.8E-231
BUD13	11	rs1263149	116,769,225	G	A	0.454560	-0.057587	0.002016	8.4E-185
BUD13	11	rs622604	116,769,346	C	T	0.303458	-0.070172	0.002185	6.5E-235
BUD13	11	rs610675	116,769,378	A	T	0.303462	-0.070172	0.002185	6.3E-235
BUD13	11	rs6589565	116,769,521	A	G	0.201420	0.111161	0.002497	7.3E-445
BUD13	11	rs623908	116,769,652	G	A	0.303581	-0.070305	0.002185	8.1E-236
BUD13	11	rs4938311	116,769,888	T	C	0.107569	0.021604	0.003232	2.9E-12
BUD13	11	rs1263151	116,770,312	T	C	0.384682	-0.021727	0.002064	1.4E-26
BUD13	11	rs181315084	116,770,469	C	T	0.012889	0.090921	0.008881	9.0E-25
BUD13	11	rs117579298	116,771,384	G	A	0.040977	-0.037820	0.005062	2.7E-14
BUD13	11	rs664059	116,771,421	T	C	0.493229	-0.012112	0.002011	2.6E-09
BUD13	11	rs79110162	116,772,295	G	A	0.040973	-0.037790	0.005062	2.7E-14
BUD13	11	rs656417	116,772,720	T	G	0.491433	-0.013235	0.002014	6.8E-11
BUD13 *	11	rs12422076	116,773,572	G	A	0.069937	-0.053403	0.003946	2.6E-44
BUD13 *	11	rs141740837	116,774,378	T	TCA	0.040979	-0.037811	0.005061	2.6E-14
BUD13 *	11	rs2041967	116,774,433	G	A	0.410447	-0.053451	0.002042	2.6E-155
BUD13 *	11	rs7118999	116,774,559	T	C	0.385423	-0.021849	0.002062	6.7E-27
BUD13 *	11	rs45443305	116,774,966	A	C	0.106166	0.020716	0.003246	2.3E-11
BUD13 *	11	rs11216135	116,775,346	G	C	0.301197	-0.070350	0.002190	9.7E-235
ZPR1 *	11	rs11602073	116,776,142	T	C	0.300770	-0.069640	0.002190	3.2E-230
ZPR1 *	11	rs11216136	116,776,404	G	T	0.303284	-0.070052	0.002185	2.9E-234
ZPR1 *	11	rs2160669	116,776,891	C	T	0.202746	0.111319	0.002489	4.7E-449
ZPR1 *	11	rs78296522	116,778,060	A	C	0.040974	-0.037840	0.005062	2.5E-14
ZPR1 *	11	rs964184	116,778,201	G	C	0.203203	0.111380	0.002487	2.2E-450
ZPR1	11	rs75198898	116,779,090	A	G	0.066151	0.168349	0.004041	1.6E-390
ZPR1	11	rs113932726	116,779,922	T	C	0.065412	0.169207	0.004064	1.2E-389
ZPR1	11	rs34248274	116,779,950	C	CTAGT	0.301000	-0.069838	0.002188	1.0E-231
ZPR1	11	rs11604424	116,780,399	C	T	0.353560	0.081153	0.002096	4.4E-339
ZPR1	11	rs200405951	116,780,493	G	C	0.011093	0.151555	0.009583	8.7E-59
ZPR1	11	rs1942478	116,780,747	G	T	0.302799	-0.070365	0.002185	1.0E-235
ZPR1	11	rs9633942	116,781,154	C	T	0.025074	-0.051973	0.006451	1.7E-15
ZPR1	11	rs139753514	116,781,213	G	GA	0.105875	0.021022	0.003255	1.9E-11
ZPR1	11	rs4417316	116,781,585	T	C	0.300735	-0.070025	0.002186	3.5E-233
ZPR1	11	rs6589566	116,781,707	G	A	0.203118	0.111405	0.002488	3.3E-450
ZPR1	11	rs190443984	116,781,741	A	G	0.014925	-0.046627	0.008314	8.3E-09
ZPR1	11	rs7483863	116,781,775	A	G	0.203118	0.111405	0.002488	3.3E-450
ZPR1	11	rs2075290	116,782,580	C	T	0.221253	0.099984	0.002411	2.0E-386

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
ZPR1	11	rs76836072	116,783,046	T	C	0.041031	-0.038082	0.005058	1.8E-14
ZPR1	11	rs603446	116,783,719	T	C	0.279084	-0.070529	0.002235	9.0E-225
ZPR1	11	rs74662600	116,784,243	A	G	0.105011	0.020875	0.003264	2.4E-11
ZPR1	11	rs139678706	116,784,368	A	G	0.018691	-0.072632	0.007442	1.5E-22
ZPR1	11	rs10750096	116,786,072	C	A	0.203153	0.111554	0.002488	3.4E-451
ZPR1	11	rs3741298	116,786,845	C	T	0.362877	0.079486	0.002081	1.5E-329
ZPR1	11	rs3741297	116,786,951	T	C	0.065051	0.173463	0.004071	1.3E-408
ZPR1	11	rs2075294	116,787,406	T	G	0.116451	0.017959	0.003118	1.7E-09
APOA5	11	rs33984246	116,789,734	G	A	0.117192	0.018104	0.003109	1.3E-09
APOA5	11	rs45596738	116,789,838	CCT	C	0.117192	0.018104	0.003109	1.3E-09
APOA5	11	rs2266788	116,789,970	G	A	0.203090	0.111804	0.002489	1.1E-452
APOA5	11	rs34089864	116,790,052	A	G	0.117187	0.018145	0.003109	1.2E-09
APOA5	11	rs2075291	116,790,676	A	C	0.065115	0.174037	0.004067	3.5E-412
APOA5	11	rs3135507	116,790,772	T	C	0.104021	0.022608	0.003287	1.3E-12
APOA5	11	rs2072560	116,791,110	T	C	0.202119	0.111950	0.002497	9.4E-451
APOA5	11	rs651821	116,791,863	C	T	0.270777	0.144797	0.002259	1.4E-919
APOA5 *	11	rs34003087	116,792,880	T	C	0.040528	-0.036267	0.005106	3.4E-13
APOA5 *	11	rs662799	116,792,991	G	A	0.271039	0.144432	0.002257	1.7E-916
APOA5 *	11	rs17120035	116,793,135	T	C	0.081843	-0.047485	0.003676	6.6E-39
APOA5 *	11	rs7103224	116,793,250	A	G	0.081813	-0.047508	0.003676	6.4E-39
APOA5 *	11	rs10750097	116,793,324	G	A	0.434506	0.028127	0.002052	2.0E-43
APOA5 *	11	rs1787680	116,794,060	A	T	0.265736	-0.072262	0.002313	1.9E-219
APOA5 *	11	rs9804646	116,794,363	T	C	0.219393	-0.064245	0.002471	8.9E-154
APOA5 *	11	rs35904674	116,795,383	T	C	0.054167	-0.042559	0.004454	6.4E-23
APOA5 *	11	chr11:116795401_C_CA	116,795,401	CA	C	0.053246	-0.042940	0.004498	8.1E-23
APOA5 *	11	rs117730008	116,795,625	A	G	0.045823	0.035093	0.004848	6.7E-14
APOA5 *	11	rs7123666	116,796,367	A	G	0.157721	0.103413	0.002787	2.0E-307
APOA5 *	11	rs75919952	116,796,829	T	C	0.041463	-0.036925	0.005057	9.5E-14
APOA5 *	11	rs35606865	116,798,127	C	T	0.053783	-0.042034	0.004470	2.8E-22
APOA5 *	11	rs11216137	116,799,112	A	G	0.050817	-0.042107	0.004598	2.8E-21
APOA5 *	11	rs11600380	116,799,466	C	T	0.053844	-0.042237	0.004468	1.8E-22
APOA5 *	11	rs12294065	116,800,824	C	G	0.050293	-0.042658	0.004626	1.7E-21
APOA5 *	11	rs116852373	116,800,861	A	G	0.022859	-0.050028	0.006703	3.1E-15
APOA5 *	11	rs188651594	116,802,375	A	G	0.027543	0.095331	0.006152	1.4E-55
APOA5 *	11	rs12791103	116,802,599	T	G	0.050167	-0.042799	0.004634	1.7E-21
APOA5 *	11	rs1263164	116,804,575	A	C	0.302201	-0.034189	0.002232	1.5E-53
APOA5 *	11	rs61499278	116,806,508	ATT	A	0.047702	-0.027026	0.004737	3.6E-09
APOA4 *	11	rs1729407	116,806,654	G	C	0.304697	-0.034555	0.002215	1.2E-55
APOA4 *	11	rs1263168	116,807,283	T	C	0.305292	-0.032866	0.002190	1.3E-51
APOA4 *	11	rs139154032	116,807,284	A	G	0.013222	-0.050949	0.008793	4.2E-10
APOA4 *	11	rs1263169	116,807,423	T	A	0.307364	-0.033760	0.002191	2.4E-54
APOA4 *	11	rs61905133	116,807,475	G	A	0.051148	-0.028747	0.004575	8.1E-11
APOA4 *	11	rs11398704	116,807,533	CA	C	0.352300	-0.036021	0.002140	1.1E-64
APOA4 *	11	rs1263170	116,807,697	C	T	0.308565	-0.033437	0.002182	8.9E-54
APOA4 *	11	rs1729405	116,808,044	T	C	0.308150	-0.033465	0.002181	6.5E-54
APOA4 *	11	rs75542613	116,808,439	A	G	0.040470	-0.070252	0.005110	1.0E-45
APOA4 *	11	rs1263171	116,809,614	A	G	0.305247	-0.031888	0.002176	3.3E-49
APOA4 *	11	rs6589571	116,809,702	T	C	0.194540	0.064688	0.002574	2.0E-142
APOA4 *	11	rs1263172	116,810,202	A	G	0.358393	-0.035561	0.002099	1.2E-65
APOA4 *	11	rs80220270	116,810,245	C	A	0.051640	-0.028575	0.004547	9.2E-11
APOA4 *	11	rs1263173	116,810,292	A	G	0.305405	-0.031848	0.002174	4.1E-49
APOA4 *	11	rs1263174	116,810,527	T	G	0.309223	-0.031659	0.002172	1.0E-48
APOA4 *	11	rs75145979	116,810,778	A	C	0.050397	-0.027418	0.004606	9.2E-10
APOA4 *	11	rs6589572	116,810,847	G	A	0.305668	0.071943	0.002178	3.5E-246
APOA4 *	11	rs79538491	116,811,203	G	A	0.060764	0.049382	0.004227	5.5E-33
APOA4 *	11	rs7927820	116,811,440	G	A	0.304529	0.072257	0.002177	1.7E-248
APOA4 *	11	rs35180165	116,811,633	C	CAG	0.304086	-0.031909	0.002181	4.6E-49
APOA4 *	11	rs76636922	116,812,279	A	G	0.335215	-0.031520	0.002132	2.9E-51
APOA4 *	11	rs2727793	116,812,658	T	C	0.304171	-0.031308	0.002185	2.9E-47
APOA4 *	11	rs75318540	116,813,146	T	C	0.219074	-0.026043	0.002447	2.5E-27
APOA4 *	11	rs7396835	116,813,312	T	C	0.305116	0.071808	0.002172	1.3E-246
APOA4 *	11	rs7396851	116,813,448	T	C	0.304777	0.072059	0.002174	6.4E-248
APOA4 *	11	rs79841374	116,813,844	T	C	0.334365	-0.031757	0.002133	6.8E-52
APOA4 *	11	rs2727791	116,813,846	G	C	0.306710	-0.032229	0.002180	3.1E-50
APOA4 *	11	rs2849167	116,814,028	A	G	0.306606	-0.032344	0.002181	1.8E-50
APOA4 *	11	rs2542063	116,814,051	A	G	0.307049	-0.032270	0.002180	2.7E-50
APOA4 *	11	rs77535577	116,814,675	A	G	0.333435	-0.032148	0.002142	1.1E-52
APOA4 *	11	rs6589573	116,815,050	C	G	0.307214	0.072697	0.002194	1.8E-247
APOA4 *	11	rs7107757	116,815,572	T	C	0.356781	0.061610	0.002108	1.5E-192
APOA4 *	11	chr11:116816190_CT_C	116,816,190	C	CT	0.314187	-0.030666	0.002198	1.0E-45
APOA4 *	11	rs9735326	116,818,049	C	A	0.326213	0.067975	0.002162	1.3E-222
APOA4 *	11	rs184316726	116,818,292	C	A	0.047382	-0.025811	0.004739	1.5E-08
APOA4 *	11	rs1263176	116,819,407	T	C	0.368407	0.059686	0.002094	1.1E-182
APOA4 *	11	rs1268354	116,819,862	C	T	0.368755	0.059646	0.002094	1.2E-182
APOA4 *	11	rs1263177	116,819,996	C	T	0.367218	0.059945	0.002098	9.2E-184
APOA4 *	11	rs2234669	116,820,795	G	GGACA	0.303478	-0.032667	0.002208	1.8E-50
APOA4 *	11	rs5104	116,821,618	C	T	0.319760	0.069993	0.002163	1.1E-235
APOA4 *	11	rs6413456	116,821,733	A	G	0.033241	-0.070575	0.005600	1.0E-38
APOA4 *	11	rs5103	116,821,836	G	A	0.048866	-0.026172	0.004667	7.4E-09
APOA4 *	11	rs5100	116,821,978	G	A	0.372586	0.059559	0.002091	1.1E-182
APOA4 *	11	rs5096	116,822,379	G	A	0.372562	0.059535	0.002091	1.8E-182
APOA4 *	11	rs2239013	116,822,637	T	C	0.040771	-0.069630	0.005088	3.8E-45
APOA4 *	11	rs5093	116,822,638	A	G	0.217399	-0.026595	0.002467	5.8E-28
APOA4 *	11	rs5092	116,822,748	C	T	0.372187	0.059347	0.002093	6.5E-181
APOA4 *	11	rs1268833	116,824,150	G	A	0.372400	0.059371	0.002092	2.0E-181
APOA4 *	11	rs10892035	116,824,222	A	G	0.371801	0.059340	0.002093	4.8E-181
APOA4 *	11	rs182352602	116,824,894	A	G	0.211429	-0.026031	0.002495	2.2E-26
APOA4 *	11	rs7111242	116,825,064	A	G	0.320577	0.069253	0.002171	6.6E-229
APOA4 *	11	rs2216311	116,825,327	G	A	0.372313	0.059597	0.002092	1.2E-182
APOA4 *	11	rs2098453	116,825,964	C	T	0.371794	0.059796	0.002094	1.7E-183
APOA4 *	11	rs7123326	116,825,965	A	G	0.048967	-0.026212	0.004661	6.7E-09
APOA4 *	11	rs2727789	116,826,171	G	T	0.373345	0.059546	0.002093	3.8E-182
APOA4 *	11	rs2849176	116,826,205	T	C	0.372385	0.059740	0.002093	3.2E-183
APOA4 *	11	rs2849174	116,826,350	A	G	0.049553	-0.025748	0.004635	1.1E-08
APOA4 *	11	rs2542050	116,826,401	C	A	0.371801	0.059838	0.002093	6.8E-184
APOC3 *	11	rs2849173	116,826,605	G	C	0.371832	0.059787	0.002093	1.6E-183
APOC3 *	11	rs2071523	116,826,628	C	T	0.371858	0.059785	0.002093	1.5E-183

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
APOC3 *	11	rs2071522	116,826,822	T	C	0.371856	0.059741	0.002093	3.1E-183
APOC3 *	11	rs2542051	116,827,022	C	A	0.372009	0.059737	0.002093	3.3E-183
APOC3 *	11	rs2071521	116,827,132	G	A	0.371961	0.059769	0.002093	1.8E-183
APOC3 *	11	rs7101528	116,827,949	A	G	0.049198	-0.026291	0.004652	6.0E-09
APOC3 *	11	rs2727788	116,828,247	A	C	0.049766	-0.025871	0.004626	9.4E-09
APOC3 *	11	rs595049	116,828,729	C	A	0.373684	0.059759	0.002086	1.9E-184
APOC3	11	rs734104	116,830,144	C	T	0.292958	0.056551	0.002222	8.4E-147
APOC3	11	rs5128	116,832,924	G	C	0.290699	0.057287	0.002210	2.8E-152
APOA1 *	11	rs10750098	116,834,852	G	T	0.290169	0.057113	0.002217	4.3E-150
APOA1 *	11	rs12718462	116,835,003	C	T	0.044319	-0.064100	0.004883	1.2E-41
APOA1 *	11	rs12721025	116,835,331	A	G	0.047623	-0.062235	0.004753	3.3E-41
APOA1 *	11	rs12721026	116,835,452	G	T	0.043068	-0.063285	0.004952	1.7E-39
APOA1	11	rs12718464	116,836,685	A	G	0.042999	-0.063068	0.004954	3.1E-39
APOA1 *	11	rs368405969	116,839,577	T	C	0.011948	-0.068717	0.009247	1.9E-14
APOA1 *	11	rs613808	116,840,252	G	A	0.276644	-0.043122	0.002280	9.7E-82
APOA1 *	11	rs2727784	116,840,425	T	C	0.257746	-0.045583	0.002336	3.7E-87
SIK3 *	11	rs480009	116,841,258	T	C	0.249675	-0.016421	0.002340	2.7E-13
SIK3 *	11	rs370143719	116,841,590	C	T	0.013613	-0.062731	0.008667	6.0E-14
SIK3 *	11	rs591592	116,842,850	T	C	0.221781	-0.033635	0.002452	3.3E-43
SIK3 *	11	rs200408997	116,842,862	A	ACCC	0.049331	0.054514	0.004632	2.4E-33
SIK3 *	11	rs579163	116,842,914	G	C	0.222198	-0.033710	0.002450	1.9E-43
SIK3	11	rs371090973	116,844,640	T	TTA	0.049512	0.051709	0.004630	2.8E-30
SIK3	11	rs201579941	116,844,674	A	ATAT	0.048465	0.053355	0.004672	1.2E-31
SIK3	11	rs142174850	116,845,068	A	G	0.081778	-0.055480	0.003667	3.3E-55
SIK3	11	rs143120617	116,846,722	T	C	0.036814	-0.051242	0.005335	3.0E-23
SIK3	11	rs61905145	116,847,699	A	G	0.050099	0.052813	0.004591	6.0E-32
SIK3	11	rs1145206	116,847,805	C	G	0.130177	0.015644	0.002984	4.3E-08
SIK3	11	rs7127590	116,848,086	G	T	0.405029	-0.021003	0.002052	1.2E-24
SIK3	11	rs532815	116,848,142	A	G	0.234563	-0.034211	0.002378	3.3E-47
SIK3	11	rs112030791	116,848,208	ATT	A	0.404217	-0.020902	0.002055	2.5E-24
SIK3	11	rs145730196	116,848,209	A	G	0.404217	-0.020902	0.002055	2.5E-24
SIK3	11	rs61905155	116,848,213	T	G	0.049954	0.052563	0.004599	1.7E-31
SIK3	11	rs2289893	116,849,373	C	T	0.350120	-0.032297	0.002109	9.3E-54
SIK3	11	rs660083	116,850,113	G	C	0.231319	-0.032896	0.002384	1.0E-43
SIK3	11	rs11216161	116,850,485	C	T	0.400907	-0.020020	0.002051	1.3E-22
SIK3	11	rs10047459	116,851,110	T	C	0.400431	-0.019946	0.002048	1.8E-22
SIK3	11	rs10047462	116,851,325	T	G	0.483333	-0.035692	0.002006	3.7E-73
SIK3	11	rs689243	116,851,977	C	G	0.230871	-0.032403	0.002385	2.0E-42
SIK3	11	rs139952838	116,852,044	T	C	0.028147	0.085984	0.006049	3.0E-47
SIK3	11	rs888245	116,853,021	G	C	0.050178	0.052996	0.004585	3.6E-32
SIK3	11	rs888246	116,853,516	T	C	0.050163	0.053315	0.004586	1.5E-32
SIK3	11	rs12099358	116,855,332	A	C	0.050316	0.052723	0.004579	5.3E-32
SIK3	11	rs112618266	116,855,993	T	C	0.079106	-0.054575	0.003707	2.3E-52
SIK3	11	rs640621	116,856,053	G	C	0.234787	-0.034203	0.002368	1.6E-47
SIK3	11	rs78857232	116,856,749	T	C	0.050131	0.052678	0.004586	7.8E-32
SIK3	11	rs1035237	116,857,134	C	G	0.484630	-0.036075	0.002014	3.7E-74
SIK3	11	rs11216162	116,857,561	A	G	0.088874	0.023431	0.003519	3.3E-11
SIK3	11	rs12225230	116,857,914	C	G	0.088856	0.023511	0.003519	2.8E-11
SIK3	11	rs6589574	116,859,922	A	G	0.311738	0.048590	0.002187	1.2E-112
SIK3	11	rs567312	116,860,022	A	G	0.233558	-0.034059	0.002373	5.5E-47
SIK3	11	rs4938315	116,860,489	A	G	0.483229	-0.035864	0.002014	3.1E-73
SIK3	11	rs2075292	116,861,796	T	G	0.482565	-0.036247	0.002017	1.0E-74
SIK3	11	rs117010832	116,861,803	A	G	0.138539	-0.022473	0.002934	4.7E-15
SIK3	11	rs484646	116,862,140	G	A	0.234890	-0.034253	0.002367	1.0E-47
SIK3	11	rs6589575	116,862,594	T	C	0.483917	-0.036067	0.002013	4.0E-74
SIK3	11	rs2080586	116,862,600	C	T	0.049964	0.053495	0.004593	1.0E-32
SIK3	11	rs476399	116,863,012	C	T	0.234847	-0.034261	0.002367	9.9E-48
SIK3	11	rs718847	116,863,430	T	C	0.483294	-0.036030	0.002013	4.4E-74
SIK3	11	rs17120099	116,864,744	C	A	0.079170	-0.054366	0.003706	5.0E-52
SIK3	11	rs6589576	116,865,072	G	C	0.483799	-0.036099	0.002013	2.5E-74
SIK3	11	rs573549	116,865,963	G	A	0.235447	-0.034460	0.002368	2.6E-48
SIK3	11	chr11:16866441_C_CTTTA	116,866,441	CTTTA	C	0.039919	0.053995	0.005152	1.0E-26
SIK3	11	rs77009426	116,867,798	T	C	0.032086	-0.034628	0.005718	1.1E-09
SIK3	11	rs17120101	116,867,872	T	C	0.032572	-0.048072	0.005657	1.4E-18
SIK3	11	rs11216168	116,870,837	A	G	0.050131	0.052911	0.004586	4.3E-32
SIK3	11	rs533556	116,870,856	C	A	0.235769	-0.034008	0.002363	3.2E-47
SIK3	11	rs17120111	116,873,302	T	C	0.049657	0.053945	0.004609	6.0E-33
SIK3	11	rs11216169	116,873,673	C	T	0.049658	0.053400	0.004611	3.0E-32
SIK3	11	rs9919599	116,874,768	G	C	0.483271	-0.035745	0.002017	2.8E-72
SIK3	11	rs17120119	116,876,566	G	C	0.077172	-0.052772	0.003751	3.8E-48
SIK3	11	rs77682889	116,876,596	T	C	0.030388	0.077014	0.005819	3.2E-41
SIK3	11	rs12278117	116,877,453	A	G	0.077168	-0.052819	0.003751	3.2E-48
SIK3	11	rs12279433	116,877,505	T	G	0.078525	-0.054068	0.003719	3.0E-51
SIK3	11	rs12279464	116,877,766	T	C	0.077168	-0.052819	0.003751	3.2E-48
SIK3	11	rs112867178	116,877,768	CTCTATT	C	0.481974	-0.035514	0.002020	3.3E-71
SIK3	11	rs12292614	116,877,799	G	A	0.077168	-0.052819	0.003751	3.2E-48
SIK3	11	rs12286581	116,878,028	C	T	0.077168	-0.052818	0.003751	3.2E-48
SIK3	11	rs61907566	116,878,189	G	C	0.233296	-0.034285	0.002380	5.0E-47
SIK3	11	rs75294699	116,878,356	A	C	0.077168	-0.052818	0.003751	3.2E-48
SIK3	11	rs76523703	116,878,793	G	T	0.049702	0.052910	0.004609	9.8E-32
SIK3	11	rs11216172	116,879,162	A	G	0.360064	-0.018413	0.002099	9.9E-18
SIK3	11	rs6589577	116,879,261	T	C	0.483247	-0.035836	0.002018	1.4E-72
SIK3	11	rs543819	116,879,357	G	A	0.083267	-0.054403	0.003629	2.0E-54
SIK3	11	rs7396061	116,880,158	C	A	0.316747	-0.032643	0.002169	1.3E-50
SIK3	11	rs74341458	116,880,833	A	G	0.049560	0.053252	0.004615	4.4E-32
SIK3	11	rs482371	116,881,447	C	T	0.228907	-0.033256	0.002395	1.2E-43
SIK3	11	rs7124741	116,881,503	T	A	0.482895	-0.035836	0.002016	9.9E-73
SIK3	11	rs12275565	116,882,836	G	A	0.082161	-0.053069	0.003653	2.7E-51
SIK3	11	rs12416987	116,883,549	C	T	0.078562	-0.054053	0.003718	2.7E-51
SIK3	11	rs1269329	116,884,325	C	T	0.234812	-0.033981	0.002375	2.3E-46
SIK3	11	rs139733873	116,884,844	G	A	0.012350	0.100452	0.009079	1.6E-28
SIK3	11	rs1827828	116,884,868	A	G	0.049707	0.052850	0.004608	1.1E-31
SIK3	11	rs2044426	116,885,467	A	G	0.076505	-0.053340	0.003768	9.7E-49
SIK3	11	rs35378097	116,886,122	G	GT	0.034134	-0.049161	0.005517	2.0E-20
SIK3	11	rs10892040	116,886,270	A	G	0.076793	-0.052992	0.003759	2.0E-48
SIK3	11	rs11216174	116,886,532	G	A	0.076798	-0.052945	0.003759	2.3E-48
SIK3	11	rs11216175	116,886,682	T	C	0.076793	-0.052992	0.003759	2.0E-48

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIK3	11	chr11:116886752_T_TA	116,886,752	TA	T	0.234130	-0.034137	0.002376	1.0E-46
SIK3	11	rs12284346	116,887,077	C	T	0.077686	-0.054481	0.003739	1.3E-51
SIK3	11	rs7106641	116,887,385	A	G	0.284986	-0.017543	0.002230	9.5E-15
SIK3	11	rs12292278	116,887,977	C	A	0.083170	-0.054388	0.003629	1.9E-54
SIK3	11	rs1473177	116,888,616	C	T	0.049595	0.053298	0.004613	3.6E-32
SIK3	11	rs17174502	116,888,939	G	A	0.483429	-0.035877	0.002018	8.6E-73
SIK3	11	rs12294191	116,889,108	G	A	0.083319	-0.054448	0.003626	1.0E-54
SIK3	11	rs10892042	116,889,829	A	G	0.049595	0.053298	0.004613	3.6E-32
SIK3	11	rs660443	116,889,977	C	T	0.229099	-0.033223	0.002394	1.3E-43
SIK3	11	rs12285074	116,891,312	G	A	0.483131	-0.036132	0.002023	1.1E-73
SIK3	11	rs72645459	116,891,441	C	A	0.482387	-0.036112	0.002020	1.1E-73
SIK3	11	chr11:116891662_AAG_A	116,891,662	AAG	A	0.481536	-0.036231	0.002018	2.8E-74
SIK3	11	rs144010715	116,891,837	AG	A	0.083270	-0.054541	0.003628	7.7E-55
SIK3	11	rs75158858	116,892,113	A	G	0.049595	0.053298	0.004613	3.6E-32
SIK3	11	rs499910	116,892,318	A	G	0.279035	-0.016798	0.002245	2.0E-13
SIK3	11	rs672058	116,893,305	T	C	0.400096	-0.033247	0.002058	5.7E-61
SIK3	11	rs74885676	116,894,221	T	G	0.136370	-0.022036	0.002953	2.3E-14
SIK3	11	rs77349713	116,894,760	C	T	0.083830	-0.054473	0.003613	4.7E-55
SIK3	11	rs11820814	116,894,984	C	T	0.049547	0.053421	0.004617	2.6E-32
SIK3	11	rs74881320	116,895,209	C	A	0.083827	-0.054508	0.003613	4.1E-55
SIK3	11	rs149874218	116,895,594	TTG	T	0.084036	-0.054519	0.003612	3.6E-55
SIK3	11	rs1216178	116,895,674	T	G	0.049504	0.053382	0.004619	3.3E-32
SIK3	11	rs10892044	116,896,183	C	T	0.049537	0.053451	0.004617	2.6E-32
SIK3	11	rs2270392	116,896,972	C	T	0.121645	-0.044208	0.003069	2.9E-51
SIK3	11	chr11:116897883_CA_C	116,897,883	C	CA	0.074164	-0.054878	0.003835	1.9E-49
SIK3	11	rs111884008	116,898,027	C	G	0.116791	-0.043482	0.003121	3.8E-48
SIK3	11	rs190051172	116,898,198	G	C	0.083832	-0.054480	0.003613	4.7E-55
SIK3	11	rs609177	116,899,801	G	A	0.235379	-0.034058	0.002376	1.0E-46
SIK3	11	rs72645460	116,900,659	A	G	0.480473	-0.035970	0.002021	6.1E-73
SIK3	11	rs1076485	116,901,725	C	T	0.443023	-0.034656	0.002030	2.0E-66
SIK3	11	rs17120131	116,901,770	C	T	0.084129	-0.054644	0.003610	1.5E-55
SIK3	11	rs518181	116,902,071	A	C	0.227929	-0.033537	0.002401	3.1E-44
SIK3	11	rs17120132	116,902,602	A	T	0.084215	-0.054621	0.003607	1.3E-55
SIK3	11	rs11216180	116,902,662	T	A	0.049553	0.053639	0.004616	1.6E-32
SIK3	11	rs17120136	116,903,045	G	T	0.082173	-0.053337	0.003653	5.9E-52
SIK3	11	rs17120139	116,903,485	G	A	0.480128	-0.036215	0.002022	7.0E-74
SIK3	11	rs78694306	116,903,528	T	G	0.077817	-0.053144	0.003735	2.2E-49
SIK3	11	rs11216181	116,903,758	T	A	0.046186	0.054973	0.004786	9.7E-32
SIK3	11	rs78832854	116,903,759	A	T	0.080857	-0.047844	0.003678	1.5E-41
SIK3	11	rs115971514	116,903,783	C	G	0.077817	-0.053144	0.003735	2.2E-49
SIK3	11	rs12280030	116,904,480	A	T	0.084000	-0.054540	0.003609	2.0E-55
SIK3	11	rs7111854	116,906,110	T	A	0.121833	-0.044267	0.003066	1.3E-51
SIK3	11	rs12273762	116,906,347	A	T	0.084000	-0.054540	0.003609	2.0E-55
SIK3	11	rs9651681	116,907,349	C	T	0.084213	-0.054619	0.003607	1.3E-55
SIK3	11	rs4938317	116,907,559	C	T	0.049549	0.053663	0.004616	1.5E-32
SIK3	11	rs35184536	116,908,097	G	A	0.084070	-0.054554	0.003610	2.4E-55
SIK3	11	rs10790166	116,908,783	G	A	0.246185	-0.015676	0.002333	1.9E-12
SIK3	11	rs200905431	116,909,318	G	GA	0.094114	-0.045884	0.003508	6.2E-42
SIK3	11	rs75920871	116,909,379	T	A	0.049634	0.055092	0.004623	3.8E-34
SIK3	11	rs11216183	116,910,829	A	C	0.075074	-0.055931	0.003790	7.2E-53
SIK3	11	rs191330880	116,911,276	A	G	0.020925	-0.040175	0.007062	1.2E-08
SIK3	11	rs7123336	116,912,103	C	T	0.162967	-0.013866	0.002713	3.4E-08
SIK3	11	rs11216185	116,912,258	G	T	0.079281	-0.054206	0.003701	3.5E-52
SIK3	11	rs983567	116,912,884	C	T	0.162954	-0.013973	0.002714	2.8E-08
SIK3	11	rs142195028	116,913,525	A	AG	0.074986	-0.056006	0.003794	6.6E-53
SIK3	11	rs11357208	116,913,587	C	CT	0.049528	0.053577	0.004618	2.0E-32
SIK3	11	rs7115583	116,913,660	T	G	0.117027	-0.043737	0.003119	7.3E-49
SIK3	11	rs149566815	116,913,905	T	TAAAC	0.075004	-0.056066	0.003794	5.0E-53
SIK3	11	rs11216186	116,913,976	C	T	0.098755	-0.053170	0.003355	7.0E-60
SIK3	11	rs10892045	116,914,108	A	C	0.046234	0.054750	0.004780	1.4E-31
SIK3	11	rs79711490	116,914,625	T	C	0.098755	-0.053172	0.003355	6.9E-60
SIK3	11	rs11216187	116,916,432	T	C	0.049518	0.053515	0.004619	2.4E-32
SIK3	11	rs12277181	116,916,604	A	G	0.098874	-0.053074	0.003355	1.5E-59
SIK3	11	rs12277092	116,916,611	T	C	0.098761	-0.053175	0.003355	7.0E-60
SIK3	11	rs7928298	116,916,811	T	A	0.073643	-0.034638	0.003881	6.9E-21
SIK3	11	rs12418208	116,916,917	T	C	0.096076	-0.053824	0.003403	1.2E-59
SIK3	11	rs12418209	116,916,925	T	C	0.096076	-0.053824	0.003403	1.2E-59
SIK3	11	rs1006176	116,917,417	C	T	0.098963	-0.053142	0.003351	6.6E-60
SIK3	11	chr11:116917733_AAGAG_A	116,917,733	A	AAGAG	0.096134	-0.051744	0.003404	5.1E-55
SIK3	11	rs76136280	116,917,775	T	C	0.049545	0.053615	0.004617	1.8E-32
SIK3	11	rs1135663	116,918,121	T	C	0.085557	-0.050857	0.003616	1.3E-47
SIK3	11	rs79530380	116,918,472	A	T	0.041004	0.061124	0.005103	3.3E-34
SIK3	11	rs78692246	116,920,591	A	G	0.099548	-0.052762	0.003341	2.4E-59
SIK3	11	rs141203891	116,921,220	C	T	0.010217	-0.077721	0.009962	5.9E-16
SIK3	11	rs7934763	116,921,641	G	T	0.049868	0.052225	0.004604	4.6E-31
SIK3	11	rs7948838	116,922,245	G	A	0.136934	-0.044390	0.002914	2.3E-56
SIK3	11	rs12225187	116,922,515	A	G	0.203038	-0.029943	0.002500	4.2E-33
SIK3	11	rs12288386	116,922,907	T	C	0.099234	-0.052671	0.003345	4.7E-59
SIK3	11	rs10892047	116,922,977	T	C	0.099147	-0.052825	0.003348	2.5E-59
SIK3	11	rs117287138	116,924,163	A	G	0.049773	0.052353	0.004609	4.0E-31
SIK3	11	rs56314469	116,924,187	A	G	0.049773	0.052353	0.004609	4.0E-31
SIK3	11	rs12292371	116,925,232	C	G	0.099335	-0.052570	0.003344	7.4E-59
SIK3	11	rs12292434	116,925,349	A	G	0.099259	-0.052700	0.003345	4.3E-59
SIK3	11	rs7121898	116,926,130	T	A	0.203380	-0.029799	0.002499	8.3E-33
SIK3	11	rs61907591	116,926,139	A	T	0.049868	0.052225	0.004604	4.6E-31
SIK3	11	rs12285956	116,926,759	A	G	0.099262	-0.052710	0.003345	4.2E-59
SIK3	11	rs11216190	116,926,968	C	T	0.136136	-0.044528	0.002923	3.1E-56
SIK3	11	chr11:116927081_AT_A	116,927,081	A	AT	0.096773	-0.051707	0.003396	2.6E-55
SIK3	11	rs1446105	116,927,828	T	C	0.203384	-0.029780	0.002498	7.7E-33
SIK3	11	rs579890	116,928,247	G	A	0.471610	-0.034634	0.002021	9.0E-68
SIK3	11	rs79157715	116,929,554	A	G	0.099362	-0.052646	0.003343	5.7E-59
SIK3	11	rs10790167	116,930,227	C	T	0.203247	-0.029728	0.002498	1.1E-32
SIK3	11	rs75776964	116,930,345	G	C	0.099345	-0.052659	0.003343	5.3E-59
SIK3	11	rs645258	116,930,485	A	C	0.313720	0.043140	0.002171	2.4E-90
SIK3	11	rs76690043	116,930,813	G	C	0.049871	0.052233	0.004604	4.5E-31
SIK3	11	rs61907594	116,931,095	T	C	0.049871	0.052237	0.004604	4.4E-31
SIK3	11	rs79974099	116,931,865	A	T	0.049871	0.052237	0.004604	4.4E-31

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIK3	11	rs74615346	116,932,256	C	A	0.099457	-0.052605	0.003342	6.1E-59
SIK3	11	chr11:116933137_CTT_C	116,933,137	C	CTT	0.051154	-0.025181	0.004602	4.2E-09
SIK3	11	rs12270974	116,933,289	T	C	0.099342	-0.052657	0.003343	5.4E-59
SIK3	11	rs7107702	116,933,428	C	T	0.187159	-0.018209	0.002568	8.1E-14
SIK3	11	rs12272491	116,933,654	T	C	0.099342	-0.052657	0.003343	5.4E-59
SIK3	11	rs12418735	116,934,046	G	T	0.099345	-0.052650	0.003343	5.6E-59
SIK3	11	rs77204473	116,934,348	G	T	0.064702	-0.050016	0.004068	3.5E-36
SIK3	11	rs562179	116,934,488	C	T	0.436613	-0.028154	0.002033	2.2E-44
SIK3	11	rs79207844	116,934,725	A	G	0.064224	-0.050644	0.004082	7.6E-37
SIK3	11	rs12274590	116,934,980	A	G	0.064224	-0.050644	0.004082	7.6E-37
SIK3	11	rs144015791	116,935,158	T	G	0.049871	0.052237	0.004604	4.4E-31
SIK3	11	rs2513095	116,935,553	C	T	0.471999	-0.034572	0.002021	1.6E-67
SIK3	11	rs2513094	116,935,696	C	T	0.266294	-0.019319	0.002272	1.4E-18
SIK3	11	rs2513093	116,935,971	G	A	0.471790	-0.034693	0.002020	4.7E-68
SIK3	11	rs12273769	116,936,457	G	T	0.099344	-0.052675	0.003343	4.8E-59
SIK3	11	rs12294657	116,936,652	C	G	0.099347	-0.052662	0.003343	5.0E-59
SIK3	11	rs77920516	116,936,711	C	T	0.088573	0.034964	0.003551	5.4E-23
SIK3	11	rs473172	116,937,254	G	A	0.471799	-0.034683	0.002020	5.1E-68
SIK3	11	rs77136879	116,937,737	T	C	0.099362	-0.052652	0.003342	5.1E-59
SIK3	11	chr11:116938204_AGAGGGGAGGGGAGGG_A	116,938,204	A	GGAGGG	0.114622	-0.035469	0.003168	5.5E-31
SIK3	11	rs142440762	116,938,378	A	G	0.143256	-0.021071	0.002885	4.2E-14
SIK3	11	rs61907600	116,938,632	G	A	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs7480278	116,939,073	G	T	0.099367	-0.052652	0.003342	5.1E-59
SIK3	11	rs61624438	116,939,229	A	C	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs80015203	116,940,190	G	A	0.099367	-0.052652	0.003342	5.1E-59
SIK3	11	rs117877581	116,940,238	G	T	0.099499	-0.052794	0.003342	2.3E-59
SIK3	11	rs116597701	116,940,771	G	C	0.097850	-0.052009	0.003367	1.3E-56
SIK3	11	rs145705809	116,940,967	A	C	0.013056	0.122973	0.008835	6.0E-45
SIK3	11	rs139127609	116,940,986	T	TTTTG	0.099367	-0.052652	0.003342	5.1E-59
SIK3	11	rs473188	116,941,313	G	C	0.471501	-0.034667	0.002020	5.3E-68
SIK3	11	rs78066444	116,941,342	C	A	0.098231	-0.052266	0.003363	1.3E-57
SIK3	11	chr11:116941408_TA_T	116,941,408	T	TA	0.480280	-0.035937	0.002042	3.1E-71
SIK3	11	rs17120157	116,941,912	C	T	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs75410648	116,942,722	T	C	0.099382	-0.052594	0.003342	6.5E-59
SIK3	11	rs510988	116,943,088	T	C	0.471476	-0.034677	0.002020	4.8E-68
SIK3	11	rs12292858	116,943,263	C	A	0.136821	-0.044485	0.002914	1.4E-56
SIK3	11	rs10892048	116,943,880	G	A	0.201426	-0.029527	0.002509	4.9E-32
SIK3	11	rs12421902	116,943,930	G	A	0.097567	-0.052547	0.003375	1.1E-57
SIK3	11	chr11:116944465_GCAAT_G	116,944,465	G	GCAAT	0.471472	-0.034671	0.002020	5.0E-68
SIK3	11	rs11216193	116,944,883	T	C	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	chr11:116944965_C_CTT	116,944,965	CTT	C	0.079486	-0.050397	0.003775	1.4E-43
SIK3	11	rs11216194	116,945,022	C	G	0.099037	-0.052229	0.003354	1.4E-57
SIK3	11	rs11216195	116,945,175	A	G	0.097251	-0.052838	0.003382	5.6E-58
SIK3	11	rs11216196	116,945,176	G	T	0.097251	-0.052838	0.003382	5.6E-58
SIK3	11	rs35485516	116,945,411	C	CAG	0.099370	-0.052630	0.003342	5.9E-59
SIK3	11	rs10892049	116,945,500	C	G	0.136810	-0.044482	0.002914	1.4E-56
SIK3	11	rs10892050	116,945,678	A	C	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs75958227	116,945,875	A	G	0.139683	-0.021605	0.002916	3.1E-14
SIK3	11	rs7924318	116,945,914	G	C	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs11216197	116,946,062	G	A	0.099608	-0.052308	0.003341	2.2E-58
SIK3	11	rs191655881	116,946,939	C	A	0.136810	-0.044482	0.002914	1.4E-56
SIK3	11	rs111327557	116,947,068	T	C	0.049596	0.051339	0.004621	8.2E-30
SIK3	11	rs1565486994	116,947,173	TATATTA	T	0.011838	-0.064678	0.009384	4.5E-13
SIK3	11	rs369504538	116,947,566	T	TG	0.014599	0.046491	0.008549	1.8E-08
SIK3	11	rs1272436324	116,947,568	T	TA	0.014599	0.046491	0.008549	1.8E-08
SIK3	11	rs146056222	116,947,627	G	A	0.136810	-0.044482	0.002914	1.4E-56
SIK3	11	rs61907604	116,947,691	G	A	0.187438	-0.018228	0.002567	7.9E-14
SIK3	11	rs112704540	116,947,811	G	A	0.187175	-0.018257	0.002568	7.0E-14
SIK3	11	rs146503809	116,948,352	G	A	0.027303	0.073468	0.006146	1.0E-33
SIK3	11	rs4316540	116,948,525	T	C	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs12293755	116,948,548	T	A	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs1241658	116,948,901	A	G	0.470865	-0.034031	0.002021	1.9E-65
SIK3	11	rs139552563	116,949,016	CAAAAT	C	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs112297132	116,949,116	GA	G	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs6589580	116,949,157	A	G	0.187175	-0.018257	0.002568	7.0E-14
SIK3	11	rs12419047	116,949,190	A	G	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs12421834	116,949,307	C	A	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs61907605	116,949,355	A	T	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs12420518	116,949,372	C	T	0.136810	-0.044482	0.002914	1.4E-56
SIK3	11	rs142344418	116,949,918	C	CAG	0.085820	0.037871	0.003604	3.2E-26
SIK3	11	rs12419437	116,949,974	A	G	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs1473324	116,951,202	G	T	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs1473325	116,951,318	T	C	0.049874	0.052211	0.004604	4.7E-31
SIK3	11	rs76538122	116,951,618	G	A	0.031800	-0.051453	0.005716	6.2E-21
SIK3	11	rs12286405	116,951,812	T	C	0.136808	-0.044444	0.002914	1.8E-56
SIK3	11	rs11605327	116,952,346	A	G	0.202737	-0.029999	0.002502	3.5E-33
SIK3	11	rs77467134	116,952,391	C	T	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs76654964	116,952,805	A	G	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs76146269	116,952,901	G	A	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs1473326	116,952,956	C	T	0.049875	0.052210	0.004604	4.7E-31
SIK3	11	rs1473327	116,953,280	T	A	0.049901	0.052240	0.004603	4.2E-31
SIK3	11	rs12275355	116,953,446	G	A	0.099394	-0.052650	0.003342	4.4E-59
SIK3	11	rs12289974	116,953,570	T	C	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs2289890	116,953,904	A	G	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs511676	116,954,168	G	T	0.471890	-0.034786	0.002020	2.1E-68
SIK3	11	rs2289892	116,954,524	A	G	0.099273	-0.052702	0.003344	4.2E-59
SIK3	11	rs12291040	116,955,901	C	T	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs12270837	116,955,927	C	A	0.099365	-0.052654	0.003342	5.1E-59
SIK3	11	rs10502221	116,956,154	T	C	0.202574	-0.029939	0.002502	4.5E-33
SIK3	11	rs17120177	116,956,653	C	T	0.099349	-0.052567	0.003344	8.7E-59
SIK3	11	rs19406626	116,957,405	C	T	0.187119	-0.018169	0.002569	9.3E-14
SIK3	11	rs682048	116,957,604	G	T	0.266253	-0.019290	0.002272	1.5E-18
SIK3	11	rs193291566	116,957,830	G	T	0.010257	-0.078839	0.009939	2.3E-16
SIK3	11	rs878692	116,958,223	A	C	0.099292	-0.052589	0.003346	9.8E-59
SIK3	11	rs6589582	116,958,484	C	A	0.204519	-0.030008	0.002493	2.4E-33
SIK3	11	rs12420857	116,958,726	T	G	0.099280	-0.052595	0.003346	9.8E-59
SIK3	11	rs7120706	116,959,371	C	T	0.204516	-0.030002	0.002493	2.5E-33

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIK3	11	rs7120963	116,959,545	C	T	0.204516	-0.030002	0.002493	2.5E-33
SIK3	11	rs11216199	116,960,300	T	C	0.099244	-0.052530	0.003347	1.4E-58
SIK3	11	rs145400227	116,960,788	CAGTAA ²	C	0.099241	-0.052562	0.003347	1.2E-58
SIK3	11	rs11216200	116,961,127	T	C	0.136764	-0.044458	0.002916	1.8E-56
SIK3	11	rs7112967	116,961,196	T	C	0.049881	0.052158	0.004603	5.3E-31
SIK3	11	rs10892051	116,962,002	A	C	0.099232	-0.052601	0.003347	9.7E-59
SIK3	11	rs117157737	116,962,297	T	G	0.017142	-0.060706	0.007763	1.4E-15
SIK3	11	rs56134734	116,962,339	A	G	0.049886	0.052049	0.004603	6.9E-31
SIK3	11	rs61905677	116,962,939	G	T	0.049886	0.052049	0.004603	6.9E-31
SIK3	11	rs493134	116,962,963	T	C	0.471246	-0.034750	0.002020	2.4E-68
SIK3	11	rs10502222	116,963,014	T	C	0.184921	-0.032306	0.002593	6.6E-36
SIK3	11	rs145388534	116,963,492	T	C	0.012734	0.055926	0.008965	1.4E-10
SIK3	11	rs10892052	116,963,597	A	G	0.184909	-0.032296	0.002594	6.8E-36
SIK3	11	rs61905678	116,964,069	T	C	0.049890	0.051993	0.004603	7.8E-31
SIK3	11	rs61905679	116,964,071	T	C	0.049890	0.051993	0.004603	7.8E-31
SIK3	11	rs1815789	116,964,237	C	T	0.186956	-0.018142	0.002570	1.2E-13
SIK3	11	rs1815788	116,964,255	C	T	0.186921	-0.018137	0.002570	1.2E-13
SIK3	11	rs201165469	116,964,853	G	GC	0.099346	-0.052657	0.003345	5.7E-59
SIK3	11	rs61905680	116,965,315	A	G	0.049890	0.051993	0.004603	7.8E-31
SIK3	11	rs76930628	116,965,385	T	A	0.020545	-0.051917	0.007092	1.9E-13
SIK3	11	rs61905681	116,965,493	C	A	0.049890	0.051993	0.004603	7.8E-31
SIK3	11	rs2513097	116,965,496	G	A	0.265664	-0.019571	0.002275	4.8E-19
SIK3	11	rs77320801	116,965,633	T	C	0.049883	0.052054	0.004603	7.0E-31
SIK3	11	rs761823852	116,965,753	A	AT	0.042507	0.052996	0.005030	4.6E-27
SIK3	11	rs78044162	116,966,737	T	C	0.136651	-0.044394	0.002917	3.3E-56
SIK3	11	rs9971422	116,966,657	C	T	0.136128	-0.044305	0.002924	5.7E-56
SIK3	11	rs113224863	116,966,687	G	GT	0.186478	-0.018050	0.002574	1.3E-13
SIK3	11	rs1241655	116,967,092	T	G	0.266270	-0.019272	0.002274	1.5E-18
SIK3	11	rs12281729	116,967,414	C	A	0.099250	-0.052567	0.003348	1.2E-58
SIK3	11	rs7941927	116,968,188	G	A	0.187004	-0.018109	0.002570	1.1E-13
SIK3	11	rs149144614	116,968,288	A	G	0.044994	0.053950	0.004851	5.2E-30
SIK3	11	rs12417152	116,968,577	C	G	0.099068	-0.052647	0.003352	1.1E-58
SIK3	11	rs11823013	116,968,819	C	T	0.049878	0.052032	0.004604	7.2E-31
SIK3	11	rs11216204	116,968,898	A	G	0.099049	-0.052726	0.003352	7.4E-59
SIK3	11	rs1241657	116,969,045	T	C	0.312384	0.043217	0.002175	1.6E-90
SIK3	11	rs12272305	116,969,222	A	G	0.095767	-0.052866	0.003411	2.8E-57
SIK3	11	rs12279266	116,969,317	C	T	0.098479	-0.052358	0.003362	8.8E-58
SIK3	11	rs201227770	116,969,542	T	3GCATTT	0.035938	0.053388	0.005449	9.1E-24
SIK3	11	rs59294170	116,970,730	T	A	0.049869	0.052170	0.004604	5.2E-31
SIK3	11	rs12418324	116,971,960	T	C	0.099002	-0.052620	0.003352	1.3E-58
SIK3	11	rs11216206	116,972,709	G	C	0.313021	-0.025507	0.002165	1.2E-33
SIK3	11	rs17120197	116,974,388	C	T	0.050021	0.052217	0.004596	3.6E-31
SIK3	11	chr11:116974556_C_CTGTT	116,974,556	CTGTT	C	0.099173	-0.052818	0.003349	4.1E-59
SIK3	11	rs74927399	116,975,550	C	T	0.099182	-0.052848	0.003349	3.5E-59
SIK3	11	rs76949321	116,975,627	A	G	0.099182	-0.052848	0.003349	3.5E-59
SIK3	11	rs11216209	116,977,470	C	T	0.099194	-0.052873	0.003349	3.0E-59
SIK3	11	rs11216210	116,977,613	T	G	0.136911	-0.044114	0.002912	1.2E-55
SIK3	11	rs7109876	116,977,932	A	C	0.050044	0.052215	0.004595	3.4E-31
SIK3	11	rs509171	116,978,141	T	C	0.266412	-0.019118	0.002268	2.7E-18
SIK3	11	chr11:116978213_C_CA	116,978,213	CA	C	0.169882	-0.037471	0.002704	3.8E-45
SIK3	11	rs11216212	116,979,635	A	T	0.099194	-0.052873	0.003349	3.0E-59
SIK3	11	rs146178826	116,980,651	G	A	0.099194	-0.052873	0.003349	3.0E-59
SIK3	11	rs7358350	116,980,892	C	T	0.136911	-0.044114	0.002912	1.2E-55
SIK3	11	rs4938321	116,981,791	T	C	0.187309	-0.017942	0.002566	1.8E-13
SIK3	11	rs11216215	116,981,971	A	T	0.099194	-0.052873	0.003349	3.0E-59
SIK3	11	rs3863304	116,982,407	A	G	0.201331	-0.031038	0.002513	3.2E-35
SIK3	11	rs3863305	116,982,408	T	C	0.201331	-0.031038	0.002513	3.2E-35
SIK3	11	rs3863306	116,982,497	T	C	0.202624	-0.029578	0.002504	2.8E-32
SIK3	11	rs7131351	116,982,890	A	G	0.202149	-0.028964	0.002506	5.8E-31
SIK3	11	rs7117123	116,982,970	A	T	0.192610	-0.028404	0.002563	1.0E-28
SIK3	11	rs10128690	116,983,206	A	G	0.093599	-0.052149	0.003457	2.3E-54
SIK3	11	rs10128570	116,983,305	G	A	0.099194	-0.052873	0.003349	3.0E-59
SIK3	11	rs10128571	116,983,465	G	A	0.099194	-0.052873	0.003349	3.0E-59
SIK3	11	rs113184611	116,984,048	A	C	0.050043	0.052243	0.004595	3.3E-31
SIK3	11	chr11:116984050_C_CAAA	116,984,050	CAAA	C	0.024794	0.045549	0.006595	1.4E-12
SIK3	11	rs374519262	116,984,705	A	AC	0.118240	-0.045316	0.003145	4.7E-50
SIK3	11	rs146725667	116,985,530	A	G	0.033798	-0.050745	0.005549	2.5E-21
SIK3	11	rs12287768	116,985,606	C	A	0.099194	-0.052820	0.003349	4.0E-59
SIK3	11	rs588918	116,985,926	C	T	0.471677	-0.034144	0.002017	2.7E-66
SIK3	11	rs12274771	116,985,982	G	C	0.099193	-0.052816	0.003349	4.1E-59
SIK3	11	rs12274773	116,985,993	T	C	0.099193	-0.052816	0.003349	4.1E-59
SIK3	11	rs75212922	116,986,276	A	T	0.099193	-0.052816	0.003349	4.1E-59
SIK3	11	rs10892053	116,986,287	T	C	0.203449	-0.029193	0.002495	1.1E-31
SIK3	11	rs11216217	116,986,936	A	G	0.099193	-0.052816	0.003349	4.1E-59
SIK3	11	chr11:116987321_TAA_T	116,987,321	T	TAA	0.100920	-0.050665	0.003332	4.1E-55
SIK3	11	rs201445271	116,987,332	AC	A	0.049783	0.050554	0.004615	3.2E-29
SIK3	11	rs10160754	116,988,278	C	A	0.136900	-0.044081	0.002913	1.4E-55
SIK3	11	rs10160755	116,988,287	G	A	0.136900	-0.044081	0.002913	1.4E-55
SIK3	11	rs11406946	116,988,385	CA	C	0.206460	-0.030627	0.002488	5.1E-35
SIK3	11	rs519794	116,988,737	C	T	0.472187	-0.034465	0.002018	2.1E-67
SIK3	11	rs10706688	116,989,575	T	TA	0.202671	-0.028867	0.002503	9.0E-31
SIK3	11	rs7939934	116,990,552	T	A	0.188447	-0.018232	0.002564	7.2E-14
SIK3	11	rs61905687	116,991,428	C	T	0.050073	0.052152	0.004593	4.0E-31
SIK3	11	rs80242245	116,991,529	G	C	0.099190	-0.052830	0.003349	3.8E-59
SIK3	11	rs11216218	116,991,945	T	C	0.099190	-0.052830	0.003349	3.8E-59
SIK3	11	rs11216219	116,992,039	T	C	0.099190	-0.052830	0.003349	3.8E-59
SIK3	11	rs607273	116,992,102	A	T	0.311564	0.043694	0.002168	6.3E-93
SIK3	11	rs12272973	116,992,331	C	A	0.099783	-0.053124	0.003351	9.2E-60
SIK3	11	rs10128682	116,992,742	T	C	0.099326	-0.052966	0.003346	1.3E-59
SIK3	11	rs6589583	116,993,050	T	C	0.266624	-0.019124	0.002266	2.5E-18
SIK3	11	rs7130531	116,993,117	T	C	0.050073	0.052152	0.004593	4.0E-31
SIK3	11	rs11216220	116,993,272	C	T	0.136909	-0.044044	0.002912	1.7E-55
SIK3	11	rs11375002	116,993,436	CA	C	0.472603	-0.034548	0.002016	7.8E-68
SIK3	11	rs75826529	116,994,384	A	T	0.099326	-0.052966	0.003346	1.3E-59
SIK3	11	rs74460214	116,994,491	C	T	0.099326	-0.052966	0.003346	1.3E-59
SIK3	11	rs79349393	116,994,651	G	A	0.099326	-0.052966	0.003346	1.3E-59
SIK3	11	rs7931665	116,995,524	G	A	0.137027	-0.044196	0.002911	5.5E-56

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
SIK3	11	rs7931770	116,995,574	T	C	0.471390	-0.034106	0.002015	3.1E-66
SIK3	11	rs7121347	116,996,493	T	G	0.471390	-0.034106	0.002015	3.1E-66
SIK3	11	rs11604866	116,996,798	T	C	0.099326	-0.052966	0.003346	1.3E-59
SIK3	11	rs10892054	116,997,505	T	C	0.187344	-0.017988	0.002565	1.5E-13
SIK3	11	rs10892055	116,997,655	A	G	0.187344	-0.017988	0.002565	1.5E-13
SIK3	11	rs7950213	116,997,938	A	C	0.050082	0.052156	0.004593	3.9E-31
SIK3	11	rs61905689	116,998,501	T	C	0.087750	0.024967	0.003537	2.3E-12
SIK3	11	chr11:116999579_G_GTTTTC	116,999,579	GTTTTC	G	0.050082	0.052156	0.004593	3.9E-31
SIK3	11	rs10892056	116,999,695	C	G	0.099326	-0.052966	0.003346	1.3E-59
SIK3	11	rs10502224	116,999,764	G	A	0.137044	-0.044161	0.002912	6.9E-56
SIK3	11	rs7930264	117,000,050	A	G	0.266695	-0.019082	0.002266	3.0E-18
SIK3	11	rs17120233	117,000,507	G	A	0.050082	0.052156	0.004593	3.9E-31
SIK3	11	rs10892057	117,001,318	C	A	0.137640	-0.044242	0.002910	3.7E-56
SIK3	11	chr11:117001505_C_CA	117,001,505	CA	C	0.280988	-0.028278	0.002247	2.6E-36
SIK3	11	rs75858236	117,001,547	G	A	0.050086	0.052116	0.004593	4.4E-31
SIK3	11	rs12278943	117,003,642	C	T	0.099193	-0.052852	0.003349	3.4E-59
SIK3	11	rs7946390	117,004,436	G	A	0.137027	-0.044162	0.002911	6.5E-56
SIK3	11	rs6589587	117,004,622	G	T	0.187360	-0.017962	0.002565	1.6E-13
SIK3	11	rs11216224	117,005,208	C	T	0.135810	-0.043950	0.002925	7.0E-55
SIK3	11	rs7114963	117,005,267	C	T	0.467103	-0.034175	0.002025	4.6E-66
SIK3	11	rs1940625	117,005,726	G	A	0.137026	-0.044159	0.002911	6.6E-56
SIK3	11	rs10892058	117,005,905	T	C	0.202853	-0.029308	0.002496	7.4E-32
SIK3	11	rs10790169	117,006,443	C	A	0.471678	-0.034277	0.002014	5.8E-67
SIK3	11	rs77250716	117,006,637	C	T	0.049578	0.052307	0.004617	5.8E-31
SIK3	11	rs11216225	117,007,298	G	A	0.137026	-0.044159	0.002911	6.6E-56
SIK3	11	rs11216226	117,007,350	G	C	0.099327	-0.052968	0.003346	1.3E-59
SIK3	11	rs11216227	117,007,881	G	C	0.203019	-0.029417	0.002497	4.6E-32
SIK3	11	rs12276805	117,008,043	C	T	0.097255	-0.054273	0.003385	8.4E-61
SIK3	11	rs57278884	117,008,464	AAAAGA	C	0.187424	-0.018035	0.002564	1.3E-13
SIK3	11	chr11:117008471_G_GAAAAAGAT	117,008,471	AAAAAGA	G	0.187253	-0.018266	0.002567	7.3E-14
SIK3	11	rs12271319	117,008,508	T	C	0.137029	-0.044160	0.002911	6.5E-56
SIK3	11	rs12284696	117,008,803	G	A	0.136151	-0.044024	0.002922	3.4E-55
SIK3	11	rs7931398	117,008,960	C	T	0.267274	-0.019114	0.002264	2.6E-18
SIK3	11	rs117901629	117,008,963	A	G	0.099201	-0.052818	0.003349	3.9E-59
SIK3	11	rs138181556	117,009,007	A	G	0.099197	-0.052849	0.003349	3.4E-59
SIK3	11	rs7112937	117,009,740	C	T	0.137046	-0.044153	0.002911	6.7E-56
SIK3	11	rs61905691	117,009,987	G	A	0.050086	0.052116	0.004593	4.4E-31
SIK3	11	rs7127881	117,010,082	A	G	0.206830	-0.029425	0.002495	4.8E-32
SIK3	11	rs58176010	117,010,731	A	G	0.019097	0.077242	0.007349	3.7E-27
SIK3	11	rs10892059	117,010,929	A	G	0.203076	-0.029239	0.002494	9.3E-32
SIK3	11	rs10892060	117,010,946	A	C	0.202724	-0.029091	0.002497	2.2E-31
SIK3	11	rs4245168	117,011,922	A	C	0.471282	-0.034244	0.002013	6.5E-67
SIK3	11	rs35123861	117,012,098	CA	C	0.203796	-0.029346	0.002492	5.6E-32
SIK3	11	rs7125788	117,012,680	C	T	0.050082	0.052092	0.004593	4.7E-31
SIK3	11	rs1442498591	117,012,824	AG	A	0.165085	-0.029922	0.002754	3.8E-28
SIK3	11	chr11:117012827_G_GTT	117,012,827	GTT	G	0.099274	-0.052953	0.003347	1.4E-59
SIK3	11	rs10790170	117,012,828	G	T	0.204073	-0.029795	0.002499	1.0E-32
SIK3	11	rs61905705	117,013,060	T	A	0.050086	0.052062	0.004593	5.2E-31
SIK3	11	rs61905706	117,013,061	T	G	0.050086	0.052062	0.004593	5.2E-31
SIK3	11	rs140947361	117,013,808	A	AC	0.050086	0.052062	0.004593	5.2E-31
SIK3	11	rs374772197	117,013,968	C	T	0.049985	0.051996	0.004597	7.0E-31
SIK3	11	rs11216230	117,014,073	A	G	0.173780	-0.027144	0.002674	3.1E-24
SIK3	11	rs35190172	117,014,597	T	TC	0.050086	0.052062	0.004593	5.2E-31
SIK3	11	rs7119185	117,015,380	T	C	0.187381	-0.018087	0.002565	1.0E-13
SIK3	11	rs10892061	117,015,398	T	C	0.203580	-0.029453	0.002494	3.7E-32
SIK3	11	chr11:117015578_AT_A	117,015,578	A	AT	0.266746	-0.019183	0.002265	1.9E-18
SIK3	11	rs79870586	117,016,005	A	G	0.099289	-0.052885	0.003346	1.8E-59
SIK3	11	rs66751419	117,017,528	T	TG	0.203800	-0.029537	0.002495	2.5E-32
SIK3	11	rs7128772	117,018,695	A	T	0.262205	-0.019174	0.002289	5.7E-18
SIK3	11	rs80054374	117,019,951	G	A	0.099292	-0.052905	0.003346	1.6E-59
SIK3	11	rs12808524	117,020,277	C	T	0.203715	-0.029341	0.002494	6.5E-32
SIK3	11	rs17120237	117,020,330	C	T	0.050090	0.052033	0.004593	5.7E-31
SIK3	11	rs77955134	117,021,652	A	G	0.099159	-0.052790	0.003349	4.1E-59
SIK3	11	rs77594377	117,021,730	A	G	0.099146	-0.052819	0.003349	3.6E-59
SIK3	11	rs112619870	117,021,940	C	A	0.026892	0.052040	0.006289	3.2E-17
SIK3	11	rs142310263	117,022,278	T	AATCTCA	0.098260	-0.052712	0.003365	2.2E-58
SIK3	11	rs4936359	117,023,008	A	T	0.050088	0.052027	0.004593	5.7E-31
SIK3	11	rs4936360	117,023,053	C	G	0.050088	0.052028	0.004593	5.7E-31
SIK3	11	rs10466590	117,023,697	G	C	0.260612	-0.019390	0.002295	2.0E-18
SIK3	11	rs143791312	117,024,639	T	C	0.062840	-0.049218	0.004132	2.5E-34
SIK3	11	rs11216239	117,024,796	G	C	0.266685	-0.019280	0.002265	1.3E-18
SIK3	11	rs10892063	117,025,439	C	A	0.204313	-0.029110	0.002490	2.0E-31
SIK3	11	rs111860754	117,025,569	C	CA	0.050083	0.052188	0.004592	3.5E-31
SIK3	11	rs10892064	117,025,837	C	G	0.203822	-0.029194	0.002490	9.8E-32
SIK3	11	rs145746824	117,025,856	G	A	0.020543	-0.042394	0.007073	2.2E-09
SIK3	11	rs2186844	117,026,197	T	C	0.099165	-0.052788	0.003349	4.2E-59
SIK3	11	rs10892065	117,026,308	C	T	0.203822	-0.029194	0.002490	9.8E-32
SIK3	11	rs61905709	117,027,118	T	C	0.050085	0.052199	0.004592	3.6E-31
SIK3	11	rs4936361	117,027,438	C	T	0.181570	-0.017254	0.002611	5.5E-12
SIK3	11	rs4938325	117,027,763	A	G	0.050091	0.052278	0.004591	2.8E-31
SIK3	11	rs7950364	117,028,170	G	C	0.471056	-0.034358	0.002013	2.7E-67
SIK3	11	rs11216240	117,028,532	T	A	0.266697	-0.019182	0.002264	2.0E-18
SIK3	11	rs11216241	117,028,533	C	A	0.266724	-0.019194	0.002264	1.8E-18
SIK3	11	rs12289032	117,028,864	T	C	0.099174	-0.052813	0.003349	3.6E-59
SIK3	11	rs141750997	117,028,962	GCTGGA1	A	0.186441	-0.017884	0.002572	2.3E-13
SIK3	11	rs7926104	117,029,066	A	G	0.203531	-0.029393	0.002492	4.4E-32
SIK3	11	rs112120205	117,029,070	A	G	0.050091	0.052278	0.004591	2.8E-31
SIK3	11	rs146943088	117,029,109	C	A	0.099174	-0.052813	0.003349	3.6E-59
SIK3	11	rs11600552	117,030,231	C	T	0.266720	-0.019228	0.002264	1.6E-18
SIK3	11	rs11216242	117,030,833	A	G	0.203542	-0.029409	0.002492	3.9E-32
SIK3	11	rs7112191	117,031,340	A	G	0.050086	0.052223	0.004592	3.4E-31
SIK3	11	chr11:117031495_C_CATTTT	117,031,495	CATTTT	C	0.471065	-0.034379	0.002013	2.2E-67
SIK3	11	rs199986368	117,031,627	C	T	0.015185	0.127260	0.008230	2.7E-55
SIK3	11	rs7481286	117,031,656	T	G	0.099293	-0.052856	0.003346	1.9E-59
SIK3	11	rs12804122	117,031,900	G	C	0.203528	-0.029169	0.002492	1.1E-31
SIK3	11	rs4548653	117,032,600	A	G	0.187360	-0.018071	0.002564	1.1E-13
SIK3	11	rs7941428	117,032,668	G	C	0.265022	-0.018245	0.002274	1.2E-16

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIK3	11	chr11:117032674_CTT_C	117,032,674	C	CTT	0.105414	-0.051582	0.003275	3.4E-59
SIK3	11	rs4575311	117,033,641	A	G	0.203585	-0.029433	0.002492	3.2E-32
SIK3	11	rs4938326	117,034,748	C	G	0.050086	0.052223	0.004592	3.4E-31
SIK3	11	rs187437651	117,034,813	A	G	0.018519	0.080912	0.007494	1.0E-27
SIK3	11	rs147518949	117,035,258	A	G	0.018519	0.080907	0.007494	1.0E-27
SIK3	11	rs4938327	117,036,012	C	T	0.187417	-0.018060	0.002563	1.1E-13
SIK3	11	rs3181	117,036,327	A	G	0.187432	-0.018036	0.002563	1.1E-13
SIK3	11	rs10732856	117,036,397	C	T	0.471454	-0.034295	0.002012	3.5E-67
SIK3	11	rs721783	117,036,733	T	C	0.187478	-0.018166	0.002563	7.7E-14
SIK3	11	rs75216569	117,036,999	G	A	0.099315	-0.052818	0.003346	2.7E-59
SIK3	11	rs7115242	117,037,567	A	G	0.312989	0.043102	0.002158	1.7E-91
SIK3	11	rs7118591	117,037,741	A	C	0.187438	-0.018087	0.002563	9.8E-14
SIK3	11	chr11:117037793_AAC_A	117,037,793	A	AAC	0.187438	-0.018087	0.002563	9.8E-14
SIK3	11	rs80273401	117,037,990	C	T	0.099315	-0.052818	0.003346	2.7E-59
SIK3	11	rs61905712	117,038,577	A	G	0.050130	0.052106	0.004591	4.9E-31
SIK3	11	rs112870705	117,038,708	T	TCAC	0.049881	0.051708	0.004603	1.4E-30
SIK3	11	rs61905713	117,038,713	T	C	0.049881	0.051708	0.004603	1.4E-30
SIK3	11	rs147501797	117,038,982	A	G	0.034507	-0.038398	0.005502	7.1E-13
SIK3	11	rs12273536	117,040,255	T	C	0.096592	-0.052722	0.003388	2.3E-57
SIK3	11	rs12273545	117,040,296	T	C	0.096592	-0.052722	0.003388	2.3E-57
SIK3	11	rs77999164	117,041,401	T	C	0.096603	-0.052738	0.003388	2.0E-57
SIK3	11	rs58194633	117,041,909	C	CT	0.263471	-0.018953	0.002274	8.7E-18
SIK3	11	rs11216244	117,042,014	T	C	0.264023	-0.018635	0.002271	2.5E-17
SIK3	11	rs11216245	117,042,486	T	C	0.264023	-0.018635	0.002271	2.5E-17
SIK3	11	rs80143284	117,042,854	A	C	0.096731	-0.052816	0.003386	1.0E-57
SIK3	11	rs12279066	117,043,193	G	C	0.263875	-0.018626	0.002272	2.6E-17
SIK3	11	rs17120241	117,044,304	C	T	0.050114	0.052112	0.004591	4.5E-31
SIK3	11	rs11351498	117,044,488	T	TA	0.263714	-0.018576	0.002274	3.6E-17
SIK3	11	rs2155583	117,044,501	G	A	0.471212	-0.034422	0.002013	1.3E-67
SIK3	11	chr11:117044615_GA_G	117,044,615	G	GA	0.219909	-0.028273	0.002470	2.7E-30
SIK3	11	rs2000614	117,045,026	T	C	0.471122	-0.034422	0.002013	1.3E-67
SIK3	11	rs2000615	117,045,103	T	C	0.471122	-0.034422	0.002013	1.3E-67
SIK3	11	rs2000616	117,045,813	T	C	0.471119	-0.034422	0.002013	1.3E-67
SIK3	11	rs76972960	117,045,962	C	T	0.050114	0.052112	0.004591	4.5E-31
SIK3	11	rs10750100	117,046,528	C	T	0.471116	-0.034418	0.002013	1.3E-67
SIK3	11	rs61905716	117,048,351	T	C	0.050114	0.052119	0.004591	4.4E-31
SIK3	11	rs12280172	117,048,557	A	G	0.097309	-0.051814	0.003378	8.9E-56
SIK3	11	rs112151056	117,048,652	A	G	0.050114	0.052119	0.004591	4.4E-31
SIK3	11	rs61905718	117,048,961	T	C	0.050114	0.052119	0.004591	4.4E-31
SIK3	11	rs75890305	117,049,253	G	A	0.096622	-0.052741	0.003388	2.0E-57
SIK3	11	rs142341972	117,049,453	T	C	0.140369	-0.022612	0.002905	2.2E-15
SIK3	11	chr11:117049961_T_TA	117,049,961	TA	T	0.473562	-0.034840	0.002023	1.6E-68
SIK3	11	rs11826651	117,049,977	A	T	0.050120	0.052087	0.004590	4.8E-31
SIK3	11	rs10892066	117,050,211	T	C	0.264020	-0.018591	0.002271	2.9E-17
SIK3	11	rs4938328	117,050,503	T	G	0.206729	-0.029931	0.002478	7.5E-34
SIK3	11	rs1815786	117,050,674	T	C	0.312810	0.043147	0.002165	7.1E-91
SIK3	11	rs1815787	117,050,681	C	T	0.471432	-0.034423	0.002013	1.2E-67
SIK3	11	rs138470332	117,051,591	T	C	0.018753	-0.061930	0.007396	1.9E-17
SIK3	11	rs111530588	117,051,870	A	G	0.096621	-0.052742	0.003388	2.0E-57
SIK3	11	rs61905719	117,051,998	T	C	0.050120	0.052087	0.004590	4.8E-31
SIK3	11	rs564325746	117,052,134	TG	T	0.092523	0.026674	0.003545	3.5E-14
SIK3	11	rs7130297	117,053,154	T	C	0.469796	-0.035390	0.002014	2.1E-71
SIK3	11	rs11216250	117,053,284	T	C	0.095873	-0.052450	0.003402	2.4E-56
SIK3	11	rs80259223	117,053,602	A	G	0.050997	0.050304	0.004557	1.7E-29
SIK3	11	rs3886960	117,054,274	T	G	0.263975	-0.018556	0.002271	3.5E-17
SIK3	11	rs723955	117,054,326	A	G	0.263975	-0.018556	0.002271	3.5E-17
SIK3	11	rs7108912	117,055,280	A	G	0.263977	-0.018558	0.002271	3.5E-17
SIK3	11	rs201829635	117,056,603	T	TC	0.049434	0.051456	0.004622	4.6E-30
SIK3	11	rs117091722	117,056,884	A	G	0.062764	-0.055747	0.004146	2.6E-42
SIK3	11	rs10790172	117,057,024	T	G	0.473252	-0.035052	0.002022	3.1E-69
SIK3	11	rs10892067	117,057,046	C	G	0.096721	-0.052873	0.003386	8.0E-58
SIK3	11	rs7124872	117,057,235	G	A	0.264092	-0.018529	0.002271	3.9E-17
SIK3	11	rs7124996	117,057,290	T	C	0.264092	-0.018529	0.002271	3.9E-17
SIK3	11	rs4938329	117,057,396	T	C	0.264085	-0.018496	0.002271	4.3E-17
SIK3	11	rs11216252	117,057,507	A	G	0.096614	-0.052774	0.003388	1.8E-57
SIK3	11	rs11216253	117,057,509	C	A	0.096614	-0.052774	0.003388	1.8E-57
SIK3	11	rs4938330	117,057,798	G	C	0.226542	-0.017797	0.002392	4.4E-14
SIK3	11	rs10892068	117,057,830	T	C	0.096719	-0.052863	0.003386	8.4E-58
SIK3	11	rs9943680	117,058,538	C	T	0.187275	-0.027572	0.002626	5.5E-26
SIK3	11	rs11216255	117,059,279	G	A	0.264157	-0.018526	0.002272	4.0E-17
SIK3	11	rs34992009	117,059,421	G	GC	0.206180	-0.030201	0.002483	2.8E-34
SIK3	11	rs4938331	117,059,966	A	C	0.206085	-0.030083	0.002483	4.7E-34
SIK3	11	rs4938332	117,060,082	G	A	0.206180	-0.030189	0.002483	2.9E-34
SIK3	11	rs4938333	117,060,172	G	A	0.050136	0.052161	0.004589	3.8E-31
SIK3	11	rs4938334	117,060,326	C	G	0.206344	-0.030169	0.002484	3.4E-34
SIK3	11	rs61903394	117,061,182	A	G	0.050133	0.052161	0.004589	3.8E-31
SIK3	11	rs11216257	117,061,845	T	C	0.372653	-0.017185	0.002081	1.0E-16
SIK3	11	rs6589590	117,065,365	C	A	0.207079	-0.029867	0.002478	1.0E-33
SIK3	11	rs56751865	117,066,155	T	C	0.115631	-0.046567	0.003152	1.3E-52
SIK3	11	rs112895963	117,066,443	T	A	0.049536	0.052560	0.004618	3.4E-31
SIK3	11	rs79955870	117,066,645	T	C	0.097440	-0.053160	0.003383	1.4E-58
SIK3	11	rs35187263	117,067,811	AC	A	0.205342	-0.031422	0.002485	4.4E-37
SIK3	11	rs368388328	117,069,182	T	TTTG	0.040781	0.049230	0.005093	2.8E-23
SIK3	11	rs11216261	117,069,494	C	T	0.096501	-0.052811	0.003391	1.7E-57
SIK3	11	rs12280210	117,069,733	C	T	0.134307	-0.043702	0.002937	8.6E-54
SIK3	11	rs9971421	117,070,824	T	C	0.095217	-0.052817	0.003416	7.2E-57
SIK3	11	rs61903398	117,070,897	T	C	0.049984	0.052274	0.004597	3.5E-31
SIK3	11	rs144942164	117,071,184	C	T	0.039195	0.053234	0.005198	1.1E-25
SIK3	11	rs202154722	117,071,196	AT	A	0.096480	-0.052601	0.003393	4.7E-57
SIK3	11	rs7101763	117,071,269	T	G	0.184331	-0.017316	0.002583	1.5E-12
SIK3	11	rs17120280	117,071,416	A	G	0.051316	0.050733	0.004545	8.3E-30
SIK3	11	rs77182215	117,071,650	A	C	0.085276	0.039752	0.003611	1.8E-28
SIK3	11	rs61903399	117,071,759	T	A	0.049536	0.052447	0.004619	3.9E-31
SIK3	11	chr11:117071926_G_GTGTT	117,071,926	GTGTT	G	0.200699	-0.031446	0.002519	6.6E-36
SIK3	11	rs116582417	117,072,350	A	G	0.096369	-0.052842	0.003393	1.8E-57
SIK3	11	rs1351452	117,072,638	C	A	0.471640	-0.034355	0.002015	2.4E-67
SIK3	11	rs7109649	117,072,828	T	C	0.263868	-0.018446	0.002274	5.1E-17

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIK3	11	rs1531706	117,073,236	A	C	0.263868	-0.018446	0.002274	5.1E-17
SIK3	11	rs77400241	117,073,331	T	C	0.017171	-0.058432	0.007751	1.7E-14
SIK3	11	rs7935913	117,073,632	A	G	0.263868	-0.018446	0.002274	5.1E-17
SIK3	11	rs7935834	117,073,721	G	C	0.263868	-0.018446	0.002274	5.1E-17
SIK3	11	rs1531707	117,073,996	A	G	0.263865	-0.018440	0.002274	5.2E-17
SIK3	11	rs17120293	117,074,130	C	T	0.096387	-0.052765	0.003393	2.4E-57
SIK3	11	rs191035489	117,074,759	T	C	0.011064	0.053975	0.009633	1.8E-08
SIK3	11	rs4620758	117,075,002	A	G	0.184156	-0.017178	0.002584	2.3E-12
SIK3	11	rs59511712	117,075,046	T	C	0.087487	0.024914	0.003544	3.4E-12
SIK3	11	rs12274388	117,075,522	T	C	0.261618	-0.017794	0.002286	8.8E-16
SIK3	11	rs7130213	117,075,936	A	C	0.183737	-0.017344	0.002587	1.4E-12
SIK3	11	rs12274725	117,076,137	T	C	0.096362	-0.052858	0.003393	1.7E-57
SIK3	11	rs7484045	117,076,174	T	C	0.263882	-0.018476	0.002274	4.6E-17
SIK3	11	rs11216265	117,076,464	C	T	0.096362	-0.052858	0.003393	1.7E-57
SIK3	11	rs12418036	117,076,590	A	G	0.096362	-0.052858	0.003393	1.7E-57
SIK3	11	rs4938335	117,076,645	C	A	0.471269	-0.034387	0.002016	2.3E-67
SIK3	11	rs4938336	117,077,726	G	A	0.049973	0.052104	0.004597	5.6E-31
SIK3	11	rs10082609	117,078,358	T	C	0.256127	-0.017498	0.002303	4.4E-15
SIK3	11	chr11:117078990_TA_T	117,078,990	T	TA	0.262200	-0.015366	0.002319	2.0E-12
SIK3	11	rs11216266	117,079,434	C	T	0.263861	-0.018443	0.002274	5.2E-17
SIK3	11	rs10736487	117,079,516	G	A	0.472632	-0.033946	0.002015	7.6E-66
SIK3	11	rs56777911	117,080,329	C	CT	0.263863	-0.018445	0.002274	5.1E-17
SIK3	11	rs7106662	117,080,669	C	T	0.263863	-0.018445	0.002274	5.1E-17
SIK3	11	rs10892070	117,080,817	A	G	0.220221	-0.029442	0.002437	8.0E-34
SIK3	11	rs10082561	117,080,868	C	A	0.091322	-0.051554	0.003476	2.8E-52
SIK3	11	rs4936362	117,081,484	T	C	0.049971	0.052008	0.004598	7.2E-31
SIK3	11	rs11216267	117,081,676	T	C	0.207874	-0.029143	0.002474	2.7E-32
SIK3	11	rs144977225	117,082,379	C	CCCA	0.263863	-0.018434	0.002274	5.3E-17
SIK3	11	rs11216270	117,082,928	A	C	0.096355	-0.052920	0.003394	1.3E-57
SIK3	11	rs1871756	117,082,929	A	G	0.184285	-0.017273	0.002583	1.7E-12
SIK3	11	rs10892071	117,083,849	T	C	0.263865	-0.018422	0.002274	5.6E-17
SIK3	11	rs61903416	117,084,333	C	T	0.267118	-0.018917	0.002268	6.5E-18
SIK3	11	rs2368149	117,085,218	A	G	0.096252	-0.052872	0.003396	2.1E-57
SIK3	11	rs61903417	117,085,441	G	T	0.049965	0.052020	0.004598	7.2E-31
SIK3	11	rs61903418	117,085,949	A	G	0.049962	0.052039	0.004598	7.0E-31
SIK3	11	rs12281358	117,086,274	C	T	0.096245	-0.052881	0.003396	2.0E-57
SIK3	11	rs12274465	117,086,473	T	C	0.263563	-0.018579	0.002276	3.3E-17
SIK3	11	rs6589592	117,087,191	C	G	0.308668	0.043515	0.002183	4.3E-91
SIK3	11	rs12277910	117,087,817	A	C	0.164592	-0.021466	0.002723	6.4E-16
SIK3	11	rs111901638	117,089,132	A	G	0.050010	0.052020	0.004596	7.0E-31
SIK3	11	rs10892072	117,089,597	A	G	0.207554	-0.029228	0.002477	2.0E-32
SIK3	11	rs11823918	117,089,781	C	G	0.050013	0.051995	0.004596	7.5E-31
SIK3	11	rs77431162	117,090,820	T	C	0.068680	0.040568	0.003958	2.7E-26
SIK3	11	rs61903421	117,091,086	T	A	0.050013	0.051993	0.004596	7.6E-31
SIK3	11	rs116861530	117,091,945	A	G	0.094923	-0.053140	0.003419	2.9E-57
SIK3	11	rs74420345	117,092,561	A	C	0.094923	-0.053186	0.003419	2.3E-57
SIK3	11	rs7946869	117,092,596	T	C	0.087399	0.025138	0.003545	2.3E-12
SIK3	11	rs7950093	117,092,803	T	G	0.262620	-0.018429	0.002279	6.3E-17
SIK3	11	rs7950381	117,093,181	A	C	0.049993	0.052071	0.004597	6.3E-31
SIK3	11	rs7950501	117,093,249	T	C	0.049993	0.052071	0.004597	6.3E-31
SIK3	11	rs57383565	117,093,678	AG	A	0.050395	0.051625	0.004587	1.5E-30
SIK3	11	rs900012	117,095,719	A	G	0.468365	-0.033813	0.002020	4.1E-65
SIK3	11	rs1320668	117,096,950	T	C	0.473357	-0.032576	0.002018	4.3E-61
SIK3	11	rs61903426	117,097,552	T	C	0.054274	0.053517	0.004427	2.0E-34
SIK3	11	rs7128071	117,098,082	A	G	0.052806	0.052837	0.004490	1.2E-32
SIK3 *	11	rs10892073	117,098,674	T	C	0.203080	-0.028729	0.002501	5.3E-31
SIK3 *	11	rs76567973	117,100,045	G	C	0.096151	-0.052785	0.003397	3.0E-57
SIK3 *	11	chr11:117100110_GT_G	117,100,110	G	GT	0.476136	-0.031919	0.002020	8.6E-59
SIK3 *	11	rs78135964	117,100,961	T	G	0.096183	-0.052716	0.003396	3.5E-57
SIK3 *	11	rs148233183	117,101,511	A	G	0.096220	-0.052657	0.003395	4.4E-57
SIK3 *	11	rs4938338	117,102,178	A	C	0.054430	0.053531	0.004419	1.8E-34
SIK3 *	11	rs4936363	117,102,219	T	C	0.054431	0.053529	0.004419	1.8E-34
SIK3 *	11	rs76942203	117,102,531	A	G	0.096249	-0.052706	0.003394	3.4E-57
SIK3 *	11	rs796725952	117,102,596	G	GA	0.018089	-0.048334	0.007525	1.1E-10
SIK3 *	11	chr11:117103138_A_AAAT	117,103,138	AAAT	A	0.096124	-0.052692	0.003399	6.0E-57
SIK3 *	11	rs12269901	117,103,213	C	G	0.268995	-0.016757	0.002258	9.6E-15
SIK3 *	11	rs149576335	117,104,420	A	G	0.096225	-0.052713	0.003394	3.2E-57
SIK3 *	11	rs11216275	117,104,988	G	T	0.092008	0.027571	0.003466	5.1E-15
SIK3 *	11	rs142395187	117,105,293	G	A	0.095620	-0.052983	0.003405	1.4E-57
SIK3 *	11	chr11:117105573_A_AT	117,105,573	AT	A	0.202437	-0.032573	0.002537	2.6E-38
SIK3 *	11	rs4388921	117,106,062	C	T	0.188486	-0.015471	0.002564	1.1E-10
SIK3 *	11	rs145671645	117,106,195	A	G	0.029016	-0.052523	0.005983	5.2E-20
SIK3 *	11	rs10160799	117,107,172	A	G	0.473503	-0.032182	0.002020	1.7E-59
SIK3 *	11	rs181104223	117,107,559	C	A	0.029310	0.072169	0.005943	3.1E-35
SIK3 *	11	rs12416941	117,108,647	A	G	0.096823	-0.051709	0.003387	2.4E-55
SIK3 *	11	rs113784559	117,108,649	G	C	0.056715	0.047445	0.004332	2.2E-28
SIK3 *	11	rs10750101	117,108,973	C	T	0.473643	-0.032204	0.002019	1.3E-59
SIK3 *	11	rs12271161	117,109,195	A	G	0.153820	-0.015275	0.002777	8.2E-09
SIK3 *	11	rs12271169	117,109,305	G	C	0.177765	-0.014967	0.002627	1.3E-09
SIK3 *	11	rs4938339	117,109,878	T	C	0.056726	0.047479	0.004332	2.0E-28
SIK3 *	11	rs4938340	117,109,906	A	G	0.057084	0.046860	0.004330	1.0E-27
SIK3 *	11	rs10892074	117,109,925	T	G	0.202747	-0.027551	0.002503	1.3E-28
SIK3 *	11	rs114221654	117,109,963	T	C	0.096823	-0.051709	0.003387	2.4E-55
SIK3 *	11	rs35172278	117,110,063	CCTG	C	0.485410	-0.033709	0.002022	4.5E-65
SIK3 *	11	rs61903427	117,110,070	C	G	0.056726	0.047479	0.004332	2.0E-28
SIK3 *	11	rs71112111	117,110,142	G	T	0.190900	-0.016938	0.002554	2.5E-12
SIK3 *	11	rs4635117	117,110,285	A	G	0.298432	0.041235	0.002215	2.1E-80
SIK3 *	11	rs148910068	117,110,595	T	C	0.018772	-0.041509	0.007401	1.5E-09
SIK3 *	11	rs6589595	117,110,619	A	G	0.056726	0.047479	0.004332	2.0E-28
SIK3 *	11	rs116770907	117,110,799	T	C	0.096823	-0.051706	0.003387	2.4E-55
SIK3 *	11	rs2127907	117,110,864	G	A	0.488260	-0.033596	0.002019	1.0E-64
SIK3 *	11	rs111677878	117,111,718	T	C	0.096807	-0.051714	0.003388	2.4E-55
SIK3 *	11	rs7104023	117,111,886	T	A	0.190853	-0.016852	0.002555	3.2E-12
SIK3 *	11	rs10892075	117,112,105	T	C	0.153789	-0.015321	0.002778	7.4E-09
SIK3 *	11	rs59700451	117,112,212	A	G	0.056723	0.047452	0.004332	2.1E-28
SIK3 *	11	rs113979111	117,112,300	A	G	0.056723	0.047447	0.004332	2.1E-28
SIK3 *	11	rs111560312	117,112,840	A	G	0.056722	0.047447	0.004332	2.1E-28

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIK3 *	11	rs55703909	117,114,150	A	G	0.056720	0.047455	0.004332	2.1E-28
SIK3 *	11	rs74882651	117,114,475	A	G	0.096803	-0.051736	0.003388	2.2E-55
SIK3 *	11	rs60834024	117,115,141	A	C	0.096815	-0.051709	0.003388	2.3E-55
SIK3 *	11	chr11:117115776_AG_A	117,115,776	A	AG	0.013985	-0.048694	0.008668	2.2E-09
SIK3 *	11	rs61903429	117,115,968	A	C	0.056731	0.047513	0.004332	1.8E-28
SIK3 *	11	rs11216277	117,116,330	A	G	0.293791	-0.027302	0.002210	1.9E-35
SIK3 *	11	rs145335872	117,116,511	A	C	0.055090	-0.047813	0.004392	1.2E-28
SIK3 *	11	rs61903430	117,116,626	C	G	0.056731	0.047521	0.004332	1.7E-28
SIK3 *	11	rs75904569	117,117,597	G	A	0.056728	0.047532	0.004332	1.7E-28
SIK3 *	11	rs80197460	117,118,074	G	C	0.096829	-0.051672	0.003387	2.8E-55
SIK3 *	11	rs10892076	117,118,220	A	G	0.292595	-0.027320	0.002214	1.7E-35
SIK3 *	11	rs74428560	117,119,266	T	C	0.056735	0.047560	0.004332	1.5E-28
SIK3 *	11	rs117300172	117,119,795	C	A	0.015625	0.073494	0.008075	4.0E-20
SIK3 *	11	chr11:117120044_G_GAAAC	117,120,044	GAAAC	G	0.429448	-0.044490	0.002038	1.8E-109
SIK3 *	11	rs200802441	117,120,056	C	A	0.415143	-0.043219	0.002072	7.9E-100
SIK3 *	11	rs12366015	117,120,135	G	A	0.429145	-0.044402	0.002037	4.4E-109
SIK3 *	11	rs138720977	117,120,356	ATAAG	A	0.288889	-0.026450	0.002229	6.7E-33
SIK3 *	11	rs142756367	117,120,357	TAAGA	T	0.293523	-0.027386	0.002211	1.2E-35
PAFAH1B2 *	11	rs74955808	117,121,969	A	G	0.097078	-0.051324	0.003383	1.2E-54
PAFAH1B2 *	11	rs71037454	117,122,203	AGAAAC	G	0.486821	-0.033372	0.002014	3.8E-64
PAFAH1B2 *	11	rs6589596	117,122,465	C	T	0.486985	-0.033286	0.002014	8.3E-64
PAFAH1B2 *	11	rs76868258	117,122,576	T	C	0.056767	0.047862	0.004330	7.0E-29
PAFAH1B2 *	11	rs12420361	117,123,072	A	G	0.096895	-0.051765	0.003385	1.7E-55
PAFAH1B2 *	11	rs10892078	117,123,213	T	A	0.203392	-0.027859	0.002496	2.5E-29
PAFAH1B2 *	11	rs11344600	117,123,743	C	CA	0.486921	-0.033290	0.002012	6.0E-64
PAFAH1B2 *	11	rs35722128	117,124,277	C	CA	0.056793	0.047685	0.004329	1.0E-28
PAFAH1B2 *	11	chr11:117125062_TAA_T	117,125,062	TAA	A	0.487199	-0.033154	0.002009	9.9E-64
PAFAH1B2 *	11	rs17120344	117,125,629	A	G	0.097127	-0.051329	0.003380	7.8E-55
PAFAH1B2 *	11	rs17120347	117,125,823	A	G	0.056873	0.047431	0.004326	1.8E-28
PAFAH1B2 *	11	rs12419454	117,125,915	T	C	0.097142	-0.051397	0.003380	5.8E-55
PAFAH1B2 *	11	rs12419459	117,125,995	T	C	0.098193	-0.049444	0.003365	2.2E-51
PAFAH1B2 *	11	rs12416691	117,126,067	T	A	0.097180	-0.051388	0.003379	5.6E-55
PAFAH1B2 *	11	rs6589597	117,127,082	T	C	0.487911	-0.033020	0.002007	1.9E-63
PAFAH1B2 *	11	rs78302396	117,127,400	G	A	0.084301	0.034303	0.003615	3.4E-22
PAFAH1B2 *	11	rs12420200	117,127,590	A	G	0.097195	-0.051446	0.003379	4.3E-55
PAFAH1B2 *	11	rs182980806	117,127,672	T	G	0.015551	0.074657	0.008095	6.0E-21
PAFAH1B2 *	11	rs145802214	117,128,196	C	A	0.097195	-0.051446	0.003379	4.3E-55
PAFAH1B2 *	11	rs141250514	117,128,309	C	T	0.097195	-0.051446	0.003379	4.3E-55
PAFAH1B2 *	11	rs4516002	117,128,343	G	A	0.487896	-0.033039	0.002007	1.6E-63
PAFAH1B2 *	11	rs9326248	117,128,509	G	T	0.352800	-0.013799	0.002095	4.2E-11
PAFAH1B2 *	11	rs7131536	117,128,730	T	C	0.488089	-0.032949	0.002008	4.4E-63
PAFAH1B2 *	11	rs7131686	117,128,843	T	C	0.487904	-0.033006	0.002007	2.1E-63
PAFAH1B2 *	11	rs138039720	117,128,884	T	C	0.097215	-0.051458	0.003379	4.1E-55
PAFAH1B2 *	11	chr11:117129006_TA_T	117,129,006	T	TA	0.444338	-0.031818	0.002036	1.8E-56
PAFAH1B2 *	11	rs146067038	117,129,463	G	A	0.097205	-0.051417	0.003380	5.2E-55
PAFAH1B2 *	11	rs10400366	117,130,239	A	G	0.293641	-0.027057	0.002202	6.0E-35
PAFAH1B2 *	11	rs199498085	117,130,739	G	A	0.090440	-0.051954	0.003509	2.5E-52
PAFAH1B2 *	11	rs12421425	117,131,244	T	C	0.097237	-0.051424	0.003379	5.1E-55
PAFAH1B2 *	11	chr11:117131317_A_AT	117,131,317	AT	A	0.441905	-0.029267	0.002049	5.1E-48
PAFAH1B2 *	11	rs142848583	117,131,334	AC	A	0.011388	0.095822	0.009444	5.2E-24
PAFAH1B2 *	11	rs191044888	117,131,336	T	G	0.011388	0.095814	0.009444	5.3E-24
PAFAH1B2 *	11	rs6589598	117,131,687	G	A	0.389991	-0.015722	0.002055	8.0E-15
PAFAH1B2 *	11	rs4938341	117,131,880	A	G	0.057138	0.046983	0.004313	6.3E-28
PAFAH1B2 *	11	rs17120367	117,132,112	T	C	0.097253	-0.051492	0.003379	3.6E-55
PAFAH1B2 *	11	rs11216284	117,132,344	T	C	0.352068	-0.013790	0.002097	4.0E-11
PAFAH1B2 *	11	chr11:117132474_CA_C	117,132,474	C	CA	0.488096	-0.032896	0.002010	7.8E-63
PAFAH1B2 *	11	rs17120370	117,132,672	C	T	0.097253	-0.051492	0.003379	3.6E-55
PAFAH1B2 *	11	rs74735277	117,132,702	T	C	0.097250	-0.051496	0.003379	3.5E-55
PAFAH1B2 *	11	rs4938342	117,132,704	G	C	0.057258	0.046748	0.004302	9.0E-28
PAFAH1B2 *	11	rs17120373	117,132,743	G	A	0.135319	-0.043433	0.002927	5.1E-53
PAFAH1B2 *	11	rs4938343	117,132,812	C	G	0.449970	-0.030901	0.002015	6.7E-55
PAFAH1B2 *	11	rs75208249	117,132,907	C	G	0.097443	-0.051182	0.003375	1.2E-54
PAFAH1B2 *	11	rs4938344	117,133,033	A	G	0.350751	-0.014695	0.002097	1.7E-12
PAFAH1B2 *	11	rs11216285	117,133,242	T	C	0.350908	-0.013556	0.002099	8.0E-11
PAFAH1B2 *	11	rs11216286	117,133,371	A	G	0.350013	-0.013670	0.002104	7.1E-11
PAFAH1B2 *	11	rs114945429	117,133,485	T	G	0.097347	-0.051414	0.003377	5.0E-55
PAFAH1B2 *	11	rs12792314	117,133,694	A	T	0.352488	-0.013949	0.002097	2.4E-11
PAFAH1B2 *	11	rs12417098	117,134,137	A	G	0.096728	-0.051001	0.003387	8.1E-54
PAFAH1B2 *	11	rs141936239	117,134,911	C	T	0.101797	-0.051041	0.003339	5.0E-55
PAFAH1B2 *	11	rs143261386	117,135,035	C	T	0.101797	-0.051048	0.003339	4.9E-55
PAFAH1B2 *	11	rs2735181	117,139,073	T	C	0.281447	-0.027923	0.002263	1.5E-35
PAFAH1B2 *	11	rs115991973	117,139,375	A	G	0.096724	-0.050629	0.003387	4.1E-53
PAFAH1B2 *	11	rs116384608	117,139,407	G	A	0.096724	-0.050629	0.003387	4.1E-53
PAFAH1B2 *	11	rs2471884	117,139,604	C	T	0.487554	-0.033095	0.002010	1.8E-63
PAFAH1B2 *	11	rs77661993	117,139,758	C	A	0.096729	-0.050653	0.003387	3.7E-53
PAFAH1B2 *	11	rs2622935	117,140,042	G	A	0.390434	-0.016174	0.002058	1.5E-15
PAFAH1B2 *	11	rs4277146	117,140,263	A	G	0.352563	-0.014206	0.002099	1.1E-11
PAFAH1B2 *	11	rs7934690	117,140,583	A	T	0.056958	0.047123	0.004323	5.4E-28
PAFAH1B2 *	11	rs7951095	117,140,724	A	C	0.352562	-0.014206	0.002099	1.1E-11
PAFAH1B2 *	11	rs2735182	117,141,494	T	A	0.352557	-0.014206	0.002099	1.1E-11
PAFAH1B2 *	11	rs11555026168	117,143,445	AAG	A	0.484670	-0.030411	0.002019	1.2E-53
PAFAH1B2 *	11	rs2622934	117,144,146	T	G	0.294688	-0.027568	0.002202	2.6E-36
PAFAH1B2 *	11	rs76904522	117,144,147	A	G	0.057506	0.046736	0.004304	6.4E-28
PAFAH1B2 *	11	rs113560866	117,144,473	C	G	0.057841	0.045753	0.004296	5.6E-27
PAFAH1B2 *	11	rs2735183	117,144,479	T	C	0.296037	-0.026960	0.002205	1.5E-34
PAFAH1B2 *	11	rs12419227	117,144,522	A	C	0.099444	-0.043086	0.003346	4.8E-40
PAFAH1B2 *	11	rs149188200	117,144,559	T	G	0.037310	0.052719	0.005332	7.0E-24
PAFAH1B2 *	11	rs11420191	117,145,447	CG	C	0.495685	-0.031589	0.002009	3.5E-58
PAFAH1B2 *	11	rs2306471	117,145,734	T	C	0.100930	-0.043345	0.003323	5.7E-41
PAFAH1B2 *	11	rs10892079	117,146,108	G	T	0.352513	-0.015642	0.002113	8.7E-14
PAFAH1B2 *	11	rs78270178	117,146,132	G	T	0.316178	-0.026559	0.002207	1.8E-34
PAFAH1B2 *	11	rs4936365	117,146,281	T	C	0.357661	-0.015011	0.002097	6.2E-13
PAFAH1B2 *	11	rs12419436	117,146,739	G	T	0.100719	-0.043153	0.003326	1.6E-40
PAFAH1B2 *	11	rs12420725	117,146,814	G	A	0.101108	-0.042841	0.003320	4.0E-40
PAFAH1B2 *	11	rs117592676	117,146,994	T	C	0.019327	0.111869	0.007313	8.8E-55
PAFAH1B2 *	11	rs12417984	117,146,998	A	G	0.100956	-0.043212	0.003323	9.6E-41
PAFAH1B2 *	11	rs139864910	117,147,046	C	A	0.100956	-0.043212	0.003323	9.6E-41

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
PAFAH1B2	11	rs2008908	117,148,294	T	C	0.357196	-0.014776	0.002093	1.3E-12
PAFAH1B2	11	rs139146464	117,149,151	G	A	0.100040	-0.042384	0.003339	6.7E-39
PAFAH1B2	11	rs71037463	117,149,256	A	AT	0.494531	-0.031679	0.002008	2.0E-58
PAFAH1B2	11	rs1461576929	117,149,430	T	G	0.021097	0.064573	0.007058	1.5E-20
PAFAH1B2	11	rs7115562	117,149,754	G	A	0.458370	-0.029671	0.002012	7.6E-51
PAFAH1B2	11	rs7116454	117,150,418	T	A	0.458367	-0.029678	0.002012	7.3E-51
PAFAH1B2	11	rs45625638	117,150,710	C	G	0.057728	0.046353	0.004295	1.3E-27
PAFAH1B2	11	chr11:117150989_GAA_G	117,150,989	G	GAA	0.100981	-0.042508	0.003335	6.5E-39
PAFAH1B2	11	rs4938347	117,151,043	A	T	0.456946	-0.029449	0.002022	1.4E-49
PAFAH1B2	11	rs4938348	117,151,161	C	G	0.455482	-0.028727	0.002018	1.7E-47
PAFAH1B2	11	rs4938349	117,151,207	T	C	0.353238	-0.014003	0.002100	2.4E-11
PAFAH1B2	11	rs4938350	117,151,560	G	A	0.455413	-0.028755	0.002018	1.7E-47
PAFAH1B2	11	rs79831695	117,151,612	G	A	0.030095	-0.057985	0.005891	2.6E-23
PAFAH1B2	11	rs4938351	117,151,636	C	A	0.296505	-0.027057	0.002199	3.9E-35
PAFAH1B2	11	rs117906059	117,151,637	T	C	0.024449	-0.037092	0.006508	3.9E-08
PAFAH1B2	11	rs146629336	117,152,290	C	G	0.020098	-0.049318	0.007151	3.9E-12
PAFAH1B2	11	rs7128382	117,152,771	C	A	0.455436	-0.028677	0.002016	2.2E-47
PAFAH1B2	11	rs143494314	117,152,990	T	C	0.100959	-0.043228	0.003323	9.0E-41
PAFAH1B2	11	rs10790174	117,153,548	A	G	0.354728	-0.014065	0.002097	1.7E-11
PAFAH1B2	11	rs7950633	117,153,586	T	C	0.494487	-0.030598	0.002010	1.9E-54
PAFAH1B2	11	rs7940310	117,153,765	C	T	0.493441	-0.030958	0.002009	8.0E-56
PAFAH1B2	11	chr11:117154119_G_GA	117,154,119	GA	G	0.453806	-0.029285	0.002021	3.2E-49
PAFAH1B2	11	rs78123099	117,154,123	G	A	0.017776	0.057778	0.007615	5.3E-15
PAFAH1B2	11	rs35500922	117,154,603	AT	A	0.097511	-0.043436	0.003384	1.4E-39
PAFAH1B2	11	rs68137714	117,154,641	G	A	0.057728	0.046353	0.004295	1.3E-27
PAFAH1B2	11	rs12418349	117,155,216	G	A	0.100959	-0.043228	0.003323	9.0E-41
PAFAH1B2	11	rs2127905	117,155,658	C	A	0.499016	-0.031736	0.002006	6.2E-59
PAFAH1B2	11	rs4936366	117,156,169	A	G	0.458384	-0.029674	0.002012	7.1E-51
PAFAH1B2	11	rs4938352	117,156,765	A	G	0.458384	-0.029674	0.002012	7.1E-51
PAFAH1B2	11	rs199763004	117,157,038	A	AG	0.500274	-0.030429	0.002018	1.1E-53
PAFAH1B2	11	rs7123517	117,157,039	A	G	0.500567	-0.030395	0.002017	1.2E-53
PAFAH1B2	11	rs117588325	117,157,577	T	A	0.027918	0.072808	0.006093	4.1E-34
PAFAH1B2	11	rs12420250	117,158,011	A	G	0.100664	-0.043109	0.003328	1.8E-40
PAFAH1B2	11	rs78166985	117,159,069	T	A	0.100783	-0.043342	0.003326	6.9E-41
PAFAH1B2	11	rs1871757	117,159,865	A	T	0.458214	-0.029646	0.002012	9.2E-51
PAFAH1B2	11	chr11:117159908_AT_A	117,159,908	A	AT	0.356284	-0.015055	0.002094	5.3E-13
PAFAH1B2	11	rs200545029	117,159,917	C	T	0.100866	-0.043129	0.003324	1.5E-40
PAFAH1B2	11	rs142017584	117,160,647	A	G	0.100962	-0.043231	0.003323	8.8E-41
PAFAH1B2	11	rs3736120	117,161,409	T	G	0.330557	-0.022659	0.002133	9.4E-27
PAFAH1B2	11	rs12281009	117,162,243	G	A	0.100962	-0.043231	0.003323	8.8E-41
PAFAH1B2	11	chr11:117162461_TC_T	117,162,461	T	TC	0.011877	-0.061792	0.009399	7.4E-12
PAFAH1B2	11	rs71037468	117,163,187	CTGAGT	A	0.455849	-0.029385	0.002019	1.5E-49
PAFAH1B2	11	rs7122944	117,163,903	T	G	0.494839	-0.032311	0.002007	6.8E-61
PAFAH1B2	11	rs10790175	117,164,013	C	T	0.357249	-0.014921	0.002090	7.5E-13
PAFAH1B2	11	rs150984554	117,164,300	A	G	0.100074	-0.043854	0.003338	1.9E-41
PAFAH1B2	11	rs12420127	117,164,603	G	A	0.100962	-0.043231	0.003323	8.8E-41
PAFAH1B2	11	rs10892080	117,164,786	G	A	0.297710	-0.027800	0.002195	3.0E-37
PAFAH1B2	11	rs149378955	117,164,863	A	G	0.045868	0.052712	0.004800	3.1E-29
PAFAH1B2	11	chr11:117164958_C_CT	117,164,958	CT	C	0.356810	-0.014072	0.002111	3.0E-11
PAFAH1B2	11	rs7931335	117,166,089	T	C	0.458395	-0.029660	0.002012	8.0E-51
PAFAH1B2	11	rs6589602	117,166,349	C	T	0.298814	-0.027997	0.002191	7.5E-38
PAFAH1B2	11	rs7112513	117,166,645	G	A	0.495722	-0.031786	0.002005	5.2E-59
PAFAH1B2	11	rs77171490	117,168,025	A	T	0.100962	-0.043231	0.003323	8.8E-41
PAFAH1B2	11	rs190482111	117,168,438	A	G	0.100956	-0.043252	0.003323	8.2E-41
PAFAH1B2	11	rs10892082	117,168,609	G	T	0.495560	-0.032077	0.002006	4.6E-60
PAFAH1B2	11	rs116773440	117,168,745	C	A	0.100566	-0.043600	0.003332	3.0E-41
PAFAH1B2	11	rs1060211	117,169,081	A	G	0.458360	-0.029684	0.002012	7.1E-51
PAFAH1B2	11	rs45628435	117,169,482	GT	G	0.298798	-0.028089	0.002191	4.4E-38
PAFAH1B2	11	rs77678768	117,169,789	C	G	0.100956	-0.043252	0.003323	8.2E-41
PAFAH1B2	11	rs10750103	117,171,522	T	C	0.298159	-0.028007	0.002193	9.6E-38
PAFAH1B2	11	rs4936367	117,171,661	A	G	0.495736	-0.031812	0.002005	4.3E-59
PAFAH1B2	11	rs10892083	117,171,864	C	G	0.208208	-0.028754	0.002472	7.1E-32
PAFAH1B2	11	rs7120309	117,172,100	A	T	0.458400	-0.029674	0.002012	7.3E-51
PAFAH1B2	11	rs7120449	117,172,183	C	T	0.458138	-0.029690	0.002012	6.6E-51
PAFAH1B2	11	rs7120565	117,172,233	C	T	0.298803	-0.028078	0.002191	4.7E-38
PAFAH1B2	11	rs56371319	117,172,251	A	C	0.057732	0.046333	0.004295	1.3E-27
PAFAH1B2	11	rs4604928	117,173,487	A	C	0.495736	-0.031813	0.002005	4.3E-59
PAFAH1B2	11	chr11:117174484_A_AT	117,174,484	AT	A	0.095608	-0.043091	0.003418	1.2E-38
PAFAH1B2	11	chr11:117174494_CT_C	117,174,494	C	CT	0.297070	-0.027947	0.002202	2.3E-37
PAFAH1B2	11	rs7925256	117,174,619	T	C	0.285679	0.040251	0.002235	8.0E-75
PAFAH1B2	11	rs146228126	117,175,016	T	G	0.015459	0.070752	0.008151	2.6E-18
PAFAH1B2	11	rs10535646	117,175,444	T	TTGC	0.298966	-0.028027	0.002191	6.0E-38
PAFAH1B2	11	rs4938353	117,175,481	A	G	0.458385	-0.029664	0.002012	7.9E-51
PAFAH1B2	11	rs10790176	117,177,136	T	G	0.458407	-0.029658	0.002012	8.2E-51
PAFAH1B2	11	rs80353869	117,177,406	A	G	0.100739	-0.043493	0.003327	4.0E-41
PAFAH1B2	11	rs10790177	117,177,701	G	A	0.357355	-0.014846	0.002091	9.7E-13
SIDT2	11	rs12419178	117,180,202	T	C	0.100630	-0.043412	0.003329	6.1E-41
SIDT2	11	rs34783152	117,180,423	A	AG	0.100634	-0.043382	0.003328	6.8E-41
SIDT2	11	rs76883864	117,181,009	T	C	0.100634	-0.043381	0.003328	6.8E-41
SIDT2	11	rs35248926	117,181,353	G	GTCTCT	0.458429	-0.029737	0.002015	5.0E-51
SIDT2	11	rs7946257	117,182,449	G	A	0.357110	-0.014946	0.002091	6.6E-13
SIDT2	11	rs2046150	117,182,717	A	C	0.102831	-0.042305	0.003297	7.1E-40
SIDT2	11	rs4938355	117,182,959	G	A	0.056313	0.046904	0.004347	1.9E-27
SIDT2	11	rs34033077	117,183,654	CT	C	0.095696	-0.040161	0.003422	1.1E-33
SIDT2	11	rs2046149	117,183,993	G	C	0.102834	-0.042306	0.003297	7.1E-40
SIDT2	11	rs10892085	117,185,065	C	T	0.338577	-0.013703	0.002153	1.9E-10
SIDT2	11	rs6589603	117,185,123	C	T	0.495351	-0.032052	0.002013	1.1E-59
SIDT2	11	rs11606672	117,185,343	T	C	0.102624	-0.042075	0.003301	2.0E-39
SIDT2	11	rs7107152	117,185,364	G	A	0.357284	-0.015032	0.002091	4.7E-13
SIDT2	11	rs2306472	117,187,346	T	C	0.100625	-0.042905	0.003329	4.2E-40
SIDT2	11	rs546506427	117,188,416	C	T	0.102632	-0.042054	0.003301	2.2E-39
SIDT2	11	rs775148500	117,188,417	TCA	T	0.100841	-0.043149	0.003324	1.4E-40
SIDT2	11	rs90192	117,188,631	T	C	0.460852	-0.028556	0.002014	4.0E-47
SIDT2	11	rs474339	117,188,836	A	G	0.357150	-0.014937	0.002091	6.6E-13
SIDT2	11	rs7933134	117,189,078	C	G	0.102844	-0.042289	0.003297	7.5E-40
SIDT2	11	rs12419470	117,191,059	T	C	0.102628	-0.042058	0.003301	2.2E-39
SIDT2	11	rs61703672	117,191,109	T	C	0.102628	-0.042058	0.003301	2.2E-39

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SIDT2	11	rs140056851	117,191,110	G	T	0.045919	0.052311	0.004798	7.8E-29
SIDT2	11	rs499713	117,191,245	C	T	0.458337	-0.029667	0.002017	1.1E-50
SIDT2	11	rs1242230	117,191,467	C	T	0.497626	-0.031866	0.002006	1.9E-59
SIDT2	11	rs1242229	117,191,654	C	T	0.497944	-0.031831	0.002005	2.6E-59
SIDT2	11	rs3213459	117,191,773	C	T	0.102843	-0.042283	0.003297	7.6E-40
SIDT2	11	rs2301174	117,192,993	G	C	0.102637	-0.041998	0.003301	2.7E-39
SIDT2	11	rs521171	117,193,977	G	C	0.357789	-0.015099	0.002092	4.2E-13
SIDT2	11	rs11605883	117,194,060	G	C	0.100837	-0.043153	0.003324	1.4E-40
SIDT2	11	rs73008568	117,194,291	G	C	0.056250	0.046761	0.004350	2.8E-27
SIDT2	11	rs3781985	117,194,350	C	G	0.100837	-0.043153	0.003324	1.4E-40
SIDT2	11	rs80183569	117,194,437	A	G	0.100837	-0.043153	0.003324	1.4E-40
SIDT2	11	rs1784042	117,194,760	A	G	0.209395	-0.028621	0.002468	1.3E-31
SIDT2	11	rs11606480	117,194,817	A	G	0.100837	-0.043153	0.003324	1.4E-40
SIDT2	11	rs112712475	117,195,056	A	C	0.099601	-0.043584	0.003348	7.3E-41
SIDT2	11	rs1794116	117,195,063	C	T	0.357034	-0.015035	0.002091	4.6E-13
LOC100652768, SIDT	11	rs2269399	117,195,637	C	G	0.100837	-0.043156	0.003324	1.3E-40
LOC100652768, SIDT	11	rs8521	117,196,983	T	C	0.357008	-0.015014	0.002091	4.9E-13
LOC100652768	11	rs74385934	117,197,728	A	G	0.100837	-0.043167	0.003324	1.3E-40
LOC100652768	11	rs588534	117,197,788	G	A	0.458081	-0.029763	0.002012	3.4E-51
LOC100652768	11	rs2075547	117,197,818	A	C	0.056240	0.046652	0.004351	3.8E-27
LOC100652768	11	rs147581841	117,197,929	T	C	0.024694	0.063443	0.006461	1.8E-23
LOC100652768	11	rs474488	117,198,261	G	A	0.458068	-0.029744	0.002012	3.9E-51
LOC100652768	11	rs7112573	117,198,307	C	T	0.102838	-0.042303	0.003297	7.5E-40
LOC100652768	11	rs585849	117,198,345	G	A	0.356446	-0.015114	0.002094	3.7E-13
LOC100652768	11	rs2269398	117,199,072	T	C	0.100823	-0.043147	0.003325	1.5E-40
LOC100652768	11	rs17523113	117,199,185	A	G	0.044172	0.052029	0.004889	1.2E-27
LOC100652768, TAGI	11	rs3833897	117,199,831	T	TGAG	0.356388	-0.015336	0.002098	2.1E-13
LOC100652768, TAGI	11	rs2239678	117,199,880	T	C	0.100807	-0.043237	0.003325	1.0E-40
LOC100652768, TAGI	11	rs2170317	117,200,024	C	A	0.100859	-0.043303	0.003325	8.6E-41
LOC100652768, TAGI	11	rs664971	117,200,141	A	G	0.357093	-0.015164	0.002096	3.7E-13
LOC100652768, TAGI	11	rs664922	117,200,179	A	C	0.356950	-0.015221	0.002096	3.0E-13
LOC100652768, TAGI	11	rs664082	117,200,354	G	C	0.356269	-0.015140	0.002099	3.9E-13
LOC100652768, TAGI	11	rs494356	117,201,254	C	T	0.469680	-0.029088	0.002025	2.2E-48
LOC100652768, TAGI	11	rs488962	117,201,809	C	T	0.357179	-0.015240	0.002096	2.7E-13
TAGLN	11	rs634960	117,202,247	T	C	0.357161	-0.015181	0.002095	3.5E-13
TAGLN	11	rs145613978	117,202,393	A	G	0.029271	0.069286	0.005964	2.6E-32
TAGLN	11	rs12970	117,203,393	A	G	0.101119	-0.042680	0.003319	6.1E-40
TAGLN	11	rs641620	117,203,513	T	C	0.437469	-0.026480	0.002040	9.4E-40
TAGLN	11	rs2269397	117,203,583	C	T	0.107234	-0.039652	0.003236	1.2E-36
PCSK7	11	rs20184697	117,206,224	A	G	0.017234	-0.043809	0.007767	3.0E-09
PCSK7	11	rs28590104	117,206,318	A	G	0.331492	-0.014730	0.002178	9.4E-12
PCSK7	11	rs659955	117,209,663	T	A	0.498881	-0.030664	0.002015	9.2E-55
PCSK7	11	rs11216315	117,209,924	G	C	0.102920	-0.041512	0.003294	9.8E-39
PCSK7	11	rs11216316	117,210,784	A	C	0.496788	-0.030487	0.002011	2.2E-54
PCSK7	11	rs171052	117,211,047	C	G	0.355597	-0.013980	0.002098	2.3E-11
PCSK7	11	rs236910	117,211,258	A	G	0.355597	-0.013980	0.002098	2.3E-11
PCSK7	11	rs12417682	117,211,393	A	G	0.103227	-0.041377	0.003290	1.5E-38
PCSK7	11	rs76169968	117,212,250	A	G	0.103389	-0.041519	0.003286	6.3E-39
PCSK7	11	rs67201490	117,212,288	G	T	0.055109	0.045129	0.004392	3.6E-25
PCSK7	11	rs4938357	117,213,324	A	G	0.055106	0.045181	0.004392	3.1E-25
PCSK7	11	rs12418705	117,213,680	T	C	0.101212	-0.042150	0.003318	4.0E-39
PCSK7	11	rs139694434	117,213,935	TTTTTC	T	0.495594	-0.030799	0.002012	2.8E-55
PCSK7	11	rs77683187	117,214,494	C	A	0.103280	-0.041357	0.003288	1.4E-38
PCSK7	11	rs236911	117,214,554	A	C	0.496084	-0.030994	0.002010	5.3E-56
PCSK7	11	rs56081989	117,214,589	A	G	0.055233	0.044818	0.004389	6.4E-25
PCSK7	11	rs36028244	117,215,198	C	CTTA	0.103065	-0.041454	0.003292	1.5E-38
PCSK7	11	rs56061158	117,216,402	C	G	0.055242	0.045012	0.004389	5.0E-25
PCSK7	11	rs150159690	117,217,269	GTCACCT	A	0.103010	-0.041272	0.003294	2.2E-38
PCSK7	11	rs2238005	117,217,366	T	C	0.103258	-0.041400	0.003289	1.3E-38
PCSK7	11	rs236915	117,217,734	A	G	0.298533	-0.026202	0.002196	4.4E-33
PCSK7	11	rs236916	117,218,912	G	A	0.460334	-0.027961	0.002016	2.3E-45
PCSK7	11	rs2239009	117,219,006	C	G	0.102983	-0.041292	0.003295	2.2E-38
PCSK7	11	rs74830	117,219,842	C	T	0.303350	-0.025749	0.002189	3.0E-32
PCSK7	11	rs35590772	117,220,535	TG	T	0.462937	-0.027887	0.002017	4.1E-45
PCSK7	11	rs236918	117,220,893	G	C	0.498464	-0.030310	0.002006	7.2E-54
PCSK7	11	rs7941150	117,221,105	A	G	0.055293	0.044772	0.004386	8.4E-25
PCSK7	11	rs78628783	117,221,335	T	C	0.103043	-0.041269	0.003295	2.5E-38
PCSK7	11	rs80351364	117,221,678	T	A	0.103432	-0.041376	0.003288	1.4E-38
PCSK7	11	rs6589606	117,222,170	T	C	0.103046	-0.041275	0.003295	2.5E-38
PCSK7	11	rs17120523	117,223,875	G	A	0.073529	-0.038153	0.003869	1.4E-23
PCSK7	11	rs236919	117,224,645	C	T	0.308773	-0.020069	0.002192	6.7E-20
PCSK7	11	rs146871029	117,225,450	T	C	0.011563	0.094664	0.009372	1.8E-23
PCSK7	11	rs75519898	117,226,533	A	G	0.025477	0.044723	0.006384	9.5E-13
PCSK7	11	chr11:17226836_T_TGGGAGCTG	117,226,836	JGGAGCT	T	0.494634	0.026288	0.002016	7.1E-41
PCSK7	11	rs2306473	117,227,236	T	C	0.059756	0.038686	0.004228	4.0E-20
PCSK7	11	rs111809212	117,228,821	C	T	0.054857	0.037383	0.004433	2.4E-17
PCSK7	11	rs4938361	117,229,225	C	G	0.058307	0.038925	0.004293	9.9E-20
PCSK7	11	rs4938362	117,229,313	A	G	0.058956	0.039541	0.004270	1.4E-20
PCSK7	11	rs11542139	117,229,541	T	C	0.043499	0.039803	0.004967	4.5E-16
RNF214	11	rs200694867	117,244,658	C	CTTTA	0.024958	0.070267	0.006467	6.3E-28
RNF214	11	rs144580263	117,253,710	T	C	0.048839	-0.035029	0.004658	3.7E-14
RNF214	11	rs145918995	117,256,488	T	C	0.015272	0.063989	0.008247	2.1E-15
BACE1, BACE1-AS	11	rs288989505	117,291,956	G	C	0.029358	0.038476	0.005958	8.0E-11
BACE1	11	rs199753343	117,310,973	A	AC	0.021756	0.042371	0.006921	2.0E-09
BACE1	11	rs3741288	117,315,499	T	C	0.030705	-0.039493	0.005856	4.2E-12
BACE1 *	11	rs1038851424	117,317,566	C	T	0.014696	0.065358	0.008416	2.2E-15
CEP164	11	rs73014327	117,325,867	C	T	0.032604	-0.040399	0.005688	3.5E-13
CEP164	11	rs11216357	117,330,037	G	T	0.034138	-0.041166	0.005531	2.5E-14
CEP164	11	rs515756	117,330,449	G	T	0.157642	0.019658	0.002796	2.2E-12
CEP164	11	chr11:17330649_CA_C	117,330,649	C	CA	0.136551	0.025367	0.002930	6.5E-18
CEP164	11	rs609663	117,331,033	G	C	0.152257	0.019383	0.002799	4.9E-12
CEP164	11	rs144584200	117,332,064	G	A	0.031793	0.066347	0.005776	1.6E-30
CEP164	11	rs371259597	117,332,128	T	C	0.015256	0.068530	0.008258	1.9E-17
CEP164	11	rs527347	117,332,917	G	A	0.152030	0.024490	0.002797	2.5E-18
CEP164	11	rs576190	117,335,050	C	T	0.151963	0.024422	0.002798	3.3E-18
CEP164	11	rs487298	117,335,128	T	G	0.151963	0.024422	0.002798	3.3E-18
CEP164	11	rs520315	117,336,910	C	T	0.155702	0.024713	0.002786	1.0E-18

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
CEP164	11	rs620848	117,336,912	G	C	0.155702	0.024713	0.002786	1.0E-18
CEP164	11	rs875209	117,337,554	A	G	0.152820	0.024539	0.002791	2.1E-18
CEP164	11	rs645305	117,338,031	C	T	0.153323	0.024807	0.002785	6.7E-19
CEP164	11	rs948181	117,338,233	T	C	0.153323	0.024807	0.002785	6.7E-19
CEP164	11	rs573801	117,338,552	T	C	0.153323	0.024780	0.002785	7.2E-19
CEP164	11	rs12221726	117,339,622	A	G	0.032103	-0.040443	0.005691	5.5E-13
CEP164	11	rs578781	117,339,991	A	G	0.152345	0.024821	0.002794	8.5E-19
CEP164	11	rs536021	117,340,185	C	T	0.153354	0.024714	0.002785	8.8E-19
CEP164	11	rs610749	117,340,524	T	G	0.153692	0.024933	0.002779	4.2E-19
CEP164	11	rs474891	117,341,621	T	G	0.173107	0.019325	0.002682	5.2E-13
CEP164	11	rs561473	117,341,924	C	T	0.150624	0.025681	0.002814	7.9E-20
CEP164	11	rs475385	117,342,176	T	C	0.153037	0.024623	0.002789	1.4E-18
CEP164	11	rs495473	117,342,192	G	A	0.137103	0.022783	0.002916	6.1E-15
CEP164	11	rs493516	117,342,444	A	G	0.153007	0.024647	0.002789	1.3E-18
CEP164	11	rs11216360	117,342,473	A	G	0.035601	-0.038933	0.005424	1.9E-13
CEP164	11	rs10892095	117,343,177	G	A	0.034314	-0.039720	0.005508	1.7E-13
CEP164	11	rs573827	117,343,375	A	G	0.153164	0.024794	0.002787	8.0E-19
CEP164	11	rs580119	117,345,497	G	T	0.153088	0.024983	0.002790	4.7E-19
CEP164	11	rs652346	117,345,883	T	C	0.137152	0.023176	0.002917	2.3E-15
CEP164	11	rs494722	117,345,887	T	A	0.137152	0.023176	0.002917	2.3E-15
CEP164	11	rs138869088	117,346,455	T	C	0.010843	0.098342	0.009750	5.8E-24
CEP164	11	rs1261744	117,347,744	C	T	0.150962	0.024509	0.002807	4.0E-18
CEP164	11	rs592828	117,348,589	C	G	0.151788	0.024834	0.002800	1.0E-18
CEP164	11	rs508871	117,349,054	A	G	0.150698	0.024104	0.002810	1.3E-17
CEP164	11	rs688207	117,351,423	T	C	0.151498	0.025061	0.002803	4.6E-19
CEP164	11	rs490262	117,351,876	A	G	0.137943	0.029582	0.002947	6.0E-24
CEP164	11	rs514806	117,352,226	T	G	0.151505	0.025010	0.002803	5.4E-19
CEP164	11	rs657666	117,353,644	A	G	0.151508	0.025018	0.002803	5.3E-19
CEP164	11	rs67060142	117,353,997	T	TCTTCTC	0.145416	0.023888	0.002864	1.5E-16
CEP164	11	rs553303	117,354,102	T	C	0.149586	0.024483	0.002823	4.7E-18
CEP164	11	rs655389	117,354,162	A	G	0.151509	0.025017	0.002803	5.4E-19
CEP164	11	rs553506	117,354,171	T	C	0.150156	0.024851	0.002816	1.2E-18
CEP164	11	rs654479	117,354,418	A	G	0.151509	0.025017	0.002803	5.4E-19
CEP164	11	rs542176	117,354,725	T	G	0.151281	0.024969	0.002805	6.3E-19
CEP164	11	rs542869	117,354,739	A	T	0.134242	0.023773	0.002948	6.1E-16
CEP164	11	rs542900	117,354,751	A	T	0.150206	0.025639	0.002816	8.4E-20
CEP164	11	rs535366	117,355,900	C	T	0.151511	0.024988	0.002803	5.8E-19
CEP164	11	rs11216364	117,355,903	T	C	0.086277	0.043973	0.003632	1.2E-34
CEP164	11	chr11:117355999_G_GAGCAGCAGC	117,355,999	G	GACAGCA	0.149380	0.023606	0.002825	6.1E-17
CEP164	11	rs537323	117,356,133	T	C	0.151511	0.024988	0.002803	5.8E-19
CEP164	11	rs528720	117,356,970	A	G	0.151243	0.025198	0.002806	3.7E-19
CEP164	11	rs595367	117,356,978	C	T	0.135292	0.023251	0.002936	2.7E-15
CEP164	11	rs534296	117,357,579	G	A	0.151516	0.025053	0.002803	4.9E-19
CEP164	11	rs12221818	117,357,803	G	A	0.034695	-0.039769	0.005477	1.1E-13
CEP164	11	rs558854	117,357,948	A	G	0.151485	0.025103	0.002803	4.1E-19
CEP164	11	rs486366	117,357,993	G	A	0.151486	0.025098	0.002803	4.1E-19
CEP164	11	rs4018864	117,358,402	AAT	A	0.151473	0.025110	0.002803	4.0E-19
CEP164	11	rs2508664	117,359,175	T	C	0.135575	0.023196	0.002933	2.6E-15
CEP164	11	rs2510450	117,359,186	T	C	0.151507	0.025095	0.002804	4.2E-19
CEP164	11	rs512730	117,360,341	A	T	0.153122	0.024240	0.002799	4.4E-18
CEP164	11	rs11216366	117,360,895	T	G	0.135915	0.022767	0.002934	7.8E-15
CEP164	11	rs12421205	117,361,440	G	C	0.151844	0.024856	0.002805	8.4E-19
CEP164	11	rs12421494	117,361,517	A	G	0.151844	0.024856	0.002805	8.4E-19
CEP164	11	rs12418678	117,361,544	G	A	0.135899	0.022780	0.002934	7.6E-15
CEP164	11	rs17500548	117,361,675	G	A	0.135899	0.022780	0.002934	7.6E-15
CEP164	11	rs2305825	117,361,776	T	C	0.151549	0.024884	0.002809	7.9E-19
CEP164	11	rs7934067	117,362,238	G	A	0.151844	0.024856	0.002805	8.4E-19
CEP164	11	rs11828506	117,362,711	T	C	0.151508	0.025093	0.002804	4.3E-19
CEP164	11	rs7945704	117,364,652	A	G	0.108852	-0.026041	0.003224	2.6E-16
CEP164	11	rs7124084	117,364,696	T	C	0.151500	0.025071	0.002804	4.5E-19
CEP164	11	rs10892097	117,365,344	T	C	0.135573	0.023190	0.002933	2.6E-15
CEP164	11	chr11:117435567_A_ATTTC	117,365,567	ATTTC	A	0.132817	0.024604	0.002966	1.2E-16
CEP164	11	rs10790179	117,365,603	T	G	0.135574	0.023189	0.002933	2.6E-15
CEP164	11	rs11606575	117,366,491	G	C	0.035241	-0.039913	0.005436	6.3E-14
CEP164	11	rs7109923	117,366,771	G	A	0.150858	0.024717	0.002812	1.5E-18
CEP164	11	rs10892098	117,367,775	T	C	0.150794	0.024564	0.002813	2.6E-18
CEP164	11	rs7115177	117,368,457	C	A	0.151432	0.023497	0.002808	6.6E-17
CEP164	11	rs7115526	117,368,474	T	G	0.151432	0.023497	0.002808	6.6E-17
CEP164	11	rs9651682	117,369,641	A	G	0.151890	0.023833	0.002805	1.8E-17
CEP164	11	rs12417440	117,370,713	T	C	0.134071	0.022559	0.002952	2.1E-14
CEP164	11	rs10790180	117,375,434	C	T	0.345883	0.015826	0.002119	9.5E-14
CEP164	11	rs7952470	117,377,552	A	G	0.134694	0.022685	0.002945	1.1E-14
CEP164	11	rs2305828	117,380,427	G	A	0.341700	0.016187	0.002128	3.6E-14
CEP164	11	rs897837	117,390,772	G	C	0.139181	0.020800	0.002915	1.0E-12
CEP164	11	rs2279013	117,412,375	T	C	0.477741	-0.014742	0.002037	2.7E-13
CEP164	11	rs9163	117,413,092	T	C	0.154806	0.020643	0.002796	1.6E-13
CEP164 *	11	rs10736488	117,414,341	G	A	0.155309	0.020422	0.002792	2.9E-13
CEP164 *	11	rs59114541	117,419,236	A	G	0.011692	0.071868	0.009314	2.9E-14
CEP164 *	11	rs74523946	117,420,199	A	G	0.033747	-0.041687	0.005560	2.5E-14
CEP164 *	11	rs11603208	117,420,247	T	G	0.035237	-0.040955	0.005448	2.5E-14
CEP164 *	11	rs180850158	117,420,250	T	C	0.014758	0.055713	0.008301	5.1E-11
DSCAML1 *	11	rs11216379	117,421,400	G	A	0.055656	-0.036610	0.004447	1.5E-16
DSCAML1 *	11	rs75493192	117,422,143	G	A	0.011874	0.068434	0.009258	3.3E-13
DSCAML1 *	11	rs11607141	117,423,306	G	T	0.033094	-0.045271	0.005637	4.3E-16
DSCAML1 *	11	chr11:117423756_AAAAC_A	117,423,756	AAAAC	A	0.011472	0.107434	0.009497	1.1E-29
DSCAML1 *	11	rs7115491	117,424,434	G	T	0.031687	-0.047168	0.005774	8.6E-17
DSCAML1 *	11	rs117229433	117,426,594	A	C	0.023671	-0.039522	0.006604	1.1E-09
NLRX1	11	rs10790286	119,183,779	C	T	0.321659	0.011322	0.002147	4.7E-08
ACACB	12	rs1013746	109,250,784	C	T	0.251422	-0.011279	0.002349	3.9E-08
ACACB	12	rs10744776	109,255,001	A	G	0.251272	-0.011303	0.002345	3.5E-08
FAM222A *	12	rs79339138	109,776,127	A	G	0.050004	0.026221	0.004692	3.3E-08
ANKRD13A	12	rs75584653	110,021,680	T	C	0.088524	0.019539	0.003572	4.0E-08
IFT81	12	rs141965732	110,144,533	T	C	0.079391	0.021084	0.003754	2.8E-08
IFT81	12	rs117624317	110,194,076	T	C	0.096818	0.020198	0.003447	5.6E-09
IFT81 *	12	rs144825998	110,237,558	T	C	0.079989	0.021121	0.003740	2.6E-08
ATP2A2 *	12	rs117121174	110,259,525	A	G	0.079484	0.021659	0.003751	1.1E-08
CUX2	12	rs11830764	111,077,216	C	G	0.097669	-0.018561	0.003417	7.7E-09

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
CUX2	12	rs7314285	111,084,222	G	T	0.099949	-0.017818	0.003373	1.3E-08
C14orf166 *	14	rs36016197	51,987,660	C	A	0.148088	-0.016557	0.002867	7.6E-09
C14orf166	14	rs56877201	51,992,899	A	G	0.147742	-0.015825	0.002867	2.7E-08
C14orf166	14	rs57358451	51,993,112	C	CAGTA	0.147759	-0.015812	0.002867	2.8E-08
C14orf166	14	rs61971506	51,996,807	A	G	0.148780	-0.015986	0.002865	1.7E-08
C14orf166	14	rs144834676	52,001,241	A	AGT	0.149474	-0.015889	0.002850	1.7E-08
NID2	14	rs2029984	52,007,011	G	A	0.159238	-0.015002	0.002783	3.6E-08
NID2	14	rs71422049	52,016,737	G	A	0.156675	-0.014996	0.002783	3.8E-08
NID2	14	rs2645750	52,036,074	C	A	0.153641	-0.015382	0.002819	2.8E-08
NID2	14	rs2645749	52,036,077	C	A	0.153641	-0.015395	0.002819	2.7E-08
NID2	14	rs2516592	52,036,827	T	C	0.154135	-0.015666	0.002810	1.4E-08
NID2	14	rs71121678	52,036,872	A	AG	0.154301	-0.015663	0.002811	1.4E-08
NID2	14	rs2749876	52,037,679	T	G	0.154582	-0.015217	0.002804	3.2E-08
NID2	14	rs904061	52,037,906	T	C	0.154627	-0.015238	0.002803	3.1E-08
NID2	14	rs753051	52,038,642	A	G	0.154726	-0.015163	0.002801	3.7E-08
NID2	14	rs753050	52,038,657	A	G	0.154777	-0.015210	0.002802	3.3E-08
NID2	14	rs2029976	52,039,093	C	T	0.154772	-0.015189	0.002801	3.3E-08
NID2	14	rs2029975	52,039,352	C	T	0.154840	-0.015218	0.002800	3.1E-08
NID2	14	rs10139288	52,039,768	T	C	0.155032	-0.015227	0.002796	2.8E-08
NID2	14	rs3742536	52,040,711	A	G	0.155123	-0.015317	0.002795	2.4E-08
NID2	14	rs1982963	52,042,383	G	A	0.155257	-0.015578	0.002791	1.3E-08
NID2	14	rs3841694	52,042,541	TA	T	0.155252	-0.015570	0.002791	1.3E-08
NID2	14	rs4898729	52,042,765	T	C	0.154890	-0.015490	0.002795	1.7E-08
NID2	14	rs4901186	52,042,766	G	A	0.155261	-0.015601	0.002791	1.3E-08
NID2	14	rs3818187	52,043,070	G	A	0.155125	-0.015650	0.002793	1.2E-08
NID2	14	rs61973203	52,043,849	G	A	0.151574	-0.016350	0.002825	3.5E-09
NID2	14	chr14:52044610_CT_C	52,044,610	CT	C	0.155084	-0.015986	0.002797	6.3E-09
NID2	14	rs1566132	52,045,118	C	T	0.155079	-0.015949	0.002794	6.2E-09
NID2	14	rs75766425	52,045,193	C	G	0.118712	-0.019996	0.003124	6.3E-11
NID2	14	rs79823890	52,045,251	T	G	0.119045	-0.020130	0.003120	4.8E-11
NID2	14	rs33921845	52,045,899	C	CTG	0.154920	-0.015746	0.002798	9.6E-09
NID2	14	rs2749880	52,046,151	G	A	0.154596	-0.015949	0.002799	6.3E-09
NID2	14	rs2645738	52,046,484	G	A	0.154574	-0.015878	0.002799	7.4E-09
NID2	14	rs1566131	52,047,966	G	A	0.154574	-0.015919	0.002800	6.4E-09
SERPINA5	14	rs6113	94,587,512	C	T	0.283052	-0.012768	0.002289	2.4E-08
SERPINA5	14	rs6118	94,587,526	T	C	0.282586	-0.012799	0.002288	2.2E-08
SERPINA5	14	rs6119	94,587,675	G	A	0.265346	-0.012586	0.002317	4.1E-08
AQP9 *	15	rs72739147	58,279,202	T	A	0.090947	-0.021060	0.003535	1.9E-10
AQP9 *	15	rs11854242	58,279,711	T	C	0.186155	-0.014994	0.002633	2.0E-09
AQP9 *	15	rs11854318	58,279,783	A	G	0.183166	-0.015973	0.002650	2.2E-10
AQP9 *	15	chr15:58279835_A_AAG	58,279,835	AAG	A	0.468431	0.011466	0.002065	1.3E-09
AQP9 *	15	rs28690720	58,281,634	G	T	0.102753	-0.021512	0.003326	1.4E-11
AQP9 *	15	rs71478659	58,281,964	G	C	0.469883	0.011733	0.002051	5.5E-10
AQP9 *	15	rs58038553	58,282,125	G	A	0.101473	-0.020921	0.003349	6.8E-11
AQP9 *	15	rs56142310	58,282,759	C	T	0.089489	-0.023096	0.003581	7.5E-12
AQP9 *	15	rs11071371	58,284,027	T	C	0.102428	-0.021938	0.003333	5.4E-12
AQP9 *	15	rs6493996	58,284,097	T	C	0.190189	-0.015515	0.002587	3.9E-10
AQP9 *	15	rs1711037	58,284,151	T	A	0.468699	0.012015	0.002029	1.3E-10
AQP9 *	15	rs10162642	58,284,964	A	G	0.104444	-0.022544	0.003306	1.2E-12
AQP9 *	15	rs12903590	58,285,578	T	A	0.466365	0.011925	0.002028	1.9E-10
AQP9 *	15	rs72294268	58,287,170	T	TATCAC	0.461065	0.011703	0.002025	4.3E-10
AQP9 *	15	rs12910051	58,288,326	G	A	0.462021	0.011525	0.002021	6.7E-10
AQP9 *	15	rs1560390	58,288,582	C	T	0.133666	-0.015596	0.002972	3.9E-08
AQP9 *	15	rs7179728	58,289,227	C	G	0.456932	0.012090	0.002028	1.4E-10
AQP9 *	15	rs938507	58,289,835	A	G	0.460268	0.011423	0.002023	8.9E-10
AQP9 *	15	rs16940017	58,289,949	A	T	0.108550	-0.020601	0.003251	5.8E-11
AQP9 *	15	rs5812930	58,290,280	C	CTT	0.107927	-0.020522	0.003260	7.0E-11
AQP9 *	15	rs1973688	58,290,341	T	C	0.194966	-0.014623	0.002562	3.4E-09
AQP9 *	15	rs1318175	58,293,930	T	C	0.105416	-0.021094	0.003304	4.0E-11
AQP9 *	15	rs1711041	58,298,422	T	G	0.476599	0.010759	0.002030	8.0E-09
AQP9 *	15	rs12899879	58,299,216	C	T	0.480150	0.010442	0.002038	2.6E-08
LIPC *	15	rs261271	58,316,595	C	T	0.281486	-0.012367	0.002294	4.7E-08
LIPC *	15	rs56080561	58,329,431	A	G	0.290457	-0.012076	0.002254	3.7E-08
LIPC *	15	rs1601934	58,379,522	G	A	0.256163	0.022209	0.002366	3.3E-21
LIPC *	15	rs1601935	58,379,566	G	T	0.317072	0.021072	0.002218	3.4E-22
LIPC *	15	rs11071376	58,379,635	C	T	0.140874	0.015973	0.002914	2.6E-08
LIPC *	15	rs74248028	58,380,169	A	G	0.370478	-0.023012	0.002134	1.1E-26
LIPC *	15	chr15:58381250_GA_G	58,381,250	G	GA	0.326272	0.024899	0.002169	1.5E-31
LIPC *	15	rs62001736	58,381,852	A	G	0.186984	0.023436	0.002591	2.3E-20
LIPC *	15	rs2043082	58,382,109	A	G	0.325383	0.025205	0.002163	1.6E-32
LIPC *	15	rs4775041	58,382,496	C	G	0.188145	0.023562	0.002581	8.3E-21
LIPC *	15	rs4775042	58,382,531	C	G	0.483458	-0.017864	0.002043	2.1E-18
LIPC *	15	rs116543766	58,382,658	C	A	0.089852	0.023907	0.003560	1.3E-11
LIPC *	15	rs75525508	58,383,286	A	G	0.369062	-0.022721	0.002122	1.5E-26
LIPC *	15	rs80123226	58,383,833	T	A	0.190870	0.023167	0.002568	2.4E-20
LIPC *	15	rs16940147	58,383,920	A	G	0.134398	0.016453	0.002966	2.1E-08
LIPC *	15	rs11858759	58,384,622	A	G	0.187659	0.023343	0.002585	2.0E-20
LIPC *	15	rs10468017	58,386,313	T	C	0.181599	0.022827	0.002619	3.3E-19
LIPC *	15	rs261290	58,386,521	T	C	0.322111	0.024680	0.002163	2.4E-31
LIPC *	15	rs7350789	58,387,469	A	G	0.322121	0.024898	0.002163	6.4E-32
LIPC *	15	rs58719229	58,387,608	C	CAGA	0.322177	0.024945	0.002163	5.5E-32
LIPC *	15	rs261291	58,387,979	C	T	0.414679	0.026795	0.002053	3.3E-40
LIPC *	15	rs7177289	58,387,985	T	C	0.322386	0.024744	0.002162	1.7E-31
LIPC *	15	rs261292	58,388,705	A	G	0.465822	-0.016792	0.002033	3.0E-16
LIPC *	15	rs2043085	58,388,755	T	C	0.441745	0.025766	0.002036	1.2E-37
LIPC *	15	rs80328086	58,388,800	G	A	0.377813	-0.022744	0.002089	2.4E-27
LIPC *	15	rs75437656	58,388,929	C	A	0.223939	0.019160	0.002435	5.5E-16
LIPC *	15	rs79745310	58,388,956	C	T	0.379515	-0.022738	0.002088	2.8E-27
LIPC *	15	chr15:58389334_G_GT	58,389,334	G	GT	0.358563	0.022282	0.002153	3.0E-26
LIPC *	15	rs261293	58,389,573	C	T	0.251535	0.017000	0.002345	1.3E-13
LIPC *	15	rs76262110	58,389,830	T	TGAA	0.222710	0.019239	0.002443	4.7E-16
LIPC *	15	rs2043084	58,390,297	C	G	0.114448	0.022143	0.003210	3.8E-12
LIPC *	15	rs1825955	58,390,584	A	C	0.247374	0.016742	0.002363	4.7E-13
LIPC *	15	rs12185071	58,391,028	T	C	0.223419	0.019278	0.002438	3.4E-16
LIPC *	15	rs1532085	58,391,167	A	G	0.441207	0.026426	0.002036	1.1E-39
LIPC *	15	rs12185072	58,391,211	T	C	0.251275	0.016841	0.002343	1.7E-13
LIPC *	15	rs12905732	58,391,343	C	G	0.111892	0.022591	0.003229	2.3E-12

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
LIPC *	15	rs28594460	58,391,386	G	A	0.274204	0.014195	0.002287	2.1E-10
LIPC *	15	rs16940167	58,391,498	C	T	0.274095	0.014239	0.002288	1.9E-10
LIPC *	15	rs11853674	58,391,858	G	A	0.111967	0.022669	0.003228	2.0E-12
LIPC *	15	rs16940168	58,391,955	T	A	0.245453	0.016142	0.002367	2.3E-12
LIPC *	15	rs16940170	58,392,083	A	G	0.244800	0.016266	0.002369	1.7E-12
LIPC *	15	rs28495863	58,392,182	A	G	0.245585	0.016060	0.002366	2.9E-12
LIPC *	15	rs12185093	58,392,477	A	G	0.244030	0.016207	0.002373	2.4E-12
LIPC *	15	rs72475921	58,392,838	G	T	0.378524	-0.023272	0.002098	1.3E-28
LIPC *	15	rs199962452	58,393,355	A	T	0.373070	-0.023147	0.002115	8.2E-28
LIPC *	15	rs28703614	58,393,361	T	C	0.245255	0.016402	0.002368	1.2E-12
LIPC *	15	rs7497636	58,393,432	T	C	0.245428	0.016377	0.002367	1.4E-12
LIPC *	15	rs1444942	58,393,614	C	G	0.245349	0.016333	0.002368	1.6E-12
LIPC *	15	rs8042174	58,393,771	C	T	0.380273	-0.023321	0.002097	9.6E-29
LIPC *	15	rs4477794	58,394,439	G	C	0.245641	0.016391	0.002368	1.3E-12
LIPC *	15	rs76679589	58,394,492	T	C	0.245634	0.016385	0.002368	1.4E-12
LIPC *	15	rs7164909	58,394,555	T	C	0.362171	-0.023227	0.002115	1.2E-27
LIPC *	15	rs7165077	58,394,610	T	C	0.387076	-0.022928	0.002085	4.7E-28
LIPC *	15	rs261301	58,394,740	T	C	0.245708	0.016437	0.002367	1.1E-12
LIPC *	15	rs75663614	58,394,841	C	T	0.363356	-0.023054	0.002111	2.4E-27
LIPC *	15	rs5812934	58,395,053	G	GA	0.109361	0.023635	0.003261	4.4E-13
LIPC *	15	rs17240832	58,395,171	G	A	0.245935	0.016537	0.002365	8.7E-13
LIPC *	15	rs74019425	58,395,266	T	G	0.245691	0.016539	0.002364	8.4E-13
LIPC *	15	rs16940181	58,395,325	C	A	0.245803	0.016504	0.002363	9.3E-13
LIPC *	15	rs7171102	58,395,331	A	G	0.109308	0.023512	0.003262	6.0E-13
LIPC *	15	rs174418	58,395,404	T	C	0.393710	0.022237	0.002080	1.9E-27
LIPC *	15	rs166359	58,395,410	G	T	0.246781	0.016083	0.002362	3.8E-12
LIPC *	15	rs495348	58,395,591	C	G	0.246235	0.016636	0.002362	5.4E-13
LIPC *	15	rs8032310	58,395,663	A	G	0.247405	0.016563	0.002363	8.0E-13
LIPC *	15	rs493987	58,395,707	T	C	0.245812	0.016619	0.002363	6.2E-13
LIPC *	15	rs76438892	58,395,733	G	A	0.362257	-0.023119	0.002113	2.4E-27
LIPC *	15	rs4238329	58,395,987	C	A	0.359926	-0.023284	0.002116	9.7E-28
LIPC *	15	rs920917	58,396,279	C	A	0.244960	0.016414	0.002368	1.2E-12
LIPC *	15	rs11855284	58,396,988	C	T	0.111246	0.022781	0.003238	2.0E-12
LIPC *	15	rs11858481	58,396,998	T	C	0.109086	0.023394	0.003267	9.5E-13
LIPC *	15	rs17821298	58,398,539	A	C	0.310095	0.014060	0.002209	5.6E-11
LIPC *	15	rs76898656	58,399,003	A	G	0.358042	-0.022820	0.002132	3.2E-26
LIPC *	15	rs74019428	58,399,009	T	C	0.358042	-0.022817	0.002132	3.2E-26
LIPC *	15	rs490098	58,399,026	C	A	0.252527	0.015812	0.002351	4.4E-12
LIPC *	15	rs2082149	58,399,190	A	G	0.258705	0.016250	0.002332	7.6E-13
LIPC *	15	rs8024755	58,399,670	A	G	0.416132	-0.022042	0.002079	6.6E-26
LIPC *	15	rs397923	58,399,919	A	T	0.368920	0.023174	0.002126	1.9E-28
LIPC *	15	rs35128881	58,399,949	T	G	0.107893	0.023210	0.003301	1.8E-12
LIPC *	15	rs12708454	58,400,003	A	C	0.467857	0.012621	0.002060	1.1E-09
LIPC *	15	rs414671	58,400,280	C	T	0.254218	0.016258	0.002343	9.9E-13
LIPC *	15	rs60900172	58,400,418	C	G	0.357380	-0.023113	0.002152	1.4E-26
LIPC *	15	rs12906722	58,400,516	T	C	0.105501	0.024070	0.003330	4.2E-13
LIPC *	15	rs16940204	58,400,737	T	C	0.103063	0.023942	0.003372	1.2E-12
LIPC *	15	rs487766	58,401,661	C	T	0.107796	0.023829	0.003312	6.0E-13
LIPC *	15	rs16940212	58,401,821	T	G	0.274056	0.016932	0.002266	4.1E-14
LIPC *	15	rs76686550	58,402,458	G	C	0.290183	0.016588	0.002269	2.2E-13
LIPC *	15	rs16940213	58,403,138	T	C	0.272755	0.017332	0.002299	3.5E-14
LIPC *	15	rs79111033	58,403,393	A	G	0.271136	0.017486	0.002310	2.8E-14
LIPC *	15	rs35980001	58,430,391	GC	G	0.341916	0.029974	0.002157	1.7E-47
LIPC *	15	rs1077835	58,431,227	G	A	0.383945	0.029580	0.002076	5.2E-50
LIPC *	15	rs1077834	58,431,280	C	T	0.383505	0.029188	0.002075	6.1E-49
LIPC *	15	rs1800588	58,431,476	T	C	0.359191	0.029100	0.002102	2.3E-47
LIPC *	15	rs2070895	58,431,740	A	G	0.382174	0.029653	0.002076	2.4E-50
LIPC	15	rs6494005	58,432,325	G	A	0.242626	-0.016250	0.002353	2.3E-13
LIPC	15	rs8034802	58,432,593	T	A	0.358495	-0.016690	0.002100	4.7E-18
LIPC	15	rs8033940	58,432,643	G	A	0.303587	-0.019266	0.002192	1.6E-21
LIPC	15	rs633695	58,433,640	A	G	0.355986	-0.016136	0.002111	7.9E-17
LIPC	15	rs261334	58,434,545	G	C	0.342107	0.027608	0.002123	3.1E-42
LIPC	15	rs71116564	58,434,769	C	CCAAAG.	0.343832	0.027468	0.002130	2.5E-41
LIPC, LOC101928694	15	rs261333	58,435,080	C	T	0.238508	-0.016074	0.002400	1.2E-12
LIPC, LOC101928694	15	rs17190517	58,436,945	T	C	0.222274	-0.015534	0.002446	3.0E-11
LIPC, LOC101928694	15	rs588136	58,438,299	C	T	0.364179	0.024861	0.002101	2.1E-35
LIPC, LOC101928694	15	rs261342	58,438,954	C	G	0.425057	-0.014871	0.002050	1.2E-14
LIPC, LOC101928694	15	rs17301746	58,439,196	T	C	0.258120	0.018949	0.002339	7.3E-18
LIPC, LOC101928694	15	rs261341	58,439,368	G	A	0.340337	-0.014038	0.002139	9.7E-13
LIPC, LOC101928694	15	rs8043310	58,439,619	A	C	0.232419	0.021419	0.002428	1.4E-20
LIPC, LOC101928694	15	rs12594375	58,440,269	A	G	0.253583	0.019086	0.002361	7.9E-18
LIPC, LOC101928694	15	rs6494007	58,442,446	T	C	0.258662	0.020006	0.002348	1.1E-19
LIPC, LOC101928694	15	rs534933	58,443,023	A	C	0.039407	0.027978	0.005253	4.5E-08
TLE3 *	15	rs4776482	69,851,564	G	C	0.405895	-0.011944	0.002087	1.1E-09
TLE3 *	15	rs305006	69,851,871	T	C	0.327456	-0.012207	0.002159	1.2E-09
TLE3 *	15	rs10468044	69,852,097	C	A	0.405812	-0.012018	0.002086	8.8E-10
TLE3 *	15	rs305007	69,853,073	G	C	0.362973	-0.011485	0.002109	4.6E-09
TLE3 *	15	rs305008	69,853,301	A	G	0.362998	-0.011470	0.002109	4.9E-09
TLE3 *	15	rs305009	69,853,419	A	G	0.327524	-0.012149	0.002150	1.1E-09
TLE3 *	15	rs305010	69,853,872	G	A	0.362975	-0.011490	0.002109	4.5E-09
TLE3 *	15	rs480441	69,855,220	C	T	0.327276	-0.012148	0.002152	1.0E-09
TLE3 *	15	rs442652	69,856,555	C	A	0.327181	-0.012308	0.002154	6.6E-10
TLE3 *	15	rs428823	69,856,745	C	T	0.327272	-0.012347	0.002153	6.0E-10
TLE3 *	15	rs28669171	69,857,361	T	G	0.309407	-0.012265	0.002233	3.1E-09
TLE3 *	15	rs435315	69,857,677	A	T	0.325050	-0.012683	0.002163	2.7E-10
TLE3 *	15	rs442784	69,857,947	T	C	0.325049	-0.012703	0.002163	2.6E-10
TLE3 *	15	rs446721	69,858,754	T	C	0.325024	-0.012641	0.002165	3.1E-10
TLE3 *	15	rs12594366	69,860,568	C	T	0.316652	-0.012299	0.002183	9.1E-10
TLE3 *	15	rs59650813	69,863,741	C	G	0.314040	-0.012526	0.002196	5.1E-10
TLE3 *	15	rs13380008	69,867,183	C	T	0.341500	-0.012287	0.002162	1.6E-09
TLE3 *	15	rs13379513	69,867,218	A	G	0.337617	-0.012705	0.002167	6.3E-10
TLE3 *	15	rs12593720	69,868,843	T	C	0.237957	-0.017186	0.002388	1.7E-14
TLE3 *	15	rs304975	69,869,121	G	C	0.347062	-0.012583	0.002143	4.7E-10
TLE3 *	15	rs304979	69,870,936	C	G	0.346379	-0.012730	0.002144	2.8E-10
TLE3 *	15	rs4777205	69,872,486	A	C	0.367785	-0.011923	0.002112	3.4E-09
TLE3 *	15	rs67972913	69,875,343	C	CT	0.449327	-0.010837	0.002057	4.5E-08
TLE3 *	15	rs10162636	69,875,502	T	G	0.241729	-0.017418	0.002392	7.9E-15

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
TLE3 *	15	rs78943073	69,876,104	A	G	0.238571	-0.017478	0.002397	6.6E-15
TLE3 *	15	rs78385799	69,878,325	A	G	0.270642	-0.014790	0.002304	5.4E-12
TLE3 *	15	rs304959	69,878,607	G	C	0.405038	-0.011301	0.002083	1.7E-08
TLE3 *	15	rs6494835	69,879,436	A	T	0.271483	-0.015317	0.002293	7.4E-13
TLE3 *	15	rs8035009	69,879,649	G	C	0.271941	-0.015541	0.002290	3.9E-13
TLE3 *	15	rs75327024	69,880,728	A	G	0.239865	-0.017500	0.002389	4.0E-15
TLE3 *	15	rs7166273	69,881,625	C	T	0.239669	-0.017754	0.002383	1.5E-15
TLE3 *	15	rs304948	69,884,491	A	G	0.348161	-0.014524	0.002130	1.0E-12
TLE3 *	15	rs1349680	69,886,868	C	T	0.376411	-0.014315	0.002089	2.5E-12
TLE3 *	15	rs1349679	69,887,061	C	T	0.376077	-0.014415	0.002088	1.6E-12
TLE3 *	15	rs304941	69,887,624	T	C	0.347007	-0.014704	0.002129	6.1E-13
TLE3 *	15	rs7175768	69,888,636	C	T	0.376131	-0.014336	0.002088	2.2E-12
TLE3 *	15	rs80287865	69,889,112	T	G	0.230273	-0.019102	0.002410	3.4E-17
TLE3 *	15	rs77648222	69,890,512	G	A	0.235274	-0.019303	0.002383	1.1E-17
TLE3 *	15	rs17756181	69,891,852	G	A	0.244714	-0.019359	0.002349	4.9E-18
TLE3 *	15	rs28521935	69,892,800	C	A	0.239626	-0.018975	0.002375	3.3E-17
TLE3 *	15	rs881053	69,894,413	A	G	0.374498	-0.014317	0.002091	2.2E-12
TLE3 *	15	rs1452725	69,895,764	T	C	0.371959	-0.014350	0.002098	1.6E-12
TLE3 *	15	rs8041139	69,896,404	G	T	0.347326	-0.014844	0.002129	3.3E-13
TLE3 *	15	rs1155996	69,897,006	C	T	0.347160	-0.014753	0.002127	4.3E-13
TLE3 *	15	rs12591142	69,897,251	C	A	0.230832	-0.018865	0.002406	7.1E-17
TLE3 *	15	rs12440731	69,899,052	A	G	0.356651	-0.014824	0.002118	5.2E-13
TLE3 *	15	rs80039904	69,901,814	T	C	0.229426	-0.018285	0.002427	6.8E-16
TLE3 *	15	rs2601882	69,902,992	T	G	0.299812	-0.012284	0.002234	2.8E-09
TLE3 *	15	rs2679629	69,903,547	C	T	0.323942	-0.011784	0.002183	1.2E-08
TLE3 *	15	rs2601883	69,903,678	C	G	0.237267	-0.018308	0.002407	7.7E-16
TLE3 *	15	rs2601885	69,904,439	T	C	0.292717	-0.011756	0.002249	1.3E-08
PCSK6 *	15	rs2084152	101,524,805	C	T	0.479430	0.011907	0.002060	2.7E-09
PCSK6 *	15	rs8025505	101,527,638	T	C	0.497672	0.011226	0.002036	1.9E-08
PCSK6 *	15	rs1037117	101,528,455	A	G	0.479279	0.012143	0.002026	1.9E-09
PCSK6 *	15	rs1037116	101,528,701	T	C	0.466273	0.012362	0.002033	1.4E-09
CETP *	16	rs12446515	56,953,103	T	C	0.159081	-0.017197	0.002783	1.4E-10
CETP *	16	rs56156922	56,953,457	C	T	0.165241	-0.016022	0.002733	6.9E-10
CETP *	16	rs56228609	56,953,853	T	C	0.164308	-0.015882	0.002728	9.7E-10
CETP *	16	rs247616	56,955,678	T	C	0.163016	-0.015575	0.002734	2.3E-09
CETP *	16	rs247617	56,956,804	A	C	0.160913	-0.015994	0.002747	1.2E-09
CETP *	16	rs183130	56,957,451	T	C	0.160534	-0.016166	0.002751	8.6E-10
CETP *	16	rs12149545	56,959,249	A	G	0.161035	-0.016225	0.002746	7.1E-10
CETP *	16	rs3764261	56,959,412	A	C	0.162676	-0.016077	0.002735	8.3E-10
CETP *	16	rs821840	56,959,974	G	A	0.135714	-0.017111	0.003007	2.6E-09
CETP *	16	rs36229491	56,960,332	TA	T	0.163609	-0.015977	0.002729	8.2E-10
CETP *	16	rs17231506	56,960,616	T	C	0.163661	-0.015979	0.002729	8.4E-10
CMIP	16	rs2925979	81,501,185	T	C	0.428822	0.013925	0.002039	3.7E-13
ZNHIT3	17	rs2306589	36,493,030	T	C	0.335792	0.011238	0.002173	4.3E-08
ZNHIT3	17	rs7222903	36,494,779	T	G	0.335896	0.011204	0.002172	4.6E-08
MYO19	17	rs1109442	36,506,381	C	T	0.340590	0.011245	0.002160	3.8E-08
MYO19	17	rs8070260	36,511,076	A	G	0.340599	0.011196	0.002159	4.2E-08
MYO19	17	rs3830270	36,511,576	A	AGT	0.342146	0.011635	0.002161	1.4E-08
PIGW	17	rs11650008	36,536,882	A	C	0.335829	0.011867	0.002166	8.2E-09
PIGW *	17	rs11263770	36,541,028	A	G	0.337258	0.011499	0.002160	1.9E-08
GGNBP2	17	rs3736166	36,544,987	C	G	0.335881	0.011556	0.002163	1.6E-08
GGNBP2	17	rs9906189	36,549,567	G	A	0.338036	0.011768	0.002155	1.0E-08
GGNBP2	17	rs2285642	36,556,904	G	C	0.337792	0.011777	0.002156	1.1E-08
GGNBP2	17	rs10707226	36,560,613	TA	T	0.338191	0.011878	0.002155	7.9E-09
GGNBP2	17	rs9903355	36,580,791	T	C	0.337652	0.011841	0.002157	8.6E-09
DHRS11	17	rs2285640	36,594,774	G	A	0.337150	0.011402	0.002165	3.3E-08
CLTC	17	rs60164173	59,645,912	A	G	0.445368	0.011063	0.002048	2.6E-08
CLTC	17	rs2877975	59,653,444	T	C	0.444761	0.010935	0.002049	3.7E-08
CLTC	17	rs7223899	59,655,224	T	C	0.445403	0.011036	0.002048	2.8E-08
CLTC	17	rs7224631	59,655,553	A	G	0.445402	0.011035	0.002048	2.8E-08
CLTC	17	rs147787850	59,655,565	CT	C	0.445402	0.011035	0.002048	2.8E-08
CLTC	17	rs16943748	59,657,329	A	G	0.445404	0.011035	0.002048	2.8E-08
CLTC	17	rs1528493	59,660,002	C	A	0.445402	0.011035	0.002048	2.8E-08
CLTC	17	rs12603541	59,661,283	T	C	0.445396	0.011044	0.002048	2.7E-08
CLTC	17	rs2014001	59,664,425	C	T	0.445550	0.011039	0.002048	2.6E-08
CLTC	17	rs12601863	59,665,475	G	A	0.445435	0.011038	0.002048	2.7E-08
CLTC	17	rs2272411	59,668,746	G	A	0.445424	0.011054	0.002048	2.6E-08
CLTC	17	rs10515171	59,670,178	G	T	0.445450	0.011101	0.002047	2.3E-08
CLTC	17	rs16943773	59,671,161	G	A	0.445480	0.011098	0.002047	2.4E-08
CLTC	17	rs28465103	59,677,230	G	A	0.448932	0.011024	0.002050	3.6E-08
CLTC	17	rs78373931	59,678,382	CTT	C	0.448636	0.011002	0.002049	3.5E-08
CLTC	17	rs3215190	59,684,023	C	CAT	0.445812	0.011039	0.002045	2.6E-08
CLTC	17	rs57592560	59,684,662	T	C	0.449702	0.010999	0.002049	3.1E-08
CLTC	17	rs2271303	59,685,510	C	T	0.449128	0.011122	0.002049	2.4E-08
CLTC	17	rs7212825	59,691,837	G	A	0.448960	0.011004	0.002049	3.2E-08
CLTC	17	rs139136427	59,695,672	C	CAAAA	0.445987	0.011037	0.002045	2.3E-08
PTRH2	17	rs58742647	59,701,700	TG	T	0.434879	0.011227	0.002052	9.8E-09
PTRH2	17	rs7226149	59,702,871	C	T	0.435875	0.011091	0.002048	1.4E-08
VMP1	17	rs111723017	59,710,070	C	G	0.435802	0.011223	0.002047	1.0E-08
VMP1	17	chr17:59711135_C_CA	59,711,135	CA	C	0.435514	0.011041	0.002057	2.1E-08
VMP1	17	rs371853860	59,711,419	A	AAC	0.405187	-0.011204	0.002068	1.3E-08
VMP1	17	rs67215819	59,711,422	T	TC	0.404899	-0.011251	0.002069	1.2E-08
VMP1	17	rs200302970	59,711,423	T	C	0.402950	-0.010964	0.002076	3.1E-08
VMP1	17	rs9903626	59,713,266	G	A	0.436006	0.011299	0.002047	7.8E-09
VMP1	17	rs12947232	59,714,483	G	A	0.406312	-0.011176	0.002066	1.5E-08
VMP1	17	rs8065615	59,720,804	T	C	0.461569	-0.011436	0.002033	2.8E-09
VMP1	17	rs76856339	59,723,605	A	G	0.434952	0.011448	0.002040	4.8E-09
VMP1	17	rs8080483	59,724,061	C	A	0.435435	0.011444	0.002042	5.0E-09
VMP1	17	rs8081108	59,724,236	T	G	0.400821	-0.010992	0.002064	1.7E-08
VMP1	17	rs8081395	59,724,400	A	G	0.401750	-0.010986	0.002062	1.6E-08
VMP1	17	rs9900133	59,724,686	G	T	0.461881	-0.011387	0.002030	2.9E-09
VMP1	17	rs11870590	59,724,791	A	C	0.462279	-0.011384	0.002030	3.1E-09
VMP1	17	rs72840511	59,728,650	T	G	0.435002	0.011427	0.002040	5.2E-09
VMP1	17	rs56384611	59,732,552	T	TGTTA	0.399246	-0.011084	0.002071	1.5E-08
VMP1	17	rs9901606	59,734,046	C	A	0.434801	0.011461	0.002038	5.0E-09
VMP1	17	rs9910518	59,734,706	C	T	0.434847	0.011487	0.002038	4.6E-09
VMP1	17	rs2271304	59,737,280	G	A	0.434858	0.011455	0.002037	4.6E-09

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
VMP1	17	rs2777898	59,738,247	C	G	0.402372	-0.010815	0.002061	2.8E-08
VMP1	17	rs28516945	59,739,217	C	T	0.426137	0.010736	0.002052	3.8E-08
VMP1	17	rs8067354	59,744,069	G	A	0.462889	-0.010851	0.002030	1.5E-08
VMP1	17	rs56236317	59,744,764	T	C	0.434793	0.011401	0.002038	5.7E-09
VMP1	17	rs7215180	59,744,993	G	A	0.434793	0.011401	0.002038	5.7E-09
VMP1	17	rs6503939	59,746,324	G	A	0.462456	-0.011229	0.002028	4.6E-09
VMP1	17	rs9907923	59,747,566	T	C	0.433742	0.011264	0.002042	9.2E-09
VMP1	17	rs9896742	59,749,169	T	G	0.464633	-0.010957	0.002035	1.2E-08
VMP1	17	rs60451858	59,749,244	G	A	0.435252	0.011453	0.002038	4.5E-09
VMP1	17	rs2665397	59,749,370	A	C	0.401912	-0.010960	0.002061	1.7E-08
VMP1	17	rs139779337	59,751,603	A	G	0.427579	0.011019	0.002063	3.2E-08
VMP1	17	rs72840522	59,752,631	A	G	0.434850	0.011399	0.002038	5.6E-09
VMP1	17	rs2777884	59,753,065	A	G	0.401921	-0.010936	0.002061	1.8E-08
VMP1	17	rs2777885	59,753,112	A	C	0.401918	-0.010941	0.002061	1.8E-08
VMP1	17	rs9899611	59,754,829	G	A	0.435088	0.011424	0.002040	4.7E-09
VMP1	17	rs2777899	59,755,030	G	T	0.402434	-0.010878	0.002063	2.6E-08
VMP1	17	rs71370116	59,759,377	A	AAAAAT	0.402217	-0.011013	0.002063	1.6E-08
VMP1	17	rs72838857	59,759,406	G	A	0.433846	0.011597	0.002041	3.5E-09
VMP1	17	rs8081468	59,759,563	A	G	0.457516	-0.011118	0.002032	6.9E-09
VMP1	17	rs2333563	59,762,207	A	G	0.456682	-0.010939	0.002030	1.0E-08
VMP1	17	rs16948388	59,762,243	T	C	0.434913	0.011434	0.002038	5.0E-09
VMP1	17	rs1874548	59,763,996	G	A	0.434590	0.011353	0.002039	6.2E-09
VMP1	17	rs2777886	59,767,960	G	A	0.434922	0.011433	0.002038	5.0E-09
VMP1	17	rs11326509	59,768,109	CA	C	0.456600	-0.011011	0.002030	8.4E-09
VMP1	17	rs2645477	59,768,263	C	A	0.402956	-0.010897	0.002061	2.1E-08
VMP1	17	rs2777889	59,770,645	A	G	0.457550	-0.010900	0.002034	1.4E-08
VMP1	17	rs2645483	59,770,823	T	G	0.456597	-0.011019	0.002030	8.2E-09
VMP1	17	rs2482455	59,772,095	G	A	0.456581	-0.011025	0.002030	8.1E-09
VMP1	17	rs11650106	59,772,890	T	C	0.401739	-0.010927	0.002061	1.9E-08
VMP1	17	chr17:59774412_TA_T	59,774,412	T	TA	0.402115	-0.010989	0.002064	1.6E-08
VMP1	17	rs116683462	59,774,420	T	A	0.397702	-0.010964	0.002081	2.3E-08
VMP1	17	rs201444735	59,774,421	A	AAAGAA/	0.429962	0.012182	0.002057	8.6E-10
VMP1	17	rs2645466	59,775,853	A	C	0.456603	-0.011084	0.002032	7.1E-09
VMP1	17	rs2645467	59,777,422	T	C	0.435273	0.011508	0.002039	4.5E-09
VMP1	17	rs2132715	59,781,013	T	A	0.435065	0.011515	0.002040	4.3E-09
VMP1	17	rs2150879	59,781,849	A	G	0.401291	-0.011016	0.002065	1.5E-08
VMP1	17	rs2173119	59,782,344	T	C	0.435073	0.011486	0.002040	4.7E-09
VMP1	17	rs2453913	59,782,789	G	T	0.457371	-0.011159	0.002036	6.9E-09
VMP1	17	rs35519306	59,782,796	A	AG	0.433125	0.011793	0.002048	2.4E-09
VMP1	17	chr17:59791184_CTTTITTT_C	59,791,184	C	CTTTITTT	0.404282	-0.011308	0.002060	6.3E-09
VMP1	17	rs2645474	59,791,240	A	G	0.427832	0.011138	0.002063	1.6E-08
VMP1	17	rs2777900	59,795,133	A	G	0.433133	0.011956	0.002037	1.1E-09
VMP1	17	rs2665405	59,797,931	A	G	0.403831	-0.011419	0.002060	4.1E-09
VMP1	17	rs2665404	59,798,035	T	C	0.403732	-0.011420	0.002058	4.1E-09
VMP1	17	rs2645492	59,798,193	A	G	0.433093	0.011947	0.002037	1.1E-09
VMP1	17	rs2102507	59,798,546	G	A	0.432978	0.011970	0.002037	1.0E-09
VMP1	17	rs2645491	59,799,688	T	C	0.433124	0.011929	0.002037	1.1E-09
VMP1	17	rs2777895	59,802,249	G	A	0.403779	-0.011442	0.002058	3.8E-09
VMP1	17	rs2665400	59,802,840	A	G	0.436330	0.012219	0.002038	4.7E-10
VMP1	17	rs77222930	59,802,913	A	AT	0.403779	-0.011442	0.002058	3.8E-09
VMP1	17	rs34890976	59,803,949	AT	A	0.398920	-0.011880	0.002077	1.4E-09
VMP1	17	rs2645489	59,806,010	G	T	0.431473	0.012087	0.002043	6.3E-10
VMP1	17	rs12449331	59,806,285	C	T	0.403802	-0.011368	0.002059	4.4E-09
VMP1	17	rs4622571	59,807,036	T	A	0.467556	-0.011045	0.002027	6.7E-09
VMP1	17	rs2645486	59,808,540	A	T	0.433167	0.011938	0.002037	1.1E-09
VMP1	17	rs2645487	59,808,764	G	T	0.433167	0.011939	0.002037	1.1E-09
VMP1	17	rs11079389	59,810,591	A	G	0.433173	0.011949	0.002037	1.1E-09
VMP1	17	rs2063353	59,811,831	G	T	0.404116	-0.011475	0.002058	3.6E-09
VMP1	17	rs2645488	59,812,044	T	G	0.467059	-0.011058	0.002026	6.5E-09
VMP1	17	rs2665402	59,812,045	T	A	0.467059	-0.011058	0.002026	6.5E-09
VMP1	17	rs2665403	59,812,624	A	G	0.433659	0.011950	0.002036	1.1E-09
VMP1	17	rs2173120	59,815,279	T	A	0.433598	0.011887	0.002036	1.3E-09
VMP1	17	chr17:59815464_ATTT_A	59,815,464	A	ATTT	0.432067	0.012017	0.002042	1.0E-09
VMP1	17	rs115869798	59,815,468	A	T	0.432067	0.012017	0.002042	1.0E-09
VMP1	17	chr17:59815689_TA_T	59,815,689	TA	T	0.469976	-0.010539	0.002036	3.9E-08
VMP1	17	rs71145576	59,815,855	C	AAAAAA/	0.434852	0.011859	0.002039	1.4E-09
VMP1	17	rs4257266	59,817,098	G	A	0.464316	-0.011001	0.002040	1.1E-08
VMP1	17	rs147970496	59,817,246	CTGGGCA	C	0.433637	0.011953	0.002036	1.0E-09
VMP1	17	chr17:59817342_C_CTTTTA	59,817,342	CTTTTA	C	0.465163	-0.010658	0.002038	2.7E-08
VMP1	17	rs11079390	59,818,580	G	C	0.467074	-0.011040	0.002026	6.8E-09
VMP1	17	rs7223793	59,818,661	G	T	0.433643	0.011954	0.002036	1.0E-09
VMP1	17	rs2333617	59,818,859	A	T	0.467074	-0.011040	0.002026	6.8E-09
VMP1	17	rs7224006	59,818,977	T	C	0.467067	-0.011041	0.002026	6.8E-09
VMP1	17	rs12938273	59,824,291	A	G	0.404186	-0.011284	0.002060	6.2E-09
VMP1	17	rs2526352	59,827,462	A	G	0.431516	0.011629	0.002042	3.5E-09
VMP1	17	rs1292065	59,828,927	G	C	0.467081	-0.011033	0.002026	7.0E-09
VMP1	17	rs1292064	59,828,957	C	A	0.403718	-0.011438	0.002058	3.7E-09
VMP1	17	rs34385574	59,829,215	T	TC	0.403880	-0.011482	0.002058	3.3E-09
VMP1	17	rs1292063	59,830,407	T	A	0.434859	0.011841	0.002040	1.5E-09
VMP1	17	rs1295926	59,832,012	G	A	0.403894	-0.011528	0.002058	2.9E-09
VMP1	17	rs1296280	59,832,068	T	A	0.403755	-0.011524	0.002058	3.0E-09
VMP1	17	chr17:59832573_ATTTGT_A	59,832,573	A	ATTTGT	0.474729	-0.011202	0.002034	5.6E-09
VMP1	17	rs1295925	59,832,902	C	T	0.467093	-0.011083	0.002026	6.1E-09
VMP1	17	rs1292061	59,833,869	G	A	0.404026	-0.011480	0.002058	3.3E-09
VMP1	17	rs1292060	59,836,488	A	G	0.467090	-0.011078	0.002026	6.1E-09
MIR21 *	17	rs1292037	59,841,547	C	T	0.433617	0.012000	0.002036	9.0E-10
MIR21 *	17	rs13137	59,841,670	T	A	0.433617	0.012000	0.002036	9.0E-10
MIR21 *	17	rs2645479	59,843,171	A	G	0.403810	-0.011617	0.002059	2.2E-09
MIR21 *	17	rs35043561	59,843,860	G	GC	0.467000	-0.011060	0.002030	6.8E-09
MIR21 *	17	rs1292072	59,848,288	G	A	0.433419	0.011827	0.002042	1.7E-09
MIR21 *	17	chr17:59849030_GT_G	59,849,030	GT	G	0.403657	-0.011177	0.002065	9.4E-09
MIR21 *	17	rs79417738	59,850,363	G	A	0.372738	0.011982	0.002129	2.3E-08
TUBD1 *	17	rs1292067	59,853,285	T	G	0.448238	0.011495	0.002042	1.7E-08
TUBD1 *	17	rs1292066	59,854,953	A	T	0.386860	0.011359	0.002091	4.6E-08
TUBD1 *	17	rs1292043	59,856,808	G	A	0.384122	0.011878	0.002087	1.2E-08
TUBD1 *	17	rs1292042	59,857,634	G	A	0.382678	0.011935	0.002087	9.7E-09
TUBD1	17	rs2526358	59,865,224	G	A	0.380167	0.011793	0.002087	1.5E-08

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
TUBD1	17	chr17:59871960_A_AT	59,871,960	AT	A	0.364262	0.011944	0.002138	2.7E-08
TUBD1	17	rs2250526	59,874,612	A	G	0.379057	0.011600	0.002083	2.3E-08
TUBD1	17	rs1292049	59,877,544	T	G	0.379056	0.011581	0.002083	2.4E-08
TUBD1	17	rs1292059	59,880,527	A	T	0.379061	0.011604	0.002083	2.2E-08
TUBD1	17	rs1292057	59,880,763	T	C	0.393398	0.011364	0.002071	2.9E-08
TUBD1	17	rs1295923	59,883,075	G	A	0.378523	0.011550	0.002084	2.6E-08
TUBD1	17	rs1292050	59,887,808	C	T	0.379139	0.011643	0.002082	2.0E-08
TUBD1	17	rs1296279	59,888,370	A	G	0.379133	0.011651	0.002082	1.9E-08
TUBD1	17	rs112149564	59,888,869	A	G	0.378018	0.011687	0.002087	1.8E-08
TUBD1	17	rs148385197	59,888,872	T	C	0.378204	0.011687	0.002087	1.8E-08
TUBD1	17	rs111282327	59,889,907	C	T	0.378351	0.011862	0.002092	1.2E-08
RPS6KB1	17	rs1292039	59,897,552	T	A	0.379265	0.011604	0.002082	2.3E-08
RPS6KB1	17	rs201550787	59,899,205	A	AG	0.443121	0.011220	0.002036	4.4E-08
RPS6KB1	17	rs2645480	59,899,206	A	G	0.443121	0.011220	0.002036	4.4E-08
RPS6KB1	17	rs2526354	59,899,297	C	T	0.379296	0.011542	0.002082	2.7E-08
RPS6KB1	17	rs2645481	59,900,581	A	G	0.379204	0.011596	0.002082	2.3E-08
RPS6KB1	17	rs7224366	59,906,904	T	G	0.377579	0.011577	0.002088	2.4E-08
RPS6KB1	17	chr17:59907006_C_CT	59,907,006	CT	C	0.383267	0.011495	0.002086	3.2E-08
RPS6KB1	17	rs2526353	59,911,246	T	G	0.379267	0.011558	0.002080	2.4E-08
RPS6KB1	17	rs1292035	59,912,196	A	G	0.379314	0.011572	0.002081	2.3E-08
RPS6KB1	17	rs1292033	59,913,236	T	A	0.379149	0.011477	0.002081	2.9E-08
RPS6KB1	17	rs3066247	59,914,784	T	TATC	0.378691	0.011550	0.002083	2.7E-08
RPS6KB1	17	rs1358683643	59,915,799	TA	T	0.441881	-0.011210	0.002047	1.9E-08
RPS6KB1	17	rs1291947	59,918,975	T	G	0.379295	0.011477	0.002081	3.1E-08
RPS6KB1	17	rs180536	59,919,445	A	G	0.443146	0.011154	0.002033	4.5E-08
RPS6KB1	17	rs1148559	59,920,166	T	C	0.379352	0.011497	0.002081	2.9E-08
RPS6KB1	17	rs1148560	59,920,253	A	G	0.379153	0.011493	0.002082	3.0E-08
RPS6KB1	17	rs2531899	59,929,832	A	G	0.378458	0.011538	0.002085	2.6E-08
RPS6KB1	17	rs2531898	59,934,990	C	G	0.379347	0.011485	0.002081	3.1E-08
RPS6KB1	17	rs2645478	59,937,351	A	G	0.379347	0.011485	0.002081	3.1E-08
RPS6KB1	17	rs72840315	59,940,781	C	G	0.379347	0.011485	0.002081	3.1E-08
RPS6KB1	17	rs9789060	59,941,209	G	A	0.378679	0.011493	0.002084	3.3E-08
RPS6KB1	17	rs145383951	59,943,933	T	TACAC	0.378820	0.011469	0.002083	3.5E-08
RPS6KB1	17	rs1051424	59,946,963	G	A	0.379471	0.011432	0.002080	3.8E-08
RNFT1	17	rs7219089	59,955,504	T	C	0.379823	0.011657	0.002081	2.0E-08
RNFT1	17	rs7221472	59,959,376	T	C	0.379379	0.011538	0.002081	2.7E-08
RNFT1	17	rs12600680	59,960,013	C	T	0.378983	0.011440	0.002083	3.8E-08
RNFT1	17	rs150771523	59,960,917	T	TAATA	0.379225	0.011528	0.002081	2.8E-08
RNFT1 *	17	rs76419616	59,964,765	C	T	0.378291	0.011639	0.002086	2.1E-08
BPTF *	17	rs3936134	67,818,266	C	G	0.374868	-0.011624	0.002130	3.4E-08
BPTF *	17	rs72631329	67,822,258	T	C	0.374318	-0.011785	0.002132	2.3E-08
BPTF	17	rs3833111	67,826,457	CAG	C	0.340432	-0.012863	0.002179	1.5E-09
BPTF	17	chr17:67829112_TTTG_T	67,829,112	TTTG	T	0.344441	-0.013048	0.002169	8.3E-10
BPTF	17	rs12603589	67,829,132	T	C	0.343835	-0.013149	0.002163	5.3E-10
BPTF	17	rs12601921	67,829,238	C	T	0.342767	-0.013495	0.002177	2.2E-10
BPTF	17	rs12601919	67,829,258	A	G	0.344266	-0.013287	0.002162	3.9E-10
BPTF	17	rs9915591	67,829,974	C	G	0.344386	-0.013038	0.002162	8.2E-10
BPTF	17	rs12602556	67,830,745	A	G	0.343716	-0.013122	0.002160	5.8E-10
BPTF	17	rs62084208	67,831,327	C	T	0.344143	-0.013225	0.002158	4.5E-10
BPTF	17	rs2080090	67,832,255	T	A	0.347440	-0.013116	0.002174	5.6E-10
BPTF	17	rs62084210	67,832,594	A	G	0.343869	-0.013363	0.002158	2.8E-10
BPTF	17	rs12449312	67,833,242	A	C	0.350329	-0.012676	0.002167	1.7E-09
BPTF	17	rs7223643	67,834,166	A	G	0.344786	-0.013231	0.002145	3.0E-10
BPTF	17	rs1976052	67,834,462	C	T	0.344958	-0.013348	0.002143	2.2E-10
BPTF	17	rs7209675	67,835,142	A	T	0.344758	-0.013259	0.002133	2.2E-10
BPTF	17	chr17:67835212_T_TA	67,835,212	T	TA	0.346173	-0.013305	0.002134	2.0E-10
BPTF	17	rs75873575	67,835,625	GT	G	0.344899	-0.013360	0.002129	1.4E-10
BPTF	17	rs142633440	67,835,663	TTTTTT	A	0.344721	-0.013299	0.002131	1.8E-10
BPTF	17	rs7218014	67,835,900	T	C	0.343895	-0.013535	0.002134	8.7E-11
BPTF	17	rs7221651	67,836,274	G	A	0.344876	-0.013318	0.002128	1.6E-10
BPTF	17	rs12452511	67,836,460	A	G	0.344876	-0.013318	0.002128	1.6E-10
BPTF	17	rs1976053	67,836,886	C	G	0.337681	-0.013570	0.002145	1.2E-10
BPTF	17	rs1976054	67,837,108	T	G	0.344876	-0.013318	0.002128	1.6E-10
BPTF	17	rs7208909	67,837,430	T	C	0.347887	-0.013138	0.002132	2.5E-10
BPTF	17	rs2052187	67,838,621	T	C	0.344876	-0.013318	0.002128	1.6E-10
BPTF	17	rs11079705	67,839,336	A	T	0.348431	-0.012852	0.002133	6.1E-10
BPTF	17	rs11079706	67,839,354	G	T	0.345168	-0.013259	0.002133	1.9E-10
BPTF	17	rs11079707	67,839,501	G	A	0.345109	-0.013300	0.002129	1.7E-10
BPTF	17	rs80135947	67,839,885	A	C	0.344874	-0.013325	0.002128	1.5E-10
BPTF	17	chr17:67840458_CTTG_C	67,840,458	CTTG	C	0.346257	-0.013310	0.002133	2.1E-10
BPTF	17	rs59252707	67,840,471	T	C	0.357273	-0.012712	0.002147	1.4E-09
BPTF	17	rs6504542	67,840,526	T	C	0.344864	-0.013306	0.002128	1.6E-10
BPTF	17	rs8082512	67,840,943	T	C	0.344864	-0.013306	0.002128	1.6E-10
BPTF	17	rs1599859	67,841,077	C	G	0.344710	-0.013228	0.002129	2.1E-10
BPTF	17	rs1966410	67,841,099	T	C	0.344710	-0.013228	0.002129	2.1E-10
BPTF	17	rs58551145	67,841,119	A	G	0.344849	-0.013158	0.002129	2.8E-10
BPTF	17	rs6504543	67,841,543	T	C	0.339096	-0.013601	0.002138	8.1E-11
BPTF	17	rs8067892	67,841,867	A	G	0.344864	-0.013306	0.002128	1.6E-10
BPTF	17	rs8074078	67,842,627	T	G	0.344864	-0.013306	0.002128	1.6E-10
BPTF	17	rs8073510	67,843,094	A	G	0.346046	-0.013167	0.002130	2.7E-10
BPTF	17	rs12450363	67,843,992	T	C	0.345408	-0.012938	0.002132	5.1E-10
BPTF	17	rs62084212	67,844,128	G	A	0.355366	-0.012490	0.002159	2.4E-09
BPTF	17	rs112222385	67,844,408	T	C	0.344279	-0.013310	0.002131	1.5E-10
BPTF	17	rs11871285	67,844,693	G	T	0.346655	-0.013243	0.002128	2.2E-10
BPTF	17	rs11868959	67,844,694	T	C	0.346655	-0.013243	0.002128	2.2E-10
BPTF	17	rs2365466	67,845,013	G	A	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs3029927	67,845,167	A	AAGT	0.340265	-0.013455	0.002139	1.5E-10
BPTF	17	rs2365467	67,845,169	A	T	0.340265	-0.013455	0.002139	1.5E-10
BPTF	17	rs2365468	67,845,202	C	T	0.339539	-0.013580	0.002137	8.3E-11
BPTF	17	rs62084213	67,845,900	A	G	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs7223930	67,846,070	G	A	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs7224923	67,846,149	T	G	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs62084214	67,847,209	C	G	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	chr17:67848171_CT_C	67,848,171	CT	C	0.333783	-0.014050	0.002169	3.3E-11
BPTF	17	rs8081517	67,849,581	A	T	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs8081856	67,849,802	A	G	0.345289	-0.013440	0.002130	1.1E-10
BPTF	17	rs62084234	67,850,944	A	G	0.345307	-0.013279	0.002127	1.7E-10

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
BPTF	17	rs7212293	67,851,209	A	G	0.339754	-0.013564	0.002137	8.6E-11
BPTF	17	chr17:67851919_CT_C	67,851,919	CT	C	0.327430	-0.012726	0.002182	9.5E-10
BPTF	17	rs34733047	67,852,002	T	TA	0.346260	-0.013357	0.002130	1.3E-10
BPTF	17	rs78452260	67,852,406	G	T	0.345406	-0.013286	0.002127	1.7E-10
BPTF	17	rs79993364	67,852,461	C	CCT	0.339539	-0.013580	0.002137	8.3E-11
BPTF	17	rs4791048	67,852,878	G	A	0.339539	-0.013580	0.002137	8.3E-11
BPTF	17	rs2086744	67,853,159	C	G	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs2046323	67,853,811	T	G	0.345319	-0.013301	0.002127	1.6E-10
BPTF	17	rs4791046	67,855,857	G	A	0.346007	-0.013372	0.002128	1.1E-10
BPTF	17	rs4790908	67,856,791	T	G	0.345307	-0.013279	0.002127	1.7E-10
BPTF	17	rs11079709	67,857,247	C	T	0.344927	-0.013447	0.002133	1.3E-10
BPTF	17	rs62084235	67,857,321	C	T	0.343176	-0.013247	0.002136	2.4E-10
BPTF	17	rs12450072	67,857,401	C	G	0.345427	-0.013286	0.002127	1.8E-10
BPTF	17	rs74541577	67,857,535	C	T	0.346281	-0.013206	0.002130	1.9E-10
BPTF	17	rs74561219	67,857,643	T	A	0.345373	-0.013289	0.002127	1.7E-10
BPTF	17	rs28609796	67,858,988	T	A	0.342699	-0.013244	0.002143	3.3E-10
BPTF	17	rs62084238	67,860,457	T	A	0.345566	-0.013238	0.002129	2.1E-10
BPTF	17	rs2128792	67,861,061	C	T	0.345325	-0.013264	0.002127	1.8E-10
BPTF	17	rs2365764	67,861,598	G	A	0.345305	-0.013275	0.002127	1.7E-10
BPTF	17	rs62084240	67,863,117	C	A	0.345297	-0.013292	0.002127	1.6E-10
BPTF	17	rs75352663	67,863,943	AT	A	0.345171	-0.013241	0.002128	2.0E-10
BPTF	17	rs60432293	67,864,291	T	C	0.345327	-0.013282	0.002127	1.7E-10
BPTF	17	rs59950564	67,864,743	A	G	0.345297	-0.013292	0.002127	1.6E-10
BPTF	17	rs8077872	67,864,943	G	T	0.339528	-0.013581	0.002137	8.2E-11
BPTF	17	rs34739687	67,865,998	TA	T	0.339528	-0.013581	0.002137	8.2E-11
BPTF	17	rs4790905	67,867,234	C	A	0.345298	-0.013289	0.002127	1.7E-10
BPTF	17	rs34872586	67,867,350	T	C	0.345547	-0.013254	0.002128	1.9E-10
BPTF	17	rs58141639	67,868,786	C	T	0.345321	-0.013272	0.002127	1.7E-10
BPTF	17	rs61067468	67,869,919	G	A	0.349117	-0.013265	0.002135	2.0E-10
BPTF	17	rs62084246	67,871,795	G	C	0.345267	-0.013247	0.002127	1.9E-10
BPTF	17	rs9912084	67,871,919	A	C	0.345294	-0.013283	0.002127	1.7E-10
BPTF	17	rs9912770	67,872,117	C	T	0.345294	-0.013283	0.002127	1.7E-10
BPTF	17	rs11869819	67,872,553	A	C	0.345268	-0.013248	0.002127	1.9E-10
BPTF	17	rs55939964	67,873,181	G	A	0.345864	-0.013396	0.002127	1.3E-10
BPTF	17	rs12602912	67,873,957	C	T	0.345475	-0.013287	0.002126	1.6E-10
BPTF	17	rs12450907	67,874,528	T	G	0.345268	-0.013248	0.002127	1.9E-10
BPTF	17	rs98906629	67,875,443	G	A	0.345268	-0.013248	0.002127	1.9E-10
BPTF	17	rs12451707	67,875,482	G	A	0.345268	-0.013248	0.002127	1.9E-10
BPTF	17	rs4569324	67,876,634	C	T	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs62084247	67,876,787	C	T	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs112651248	67,876,819	AAG	A	0.339528	-0.013585	0.002137	8.1E-11
BPTF	17	rs9915108	67,878,347	T	C	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs9913471	67,878,379	C	T	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs62084248	67,878,425	C	T	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs12451511	67,878,745	T	G	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs62084249	67,878,882	A	G	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs73352808	67,879,041	G	A	0.359412	-0.012071	0.002152	9.0E-09
BPTF	17	rs11867517	67,879,210	C	T	0.346010	-0.013333	0.002131	1.5E-10
BPTF	17	rs11867537	67,879,376	A	G	0.346290	-0.013252	0.002127	2.0E-10
BPTF	17	rs11867618	67,879,471	G	A	0.346614	-0.013130	0.002127	2.9E-10
BPTF	17	rs35243555	67,880,361	G	C	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs58122682	67,880,799	T	C	0.346060	-0.013294	0.002129	1.7E-10
BPTF	17	rs8074644	67,882,101	G	C	0.345367	-0.013271	0.002127	1.7E-10
BPTF	17	rs62084251	67,882,620	G	A	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs9892803	67,883,127	T	G	0.345295	-0.013284	0.002127	1.7E-10
BPTF	17	rs140912776	67,883,456	TA	T	0.347103	-0.013186	0.002128	2.7E-10
BPTF	17	rs62084252	67,883,462	G	C	0.347103	-0.013186	0.002128	2.7E-10
BPTF	17	rs9897982	67,883,476	G	T	0.340667	-0.013609	0.002138	8.2E-11
BPTF	17	rs6504545	67,884,251	A	G	0.345948	-0.013401	0.002130	1.0E-10
BPTF	17	rs6504546	67,884,269	A	C	0.346146	-0.013540	0.002127	6.9E-11
BPTF	17	rs7213292	67,884,327	A	G	0.345983	-0.013374	0.002127	1.3E-10
BPTF	17	rs115210018	67,884,423	T	C	0.358234	-0.011593	0.002155	2.4E-08
BPTF	17	rs3935969	67,885,843	A	G	0.345283	-0.013302	0.002127	1.6E-10
BPTF	17	rs4318247	67,886,056	A	G	0.345283	-0.013302	0.002127	1.6E-10
BPTF	17	rs75360723	67,886,426	A	AT	0.345025	-0.013515	0.002129	9.3E-11
BPTF	17	rs8082661	67,888,585	G	A	0.345694	-0.012676	0.002158	2.2E-09
BPTF	17	rs7208663	67,889,055	T	C	0.345283	-0.013302	0.002127	1.6E-10
BPTF	17	rs75231441	67,889,369	A	G	0.345283	-0.013302	0.002127	1.6E-10
BPTF	17	rs12452823	67,889,667	G	A	0.345282	-0.013298	0.002127	1.6E-10
BPTF	17	rs11079710	67,889,795	C	T	0.314619	-0.012058	0.002180	1.1E-08
BPTF	17	rs6504548	67,889,932	T	C	0.339485	-0.013590	0.002137	8.0E-11
BPTF	17	rs8079291	67,891,506	A	G	0.344343	-0.013270	0.002131	1.8E-10
BPTF	17	rs8079754	67,891,780	A	G	0.345266	-0.013283	0.002127	1.7E-10
BPTF	17	rs6504549	67,892,668	A	G	0.339463	-0.013578	0.002137	8.4E-11
BPTF	17	rs61676547	67,896,391	G	C	0.334620	-0.013836	0.002162	8.6E-11
BPTF	17	rs56148300	67,896,636	T	C	0.326956	-0.014340	0.002159	1.4E-11
BPTF	17	rs3206817	67,896,718	A	G	0.332979	-0.014036	0.002148	3.0E-11
BPTF	17	rs56404791	67,896,903	T	G	0.327581	-0.014330	0.002157	1.5E-11
BPTF	17	rs145606454	67,897,173	AC	A	0.332124	-0.014150	0.002149	2.1E-11
BPTF	17	rs60477798	67,897,174	C	A	0.355808	-0.014259	0.002156	2.6E-11
BPTF	17	rs6504550	67,898,426	A	G	0.294745	-0.013169	0.002222	1.4E-09
BPTF	17	chr17:67898661_CT_C	67,898,661	CT	C	0.330670	-0.013808	0.002176	9.3E-11
BPTF	17	rs7216064	67,902,693	G	A	0.334179	-0.013733	0.002145	8.0E-11
BPTF	17	rs8065906	67,906,529	G	A	0.346129	-0.013216	0.002128	1.8E-10
BPTF	17	rs6504551	67,907,210	T	G	0.294796	-0.012995	0.002221	2.2E-09
BPTF	17	rs12602655	67,913,326	A	G	0.344873	-0.013139	0.002131	2.3E-10
BPTF	17	rs8072225	67,916,844	A	G	0.326313	-0.014263	0.002160	2.0E-11
BPTF	17	rs55896768	67,917,242	T	C	0.326751	-0.014207	0.002161	2.3E-11
BPTF	17	rs12600941	67,922,691	A	G	0.345467	-0.013249	0.002130	1.6E-10
BPTF	17	rs62085991	67,924,392	G	A	0.346129	-0.013168	0.002128	1.9E-10
BPTF	17	rs62085992	67,926,967	T	A	0.346545	-0.013190	0.002129	2.0E-10
BPTF	17	rs62085993	67,927,036	T	C	0.333196	-0.013993	0.002146	3.3E-11
BPTF	17	rs73338706	67,930,488	T	C	0.331954	-0.013841	0.002151	6.1E-11
BPTF	17	rs4271626	67,934,017	G	A	0.333002	-0.014050	0.002146	2.9E-11
BPTF	17	rs4791300	67,934,656	A	G	0.327896	-0.014849	0.002168	4.0E-12
BPTF	17	rs4791299	67,934,821	A	G	0.327251	-0.014799	0.002168	4.5E-12
BPTF	17	rs56393562	67,937,802	C	T	0.332342	-0.014301	0.002150	1.5E-11

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
BPTF	17	rs5821447	67,940,063	TATTAA	T	0.333053	-0.014454	0.002150	1.0E-11
BPTF	17	rs8071463	67,942,539	A	G	0.331960	-0.013947	0.002149	3.9E-11
BPTF	17	rs12451721	67,942,959	G	A	0.345925	-0.013245	0.002128	1.6E-10
BPTF	17	rs6504555	67,944,611	G	A	0.329349	-0.014377	0.002167	2.0E-11
BPTF	17	rs11870068	67,948,399	A	C	0.331884	-0.013804	0.002150	6.3E-11
BPTF	17	rs7223357	67,949,420	C	G	0.332643	-0.013828	0.002147	6.2E-11
BPTF	17	rs7223813	67,949,724	A	G	0.332643	-0.013828	0.002147	6.2E-11
BPTF	17	rs12449442	67,951,524	G	A	0.343629	-0.013854	0.002145	6.3E-11
BPTF	17	rs11867401	67,951,854	A	G	0.327014	-0.014211	0.002158	2.3E-11
BPTF	17	rs9907491	67,953,877	A	G	0.326996	-0.014238	0.002158	2.1E-11
BPTF	17	rs71142114	67,954,174	G	GT	0.324365	-0.014053	0.002171	5.6E-11
BPTF	17	rs4790974	67,954,991	T	A	0.327086	-0.014239	0.002158	2.1E-11
BPTF	17	rs4790973	67,955,017	C	T	0.333034	-0.013921	0.002147	4.4E-11
BPTF	17	rs77706698	67,957,232	G	A	0.346109	-0.013171	0.002130	2.2E-10
BPTF	17	rs12601759	67,959,168	A	G	0.332531	-0.013996	0.002149	3.8E-11
BPTF	17	rs9899520	67,961,452	G	A	0.322888	-0.014359	0.002175	1.9E-11
BPTF	17	rs146879804	67,961,470	C	CT	0.347250	-0.013225	0.002137	2.1E-10
BPTF	17	chr17:67961971_CA_C	67,961,971	CA	C	0.294253	-0.013188	0.002225	1.4E-09
BPTF	17	rs148803332	67,962,134	C	AAAAGA/	0.314024	-0.014139	0.002219	1.3E-10
BPTF	17	rs60626066	67,965,117	G	A	0.352581	-0.014829	0.002146	3.0E-12
BPTF	17	rs10445361	67,966,122	T	G	0.333863	-0.015226	0.002148	6.0E-13
BPTF	17	rs5821446	67,966,422	AT	A	0.332525	-0.015149	0.002148	9.3E-13
BPTF	17	rs77596502	67,968,054	TAGG	T	0.341300	-0.013410	0.002140	9.3E-11
BPTF	17	rs62086042	67,971,327	T	C	0.286656	-0.012742	0.002243	4.9E-09
BPTF	17	rs62086043	67,971,887	A	G	0.328247	-0.014022	0.002166	3.7E-11
BPTF	17	rs62086044	67,974,721	G	T	0.328374	-0.013992	0.002161	3.0E-11
BPTF	17	rs62086045	67,977,615	G	A	0.327275	-0.014196	0.002164	1.9E-11
BPTF	17	rs4791212	67,979,269	C	T	0.339663	-0.013411	0.002147	1.0E-10
BPTF	17	rs7210027	67,980,937	T	C	0.326762	-0.014205	0.002166	1.9E-11
BPTF	17	rs4790941	67,981,016	G	A	0.327167	-0.014208	0.002164	1.8E-11
BPTF	17	rs11656743	67,984,173	A	G	0.325395	-0.014188	0.002169	2.3E-11
BPTF *	17	rs62086046	67,986,827	C	T	0.328042	-0.014163	0.002165	2.1E-11
C17orf58 *	17	rs75772932	67,988,421	G	A	0.343133	-0.012966	0.002145	3.9E-10
C17orf58	17	rs5821444	67,991,393	T	TTAA	0.323632	-0.014548	0.002192	1.2E-11
C17orf58	17	rs9891146	67,991,933	C	T	0.285256	-0.013291	0.002268	1.5E-09
C17orf58 *	17	rs7502307	67,993,845	C	G	0.343012	-0.013635	0.002176	8.4E-11
C17orf58 *	17	rs113985803	67,993,855	A	G	0.326566	-0.014491	0.002198	1.5E-11
C17orf58 *	17	rs56305452	67,994,384	A	C	0.325001	-0.014329	0.002198	2.5E-11
C17orf58 *	17	rs56315139	67,994,455	G	C	0.283810	-0.013158	0.002283	2.8E-09
C17orf58 *	17	rs62086884	67,998,284	G	C	0.345929	-0.013549	0.002157	7.9E-11
C17orf58 *	17	rs4791295	68,001,201	G	A	0.337558	-0.014425	0.002151	5.3E-12
C17orf58 *	17	rs28855509	68,002,051	T	C	0.337820	-0.014074	0.002149	1.7E-11
C17orf58 *	17	rs74564337	68,003,451	C	T	0.337523	-0.014434	0.002156	6.0E-12
C17orf58 *	17	rs6504568	68,003,532	T	C	0.337175	-0.014423	0.002152	5.7E-12
C17orf58 *	17	rs75756093	68,004,462	TAGTC	T	0.340046	-0.014063	0.002156	2.2E-11
C17orf58 *	17	rs62086889	68,004,487	C	T	0.338982	-0.014281	0.002155	1.0E-11
C17orf58 *	17	rs8081714	68,005,014	G	A	0.337901	-0.014358	0.002152	7.7E-12
C17orf58 *	17	chr17:68007425_G_GT	68,007,425	G	GT	0.309413	-0.013310	0.002239	3.5E-09
C17orf58 *	17	rs28437386	68,008,555	T	A	0.349708	-0.013900	0.002167	5.5E-11
C17orf58 *	17	rs78186330	68,008,599	G	A	0.342887	-0.013650	0.002161	9.6E-11
C17orf58 *	17	chr17:68011432_TTTTG_T	68,011,432	TTTTG	T	0.339504	-0.014204	0.002156	1.3E-11
C17orf58 *	17	rs62086897	68,011,928	A	C	0.334922	-0.013395	0.002152	2.1E-10
C17orf58 *	17	rs62086898	68,013,004	A	G	0.334922	-0.013395	0.002152	2.1E-10
C17orf58 *	17	rs62086899	68,013,018	C	T	0.334922	-0.013395	0.002152	2.1E-10
KPNA2 *	17	rs7225959	68,018,993	T	A	0.339232	-0.013580	0.002148	9.9E-11
KPNA2 *	17	rs62086903	68,019,890	T	C	0.323031	-0.013523	0.002168	2.2E-10
KPNA2 *	17	rs62086904	68,019,980	C	T	0.337322	-0.013175	0.002144	2.7E-10
KPNA2 *	17	rs8182243	68,022,389	C	T	0.298669	-0.012454	0.002206	5.8E-09
KPNA2 *	17	rs8065296	68,022,446	A	T	0.298724	-0.012398	0.002206	6.8E-09
KPNA2 *	17	rs62086906	68,023,810	T	C	0.336324	-0.013306	0.002145	1.9E-10
KPNA2 *	17	rs145520076	68,024,495	G	A	0.342858	-0.013655	0.002161	1.1E-10
KPNA2 *	17	rs189628481	68,024,502	C	T	0.344026	-0.013471	0.002162	1.7E-10
KPNA2 *	17	rs192988621	68,024,504	C	T	0.342172	-0.013403	0.002156	2.5E-10
KPNA2 *	17	rs183763906	68,024,506	C	T	0.342172	-0.013403	0.002156	2.5E-10
KPNA2 *	17	rs200026262	68,024,507	A	G	0.344026	-0.013471	0.002162	1.7E-10
KPNA2 *	17	rs62086907	68,025,051	A	G	0.334626	-0.012878	0.002175	7.3E-10
KPNA2 *	17	rs62086908	68,025,098	G	C	0.336304	-0.013081	0.002152	4.3E-10
KPNA2 *	17	rs7405987	68,025,278	A	G	0.336858	-0.013418	0.002145	1.3E-10
KPNA2 *	17	rs7406031	68,025,637	T	C	0.298593	-0.012401	0.002206	6.7E-09
KPNA2 *	17	rs7406141	68,025,870	C	T	0.298593	-0.012401	0.002206	6.7E-09
KPNA2 *	17	rs8076753	68,026,725	G	A	0.336588	-0.013329	0.002145	1.9E-10
KPNA2 *	17	rs6504574	68,026,895	A	G	0.298593	-0.012401	0.002206	6.7E-09
KPNA2 *	17	rs79778350	68,027,670	C	T	0.324344	-0.013252	0.002209	8.7E-10
KPNA2 *	17	rs62084669	68,028,054	A	G	0.336463	-0.013336	0.002145	1.8E-10
KPNA2 *	17	rs7211282	68,028,479	A	G	0.298275	-0.012310	0.002207	8.6E-09
KPNA2 *	17	rs62084675	68,030,909	G	A	0.295881	-0.012483	0.002212	8.3E-09
KPNA2 *	17	rs77536355	68,032,115	T	A	0.344886	-0.012377	0.002136	2.7E-09
KPNA2 *	17	chr17:68032921_CT_C	68,032,921	CT	C	0.352987	-0.012603	0.002145	1.4E-09
KPNA2 *	17	rs35229997	68,033,474	T	G	0.338538	-0.012899	0.002141	9.2E-10
KPNA2 *	17	rs62084679	68,033,977	A	G	0.295718	-0.012469	0.002213	8.7E-09
KPNA2 *	17	rs202202345	68,034,430	G	GGCT	0.299043	-0.012201	0.002209	1.5E-08
KPNA2 *	17	rs10636181	68,034,433	T	TGC	0.295359	-0.012411	0.002214	1.0E-08
KPNA2 *	17	rs7226002	68,034,719	T	C	0.338265	-0.012846	0.002142	1.0E-09
KPNA2 *	17	rs62084681	68,034,876	G	A	0.338265	-0.012846	0.002142	1.0E-09
KPNA2 *	17	rs75236169	68,035,083	T	C	0.295944	-0.012402	0.002213	1.0E-08
KPNA2 *	17	rs62084682	68,035,405	G	C	0.340312	-0.012598	0.002138	1.6E-09
KPNA2 *	17	rs62084683	68,035,609	G	A	0.297930	-0.012217	0.002207	1.3E-08
KPNA2	17	rs12752	68,035,784	T	C	0.295426	-0.012376	0.002214	9.9E-09
KPNA2	17	rs7214869	68,036,141	T	C	0.295936	-0.012427	0.002212	9.7E-09
KPNA2	17	rs7214119	68,036,182	G	A	0.338334	-0.012828	0.002142	1.1E-09
KPNA2	17	rs8075764	68,036,993	C	A	0.338265	-0.012846	0.002142	1.0E-09
KPNA2	17	rs7503834	68,037,868	A	G	0.294476	-0.012349	0.002217	1.3E-08
KPNA2	17	rs6504576	68,038,360	T	C	0.295216	-0.012384	0.002214	1.1E-08
KPNA2	17	rs146286181	68,039,012	CTA	C	0.337913	-0.012708	0.002144	1.6E-09
KPNA2	17	rs62084689	68,039,173	T	C	0.338108	-0.012685	0.002146	1.7E-09
KPNA2	17	rs62084691	68,039,402	C	T	0.295216	-0.012384	0.002214	1.1E-08
KPNA2	17	rs62084692	68,039,728	C	T	0.338958	-0.012885	0.002146	1.1E-09

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
KPNA2	17	rs62084693	68,039,994	T	C	0.293697	-0.012230	0.002221	1.6E-08
KPNA2	17	chr17:68040078_C_CA	68,040,078	C	CA	0.347355	-0.013041	0.002155	7.2E-10
KPNA2	17	chr17:68040818_A_AT	68,040,818	A	AT	0.296443	-0.012399	0.002215	9.9E-09
KPNA2	17	rs8078543	68,041,135	T	G	0.295216	-0.012384	0.002214	1.1E-08
KPNA2	17	rs62084694	68,041,478	G	T	0.337611	-0.012759	0.002143	1.3E-09
KPNA2	17	rs62084696	68,042,065	G	C	0.295216	-0.012384	0.002214	1.1E-08
KPNA2	17	rs62084697	68,042,440	G	A	0.337611	-0.012759	0.002143	1.3E-09
KPNA2	17	rs4638	68,043,234	G	A	0.295216	-0.012384	0.002214	1.1E-08
KPNA2	17	rs35594666	68,043,502	A	G	0.295216	-0.012384	0.002214	1.1E-08
KPNA2	17	rs354533056	68,043,552	G	A	0.294699	-0.012282	0.002216	1.4E-08
KPNA2	17	chr17:68045755_AT_A	68,045,755	AT	A	0.340969	-0.012336	0.002162	5.4E-09
KPNA2	17	rs62084701	68,046,122	T	C	0.295030	-0.012458	0.002214	9.5E-09
KPNA2 *	17	rs62084702	68,047,041	T	C	0.295216	-0.012384	0.002214	1.1E-08
KPNA2 *	17	rs62084703	68,047,268	C	T	0.337678	-0.012708	0.002142	1.5E-09
KPNA2 *	17	rs7405743	68,047,422	T	C	0.295216	-0.012384	0.002214	1.1E-08
KPNA2 *	17	rs62084704	68,048,913	A	G	0.295216	-0.012384	0.002214	1.1E-08
KPNA2 *	17	rs78496681	68,049,047	C	CA	0.336606	-0.012737	0.002147	1.5E-09
KPNA2 *	17	rs74354868	68,049,715	G	A	0.337658	-0.012768	0.002143	1.3E-09
KPNA2 *	17	rs75885145	68,050,690	G	C	0.295272	-0.012397	0.002214	1.0E-08
KPNA2 *	17	rs7214557	68,051,614	T	C	0.295267	-0.012395	0.002215	1.1E-08
KPNA2 *	17	rs145024643	68,052,216	G	GC	0.294993	-0.012527	0.002215	8.0E-09
KPNA2 *	17	rs7503050	68,052,346	G	T	0.337519	-0.012801	0.002143	1.1E-09
KPNA2 *	17	rs7503056	68,052,533	C	G	0.295045	-0.012450	0.002214	9.0E-09
KPNA2 *	17	rs34503060	68,052,563	G	A	0.295045	-0.012450	0.002214	9.0E-09
KPNA2 *	17	rs7503096	68,052,679	C	T	0.295085	-0.012422	0.002214	9.8E-09
KPNA2 *	17	rs35670842	68,052,729	ACT	A	0.294130	-0.012237	0.002217	1.5E-08
KPNA2 *	17	rs7503206	68,053,058	G	A	0.295120	-0.012451	0.002214	9.2E-09
KPNA2 *	17	rs75033810	68,053,415	G	A	0.333352	-0.013134	0.002149	5.3E-10
KPNA2 *	17	rs62084708	68,053,591	G	A	0.333219	-0.013123	0.002149	5.3E-10
KPNA2 *	17	rs7209959	68,054,289	T	C	0.295120	-0.012451	0.002214	9.2E-09
KPNA2 *	17	rs62084711	68,054,795	T	C	0.295120	-0.012451	0.002214	9.2E-09
KPNA2 *	17	rs28592929	68,056,618	C	T	0.295124	-0.012447	0.002214	9.2E-09
KPNA2 *	17	rs3890640	68,056,912	T	C	0.295124	-0.012447	0.002214	9.2E-09
KPNA2 *	17	rs34843489	68,057,215	T	C	0.294432	-0.012575	0.002217	7.4E-09
KPNA2 *	17	rs139345647	68,057,409	CA	C	0.295084	-0.012476	0.002214	8.5E-09
KPNA2 *	17	rs72318931	68,058,249	CTCTT	C	0.336459	-0.012502	0.002187	8.7E-09
KPNA2 *	17	rs78429175	68,058,655	G	A	0.294836	-0.012495	0.002215	8.4E-09
KPNA2 *	17	rs76542911	68,059,778	G	A	0.295383	-0.012403	0.002214	9.8E-09
KPNA2 *	17	rs62084734	68,060,081	C	T	0.295277	-0.012561	0.002215	6.8E-09
KPNA2 *	17	rs35040337	68,060,566	A	G	0.333181	-0.013175	0.002150	4.4E-10
KPNA2 *	17	rs8072723	68,060,854	A	T	0.295084	-0.012476	0.002214	8.5E-09
KPNA2 *	17	rs6504578	68,061,850	A	G	0.295084	-0.012476	0.002214	8.5E-09
KPNA2 *	17	rs200647245	68,062,663	A	AT	0.340534	-0.012508	0.002157	3.5E-09
KPNA2 *	17	rs62084738	68,063,664	T	C	0.295084	-0.012476	0.002214	8.5E-09
KPNA2 *	17	rs74976757	68,064,790	G	T	0.337575	-0.012871	0.002143	9.4E-10
KPNA2 *	17	rs62084740	68,065,068	C	T	0.337575	-0.012871	0.002143	9.4E-10
KPNA2 *	17	rs77194282	68,065,510	C	T	0.295084	-0.012476	0.002214	8.5E-09
KPNA2 *	17	rs7213585	68,066,200	T	A	0.294997	-0.012493	0.002215	8.1E-09
KPNA2 *	17	rs62084741	68,066,544	T	C	0.295084	-0.012476	0.002214	8.5E-09
KPNA2 *	17	rs74900486	68,066,757	C	T	0.337575	-0.012871	0.002143	9.4E-10
KPNA2 *	17	rs8075604	68,066,985	C	T	0.290646	-0.012503	0.002227	9.3E-09
KPNA2 *	17	rs28850355	68,068,281	T	C	0.291469	-0.012672	0.002232	7.2E-09
KPNA2 *	17	chr17:68069522_AT_A	68,069,522	AT	A	0.295058	-0.012463	0.002219	8.0E-09
KPNA2 *	17	rs75544834	68,070,322	T	C	0.333821	-0.012953	0.002154	1.2E-09
KPNA2 *	17	rs79415988	68,070,853	C	T	0.294543	-0.012283	0.002218	1.7E-08
KPNA2 *	17	rs9674669	68,071,338	G	A	0.294951	-0.012050	0.002220	3.2E-08
KPNA2 *	17	rs184478609	68,071,576	T	C	0.335277	-0.012883	0.002155	7.6E-10
KPNA2 *	17	rs190151381	68,071,898	G	A	0.299709	-0.012219	0.002224	2.0E-08
KPNA2 *	17	rs9747971	68,073,082	C	G	0.294387	-0.012224	0.002219	1.9E-08
KPNA2 *	17	rs9330556	68,073,785	T	G	0.295256	-0.012274	0.002218	1.8E-08
KPNA2 *	17	rs62084742	68,079,426	A	G	0.294480	-0.012241	0.002219	1.8E-08
KPNA2 *	17	rs34937122	68,079,772	A	G	0.294011	-0.012218	0.002221	2.0E-08
KPNA2 *	17	rs147170518	68,079,918	T	AAATCCT	0.339677	-0.012770	0.002145	1.5E-09
KPNA2 *	17	rs78352159	68,082,103	C	G	0.339481	-0.012905	0.002144	1.5E-09
KPNA2 *	17	rs75428197	68,082,271	A	G	0.296530	-0.012551	0.002212	8.5E-09
KPNA2 *	17	rs62084744	68,082,412	T	C	0.340622	-0.012907	0.002148	1.5E-09
KPNA2 *	17	rs869223723	68,082,741	T	TTA	0.340281	-0.012741	0.002145	2.5E-09
KPNA2 *	17	rs62084746	68,083,430	T	C	0.294863	-0.012345	0.002220	2.0E-08
KPNA2 *	17	rs62084747	68,083,493	T	C	0.294863	-0.012345	0.002220	2.0E-08
KPNA2 *	17	rs62084748	68,084,098	T	C	0.296124	-0.012185	0.002220	3.1E-08
KPNA2 *	17	rs111730207	68,087,657	G	C	0.296169	-0.012456	0.002214	1.2E-08
KPNA2 *	17	rs62084750	68,089,067	T	C	0.293775	-0.012054	0.002226	4.8E-08
KPNA2 *	17	rs12943289	68,089,425	G	A	0.294276	-0.012147	0.002224	4.0E-08
KPNA2 *	17	rs12940060	68,089,562	G	C	0.294121	-0.012227	0.002225	3.4E-08
KPNA2 *	17	rs76877263	68,092,945	G	C	0.338279	-0.012747	0.002149	2.7E-09
KPNA2 *	17	rs62084752	68,093,252	G	C	0.338787	-0.012629	0.002149	4.0E-09
KPNA2 *	17	rs28512206	68,093,732	A	T	0.338564	-0.012704	0.002152	3.0E-09
KPNA2 *	17	rs62084755	68,099,765	G	A	0.343253	-0.012022	0.002146	1.8E-08
KPNA2 *	17	rs62084759	68,101,151	G	A	0.294585	-0.012097	0.002225	4.8E-08
LINC00674	17	rs75868869	68,102,013	G	A	0.344136	-0.012159	0.002144	1.3E-08
INSR	19	rs81110533	7,138,817	G	T	0.495927	-0.011723	0.002025	1.1E-08
INSR	19	rs12461909	7,145,620	G	C	0.488448	-0.012532	0.002032	9.6E-10
INSR	19	rs12460478	7,145,951	T	C	0.488573	-0.012603	0.002032	7.8E-10
INSR	19	rs16994221	7,147,505	G	C	0.488398	-0.012796	0.002040	4.1E-10
INSR	19	rs7256994	7,180,811	A	G	0.180620	-0.014185	0.002645	3.7E-08
ANGPTL4 *	19	rs11881114	8,356,174	C	T	0.016194	-0.048755	0.008017	3.7E-09
ANGPTL4 *	19	rs113472294	8,356,384	A	G	0.016198	-0.048646	0.008016	4.0E-09
ANGPTL4 *	19	rs111651803	8,356,534	G	A	0.016201	-0.048439	0.008015	4.7E-09
ANGPTL4 *	19	rs62117487	8,359,176	G	A	0.029370	-0.037427	0.006033	2.8E-09
ANGPTL4 *	19	rs112090257	8,359,426	A	G	0.016244	-0.048394	0.008005	4.6E-09
ANGPTL4 *	19	rs112365616	8,360,096	T	C	0.015827	-0.048675	0.008110	7.9E-09
ANGPTL4 *	19	rs111500536	8,360,674	A	G	0.031865	-0.040301	0.005781	1.2E-11
ANGPTL4 *	19	rs112634335	8,361,765	C	G	0.016383	-0.049205	0.007968	2.3E-09
ANGPTL4 *	19	rs112822112	8,363,947	A	G	0.015256	-0.050204	0.008268	2.1E-09
ANGPTL4	19	rs113446232	8,368,117	T	C	0.016637	-0.048676	0.007907	2.2E-09
ANGPTL4	19	rs77439987	8,369,178	A	G	0.016917	-0.047762	0.007839	2.6E-09
ANGPTL4	19	rs35061979	8,371,316	A	G	0.016794	-0.048115	0.007868	2.3E-09

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
ANGPTL4	19	rs112625532	8,372,050	A	G	0.016745	-0.048798	0.007877	1.3E-09
RAB11B-AS1	19	rs111313909	8,374,409	C	T	0.016740	-0.049376	0.007879	8.8E-10
RAB11B-AS1	19	rs113896502	8,375,087	G	C	0.016739	-0.049371	0.007879	8.9E-10
RAB11B-AS1	19	rs111910861	8,376,434	A	T	0.016739	-0.049371	0.007879	8.9E-10
RAB11B-AS1	19	rs113687395	8,377,181	A	C	0.016739	-0.049371	0.007879	8.9E-10
RAB11B-AS1	19	rs112381844	8,380,361	T	C	0.016740	-0.049361	0.007879	8.9E-10
RAB11B-AS1	19	rs149784573	8,382,281	A	G	0.016744	-0.049509	0.007878	8.1E-10
RAB11B-AS1	19	rs113937955	8,385,469	C	T	0.016563	-0.049271	0.007921	1.2E-09
RAB11B	19	rs112981054	8,390,708	A	G	0.016024	-0.049833	0.008069	1.3E-09
RAB11B	19	rs113090151	8,390,816	A	G	0.016024	-0.049829	0.008069	1.3E-09
RAB11B	19	rs10403402	8,401,621	A	G	0.015171	-0.051997	0.008286	7.5E-10
RAB11B *	19	rs10426486	8,405,069	A	G	0.015212	-0.050781	0.008268	1.5E-09
RAB11B *	19	rs6603067	8,405,680	C	T	0.015462	-0.052074	0.008198	4.0E-10
MARCHF2 *	19	rs71175850	8,409,899	CA	C	0.015432	-0.052246	0.008206	3.6E-10
MARCHF2 *	19	rs62117520	8,411,923	A	G	0.015433	-0.052403	0.008207	3.3E-10
MARCHF2 *	19	rs368888811	8,413,049	T	C	0.015166	-0.050677	0.008282	1.7E-09
MARCHF2	19	rs62117522	8,416,119	A	G	0.015431	-0.052311	0.008207	3.5E-10
MARCHF2	19	rs112826244	8,422,486	G	A	0.015179	-0.051176	0.008279	1.2E-09
MARCHF2	19	rs77968216	8,422,767	C	T	0.014247	-0.051693	0.008545	1.9E-09
MARCHF2	19	rs61499007	8,428,930	T	C	0.013387	-0.053771	0.008783	1.3E-09
MARCHF2	19	rs17159300	8,429,250	T	C	0.013360	-0.053282	0.008792	2.0E-09
MARCHF2	19	rs34344658	8,430,227	C	G	0.013373	-0.052982	0.008788	2.5E-09
MARCHF2	19	rs34350946	8,430,231	T	C	0.013408	-0.053311	0.008789	1.8E-09
MARCHF2	19	rs113550925	8,435,655	G	C	0.013396	-0.053108	0.008780	2.2E-09
MARCHF2	19	rs60748247	8,435,690	CACCTGT	C	0.013658	-0.054905	0.008691	4.0E-10
MARCHF2	19	rs6603071	8,435,751	T	G	0.013396	-0.053108	0.008780	2.2E-09
MARCHF2	19	rs112363339	8,437,217	C	T	0.013238	-0.051311	0.008828	1.0E-08
MARCHF2	19	rs7408526	8,437,225	A	C	0.013238	-0.051311	0.008828	1.0E-08
MARCHF2	19	rs7408547	8,437,349	A	T	0.013238	-0.051318	0.008828	1.0E-08
MARCHF2	19	rs12976614	8,437,541	T	C	0.013321	-0.050804	0.008805	1.2E-08
MARCHF2	19	rs11259981	8,438,690	A	G	0.013247	-0.051340	0.008825	1.0E-08
MARCHF2 *	19	rs7251323	8,440,340	T	C	0.013254	-0.051110	0.008822	1.2E-08
MARCHF2 *	19	rs6603074	8,440,448	C	T	0.013529	-0.052293	0.008728	3.5E-09
MARCHF2 *	19	rs11259982	8,441,103	T	C	0.013282	-0.050601	0.008814	1.5E-08
HNRNPM *	19	rs10796330	8,442,955	A	G	0.013289	-0.049986	0.008811	2.4E-08
HNRNPM	19	rs11881939	8,445,260	T	C	0.013296	-0.049711	0.008808	2.8E-08
HNRNPM	19	rs7245737	8,445,529	T	G	0.013300	-0.049347	0.008807	3.6E-08
HNRNPM	19	rs6603078	8,446,441	C	G	0.013577	-0.049134	0.008722	3.0E-08
HNRNPM	19	rs78136847	8,447,444	T	A	0.013303	-0.049367	0.008806	3.4E-08
HNRNPM	19	rs76586439	8,448,918	A	G	0.013303	-0.049380	0.008806	3.4E-08
HNRNPM	19	rs11259984	8,450,593	T	G	0.013303	-0.049380	0.008806	3.4E-08
HNRNPM	19	rs113420240	8,450,730	A	T	0.010702	-0.056072	0.009832	4.5E-08
HNRNPM	19	rs7253907	8,452,130	G	A	0.013310	-0.049178	0.008804	3.7E-08
HNRNPM	19	rs6603081	8,454,016	C	T	0.013349	-0.048981	0.008791	4.0E-08
HNRNPM	19	rs1151032440	8,458,266	C	A	0.013346	-0.048942	0.008792	4.1E-08
HNRNPM	19	rs372974746	8,460,844	C	CTA	0.013346	-0.048938	0.008792	4.1E-08
HNRNPM	19	rs1057253	8,461,561	C	G	0.013600	-0.050683	0.008705	9.4E-09
HNRNPM	19	rs8102587	8,463,426	A	G	0.013346	-0.048943	0.008792	4.1E-08
HNRNPM	19	rs11878480	8,465,813	C	T	0.013345	-0.048926	0.008792	4.2E-08
HNRNPM	19	rs11259987	8,467,885	G	A	0.013624	-0.050645	0.008697	8.9E-09
HNRNPM	19	rs11259988	8,468,021	T	C	0.013370	-0.048907	0.008784	3.9E-08
HNRNPM	19	rs7258281	8,468,620	T	C	0.013370	-0.048907	0.008784	3.9E-08
HNRNPM	19	rs10421511	8,469,041	A	G	0.014041	-0.050122	0.008562	9.4E-09
HNRNPM	19	rs113957806	8,470,495	G	T	0.013370	-0.048907	0.008784	3.9E-08
HNRNPM	19	rs7507730	8,470,498	T	G	0.013389	-0.048786	0.008782	4.4E-08
HNRNPM	19	rs145645068	8,471,306	G	T	0.014368	-0.046097	0.008486	3.3E-08
HNRNPM	19	rs77540833	8,472,481	G	A	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs7507621	8,475,376	T	C	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs7408534	8,476,906	G	T	0.013624	-0.050646	0.008697	8.9E-09
HNRNPM	19	rs12611110	8,477,456	A	G	0.013624	-0.050646	0.008697	8.9E-09
HNRNPM	19	rs7255548	8,477,853	C	T	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs111364559	8,481,241	C	T	0.013451	-0.048902	0.008762	3.8E-08
HNRNPM	19	rs6603083	8,482,573	A	G	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs7508561	8,483,613	A	T	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs7409317	8,483,991	C	T	0.013624	-0.050647	0.008697	8.9E-09
HNRNPM	19	rs6603084	8,484,333	T	C	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs7250951	8,484,576	A	T	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs10412549	8,485,223	G	C	0.013624	-0.050647	0.008697	8.9E-09
HNRNPM	19	rs2230647	8,486,210	T	C	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs55635857	8,486,649	CTGAT	C	0.013624	-0.050647	0.008697	8.9E-09
HNRNPM	19	rs11669139	8,486,968	A	G	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs12608524	8,487,283	C	T	0.013370	-0.048908	0.008784	3.9E-08
HNRNPM	19	rs7507526	8,488,438	C	T	0.013631	-0.050683	0.008695	8.5E-09
HNRNPM	19	rs6992	8,488,746	C	T	0.013383	-0.049019	0.008781	3.5E-08
PRAM1	19	rs58034536	8,493,082	A	G	0.013360	-0.049230	0.008788	3.2E-08
NCAN	19	rs145876852	19,248,021	C	A	0.014551	-0.054875	0.008416	1.7E-10
HAPLN4	19	rs150641967	19,259,531	T	TGACA	0.060710	-0.050538	0.004236	3.0E-33
HAPLN4 *	19	rs2074296	19,262,880	G	A	0.317945	-0.013423	0.002178	2.4E-10
HAPLN4 *	19	rs8105094	19,263,252	T	C	0.298031	-0.012996	0.002220	1.3E-09
HAPLN4 *	19	rs8105984	19,263,259	C	T	0.298031	-0.012996	0.002220	1.3E-09
TM6SF2 *	19	rs10684386	19,263,737	AAG	A	0.298902	-0.013083	0.002216	8.7E-10
TM6SF2	19	rs10426780	19,265,074	C	T	0.318349	-0.013207	0.002170	4.2E-10
TM6SF2	19	rs56831097	19,265,416	G	A	0.298846	-0.012984	0.002209	1.5E-09
TM6SF2	19	rs2074298	19,266,907	G	C	0.319204	-0.013114	0.002162	4.9E-10
TM6SF2	19	rs68050962	19,267,386	G	GAA	0.300012	-0.012938	0.002202	1.5E-09
TM6SF2	19	rs58542926	19,268,740	T	C	0.066469	-0.052502	0.004046	1.4E-39
TM6SF2	19	rs2074299	19,269,837	C	T	0.318622	-0.013011	0.002163	6.5E-10
TM6SF2	19	rs2074300	19,270,187	T	G	0.299528	-0.012917	0.002201	1.5E-09
TM6SF2	19	rs2074301	19,270,906	A	G	0.299425	-0.012831	0.002201	1.9E-09
TM6SF2	19	rs2074303	19,270,946	T	C	0.318389	-0.013017	0.002163	6.4E-10
TM6SF2	19	chr19:19271498_C_CTCTT	19,271,498	CTCTT	C	0.316656	-0.012924	0.002170	9.2E-10
TM6SF2	19	rs10419245	19,272,946	A	G	0.319923	-0.012423	0.002161	3.6E-09
TM6SF2 *	19	rs735273	19,274,602	C	T	0.319397	-0.012922	0.002162	8.3E-10
SUGP1 *	19	rs8103496	19,275,206	G	A	0.318405	-0.012960	0.002162	7.5E-10
SUGP1 *	19	rs11882123	19,275,530	G	A	0.318404	-0.012965	0.002162	7.4E-10
SUGP1 *	19	rs2017964	19,276,340	C	T	0.318406	-0.012960	0.002162	7.5E-10
SUGP1	19	rs2074550	19,276,934	C	A	0.318406	-0.012960	0.002162	7.5E-10

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SUGP1	19	rs2074551	19,277,248	C	G	0.324236	-0.012732	0.002178	1.2E-09
SUGP1	19	rs8107974	19,277,691	T	A	0.095896	-0.033109	0.003416	2.2E-23
SUGP1	19	rs8101938	19,279,688	A	G	0.318411	-0.012961	0.002162	7.5E-10
SUGP1	19	rs2301784	19,279,940	A	G	0.318566	-0.012876	0.002163	9.9E-10
SUGP1	19	rs6511026	19,280,593	T	C	0.318413	-0.012957	0.002162	7.6E-10
SUGP1	19	rs2269873	19,281,592	C	T	0.319064	-0.013180	0.002164	4.2E-10
SUGP1	19	rs8100204	19,282,905	A	G	0.223054	-0.013396	0.002465	1.5E-08
SUGP1	19	chr19:19283076_C_CA	19,283,076	CA	C	0.333618	-0.012149	0.002177	7.6E-09
SUGP1	19	rs200210321	19,283,081	AG	A	0.102399	-0.031808	0.003332	1.3E-22
SUGP1	19	chr19:19283440_GTT_G	19,283,440	G	GTT	0.318571	-0.012576	0.002168	2.8E-09
SUGP1	19	rs10407952	19,283,587	T	C	0.316939	-0.012619	0.002171	2.7E-09
SUGP1	19	rs6511028	19,285,158	C	T	0.317925	-0.012553	0.002165	2.6E-09
SUGP1	19	rs7254748	19,286,670	C	A	0.317984	-0.012549	0.002163	2.5E-09
SUGP1	19	rs10418051	19,286,980	T	C	0.317216	-0.012672	0.002166	1.8E-09
SUGP1	19	rs4808937	19,287,196	G	A	0.318103	-0.012539	0.002163	2.6E-09
SUGP1	19	rs4808938	19,290,409	A	G	0.318103	-0.012539	0.002163	2.6E-09
SUGP1	19	rs10409234	19,292,601	G	A	0.318054	-0.012502	0.002163	2.9E-09
SUGP1	19	chr19:19293578_CA_C	19,293,578	C	CA	0.313046	-0.012313	0.002191	9.1E-09
SUGP1	19	rs7254927	19,293,977	G	C	0.318103	-0.012539	0.002163	2.6E-09
SUGP1	19	rs2023882	19,294,596	C	T	0.318092	-0.012497	0.002163	3.0E-09
SUGP1	19	rs2023883	19,294,671	A	G	0.299380	-0.012579	0.002202	4.0E-09
SUGP1	19	rs12979148	19,296,060	C	T	0.220619	-0.013353	0.002439	2.3E-08
SUGP1	19	rs11666553	19,296,362	A	C	0.299301	-0.012547	0.002201	4.4E-09
SUGP1	19	rs10401969	19,296,909	C	T	0.096251	-0.032035	0.003413	4.3E-22
SUGP1	19	rs10665929	19,298,212	CAG	C	0.318100	-0.012614	0.002163	2.1E-09
SUGP1	19	chr19:19298215_A_AGG	19,298,215	AGG	A	0.318100	-0.012614	0.002163	2.1E-09
SUGP1	19	rs5827440	19,299,374	TC	T	0.315213	-0.012799	0.002174	1.6E-09
SUGP1	19	rs4808939	19,299,671	T	C	0.299571	-0.012956	0.002205	1.7E-09
SUGP1	19	rs4808193	19,299,813	C	T	0.317851	-0.012618	0.002164	2.2E-09
SUGP1	19	rs4808940	19,300,139	G	C	0.318112	-0.012673	0.002163	1.8E-09
SUGP1	19	rs4808941	19,300,327	C	T	0.317025	-0.012695	0.002168	1.8E-09
SUGP1	19	rs2315022	19,302,572	G	A	0.316623	-0.012353	0.002168	4.5E-09
SUGP1	19	rs2301786	19,303,138	G	A	0.317922	-0.012593	0.002163	2.3E-09
SUGP1	19	rs1010207	19,305,236	C	T	0.317644	-0.012723	0.002163	1.5E-09
SUGP1	19	rs2240117	19,308,107	T	C	0.221149	-0.013165	0.002435	3.6E-08
SUGP1	19	rs739846	19,308,262	A	G	0.095875	-0.032350	0.003416	2.6E-22
SUGP1	19	rs12983137	19,309,001	A	G	0.299355	-0.012529	0.002202	4.8E-09
SUGP1	19	rs4808942	19,309,772	T	C	0.316003	-0.012289	0.002169	6.1E-09
SUGP1	19	chr19:19311343_CA_C	19,311,343	C	CA	0.307841	-0.012590	0.002204	4.4E-09
SUGP1	19	rs1859287	19,311,378	C	T	0.298760	-0.012241	0.002215	1.3E-08
SUGP1	19	rs2285859	19,311,676	G	A	0.315691	-0.012464	0.002175	4.3E-09
SUGP1	19	rs2315024	19,313,008	A	T	0.299927	-0.012353	0.002200	7.7E-09
SUGP1	19	rs57962361	19,314,216	T	C	0.164400	-0.020070	0.002715	2.9E-14
SUGP1	19	rs12459676	19,314,332	T	A	0.286323	-0.012769	0.002255	5.5E-09
SUGP1	19	rs11668104	19,315,372	A	G	0.164398	-0.020072	0.002715	2.8E-14
SUGP1	19	rs2315025	19,315,800	T	C	0.318454	-0.012438	0.002162	3.3E-09
SUGP1	19	rs8108647	19,316,814	G	A	0.318127	-0.012442	0.002163	3.0E-09
SUGP1	19	rs7259434	19,317,996	T	A	0.297968	-0.012285	0.002208	1.1E-08
SUGP1	19	rs186896134	19,318,143	T	G	0.012393	-0.056154	0.009141	9.8E-10
SUGP1	19	rs12976025	19,318,411	T	C	0.299563	-0.012382	0.002201	6.7E-09
SUGP1	19	rs12977937	19,319,166	G	C	0.317461	-0.012447	0.002165	3.3E-09
SUGP1 *	19	rs3934667	19,320,614	T	G	0.314016	-0.012713	0.002191	2.3E-09
MAU2	19	rs12460764	19,321,154	G	T	0.317461	-0.012447	0.002165	3.3E-09
MAU2	19	rs10402661	19,322,150	G	A	0.302251	-0.012567	0.002209	4.4E-09
MAU2	19	rs7246748	19,322,296	C	T	0.321092	-0.012567	0.002171	2.5E-09
MAU2	19	rs58833986	19,323,233	TCACCA	T	0.296228	-0.012006	0.002216	2.7E-08
MAU2	19	rs7254230	19,323,541	C	T	0.318021	-0.012446	0.002164	3.2E-09
MAU2	19	rs4808194	19,324,871	G	T	0.299390	-0.012571	0.002201	4.2E-09
MAU2	19	rs111234557	19,325,420	G	C	0.164109	-0.020285	0.002718	1.6E-14
MAU2	19	rs62135552	19,326,045	G	A	0.318196	-0.012503	0.002163	2.9E-09
MAU2	19	rs7247309	19,328,822	A	T	0.317862	-0.012608	0.002163	2.1E-09
MAU2	19	rs11411903	19,329,255	TA	T	0.167063	-0.020259	0.002701	1.2E-14
MAU2	19	rs3764567	19,329,257	C	T	0.300037	-0.012669	0.002199	2.9E-09
MAU2	19	rs1009136	19,329,619	A	G	0.318378	-0.012517	0.002164	2.5E-09
MAU2	19	rs67720221	19,330,055	C	T	0.299017	-0.012333	0.002205	7.5E-09
MAU2	19	chr19:19331501_C_CA	19,331,501	C	CA	0.330204	-0.012645	0.002165	1.3E-09
MAU2	19	rs12985655	19,331,625	G	A	0.325112	-0.012638	0.002150	1.2E-09
MAU2	19	rs10640109	19,332,597	C	CAAG	0.299425	-0.012622	0.002201	4.0E-09
MAU2	19	rs8103197	19,332,657	C	T	0.324992	-0.012649	0.002150	1.2E-09
MAU2	19	rs11085259	19,335,047	T	C	0.299071	-0.012706	0.002201	3.0E-09
MAU2	19	rs769267	19,336,127	G	A	0.325242	-0.012687	0.002150	1.1E-09
MAU2	19	rs757000	19,337,492	G	A	0.298591	-0.012587	0.002203	4.4E-09
MAU2	19	rs757001	19,337,999	A	G	0.299061	-0.012719	0.002201	2.9E-09
MAU2	19	rs2074090	19,338,877	G	T	0.324961	-0.012619	0.002150	1.4E-09
MAU2	19	rs2074091	19,339,271	A	G	0.324890	-0.012606	0.002151	1.4E-09
MAU2	19	chr19:19339445_CA_C	19,339,445	C	CA	0.154536	-0.018443	0.002830	8.7E-12
MAU2	19	rs8111511	19,340,184	T	A	0.327596	-0.012488	0.002160	1.8E-09
MAU2	19	rs2301668	19,341,440	A	G	0.298909	-0.012675	0.002202	3.4E-09
MAU2	19	rs2965191	19,342,712	T	G	0.324905	-0.012505	0.002151	1.8E-09
MAU2	19	rs2301669	19,342,751	C	A	0.324807	-0.012565	0.002151	1.6E-09
MAU2	19	rs2965193	19,344,019	G	A	0.327098	-0.012717	0.002147	1.2E-09
MAU2	19	rs58489806	19,346,108	T	C	0.164820	-0.020548	0.002714	9.0E-15
MAU2	19	rs968525	19,348,406	T	C	0.299082	-0.012834	0.002201	2.2E-09
MAU2	19	rs10421505	19,348,745	T	C	0.324421	-0.012825	0.002152	7.1E-10
MAU2	19	rs12982276	19,348,991	C	T	0.323946	-0.012902	0.002153	6.2E-10
MAU2	19	chr19:19350607_C_CA	19,350,607	CA	C	0.287706	-0.014395	0.002247	6.5E-11
MAU2	19	rs12459854	19,350,628	T	C	0.324646	-0.012842	0.002151	7.1E-10
MAU2	19	rs11085261	19,351,797	A	G	0.298463	-0.012653	0.002204	3.6E-09
MAU2	19	rs11672355	19,351,893	C	G	0.162434	-0.020447	0.002744	2.2E-14
MAU2	19	rs9304960	19,354,720	A	G	0.299086	-0.012834	0.002201	2.2E-09
MAU2	19	rs2301671	19,355,460	T	C	0.299086	-0.012834	0.002201	2.2E-09
MAU2	19	rs2285626	19,356,736	T	C	0.173991	-0.022254	0.002660	5.8E-18
MAU2	19	rs2285627	19,357,128	T	C	0.295725	-0.013367	0.002212	5.8E-10
MAU2	19	rs2285628	19,357,187	A	T	0.301189	-0.012434	0.002205	8.5E-09
MAU2	19	rs117970794	19,357,846	T	C	0.090624	-0.029540	0.003504	4.5E-18
MAU2	19	rs13964	19,357,901	C	G	0.325462	-0.012545	0.002154	1.9E-09
MAU2	19	rs15622	19,357,925	G	A	0.326600	-0.012203	0.002152	5.6E-09

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
MAU2	19	rs10403731	19,358,487	A	G	0.298699	-0.012681	0.002206	4.1E-09
MAU2 *	19	rs2965197	19,360,101	C	T	0.327790	-0.012524	0.002185	3.2E-09
MAU2 *	19	rs10419672	19,360,432	C	T	0.323731	-0.012436	0.002157	2.6E-09
MAU2 *	19	rs6511030	19,360,637	G	A	0.330579	-0.011915	0.002194	1.6E-08
MAU2 *	19	rs6511032	19,360,874	C	T	0.323721	-0.012644	0.002156	1.5E-09
MAU2 *	19	rs2905423	19,360,996	G	A	0.325103	-0.012478	0.002154	2.7E-09
MAU2 *	19	rs8101499	19,366,175	A	G	0.301718	-0.012038	0.002199	4.3E-08
MAU2 *	19	rs56255430	19,367,068	C	A	0.066193	-0.042068	0.004057	1.7E-25
MAU2 *	19	rs2074088	19,367,586	T	C	0.298200	-0.012121	0.002215	3.9E-08
GATAD2A *	19	rs59148799	19,373,199	G	A	0.136267	-0.022521	0.002936	7.0E-15
GATAD2A *	19	rs12052117	19,374,296	T	C	0.136244	-0.022401	0.002937	9.2E-15
GATAD2A *	19	rs2965180	19,381,164	T	C	0.300596	-0.012060	0.002200	3.8E-08
GATAD2A *	19	rs2905435	19,385,145	G	A	0.300157	-0.012069	0.002201	4.0E-08
GATAD2A	19	rs10408875	19,392,764	C	T	0.136368	-0.022560	0.002935	4.5E-15
GATAD2A	19	rs56241616	19,395,283	T	C	0.136362	-0.022560	0.002935	4.4E-15
GATAD2A	19	rs10424702	19,397,204	G	A	0.220271	-0.013557	0.002438	4.6E-08
GATAD2A	19	rs10408596	19,401,848	T	A	0.136344	-0.022571	0.002936	4.2E-15
GATAD2A	19	rs34324111	19,402,759	G	T	0.140575	-0.021151	0.002941	9.6E-14
GATAD2A	19	rs113460678	19,402,771	G	T	0.128937	-0.021972	0.003012	1.0E-13
GATAD2A	19	rs188552254	19,406,360	G	A	0.134033	-0.022448	0.002963	9.6E-15
GATAD2A	19	rs2965185	19,414,983	C	T	0.160309	-0.024396	0.002746	1.8E-19
GATAD2A	19	rs11668386	19,421,101	G	A	0.136476	-0.022488	0.002933	5.1E-15
GATAD2A	19	rs8182472	19,429,082	C	T	0.136593	-0.022552	0.002932	4.2E-15
GATAD2A	19	rs2916076	19,435,181	C	T	0.301394	-0.011915	0.002197	4.9E-08
GATAD2A	19	rs79954596	19,437,834	G	T	0.136494	-0.022490	0.002933	4.8E-15
GATAD2A	19	rs4808957	19,456,439	G	A	0.301112	-0.011993	0.002197	4.2E-08
GATAD2A	19	rs4808203	19,457,850	C	T	0.301232	-0.011921	0.002197	4.9E-08
GATAD2A	19	rs4808959	19,461,299	G	T	0.302078	-0.012017	0.002196	3.3E-08
GATAD2A	19	rs28720066	19,461,411	T	G	0.135709	-0.022671	0.002943	3.6E-15
GATAD2A	19	rs73002956	19,467,934	G	A	0.070092	-0.039239	0.003948	9.9E-24
GATAD2A	19	rs145702982	19,468,917	T	A	0.066222	-0.037974	0.004053	1.8E-21
GATAD2A	19	rs73002960	19,472,183	T	C	0.139705	-0.022474	0.002908	3.2E-15
GATAD2A	19	rs10404728	19,484,205	T	C	0.296931	-0.012016	0.002209	3.7E-08
GATAD2A	19	rs10419912	19,486,246	A	G	0.311623	-0.012117	0.002177	1.9E-08
GATAD2A	19	rs2315610	19,486,431	C	T	0.311725	-0.012277	0.002177	1.3E-08
GATAD2A	19	rs751858	19,492,012	C	G	0.300887	-0.012073	0.002198	3.1E-08
GATAD2A	19	rs2288852	19,494,539	C	T	0.301265	-0.011969	0.002197	4.3E-08
GATAD2A	19	rs1047361	19,495,825	A	G	0.301264	-0.012012	0.002197	4.1E-08
GATAD2A	19	rs6511038	19,496,755	C	A	0.301274	-0.011961	0.002197	4.4E-08
GATAD2A	19	rs10402451	19,497,728	G	A	0.301407	-0.011997	0.002197	3.9E-08
GATAD2A	19	rs3794990	19,499,221	G	A	0.301425	-0.011922	0.002197	4.8E-08
GATAD2A	19	rs3794991	19,499,787	T	C	0.073207	-0.041344	0.003865	3.6E-27
GATAD2A	19	rs3794993	19,500,741	A	C	0.301259	-0.011923	0.002197	4.8E-08
GATAD2A	19	rs57009615	19,502,813	G	A	0.147995	-0.025203	0.002836	1.2E-19
GATAD2A	19	chr19:19507571_C_CCCCCAG	19,507,571	CCCCCAC	C	0.024285	-0.045941	0.006550	2.5E-12
GATAD2A	19	rs148458424	19,507,589	T	G	0.024754	-0.045309	0.006486	3.2E-12
GATAD2A *	19	rs56273306	19,510,195	C	T	0.138802	-0.022227	0.002914	7.8E-15
GATAD2A *	19	rs113365218	19,510,388	A	G	0.138238	-0.021736	0.002921	3.9E-14
NDUFA13	19	rs67644947	19,524,054	GCGGCC.	C	0.299941	-0.012183	0.002205	2.8E-08
YJEFN3	19	rs56397647	19,531,986	T	C	0.136611	-0.022289	0.002937	1.1E-14
CILP2 *	19	rs10402308	19,546,691	A	G	0.298339	-0.012300	0.002218	2.4E-08
CILP2 *	19	rs7245983	19,546,823	C	A	0.299379	-0.012189	0.002214	2.8E-08
CILP2 *	19	rs16996148	19,547,663	T	G	0.069331	-0.043469	0.003965	1.4E-28
CILP2 *	19	rs17216525	19,551,411	T	C	0.075453	-0.040386	0.003813	7.5E-27
CILP2 *	19	rs17216588	19,553,268	T	C	0.073819	-0.034748	0.003876	7.2E-20
PBX4 *	19	rs143988316	19,556,445	T	C	0.076254	-0.035331	0.003814	2.2E-21
PBX4 *	19	rs78916915	19,558,399	A	G	0.075684	-0.032104	0.003817	8.6E-18
PBX4 *	19	rs150824230	19,559,801	A	G	0.074789	-0.033363	0.003841	4.5E-19
PBX4 *	19	rs73004926	19,560,457	T	C	0.074789	-0.033363	0.003841	4.5E-19
PBX4	19	rs73004933	19,564,887	T	C	0.074317	-0.034409	0.003850	5.8E-20
PBX4	19	rs141756246	19,574,661	GT	G	0.070799	-0.034585	0.003963	1.1E-18
PBX4	19	rs73004951	19,584,419	T	C	0.094695	-0.030983	0.003459	9.5E-20
PBX4	19	rs374807806	19,584,623	T	G	0.010868	-0.057517	0.009739	3.7E-09
PBX4	19	rs12608729	19,589,743	T	C	0.092133	-0.031315	0.003490	1.1E-19
PBX4	19	rs73004959	19,600,330	T	C	0.092161	-0.031288	0.003489	1.4E-19
PBX4	19	rs73004962	19,602,260	T	A	0.084434	-0.030639	0.003627	8.5E-18
PBX4	19	rs73004966	19,605,749	T	C	0.080560	-0.033731	0.003705	2.3E-20
PBX4	19	rs57504626	19,609,590	T	C	0.084140	-0.031697	0.003633	5.2E-19
PBX4	19	rs16996185	19,609,979	G	T	0.085501	-0.030945	0.003601	2.4E-18
PBX4	19	rs12610185	19,610,913	A	G	0.085463	-0.031089	0.003602	1.4E-18
PBX4	19	rs12610191	19,611,167	T	C	0.085456	-0.031063	0.003603	1.5E-18
PBX4	19	rs10500212	19,612,406	T	C	0.085742	-0.030727	0.003600	3.4E-18
PBX4	19	rs58847337	19,615,213	A	G	0.078771	-0.034296	0.003742	1.1E-20
PBX4	19	rs73004975	19,616,343	G	A	0.097278	-0.028821	0.003403	6.5E-18
GMIP	19	rs2304128	19,635,342	T	G	0.053709	-0.026724	0.004501	5.9E-10
CEBPA *	19	rs11308479	33,321,108	C	CA	0.164081	0.019856	0.002757	1.6E-12
CEBPA *	19	rs10403076	33,322,595	T	C	0.159052	0.020031	0.002781	1.3E-12
CEBPA *	19	rs10403125	33,322,664	T	C	0.159234	0.019915	0.002780	1.7E-12
CEBPA *	19	rs10402014	33,322,870	A	G	0.170288	0.020648	0.002704	5.5E-14
CEBPA *	19	rs10411163	33,323,488	G	A	0.166029	0.020309	0.002729	2.2E-13
CEBPA *	19	rs28885440	33,323,563	A	G	0.165905	0.020202	0.002729	2.9E-13
CEBPA *	19	rs113811498	33,323,649	A	ATAT	0.159715	0.020092	0.002767	7.6E-13
CEBPA *	19	rs7254869	33,323,787	C	T	0.159833	0.020155	0.002765	5.9E-13
CEBPA *	19	rs7253713	33,324,221	A	G	0.166343	0.020207	0.002722	2.4E-13
CEBPA *	19	rs10415737	33,324,300	C	G	0.166350	0.020198	0.002722	2.4E-13
CEBPA *	19	rs10415770	33,324,336	A	G	0.166355	0.020213	0.002722	2.3E-13
CEBPA *	19	rs60656848	33,325,591	C	T	0.160194	0.020205	0.002761	5.4E-13
CEBPA *	19	rs12608723	33,326,227	G	A	0.171552	0.020960	0.002683	1.4E-14
CEBPA *	19	rs112167957	33,326,622	GA	G	0.171559	0.020945	0.002683	1.4E-14
CEBPA *	19	rs7251395	33,327,226	C	G	0.165101	0.020815	0.002723	5.1E-14
CEBPA *	19	rs7256107	33,327,250	C	T	0.171380	0.020872	0.002684	1.9E-14
CEBPA *	19	rs10413354	33,327,308	G	C	0.171582	0.020835	0.002683	2.0E-14
CEBPA *	19	rs10414141	33,327,311	T	A	0.165103	0.020804	0.002723	5.3E-14
CEBPA *	19	rs7251758	33,327,479	A	G	0.171723	0.020864	0.002682	1.9E-14
CEBPA *	19	rs112432604	33,328,149	G	A	0.169619	0.020930	0.002711	4.0E-14
CEBPA *	19	rs10421445	33,328,331	G	A	0.171741	0.020680	0.002682	3.1E-14
CEBPA *	19	rs10426997	33,328,338	C	T	0.164646	0.020739	0.002727	6.7E-14

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
CEBPA *	19	rs7253865	33,330,342	G	T	0.167084	0.002065	0.002717	2.0E-13
CEBPA *	19	rs149222436	33,336,002	T	C	0.159036	0.020327	0.002770	5.2E-13
CEBPA *	19	rs141706710	33,336,121	T	C	0.159080	0.020325	0.002770	5.2E-13
CEBPG *	19	rs16967971	33,339,692	T	G	0.159714	0.020312	0.002766	3.6E-13
CEBPG *	19	rs12610763	33,350,705	A	G	0.159482	0.019880	0.002767	1.4E-12
CEBPG *	19	rs10417389	33,350,819	T	C	0.159465	0.019834	0.002767	1.6E-12
CEBPG *	19	rs10409981	33,358,189	T	C	0.159468	0.019796	0.002768	2.0E-12
CEBPG *	19	rs10416682	33,358,955	T	C	0.180527	0.019143	0.002645	1.4E-12
CEBPG *	19	rs4805872	33,358,978	C	T	0.181329	0.018912	0.002639	2.3E-12
CEBPG *	19	rs1423065	33,359,589	T	C	0.172626	0.020322	0.002674	7.4E-14
CEBPG *	19	chr19:33360112_C_CT	33,360,112	CT	C	0.163399	0.021669	0.002762	8.5E-15
CEBPG *	19	rs10425856	33,361,416	C	T	0.175312	0.020536	0.002657	2.9E-14
CEBPG *	19	rs11878996	33,366,074	C	T	0.172509	0.020742	0.002676	2.3E-14
CEBPG *	19	rs2112820	33,371,182	C	T	0.172549	0.020653	0.002675	2.7E-14
CEBPG *	19	rs77592544	33,372,029	G	T	0.171935	0.020686	0.002684	2.3E-14
CEBPG *	19	rs78230685	33,372,898	C	A	0.171729	0.020363	0.002683	5.5E-14
CEBPG	19	rs116494882	33,374,217	T	C	0.172237	0.020351	0.002683	5.2E-14
CEBPG	19	rs151086462	33,376,066	TG	T	0.172033	0.019880	0.002688	2.0E-13
CEBPG	19	rs77152611	33,378,116	T	C	0.171720	0.019868	0.002687	2.1E-13
HPN	19	rs12461158	35,049,978	A	G	0.138445	-0.020437	0.002983	6.2E-13
HPN	19	rs10406943	35,050,344	T	G	0.130127	-0.022648	0.003046	6.5E-15
HPN	19	rs57035236	35,050,426	TA	T	0.128280	-0.021928	0.003062	6.3E-14
HPN	19	rs1688025	35,054,215	T	C	0.148526	-0.020023	0.002842	1.1E-13
HPN	19	rs73597479	35,054,481	T	C	0.108149	-0.019221	0.003286	3.9E-10
HPN	19	rs1672981	35,056,147	T	C	0.137653	-0.021168	0.002932	3.6E-14
HPN	19	rs1672980	35,056,214	T	C	0.143561	-0.020064	0.002883	2.4E-13
HPN, HPN-AS1	19	rs8103570	35,059,337	T	C	0.149908	-0.019955	0.002832	1.3E-13
HPN, HPN-AS1	19	rs1688044	35,061,175	C	G	0.171667	-0.019681	0.002686	2.5E-14
HPN, HPN-AS1	19	rs60291566	35,062,059	TA	T	0.163651	-0.020274	0.002731	1.2E-14
HPN, HPN-AS1	19	rs55726903	35,062,418	T	TA	0.162979	-0.020275	0.002734	1.4E-14
HPN, HPN-AS1	19	rs1688043	35,062,437	C	T	0.139066	-0.020606	0.002918	9.2E-14
HPN, HPN-AS1	19	rs2445818	35,062,545	A	G	0.163219	-0.020341	0.002736	1.2E-14
HPN, HPN-AS1	19	rs1688042	35,062,684	A	T	0.163126	-0.020132	0.002735	2.1E-14
HPN, HPN-AS1	19	rs1672979	35,062,693	G	A	0.163128	-0.020138	0.002735	2.0E-14
HPN, HPN-AS1	19	rs1350292	35,062,852	C	T	0.162999	-0.020265	0.002734	1.4E-14
HPN, HPN-AS1	19	rs1350291	35,062,860	T	G	0.162999	-0.020265	0.002734	1.4E-14
HPN, HPN-AS1	19	rs3074472	35,062,896	TAAACGG	A	0.163196	-0.020154	0.002737	2.1E-14
HPN, HPN-AS1	19	rs1688040	35,062,926	G	C	0.162966	-0.020306	0.002736	1.4E-14
HPN, HPN-AS1	19	rs1350290	35,063,068	C	T	0.162845	-0.020250	0.002735	1.5E-14
HPN, HPN-AS1	19	rs2452000	35,063,480	G	A	0.162871	-0.020302	0.002734	1.2E-14
HPN, HPN-AS1	19	rs2445819	35,063,499	G	A	0.162852	-0.020348	0.002734	1.1E-14
HPN, HPN-AS1	19	rs1615767	35,063,863	C	T	0.162904	-0.020225	0.002734	1.5E-14
HPN, HPN-AS1	19	rs10567974	35,064,149	CAGCAG	T	0.164294	-0.020298	0.002739	1.5E-14
HPN, HPN-AS1	19	rs4806073	35,064,286	T	C	0.163078	-0.020312	0.002732	1.1E-14
HPN, HPN-AS1	19	rs2305746	35,065,396	A	G	0.160373	-0.020818	0.002754	4.0E-15
HPN, HPN-AS1	19	rs1688031	35,065,736	T	C	0.160537	-0.020828	0.002755	4.2E-15
HPN, HPN-AS1	19	rs1672991	35,065,755	A	G	0.159613	-0.021043	0.002762	2.9E-15
HPN, HPN-AS1	19	rs3835126	35,065,811	GT	G	0.160531	-0.020844	0.002755	4.0E-15
HPN, HPN-AS1	19	rs1672992	35,065,825	C	T	0.160536	-0.020854	0.002755	3.9E-15
HPN, HPN-AS1	19	rs1688030	35,065,840	T	C	0.160364	-0.020898	0.002756	3.6E-15
HPN-AS1	19	rs10411370	35,070,896	T	C	0.100115	-0.017633	0.003403	2.5E-08
NECTIN2 *	19	rs111371860	44,842,530	T	A	0.024338	0.040435	0.006606	1.6E-09
NECTIN2	19	rs11667610	44,852,338	T	C	0.036261	0.039182	0.005490	8.1E-13
NECTIN2	19	rs10421035	44,853,417	G	A	0.036697	0.038099	0.005458	2.8E-12
NECTIN2	19	rs12971462	44,853,638	A	G	0.036633	0.038007	0.005463	3.6E-12
NECTIN2	19	rs11454806	44,864,023	C	A	0.014920	-0.048390	0.008375	2.7E-08
NECTIN2	19	rs8105340	44,864,520	C	T	0.063843	0.027589	0.004124	2.0E-11
NECTIN2	19	rs3112439	44,864,715	G	C	0.060868	0.025316	0.004219	2.9E-09
NECTIN2	19	rs3112440	44,864,753	A	G	0.063462	0.027432	0.004137	2.9E-11
NECTIN2	19	rs147906601	44,866,575	T	G	0.012028	0.053194	0.009272	9.1E-09
NECTIN2	19	rs12610605	44,867,581	G	A	0.484665	0.023157	0.002023	3.0E-31
NECTIN2	19	rs4803766	44,867,911	A	G	0.371039	0.017941	0.002088	8.6E-19
NECTIN2	19	rs34165484	44,868,428	A	AT	0.485060	0.022827	0.002045	8.1E-30
NECTIN2	19	rs200149544	44,868,448	T	TTTTTC	0.486291	0.022750	0.002046	1.3E-29
NECTIN2	19	rs404935	44,869,537	A	G	0.138202	0.023100	0.002930	8.9E-16
NECTIN2	19	rs79954154	44,870,118	A	G	0.021941	0.049633	0.006898	1.6E-13
NECTIN2	19	rs395908	44,870,308	A	G	0.131744	0.022057	0.003000	9.8E-14
NECTIN2	19	rs148251724	44,872,787	TATTATTA	G	0.467120	0.023967	0.002039	2.5E-33
NECTIN2	19	rs519113	44,873,027	G	C	0.157494	0.023165	0.002766	1.2E-17
NECTIN2	19	rs393584	44,874,077	G	A	0.316185	0.016725	0.002173	2.4E-15
NECTIN2	19	rs34278513	44,874,887	T	C	0.133751	0.023792	0.002963	1.2E-16
NECTIN2	19	rs387976	44,875,803	A	C	0.314879	0.016449	0.002171	6.5E-15
NECTIN2	19	rs369599	44,876,079	C	T	0.314867	0.016421	0.002171	7.1E-15
NECTIN2	19	rs412776	44,876,259	A	G	0.130801	0.030845	0.002996	7.3E-26
NECTIN2	19	rs3837923	44,876,309	AC	A	0.315608	0.016199	0.002171	1.5E-14
NECTIN2	19	rs370705	44,876,381	C	T	0.315402	0.016567	0.002171	3.9E-15
NECTIN2	19	rs385982	44,876,425	A	C	0.314779	0.016382	0.002172	7.9E-15
NECTIN2	19	rs419925	44,876,869	G	C	0.315701	0.016502	0.002172	4.9E-15
NECTIN2	19	rs421812	44,877,288	G	T	0.315742	0.016365	0.002176	8.8E-15
NECTIN2	19	rs3865427	44,877,704	A	C	0.125964	0.029527	0.003047	3.4E-23
NECTIN2	19	rs11668861	44,877,713	G	T	0.209093	0.034082	0.002495	6.1E-44
NECTIN2	19	rs6859	44,878,777	A	G	0.297356	0.025559	0.002211	7.0E-32
NECTIN2	19	rs406456	44,879,460	G	A	0.104435	0.030117	0.003320	4.8E-20
NECTIN2	19	rs3852860	44,879,709	C	T	0.213787	0.038901	0.002474	3.0E-57
NECTIN2	19	rs71352237	44,879,822	C	T	0.118784	0.032753	0.003132	1.0E-26
NECTIN2	19	rs71171301	44,879,834	AC	A	0.118768	0.032751	0.003132	1.0E-26
NECTIN2	19	rs34224078	44,879,858	G	A	0.118751	0.032818	0.003132	8.9E-27
NECTIN2	19	rs35879138	44,879,882	A	T	0.118735	0.032865	0.003132	7.6E-27
NECTIN2	19	rs11083749	44,880,848	C	T	0.091670	0.037470	0.003540	1.5E-26
NECTIN2	19	rs406315	44,880,859	G	A	0.085337	0.035609	0.003655	5.6E-23
NECTIN2	19	rs34994196	44,881,075	GC	G	0.091062	0.037466	0.003547	1.5E-26
NECTIN2	19	rs142042446	44,883,210	GTAA	G	0.085621	0.050124	0.003599	1.9E-47
NECTIN2	19	rs283808	44,883,777	C	A	0.085351	0.044071	0.003636	4.4E-35
NECTIN2	19	rs283809	44,883,800	G	A	0.085919	0.044509	0.003622	4.0E-36
NECTIN2	19	rs12972156	44,884,202	G	C	0.080812	0.053334	0.003708	6.7E-51
NECTIN2	19	rs12972970	44,884,339	A	G	0.080824	0.053359	0.003707	5.9E-51
NECTIN2	19	rs34342646	44,884,873	A	G	0.080929	0.053219	0.003704	9.9E-51

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
NECTIN2	19	rs283810	44,884,984	G	T	0.087307	0.044433	0.003593	1.4E-36
NECTIN2	19	rs283811	44,885,243	G	A	0.168748	0.053945	0.002701	1.6E-94
NECTIN2	19	rs283813	44,885,917	A	T	0.087868	0.045219	0.003571	3.0E-38
NECTIN2	19	rs7254892	44,886,339	A	G	0.061867	0.055784	0.004203	7.9E-43
NECTIN2	19	rs283815	44,887,076	G	A	0.173189	0.052013	0.002666	7.6E-90
NECTIN2	19	rs148665049	44,887,875	T	C	0.022448	0.051333	0.006825	8.2E-15
NECTIN2	19	rs6857	44,888,997	T	C	0.082597	0.052271	0.003665	3.1E-50
TOMM40 *	19	rs71352238	44,891,079	C	T	0.082502	0.053109	0.003667	1.4E-51
TOMM40	19	rs184017	44,891,712	G	T	0.175158	0.050762	0.002657	4.9E-87
TOMM40	19	rs157580	44,892,009	A	G	0.433002	0.033190	0.002031	2.2E-64
TOMM40	19	rs2075650	44,892,362	G	A	0.082839	0.052467	0.003661	1.2E-50
TOMM40	19	rs34404554	44,892,652	G	C	0.082187	0.053237	0.003672	1.2E-51
TOMM40	19	rs11556505	44,892,887	T	C	0.082248	0.053245	0.003672	1.3E-51
TOMM40	19	rs157582	44,892,962	T	C	0.173342	0.053079	0.002666	7.5E-94
TOMM40	19	rs157584	44,893,642	C	T	0.315372	0.023282	0.002173	4.3E-28
TOMM40	19	rs1160983	44,893,972	A	G	0.066649	0.051031	0.004073	2.9E-38
TOMM40	19	rs157585	44,894,255	C	A	0.320627	0.024111	0.002167	2.9E-30
TOMM40	19	rs157588	44,895,007	T	C	0.315609	0.024282	0.002171	1.9E-30
TOMM40	19	rs157590	44,895,459	C	A	0.322705	0.023942	0.002157	2.0E-30
TOMM40	19	rs61679753	44,897,490	A	T	0.074245	0.058943	0.003862	9.9E-56
TOMM40	19	rs111784051	44,899,005	G	T	0.073139	0.058179	0.003890	1.1E-53
TOMM40	19	chr19:44899618_ATT_A	44,899,618	A	ATT	0.314066	0.022348	0.002180	2.0E-26
TOMM40	19	rs1160985	44,900,155	T	C	0.313025	0.022355	0.002179	2.1E-26
TOMM40	19	rs760136	44,900,601	G	A	0.313045	0.022368	0.002179	1.9E-26
TOMM40	19	rs189407352	44,900,873	T	C	0.012146	-0.053534	0.009250	3.1E-09
TOMM40	19	rs741780	44,901,174	C	T	0.313314	0.022363	0.002178	1.8E-26
TOMM40	19	rs405697	44,901,434	G	A	0.401007	0.040179	0.002062	2.7E-90
TOMM40	19	rs1038025	44,901,715	C	T	0.312606	0.022557	0.002181	8.1E-27
TOMM40	19	rs1038026	44,901,805	G	A	0.313266	0.022428	0.002178	1.3E-26
TOMM40	19	rs34215622	44,903,281	CG	C	0.292446	0.022691	0.002223	3.1E-26
TOMM40	19	rs101119	44,903,416	A	G	0.086980	0.060627	0.003591	8.3E-68
TOMM40 *	19	rs7259620	44,904,531	A	G	0.311711	0.022225	0.002182	5.7E-26
APOE *	19	rs769446	44,905,371	C	T	0.070568	0.057973	0.003985	1.8E-51
APOE *	19	rs405509	44,905,579	G	T	0.295510	0.027338	0.002213	1.2E-36
APOE	19	rs440446	44,905,910	G	C	0.388629	0.044280	0.002073	1.7E-106
APOE	19	rs769449	44,906,745	A	G	0.076398	0.062235	0.003798	2.3E-64
APOE	19	rs429358	44,908,684	C	T	0.086461	0.062389	0.003594	5.6E-72
APOE	19	rs7412	44,908,822	T	C	0.072738	0.060049	0.003894	8.7E-57
APOE *	19	rs1065853	44,909,976	T	G	0.072700	0.060299	0.003895	3.0E-57
APOE *	19	rs376097536	44,909,977	G	GGT	0.086609	0.058468	0.003625	1.4E-62
APOE *	19	rs75627662	44,910,319	T	C	0.168145	0.057914	0.002705	1.2E-106
APOE *	19	rs72654473	44,911,142	A	C	0.076039	0.058275	0.003813	2.3E-56
APOE *	19	rs439401	44,911,194	C	T	0.406615	0.042738	0.002055	5.7E-100
APOC1 *	19	rs445925	44,912,383	A	G	0.083208	0.059805	0.003656	1.1E-63
APOC1 *	19	rs10414043	44,912,456	A	G	0.090569	0.051786	0.003517	3.9E-51
APOC1 *	19	rs7256200	44,912,678	T	G	0.090759	0.051807	0.003516	3.8E-51
APOC1 *	19	rs483082	44,912,921	T	G	0.173985	0.061444	0.002664	1.3E-123
APOC1 *	19	rs584007	44,913,221	G	A	0.405764	0.042915	0.002058	7.8E-101
APOC1 *	19	rs438811	44,913,484	T	C	0.174019	0.061386	0.002665	2.1E-123
APOC1 *	19	rs390082	44,913,574	G	T	0.082995	0.059633	0.003663	3.1E-63
APOC1 *	19	rs11568822	44,914,381	CTTCG	C	0.168403	0.059901	0.002701	1.4E-114
APOC1	19	rs5117	44,915,533	C	T	0.168995	0.058979	0.002707	2.8E-111
APOC1	19	rs3826688	44,915,704	C	T	0.410536	0.042699	0.002064	3.1E-99
APOC1	19	rs73052335	44,916,825	C	A	0.092278	0.051556	0.003520	4.7E-50
APOC1	19	rs12721046	44,917,997	A	G	0.100803	0.051819	0.003361	2.0E-55
APOC1	19	rs484195	44,918,620	G	A	0.405746	0.042154	0.002077	5.5E-96
APOC1	19	rs12721051	44,918,903	G	C	0.101358	0.050895	0.003347	2.6E-54
APOC1 *	19	rs56131196	44,919,589	A	G	0.101651	0.050718	0.003341	3.5E-54
APOC1 *	19	rs4420638	44,919,689	G	A	0.101697	0.050666	0.003340	4.2E-54
APOC1 *	19	rs117569256	44,920,073	G	A	0.035137	0.060156	0.005504	1.1E-28
APOC1 *	19	chr19:44920730_C_CA	44,920,730	CA	C	0.087890	0.051722	0.003625	2.5E-47
APOC1 *	19	rs199769815	44,921,765	A	G	0.023285	0.060634	0.006740	8.6E-20
APOC1 *	19	rs190712692	44,921,921	A	G	0.073136	0.057544	0.003899	1.1E-52
APOC1 *	19	rs141622900	44,923,535	A	G	0.073485	0.056853	0.003878	6.9E-52
APOC1P1	19	rs114448690	44,928,196	A	G	0.219765	0.038177	0.002489	2.3E-55
APOC1P1	19	rs113345881	44,928,379	G	A	0.230095	0.037843	0.002443	8.4E-57
APOC1P1	19	rs112871012	44,928,640	A	G	0.228018	0.036889	0.002444	4.9E-54
APOC1P1	19	rs111271293	44,928,832	C	T	0.231416	0.036896	0.002418	2.1E-55
APOC1P1	19	chr19:44928869_AAAAAC_A	44,928,869	A	AAAAAC	0.230667	0.036609	0.002421	1.5E-54
APOC1P1	19	rs7259350	44,929,021	C	T	0.240883	0.037397	0.002363	2.3E-59
APOC1P1	19	rs7259004	44,929,300	C	G	0.242096	0.037224	0.002354	2.0E-59
APOC1P1	19	chr19:44930070_T_TA	44,930,070	TA	T	0.222448	0.036621	0.002466	2.9E-52
APOC2, APOC4-APOE	19	rs2288911	44,946,027	T	G	0.357315	-0.013583	0.002142	2.8E-10
LINC00261	20	rs11087387	22,568,541	C	T	0.154261	-0.015956	0.002818	2.0E-08
LINC00261	20	rs1203894	22,568,731	C	T	0.191995	-0.014004	0.002592	3.4E-08
LINC00261	20	rs11087388	22,568,799	A	C	0.154313	-0.016064	0.002819	1.6E-08
LINC00261	20	rs6048197	22,569,319	A	G	0.154299	-0.015980	0.002820	2.0E-08
LINC00261	20	rs1203895	22,569,788	C	T	0.192697	-0.013877	0.002591	4.3E-08
LINC00261	20	rs6048199	22,569,807	C	T	0.154290	-0.015951	0.002820	2.0E-08
LINC00261	20	rs6048200	22,569,896	C	T	0.154326	-0.015944	0.002821	2.1E-08
LINC00261	20	rs73300990	22,570,221	A	G	0.153621	-0.016129	0.002828	1.5E-08
LINC00261	20	rs1203896	22,570,456	G	A	0.168680	-0.015769	0.002716	3.0E-09
LINC00261	20	rs73300991	22,570,688	T	C	0.131195	-0.018621	0.003002	7.6E-10
LINC00261	20	rs73300993	22,570,865	A	G	0.131190	-0.018697	0.003002	6.7E-10
LINC00261	20	rs6048202	22,571,368	A	G	0.131228	-0.018649	0.003002	7.3E-10
LINC00261	20	rs1203898	22,572,502	C	T	0.169506	-0.017714	0.002712	3.7E-11
LINC00261	20	rs1203899	22,572,658	T	C	0.169331	-0.017777	0.002712	3.0E-11
LINC00261	20	rs148030607	22,572,923	C	CTT	0.133367	-0.021143	0.002980	1.9E-12
LINC00261	20	rs11477526	22,574,444	A	AT	0.133416	-0.021174	0.002979	1.8E-12
LINC00261	20	rs6036152	22,575,955	C	A	0.141931	-0.020648	0.002892	8.2E-13
LINC00261	20	rs6113722	22,576,461	A	G	0.141760	-0.020607	0.002893	9.0E-13
LINC00261	20	rs1203902	22,578,486	C	T	0.198922	-0.015630	0.002563	4.3E-10
FOXA2 *	20	chr20:22578744_C_CAAA	22,578,744	CAAA	C	0.169933	-0.018542	0.002714	4.0E-12
FOXA2 *	20	rs6048205	22,578,963	G	A	0.142275	-0.020153	0.002887	3.0E-12
FOXA2 *	20	rs1203905	22,580,051	G	A	0.176554	-0.017435	0.002663	3.0E-11
FOXA2 *	20	rs72470563	22,580,294	A	T	0.140995	-0.020344	0.002911	3.7E-12
FOXA2 *	20	rs1203907	22,580,333	C	T	0.177043	-0.017411	0.002662	3.0E-11

GENE	CHR	SNP	Pos (h38)	EA	NEA	EAF	BETA	SE	P
FOXA2 *	20	rs6048206	22,580,744	C	T	0.140945	-0.020503	0.002911	2.6E-12
FOXA2	20	rs112021763	22,581,333	CT	C	0.176942	-0.017598	0.002667	1.9E-11
FOXA2	20	rs1974	22,581,673	A	G	0.137139	-0.020857	0.002953	2.7E-12
FOXA2	20	rs3833331	22,581,688	AG	A	0.137090	-0.020924	0.002954	2.3E-12
FOXA2	20	rs1055080	22,581,800	A	G	0.177250	-0.017871	0.002665	8.9E-12
FOXA2	20	rs1203910	22,582,387	C	T	0.181117	-0.017017	0.002644	8.3E-11
FOXA2	20	rs1800847	22,582,933	A	G	0.136044	-0.021356	0.002965	9.8E-13
FOXA2 *	20	rs2277764	22,585,486	C	T	0.136371	-0.020897	0.002961	2.9E-12
FOXA2 *	20	rs1337918	22,586,970	A	C	0.138488	-0.020826	0.002931	2.4E-12
FOXA2 *	20	rs1209523	22,587,304	T	C	0.181017	-0.017020	0.002625	4.9E-11
LOC101929685	20	rs1337919	22,587,957	T	G	0.137749	-0.020775	0.002937	2.8E-12
LOC101929685	20	rs6048209	22,590,445	G	A	0.139269	-0.020432	0.002923	4.7E-12
LOC101929685	20	rs1337920	22,590,566	T	A	0.181473	-0.016543	0.002623	1.4E-10
LOC101929685	20	rs1337921	22,590,570	G	T	0.181473	-0.016543	0.002623	1.4E-10
LOC101929685	20	rs1203915	22,591,866	C	T	0.180078	-0.016645	0.002629	1.2E-10
LOC101929685	20	rs8123991	22,592,696	T	C	0.137876	-0.020730	0.002934	2.9E-12
LOC101929685	20	rs6048211	22,593,298	A	C	0.137477	-0.020747	0.002942	3.3E-12
LOC101929685	20	rs200638849	22,595,154	G	T	0.134575	-0.020684	0.002980	8.5E-12
LOC101929685	20	rs1203916	22,595,643	C	G	0.179708	-0.016691	0.002650	1.7E-10
LOC101929685	20	rs1203917	22,595,877	C	T	0.177593	-0.017224	0.002659	5.2E-11
LOC101929685	20	rs7266093	22,596,998	G	A	0.137077	-0.021015	0.002941	1.5E-12
LOC101929685	20	rs910958	22,597,366	A	G	0.177603	-0.017508	0.002660	2.5E-11
LOC101929685	20	rs910959	22,597,373	C	T	0.137010	-0.021027	0.002941	1.5E-12
LOC101929685	20	rs6036157	22,597,777	A	G	0.137013	-0.021026	0.002941	1.5E-12
LOC101929685	20	rs1203918	22,598,869	G	A	0.177136	-0.017697	0.002662	1.8E-11
LOC101929685	20	rs2003076	22,598,907	A	G	0.136622	-0.021194	0.002944	1.1E-12
LOC101929685	20	rs16984154	22,600,263	A	G	0.136565	-0.021322	0.002944	8.6E-13
LOC101929685	20	rs6036158	22,600,422	C	T	0.136677	-0.021297	0.002943	8.7E-13
LOC101929685	20	rs6048216	22,600,630	C	T	0.137244	-0.021060	0.002941	1.6E-12
LOC101929685	20	rs1203919	22,602,316	T	G	0.174047	-0.017501	0.002690	3.6E-11
LOC101929685	20	rs1203921	22,604,846	T	G	0.154788	-0.016352	0.002795	6.9E-09
LOC101929685	20	rs1203922	22,605,062	G	T	0.156888	-0.016800	0.002775	2.1E-09
LOC101929685	20	rs1203923	22,605,190	T	G	0.156879	-0.016812	0.002775	2.0E-09
LOC101929685	20	rs11480708	22,605,448	C	CT	0.156888	-0.016800	0.002775	2.1E-09
LOC101929685	20	rs1203924	22,605,670	G	A	0.157088	-0.016896	0.002773	1.6E-09
LOC101929685	20	rs11474135	22,605,991	C	CAA	0.157086	-0.016909	0.002773	1.6E-09
LOC101929685	20	rs11087391	22,606,202	GC	G	0.157086	-0.016909	0.002773	1.6E-09
LOC101929685	20	rs1007458	22,607,038	G	A	0.157591	-0.016710	0.002768	2.3E-09
LOC101929685	20	rs995734	22,607,370	G	T	0.157091	-0.016914	0.002773	1.6E-09
FOXA2 *	20	rs1203925	22,608,135	G	A	0.157083	-0.016889	0.002773	1.7E-09
FOXA2 *	20	rs1203926	22,608,279	A	T	0.158441	-0.016654	0.002770	2.2E-09
FOXA2 *	20	rs1007202	22,608,882	T	G	0.156820	-0.016841	0.002775	1.9E-09
FOXA2 *	20	rs1203928	22,609,245	G	A	0.157033	-0.016917	0.002773	1.6E-09
FOXA2 *	20	rs1203929	22,609,266	C	G	0.157033	-0.016917	0.002773	1.6E-09
FOXA2 *	20	rs2424435	22,609,912	C	T	0.157072	-0.016856	0.002774	1.8E-09
FOXA2 *	20	rs2424436	22,609,914	G	T	0.157072	-0.016856	0.002774	1.8E-09
FOXA2 *	20	rs1203930	22,610,197	A	G	0.158855	-0.016871	0.002766	1.6E-09
FOXA2 *	20	rs1203931	22,610,325	A	G	0.156911	-0.016804	0.002775	1.9E-09
FOXA2 *	20	chr20:22610445_ATTT_A	22,610,445	ATTT	A	0.161289	-0.016421	0.002766	3.9E-09
FOXA2 *	20	rs1203932	22,610,530	T	G	0.156897	-0.016748	0.002775	2.2E-09
FOXA2 *	20	rs1203933	22,610,551	T	C	0.156897	-0.016748	0.002775	2.2E-09
FOXA2 *	20	rs1203934	22,611,326	A	C	0.156869	-0.016836	0.002776	1.8E-09
FOXA2 *	20	rs1203936	22,611,792	G	T	0.156883	-0.016848	0.002776	1.7E-09
FOXA2 *	20	rs1203937	22,612,728	T	C	0.156767	-0.016788	0.002777	2.1E-09
FOXA2 *	20	rs1203938	22,614,320	G	A	0.156988	-0.016897	0.002776	1.8E-09
FOXA2 *	20	rs1203939	22,614,618	A	G	0.156920	-0.017038	0.002777	1.3E-09
FOXA2 *	20	rs1203940	22,615,005	T	C	0.156871	-0.017004	0.002778	1.4E-09
FOXA2 *	20	rs61186493	22,615,369	TG	T	0.156776	-0.016982	0.002779	1.5E-09
FOXA2 *	20	rs1203941	22,615,951	T	C	0.156527	-0.017078	0.002782	1.3E-09
FOXA2 *	20	rs1203942	22,615,997	C	G	0.156522	-0.017074	0.002782	1.3E-09
FOXA2 *	20	rs1203943	22,616,187	T	C	0.156507	-0.017018	0.002782	1.5E-09
FOXA2 *	20	rs1203944	22,616,241	T	C	0.156499	-0.017002	0.002782	1.5E-09
FOXA2 *	20	rs1203945	22,616,255	G	T	0.156497	-0.017002	0.002782	1.5E-09
FOXA2 *	20	rs5840968	22,617,806	G	GA	0.156466	-0.017040	0.002782	1.5E-09
FOXA2 *	20	rs1203946	22,620,340	A	C	0.156397	-0.017090	0.002783	1.3E-09
FOXA2 *	20	chr20:22621385_GA_G	22,621,385	GA	G	0.156417	-0.017095	0.002783	1.3E-09
FOXA2 *	20	rs1203947	22,621,725	C	T	0.156371	-0.017005	0.002783	1.6E-09
FOXA2 *	20	rs1203948	22,624,134	G	A	0.157957	-0.016753	0.002772	2.0E-09
FOXA2 *	20	rs1203949	22,625,059	T	C	0.157948	-0.016738	0.002772	2.1E-09
FOXA2 *	20	rs1203952	22,633,494	G	A	0.191257	-0.015998	0.002605	9.9E-10
FOXA2 *	20	rs1203953	22,635,505	T	C	0.155264	-0.016502	0.002788	4.1E-09
FOXA2 *	20	rs6137704	22,639,060	A	T	0.155218	-0.016664	0.002789	3.0E-09
FOXA2 *	20	rs2424439	22,639,402	G	A	0.155218	-0.016664	0.002789	3.0E-09
FOXA2 *	20	rs2208168	22,642,628	C	T	0.157480	-0.017172	0.002776	5.4E-10
FOXA2 *	20	rs2424440	22,643,338	C	T	0.157469	-0.017177	0.002776	5.4E-10
FOXA2 *	20	rs2208169	22,643,647	T	C	0.112814	-0.018431	0.003203	2.0E-08
FOXA2 *	20	rs2424442	22,644,151	C	T	0.157406	-0.017134	0.002777	6.1E-10
FOXA2 *	20	rs6082762	22,644,378	A	T	0.157409	-0.017134	0.002777	6.2E-10
FOXA2 *	20	rs2424443	22,644,497	G	A	0.157483	-0.017021	0.002776	8.0E-10
FOXA2 *	20	rs6075931	22,644,757	C	A	0.162496	-0.015720	0.002750	1.0E-08
FOXA2 *	20	rs910960	22,647,249	G	C	0.113697	-0.018058	0.003191	4.2E-08
FOXA2 *	20	rs2424444	22,648,681	C	T	0.113734	-0.018044	0.003190	4.3E-08
FOXA2 *	20	rs2180553	22,651,781	C	T	0.166024	-0.015516	0.002715	2.3E-08
FOXA2 *	20	rs10534088	22,651,939	GCCAGC	G	0.166001	-0.015508	0.002716	2.4E-08
FOXA2 *	20	rs4815131	22,658,994	T	C	0.122671	-0.017687	0.003086	2.4E-08
FOXA2 *	20	rs975525	22,659,774	G	A	0.122704	-0.017724	0.003085	2.3E-08
FOXA2 *	20	rs2145058	22,660,132	T	C	0.122757	-0.017689	0.003085	2.5E-08
FOXA2 *	20	rs4815132	22,661,195	T	C	0.125954	-0.017526	0.003057	3.4E-08
FOXA2 *	20	rs6036168	22,662,688	G	A	0.123041	-0.017664	0.003078	2.4E-08
FOXA2 *	20	rs2424456	22,663,024	C	A	0.123047	-0.017674	0.003078	2.3E-08
FOXA2 *	20	rs4815134	22,663,923	C	T	0.123043	-0.017670	0.003078	2.3E-08
FOXA2 *	20	rs4815135	22,663,951	C	G	0.123043	-0.017670	0.003078	2.3E-08
FOXA2 *	20	rs55803110	22,664,344	C	T	0.123494	-0.017419	0.003073	3.4E-08
FOXA2 *	20	rs2424457	22,664,411	C	T	0.123684	-0.017597	0.003071	2.4E-08
FOXA2 *	20	rs2424458	22,664,505	C	T	0.123687	-0.017572	0.003071	2.5E-08
FOXA2 *	20	rs2145059	22,664,889	C	T	0.123071	-0.017513	0.003077	2.5E-08
FOXA2 *	20	rs2145060	22,664,994	T	A	0.123071	-0.017513	0.003077	2.5E-08

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
FOXA2 *	20	rs2145061	22,665,097	A	G	0.123071	-0.017513	0.003077	2.5E-08
FOXA2 *	20	rs6036169	22,665,239	G	A	0.123124	-0.017477	0.003076	2.6E-08
FOXA2 *	20	rs35336166	22,666,799	TC	T	0.122898	-0.017620	0.003079	2.3E-08
FOXA2 *	20	rs6036170	22,666,949	T	C	0.122898	-0.017620	0.003079	2.3E-08
FOXA2 *	20	rs6113758	22,667,010	C	T	0.122898	-0.017620	0.003079	2.3E-08
FOXA2 *	20	rs2424459	22,667,434	C	A	0.122899	-0.017627	0.003079	2.2E-08
FOXA2 *	20	rs11087394	22,669,346	TC	T	0.122895	-0.017650	0.003079	2.1E-08
FOXA2 *	20	rs6082774	22,669,410	G	A	0.122895	-0.017650	0.003079	2.1E-08
FOXA2 *	20	rs6048241	22,669,505	T	C	0.166146	-0.015117	0.002706	4.4E-08
FOXA2 *	20	rs6137721	22,670,000	G	A	0.122895	-0.017650	0.003079	2.1E-08
FOXA2 *	20	rs6036172	22,670,551	A	G	0.166143	-0.015123	0.002706	4.4E-08
FOXA2 *	20	rs7273357	22,671,324	T	C	0.122895	-0.017650	0.003079	2.1E-08
FOXA2 *	20	rs6082777	22,672,079	A	G	0.166232	-0.015108	0.002707	4.5E-08
FOXA2 *	20	rs6113762	22,672,946	C	T	0.166165	-0.015145	0.002708	4.1E-08
FOXA2 *	20	rs6132536	22,673,262	T	C	0.122692	-0.017504	0.003081	2.9E-08
FOXA2 *	20	rs6082778	22,673,436	T	C	0.123111	-0.017443	0.003077	3.1E-08
FOXA2 *	20	rs6075934	22,673,477	G	T	0.166069	-0.015135	0.002709	4.3E-08
FOXA2 *	20	rs73304706	22,673,756	A	G	0.166013	-0.015099	0.002710	4.8E-08
FOXA2 *	20	rs73304707	22,673,921	A	C	0.122882	-0.017735	0.003079	1.8E-08
FOXA2 *	20	rs6048245	22,674,559	A	C	0.122849	-0.017839	0.003080	1.5E-08
FOXA2 *	20	rs6082779	22,675,057	T	C	0.122760	-0.017706	0.003081	2.1E-08
FOXA2 *	20	rs6132537	22,675,285	C	T	0.122646	-0.017769	0.003084	2.1E-08
PLTP	20	rs6065904	45,906,012	A	G	0.298080	0.018325	0.002206	1.1E-18
PLTP	20	rs148753678	45,907,567	C	CACA	0.066736	0.043358	0.004076	2.3E-28
PLTP	20	rs3091649	45,909,058	G	A	0.438665	-0.012500	0.002045	1.9E-10
PLTP	20	rs3781114	45,909,788	T	C	0.406332	-0.015387	0.002058	8.9E-15
PLTP	20	rs435306	45,909,845	G	T	0.408868	-0.015536	0.002054	3.6E-15
PLTP	20	rs441346	45,910,853	G	C	0.430975	-0.012061	0.002051	1.0E-09
PLTP	20	rs394643	45,911,539	A	G	0.425063	-0.011292	0.002057	1.0E-08
PLTP	20	rs2294212	45,911,925	G	C	0.354529	-0.013241	0.002125	7.4E-11
PLTP	20	rs2294213	45,912,053	G	C	0.353177	-0.013019	0.002129	1.7E-10
PLTP	20	rs200238866	45,912,201	C	CCCT	0.066837	0.042834	0.004053	5.8E-28
PLTP	20	rs3092096	45,912,327	A	AC	0.462395	-0.011334	0.002036	6.1E-09
PLTP *	20	rs76083992	45,916,159	T	C	0.067296	0.042458	0.004038	8.7E-28
PLTP *	20	rs4810479	45,916,409	T	C	0.398741	-0.015839	0.002063	6.1E-16
PLTP *	20	rs4812975	45,916,821	A	G	0.398944	-0.015821	0.002063	6.5E-16
PLTP *	20	rs6130967	45,919,050	A	G	0.067307	0.042500	0.004037	8.3E-28
PLTP *	20	rs2868346	45,919,331	T	C	0.398111	-0.015835	0.002068	8.2E-16
PLTP *	20	rs3843763	45,919,554	T	C	0.397753	-0.015476	0.002070	3.2E-15
PLTP *	20	rs6130969	45,920,383	T	G	0.067174	0.042151	0.004040	2.2E-27
PLTP *	20	rs6073958	45,923,216	C	T	0.126562	0.031638	0.003049	2.1E-27
PCIF1 *	20	rs2903809	45,924,256	A	C	0.396170	-0.015280	0.002085	8.2E-15
PCIF1 *	20	rs1810322	45,925,065	A	G	0.065124	0.042260	0.004106	1.2E-26
PCIF1 *	20	rs111859808	45,930,210	A	G	0.066760	0.042074	0.004055	4.5E-27
PCIF1 *	20	rs6032589	45,930,959	C	T	0.361373	-0.014871	0.002109	1.3E-13
PCIF1 *	20	rs113232549	45,931,069	T	C	0.066763	0.042078	0.004055	4.4E-27
PCIF1	20	rs74436333	45,937,405	G	A	0.066760	0.042092	0.004055	4.3E-27
PCIF1	20	rs6032597	45,938,696	T	G	0.360334	-0.014779	0.002109	1.5E-13
PCIF1	20	rs6094229	45,941,824	G	C	0.360792	-0.014775	0.002109	1.6E-13
PCIF1	20	rs2297194	45,945,077	G	A	0.066769	0.042161	0.004054	3.5E-27
PCIF1	20	rs11111750	45,945,599	C	T	0.066793	0.042142	0.004054	3.4E-27
ZNF335 *	20	rs6130975	45,948,343	A	G	0.066768	0.042162	0.004054	3.5E-27
ZNF335 *	20	rs6124759	45,948,363	G	C	0.383694	-0.013341	0.002080	6.0E-12
ZNF335	20	rs3363	45,948,675	T	C	0.360286	-0.014940	0.002105	8.5E-14
ZNF335	20	rs16990951	45,950,035	A	T	0.384205	-0.013416	0.002080	4.8E-12
ZNF335	20	rs3746503	45,950,322	G	A	0.383294	-0.013357	0.002078	6.6E-12
ZNF335	20	rs6130976	45,950,933	T	C	0.066630	0.042382	0.004058	1.7E-27
ZNF335	20	rs34240177	45,951,651	C	G	0.066910	0.042186	0.004049	2.5E-27
ZNF335	20	rs6124760	45,952,814	G	C	0.067171	0.042506	0.004040	8.4E-28
ZNF335	20	rs6032601	45,956,315	A	G	0.381368	-0.013629	0.002084	2.7E-12
ZNF335	20	rs3848718	45,957,124	A	G	0.065580	0.042478	0.004086	3.6E-27
ZNF335	20	rs111434827	45,958,597	T	C	0.066986	0.042673	0.004045	5.4E-28
ZNF335	20	rs6032602	45,958,731	C	T	0.382218	-0.013527	0.002081	3.7E-12
ZNF335	20	rs6130977	45,959,191	A	C	0.066986	0.042673	0.004045	5.4E-28
ZNF335	20	rs3746508	45,959,540	A	G	0.385443	-0.013395	0.002080	6.2E-12
ZNF335	20	rs3746509	45,959,602	C	T	0.382176	-0.013576	0.002081	3.0E-12
ZNF335	20	rs6130978	45,959,766	G	A	0.066984	0.042677	0.004045	5.4E-28
ZNF335	20	rs79645412	45,960,177	C	G	0.066916	0.042718	0.004048	5.6E-28
ZNF335	20	rs6104404	45,961,203	A	C	0.382542	-0.013542	0.002082	3.7E-12
ZNF335	20	rs16990964	45,962,093	A	G	0.067013	0.042673	0.004045	5.3E-28
ZNF335	20	rs147204976	45,963,071	A	G	0.096162	0.031081	0.003444	7.7E-21
ZNF335	20	rs3746511	45,963,725	T	C	0.380920	-0.013645	0.002088	3.2E-12
ZNF335	20	rs3746512	45,963,997	T	C	0.380729	-0.013589	0.002089	3.9E-12
ZNF335	20	rs74880664	45,965,956	A	G	0.067003	0.042685	0.004045	5.2E-28
ZNF335	20	rs143167649	45,966,533	C	CTCTGTT	0.065129	0.041926	0.004103	2.3E-26
ZNF335	20	rs3092073	45,967,010	A	G	0.448103	-0.010976	0.002054	8.0E-09
ZNF335	20	rs76907877	45,967,688	T	C	0.066764	0.042214	0.004053	2.3E-27
ZNF335	20	rs78558150	45,970,350	T	C	0.052751	0.040097	0.004547	2.4E-20
ZNF335 *	20	rs16990971	45,972,654	G	A	0.067326	0.040901	0.004045	4.8E-26
ZNF335 *	20	rs11469011	45,973,042	G	GCCTAT,	0.378798	-0.014120	0.002110	1.1E-12
ZNF335 *	20	rs6017717	45,975,324	C	G	0.378816	-0.013770	0.002112	3.3E-12
MMP9 *	20	rs78295912	45,993,859	T	C	0.065687	0.038698	0.004113	3.4E-22
MMP9 *	20	rs1888235	45,995,328	T	C	0.117195	0.025395	0.003177	3.5E-16
MMP9 *	20	rs145026700	45,996,044	T	C	0.065172	0.038399	0.004128	7.9E-22
MMP9 *	20	rs6073984	46,002,014	G	A	0.115386	0.025275	0.003193	7.5E-16
MMP9 *	20	rs3918241	46,007,096	A	T	0.120950	0.023305	0.003120	1.9E-14
MMP9 *	20	rs3918242	46,007,337	T	C	0.120956	0.023295	0.003119	2.0E-14
MMP9	20	rs2274755	46,011,053	T	G	0.123040	0.023377	0.003084	1.1E-14
MMP9	20	rs2236416	46,011,936	G	A	0.123716	0.022959	0.003072	2.8E-14
MMP9	20	rs17577	46,014,472	A	G	0.125890	0.022483	0.003041	3.6E-14
MMP9	20	rs3918261	46,014,953	G	A	0.125903	0.022485	0.003041	3.6E-14
MMP9	20	rs13925	46,016,326	A	G	0.125902	0.022482	0.003041	3.5E-14
MMP9 *	20	rs3918270	46,016,700	A	G	0.122002	0.021760	0.003100	6.0E-13
MMP9 *	20	rs8184490	46,016,794	G	C	0.071086	0.033155	0.003944	2.8E-18
MMP9 *	20	rs3918271	46,016,954	A	G	0.119407	0.022912	0.003129	7.1E-14
SLC12A5 *	20	rs10432735	46,021,679	T	A	0.125385	0.022287	0.003044	6.1E-14
SLC12A5	20	rs62215576	46,023,758	T	C	0.125931	0.022396	0.003040	4.1E-14

GENE	CHR	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
SLC12A5	20	rs6124764	46,027,498	A	T	0.122906	0.022862	0.003091	1.9E-14
SLC12A5	20	rs11908352	46,027,501	A	C	0.122903	0.022868	0.003091	1.9E-14
SLC12A5	20	rs6124765	46,039,572	T	C	0.123908	0.023440	0.003123	2.1E-14
SLC12A5	20	rs116878061	46,057,452	T	G	0.068687	0.030037	0.004004	1.9E-15
MIRLET7BHG	22	rs8135478	46,086,105	C	T	0.128740	-0.017083	0.003026	6.3E-09
MIRLET7BHG	22	rs9626891	46,087,068	C	T	0.124602	-0.016626	0.003053	2.2E-08
MIRLET7BHG	22	rs58280444	46,088,037	A	G	0.115302	-0.017484	0.003194	1.6E-08
MIRLET7BHG	22	rs7290267	46,088,855	G	A	0.119061	-0.017025	0.003153	2.8E-08
MIRLET7BHG	22	rs7291040	46,089,093	C	T	0.118368	-0.017007	0.003168	3.2E-08
PPARA	22	rs1800234	46,219,983	C	T	0.043950	-0.028196	0.004937	2.7E-09

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error
This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.
The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 5. Summary of top variants exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

Rank	CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	GCKR	2	rs1260326	27,508,073	T	C	0.492771	0.059432	0.002013	4.3E-204
10	C2orf16	2	rs1919127	27,578,626	C	T	0.471991	0.044690	0.002016	6.9E-114
9	ZNF512	2	rs12989678	27,598,615	T	C	0.472286	0.045241	0.002022	1.3E-115
19	BCL7B	7	rs7793710	73,557,201	G	C	0.095197	-0.064425	0.003437	1.1E-83
18	TBL2	7	rs13246490	73,578,020	T	C	0.095198	-0.064739	0.003438	2.6E-84
14	MLXIPL	7	rs3812316	73,606,007	G	C	0.086346	-0.075923	0.003591	8.5E-105
6	LPL	8	rs75278536	19,963,914	G	T	0.103029	-0.084222	0.003311	2.0E-153
17	SLC18A1 *	8	rs9644568	20,071,071	A	G	0.112729	-0.060751	0.003184	2.8E-90
3	BUD13	11	rs6589565	116,769,521	A	G	0.201420	0.111161	0.002497	7.3E-445
2	ZPR1	11	rs10750096	116,786,072	C	A	0.203153	0.111554	0.002488	3.4E-451
1	APOA5	11	rs651821	116,791,863	C	T	0.270777	0.144797	0.002259	1.4E-919
4	APOA4	11	rs5104	116,821,618	C	T	0.319760	0.069993	0.002163	1.1E-235
7	APOC3	11	rs5128	116,832,924	G	C	0.290699	0.057287	0.002210	2.8E-152
8	APOA1 *	11	rs10750098	116,834,852	G	T	0.290169	0.057113	0.002217	4.3E-150
11	SIK3	11	rs6589574	116,859,922	A	G	0.311738	0.048590	0.002187	1.2E-112
20	PAFAH1B2	11	rs7925256	117,174,619	T	C	0.285679	0.040251	0.002235	8.0E-75
15	NECTIN2	19	rs283811	44,885,243	G	A	0.168748	0.053945	0.002701	1.6E-94
16	TOMM40	19	rs157582	44,892,962	T	C	0.173342	0.053079	0.002666	7.5E-94
13	APOE	19	rs440446	44,905,910	G	C	0.388629	0.044280	0.002073	1.7E-106
12	APOC1	19	rs5117	44,915,533	C	T	0.168995	0.058979	0.002707	2.8E-111

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error
This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.
The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 6. Summary of variants exhibiting genome-wide significance for the TG:HDL-C ratio, a marker of insulin resistance, identified within the Taiwan Biobank.

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAf	BETA	SE	P
1	SFPQ *	rs79395015	35170115	T	C	0.3768560	0.0335955	0.0063656	2.70E-08
1	SFPQ *	rs77686522	35171992	T	A	0.3920650	0.0347484	0.0062731	5.60E-09
1	SFPQ *	rs80099351	35177518	G	A	0.3923310	0.0347229	0.0062635	6.60E-09
1	SFPQ	rs3768339	35184401	C	T	0.3905020	0.0342677	0.0062761	1.00E-08
1	SFPQ	rs3738696	35186666	C	A	0.3894150	0.0363352	0.0062726	1.30E-09
1	SFPQ	rs12075530	35188306	T	C	0.3894480	0.0363485	0.0062735	1.30E-09
1	SFPQ	rs142470364	35192209	C	CAT	0.4098280	0.0358186	0.0062560	2.20E-09
1	SFPQ *	rs12075169	35193419	G	C	0.4100570	0.0360031	0.0062534	1.90E-09
1	SFPQ *	rs77084091	35194249	T	C	0.4084520	0.0347937	0.0062937	6.50E-09
1	SFPQ *	rs77086052	35197007	G	A	0.4105000	0.0361604	0.0062732	1.60E-09
1	SFPQ *	rs12083658	35198902	A	C	0.4130730	0.0356033	0.0063030	2.80E-09
1	SFPQ *	rs80332318	35199001	G	A	0.4047360	0.0351338	0.0063361	5.10E-09
1	SFPQ *	rs11264116	35200158	T	C	0.3964150	0.0355970	0.0062879	2.70E-09
1	SFPQ *	chr1:35200449_A_ATTGTT	35200449	ATTGTT	A	0.3961910	0.0360447	0.0062935	1.90E-09
1	SFPQ *	rs12081295	35200520	A	G	0.3965250	0.0356570	0.0062905	2.50E-09
1	SFPQ *	rs7542630	35202061	C	T	0.4088360	0.0358555	0.0062749	2.00E-09
1	SFPQ *	rs145536651	35203297	T	TATA	0.4070200	0.0349328	0.0062902	5.30E-09
1	SFPQ *	chr1:35206901_C_CAA	35206901	C	CAA	0.4993070	-0.0337181	0.0062215	1.50E-08
1	SFPQ *	rs35520620	35207155	T	C	0.4980970	-0.0347843	0.0062368	5.30E-09
1	SFPQ *	rs28673907	35207726	T	C	0.4108700	0.0352666	0.0063049	4.70E-09
1	SFPQ *	rs925718	35210163	G	C	0.4865030	-0.0323727	0.0062117	3.60E-08
1	SFPQ *	rs10908387	35211438	C	T	0.4839570	-0.0321258	0.0062138	4.40E-08
1	SFPQ *	rs7512559	35212152	T	C	0.4833540	-0.0322976	0.0062158	4.00E-08
1	SFPQ *	rs7520747	35212538	G	T	0.4833250	-0.0322937	0.0062159	4.00E-08
1	SFPQ *	rs10752602	35212644	G	A	0.4842790	-0.0327455	0.0062239	2.80E-08
1	SFPQ *	rs10796919	35213148	T	C	0.3944270	0.0348665	0.0063233	6.20E-09
1	SFPQ *	rs58482098	35213593	G	T	0.3940190	0.0347364	0.0063231	7.40E-09
1	SFPQ *	rs12096175	35215884	C	T	0.4136720	0.0351201	0.0063323	7.80E-09
1	SFPQ *	rs12568606	35216695	A	C	0.4128620	0.0358727	0.0063254	3.00E-09
1	SFPQ *	rs74224909	35218456	G	A	0.4150140	0.0354681	0.0063020	3.30E-09
1	SFPQ *	rs58534131	35220920	T	C	0.3945320	0.0346598	0.0063207	8.10E-09
1	SFPQ *	rs78157661	35221488	C	T	0.3947040	0.0350651	0.0063208	5.40E-09
1	SFPQ *	rs11264122	35224074	A	G	0.4195400	0.0331112	0.0062595	2.00E-08
1	SFPQ *	rs75178217	35226309	A	G	0.4214950	0.0329781	0.0062538	2.30E-08
1	ZMYM4 *	rs72910977	35233068	A	G	0.4506000	0.0329666	0.0062488	1.70E-08
1	ZMYM4 *	rs72893303	35233650	T	C	0.4520420	0.0330766	0.0062460	1.50E-08
1	ZMYM4 *	rs72895281	35235423	G	A	0.4529030	0.0326162	0.0062447	2.70E-08
1	ZMYM4 *	rs77968776	35235523	G	A	0.4422480	0.0338076	0.0062613	1.40E-08
1	ZMYM4 *	rs74791659	35236875	G	A	0.4425680	0.0341424	0.0062680	1.00E-08
1	ZMYM4 *	rs59854554	35237683	G	A	0.4420970	0.0341149	0.0062763	1.30E-08
1	MACF1	rs2036465	39110310	A	C	0.2009580	0.0422796	0.0076274	4.70E-08
1	MACF1	rs11348708	39112680	C	CA	0.1951260	0.0435290	0.0077208	2.00E-08
1	MACF1	rs4660165	39112860	G	A	0.1950390	0.0435040	0.0077245	2.20E-08
1	MACF1	rs4660416	39113314	G	A	0.1944790	0.0448037	0.0077410	1.20E-08
1	MACF1	chr1:39117533_GGTGTGTGTGTGT_G	39117533	G	GTGTGTG	0.1941990	0.0457203	0.0077554	7.70E-09
1	MACF1	rs112205225	39121716	C	A	0.1975670	0.0456321	0.0077057	5.90E-09
1	MACF1	rs1472662	39124737	T	G	0.1963550	0.0455980	0.0077192	5.00E-09
1	MACF1	rs4660443	39126107	T	C	0.1971120	0.0453094	0.0077115	6.90E-09
1	MACF1	rs67916282	39137083	A	T	0.1966790	0.0455289	0.0077069	6.50E-09
1	MACF1	rs56809193	39143626	A	T	0.1978500	0.0453901	0.0076866	7.70E-09
1	MACF1	chr1:39145519_C_CT	39145519	CT	C	0.2066600	0.0441156	0.0075725	1.60E-08
1	MACF1	rs4660475	39146568	G	A	0.1974320	0.0458387	0.0076861	4.70E-09
1	MACF1	rs66848709	39146885	C	T	0.1974320	0.0458387	0.0076861	4.70E-09
1	MACF1	rs67062906	39151018	G	C	0.1962280	0.0463726	0.0077027	2.80E-09
1	MACF1	rs67408364	39152884	G	A	0.1969850	0.0458051	0.0076939	5.30E-09
1	MACF1	chr1:39154721_A_AT	39154721	AT	A	0.1918420	0.0490727	0.0078193	1.10E-09
1	MACF1	rs66531516	39163390	A	G	0.1959790	0.0432520	0.0077311	4.80E-08
1	MACF1	rs1537817	39173981	T	C	0.2001870	0.0445165	0.0076240	7.70E-09
1	MACF1	rs1126313	39174072	A	C	0.2001870	0.0445165	0.0076240	7.70E-09
1	MACF1	rs16825887	39177710	A	G	0.2001740	0.0446164	0.0076241	7.20E-09
1	MACF1	rs16825889	39178541	A	G	0.1353240	0.0552993	0.0089795	1.20E-09
1	MACF1	rs112672438	39181115	T	C	0.2002240	0.0445864	0.0076227	7.10E-09
1	MACF1	rs112824904	39181948	T	C	0.2002260	0.0445356	0.0076223	7.50E-09
1	MACF1	rs16825921	39183526	T	A	0.2002400	0.0445599	0.0076224	7.40E-09
1	MACF1	rs57214150	39188700	C	G	0.2006110	0.0443693	0.0076179	9.90E-09
1	MACF1	rs16825939	39196836	A	G	0.2002300	0.0445596	0.0076223	7.30E-09
1	MACF1	rs16825942	39196946	A	G	0.2002300	0.0445596	0.0076223	7.30E-09
1	MACF1	rs67020650	39202343	C	T	0.1996890	0.0451248	0.0076329	5.00E-09
1	MACF1	rs72637904	39203010	T	C	0.2002320	0.0445512	0.0076224	7.40E-09
1	MACF1	rs72661925	39203865	A	T	0.2002440	0.0444641	0.0076222	7.80E-09
1	MACF1	rs17491275	39206873	G	T	0.2003280	0.0442919	0.0076236	9.20E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	MACF1	rs72661927	39209650	G	A	0.2002450	0.0444108	0.0076222	8.10E-09
1	MACF1	rs4660543	39213318	G	A	0.2002550	0.0443396	0.0076219	8.40E-09
1	MACF1	rs4660546	39213730	C	T	0.2000720	0.0444227	0.0076260	8.00E-09
1	MACF1	rs72637905	39217626	T	C	0.2002430	0.0443232	0.0076223	8.50E-09
1	MACF1	rs112139327	39220538	C	A	0.1952670	0.0428889	0.0077404	2.70E-08
1	MACF1	rs2036463	39222403	A	G	0.2002510	0.0443681	0.0076224	8.30E-09
1	MACF1	rs2036464	39222570	G	A	0.2002510	0.0443681	0.0076224	8.30E-09
1	MACF1	rs905381	39222880	G	T	0.2002510	0.0443681	0.0076224	8.30E-09
1	MACF1	rs111701080	39228846	T	G	0.2002490	0.0443764	0.0076224	8.20E-09
1	MACF1	rs16837533	39238175	A	G	0.2002420	0.0442684	0.0076187	8.40E-09
1	MACF1	rs72637906	39242630	A	G	0.1997350	0.0440138	0.0076301	1.10E-08
1	MACF1	rs67886352	39243031	A	G	0.2003240	0.0439614	0.0076187	1.10E-08
1	MACF1	rs60323161	39244787	C	T	0.2004490	0.0446721	0.0076227	6.60E-09
1	MACF1	rs66727439	39246258	T	C	0.2002440	0.0442428	0.0076187	8.60E-09
1	MACF1	rs111254532	39247976	C	T	0.2002300	0.0437331	0.0076233	1.30E-08
1	MACF1	rs16826000	39248188	T	G	0.2002880	0.0435964	0.0076224	1.40E-08
1	MACF1	chr1:39251172_C_CT	39251172	CT	C	0.1993280	0.0430756	0.0076438	2.20E-08
1	MACF1	rs16826009	39251230	G	A	0.1998530	0.0431371	0.0076326	2.00E-08
1	MACF1	rs16826012	39253847	C	T	0.2002220	0.0435098	0.0076244	1.50E-08
1	MACF1	rs66880209	39254140	A	G	0.2002220	0.0435098	0.0076244	1.50E-08
1	MACF1	rs4660208	39256542	G	A	0.1987890	0.0430668	0.0076527	2.50E-08
1	MACF1	rs72661940	39262975	G	C	0.2035660	0.0451447	0.0076939	4.10E-09
1	MACF1	rs4660214	39265878	C	T	0.2085200	0.0410890	0.0075160	4.20E-08
1	MACF1	rs4660603	39270662	G	C	0.2000830	0.0437971	0.0076213	1.30E-08
1	MACF1	rs56658816	39270791	GATAT	G	0.2000830	0.0437971	0.0076213	1.30E-08
1	MACF1	rs3818806	39282599	A	G	0.1999970	0.0438975	0.0076239	1.20E-08
1	MACF1	rs41270799	39282990	A	G	0.1999990	0.0438245	0.0076236	1.30E-08
1	MACF1	rs16826036	39292127	C	G	0.1998270	0.0433664	0.0076301	2.10E-08
1	MACF1	rs16826038	39292962	A	G	0.1998210	0.0433996	0.0076304	2.00E-08
1	MACF1	rs111797516	39296531	G	A	0.1998210	0.0433996	0.0076304	2.00E-08
1	MACF1	rs61782157	39297217	T	C	0.2001710	0.0437171	0.0076263	1.40E-08
1	MACF1	rs41270803	39300369	G	A	0.1998210	0.0433996	0.0076304	2.00E-08
1	MACF1	rs61783376	39303328	C	T	0.1998310	0.0433713	0.0076306	2.10E-08
1	MACF1	rs4660636	39304555	C	T	0.1943000	0.0455209	0.0077530	7.00E-09
1	MACF1	rs4660637	39304606	T	C	0.1937480	0.0452399	0.0077721	1.40E-08
1	MACF1	rs61783378	39311487	A	G	0.1978860	0.0426282	0.0076687	4.10E-08
1	MACF1	rs72661956	39319216	C	G	0.1844360	0.0455885	0.0078626	7.70E-09
1	MACF1	rs16826068	39326204	C	G	0.1850320	0.0461320	0.0078453	4.30E-09
1	MACF1	rs41270807	39336143	C	A	0.1842550	0.0463198	0.0078615	4.10E-09
1	MACF1	rs111623477	39345533	T	C	0.1850310	0.0461007	0.0078449	4.60E-09
1	MACF1	rs16826087	39346846	T	C	0.1851220	0.0462460	0.0078417	4.10E-09
1	MACF1	rs3754346	39349288	T	C	0.1852340	0.0462372	0.0078457	4.10E-09
1	MACF1	rs16826093	39349471	A	T	0.1850320	0.0460517	0.0078448	4.70E-09
1	MACF1	rs41270811	39349672	A	G	0.1850320	0.0460517	0.0078448	4.70E-09
1	MACF1	rs61779274	39351269	G	C	0.1850320	0.0460517	0.0078448	4.70E-09
1	MACF1	rs17264671	39352380	C	A	0.1850540	0.0459788	0.0078443	4.90E-09
1	MACF1	rs4660690	39353831	A	G	0.1850540	0.0459788	0.0078443	4.90E-09
1	MACF1	rs61779275	39354638	T	C	0.1850590	0.0459492	0.0078443	5.00E-09
1	MACF1	chr1:39357360_A_AT	39357360	AT	A	0.1846980	0.0464261	0.0078539	4.10E-09
1	MACF1	rs61779276	39359766	T	C	0.1850590	0.0459492	0.0078443	5.00E-09
1	MACF1	rs72661961	39366096	G	A	0.1852420	0.0455131	0.0078375	7.30E-09
1	MACF1	rs61779277	39367863	A	G	0.1851280	0.0457825	0.0078401	6.10E-09
1	MACF1	rs61779278	39368945	G	A	0.1852420	0.0455131	0.0078375	7.30E-09
1	MACF1	rs2296172	39370145	G	A	0.1853390	0.0454190	0.0078361	7.80E-09
1	MACF1	rs61779279	39371430	T	C	0.1852420	0.0455131	0.0078375	7.30E-09
1	MACF1	rs61779282	39374632	G	C	0.1854320	0.0456402	0.0078407	6.50E-09
1	MACF1	rs61779283	39375096	T	C	0.1852420	0.0455131	0.0078375	7.30E-09
1	MACF1	rs76111861	39377018	T	G	0.1852420	0.0455131	0.0078375	7.30E-09
1	MACF1	rs72661965	39380918	C	A	0.1852420	0.0455131	0.0078375	7.30E-09
1	MACF1	rs6668369	39382675	G	C	0.1847390	0.0458622	0.0078503	6.10E-09
1	MACF1	rs61779284	39389505	A	G	0.1845780	0.0463570	0.0078509	4.50E-09
1	MACF1	rs3768299	39391520	A	G	0.1846740	0.0459939	0.0078483	5.60E-09
1	MACF1	rs4660732	39397543	T	C	0.1850830	0.0459653	0.0078485	5.10E-09
1	MACF1	rs61779285	39401383	T	C	0.1844680	0.0465704	0.0078574	3.60E-09
1	MACF1	rs146152783	39402073	T	TTGG	0.1822360	0.0455955	0.0079005	8.00E-09
1	MACF1	rs78203103	39402949	G	GTCTC1	0.1839030	0.0467173	0.0078719	3.20E-09
1	MACF1	rs111411108	39404153	G	A	0.1747890	0.0452603	0.0081185	2.40E-08
1	MACF1	rs3768301	39405121	T	C	0.1844200	0.0465157	0.0078595	3.70E-09
1	MACF1	rs113214136	39408867	T	G	0.1843580	0.0462174	0.0078592	4.60E-09
1	KIAA0754, lrs3768302		39414647	G	T	0.1843420	0.0463314	0.0078595	4.20E-09
1	KIAA0754, lrs17343193		39415796	A	T	0.1843420	0.0463314	0.0078595	4.20E-09
1	MACF1	rs144172969	39417348	G	GA	0.1844020	0.0463284	0.0078604	4.40E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	MACF1	rs61779300	39420091	A	G	0.1843440	0.0463130	0.0078594	4.30E-09
1	MACF1	rs2018212	39439916	C	T	0.1817290	0.0457014	0.0079028	7.40E-09
1	MACF1	rs4660751	39440201	T	C	0.1805160	0.0447424	0.0079455	1.70E-08
1	MACF1	rs2296173	39447679	G	A	0.1841580	0.0463760	0.0078645	4.40E-09
1	MACF1	rs3118014	39448418	A	G	0.1842070	0.0462588	0.0078662	4.80E-09
1	MACF1	rs1985076	39449537	C	T	0.1841310	0.0464216	0.0078649	4.30E-09
1	MACF1	rs61779306	39456754	A	G	0.1494210	0.0568734	0.0085586	4.00E-11
1	MACF1	rs41270821	39458060	C	T	0.1501460	0.0564739	0.0085349	5.30E-11
1	MACF1	rs2296175	39458726	A	G	0.1501460	0.0564739	0.0085349	5.30E-11
1	MACF1	rs61226452	39471127	C	CTG	0.1501380	0.0568793	0.0085294	3.80E-11
1	MACF1	rs61779308	39472585	T	C	0.1461880	0.0605733	0.0086253	4.30E-12
1	MACF1	rs61779309	39474827	C	T	0.1448360	0.0610608	0.0086840	3.30E-12
1	MACF1	chr1:39476570_C_CA	39476570	CA	C	0.1386230	0.0549572	0.0089473	7.80E-10
1	MACF1	rs61779310	39476625	G	C	0.1474890	0.0563930	0.0086409	8.50E-11
1	MACF1	rs61779313	39478577	C	T	0.1481350	0.0585835	0.0086148	1.40E-11
1	MACF1	rs1386747518	39480077	AGTGA	T	0.1479010	0.0582414	0.0086214	1.90E-11
1	MACF1	chr1:39482510_TTTTG_T	39482510	T	TTTTG	0.1486830	0.0584074	0.0086144	1.50E-11
1	MACF1	rs61779314	39482667	T	C	0.1484350	0.0586583	0.0086049	1.20E-11
1	MACF1	chr1:39484331_AT_A	39484331	AT	A	0.1538000	0.0551341	0.0086586	1.90E-10
1	MACF1 *	rs61779328	39487795	G	A	0.1484210	0.0583891	0.0086000	1.60E-11
1	BMP8A	rs60069508	39499240	C	G	0.1485040	0.0575655	0.0085997	3.20E-11
1	BMP8A	rs61779330	39501551	A	G	0.1486060	0.0576230	0.0085811	2.80E-11
1	BMP8A	rs72662001	39501608	C	T	0.1486650	0.0573347	0.0085807	3.70E-11
1	BMP8A	rs72663503	39503387	T	C	0.1486810	0.0585047	0.0085796	1.50E-11
1	BMP8A	rs61779331	39505256	A	C	0.1483000	0.0581219	0.0086021	2.70E-11
1	BMP8A, PP1	rs755249	39529402	T	C	0.1365360	0.0617251	0.0088928	3.70E-12
1	PPIEL	rs12141058	39534682	T	C	0.1415290	0.0617433	0.0087755	3.10E-12
1	PPIEL	rs143948354	39536713	G	GA	0.1220780	0.0676210	0.0093424	3.20E-13
1	PPIEL	rs72663520	39537738	T	C	0.1234230	0.0683992	0.0092975	1.50E-13
1	PPIEL	rs72663521	39540231	A	G	0.1128150	0.0697156	0.0096468	3.00E-13
1	PPIEL	rs61779359	39544563	C	T	0.1131820	0.0685524	0.0096315	6.40E-13
1	PPIEL	rs41270829	39546018	T	G	0.1131250	0.0694829	0.0096294	3.40E-13
1	PPIEL	rs61781362	39546558	T	C	0.1136280	0.0687291	0.0096100	5.20E-13
1	PPIEL	rs61781363	39546761	T	C	0.1134840	0.0685331	0.0096125	6.20E-13
1	PPIEL	rs4660808	39552837	T	C	0.1135500	0.0685687	0.0096115	5.90E-13
1	PPIEL	rs61781364	39553919	G	A	0.1046610	0.0698352	0.0100361	1.80E-12
1	PPIEL	rs1180333	39554832	T	C	0.1153510	0.0690958	0.0095506	2.60E-13
1	PPIEL	rs76207570	39556810	T	C	0.1123720	0.0687026	0.0096621	6.60E-13
1	PPIEL	rs17264866	39557105	G	C	0.1134840	0.0685331	0.0096125	6.20E-13
1	PPIEL	rs138909742	39559525	T	TG	0.1134790	0.0685225	0.0096125	6.30E-13
1	PABPC4	rs4660293	39562508	G	A	0.1138620	0.0690051	0.0096002	3.40E-13
1	PABPC4	rs3768320	39566567	T	C	0.1183160	0.0653659	0.0094450	4.20E-12
1	PABPC4	rs58302493	39568233	A	G	0.1109190	0.0680101	0.0097124	2.10E-12
1	PABPC4	rs17513135	39570014	T	C	0.1110830	0.0681640	0.0097067	1.80E-12
1	PABPC4	rs3768321	39570256	T	G	0.1111990	0.0669362	0.0097078	4.70E-12
1	PABPC4	rs2293476	39571175	C	G	0.1110050	0.0673101	0.0097092	3.40E-12
1	PABPC4	rs41264487	39571682	G	C	0.1133800	0.0692009	0.0096164	3.80E-13
1	PABPC4	rs2068663	39572899	T	C	0.1133650	0.0687729	0.0096202	5.30E-13
1	PABPC4	rs79094524	39575699	GA	G	0.1130940	0.0688803	0.0096340	5.50E-13
1	PABPC4	rs76113306	39576027	CGGAG	T	0.1119400	0.0694608	0.0096724	4.30E-13
1	PABPC4 *	rs61781368	39578080	G	C	0.1109930	0.0683459	0.0097170	1.70E-12
1	PABPC4 *	rs12064914	39578100	A	G	0.1115850	0.0673657	0.0097054	3.70E-12
1	PABPC4 *	rs7520271	39579041	A	C	0.1198060	0.0657638	0.0094123	1.90E-12
1	PABPC4 *	rs61781370	39579628	C	A	0.1107890	0.0686551	0.0097215	9.40E-13
1	PABPC4 *	rs12740105	39579796	A	G	0.1193890	0.0667953	0.0094071	8.60E-13
1	PABPC4 *	rs111768751	39580421	A	G	0.1119810	0.0692128	0.0096697	5.10E-13
1	PABPC4 *	chr1:39580875_A_AT	39580875	A	AT	0.1192840	0.0664106	0.0094101	1.10E-12
1	PABPC4 *	rs12037073	39581225	C	T	0.1191200	0.0665315	0.0094127	1.00E-12
1	PABPC4 *	rs11206374	39582337	A	G	0.1115630	0.0685167	0.0096844	9.40E-13
1	PABPC4 *	rs4660846	39583839	C	T	0.1192470	0.0663767	0.0094057	1.00E-12
1	PABPC4 *	rs7539261	39584831	A	T	0.1192680	0.0664680	0.0094053	9.40E-13
1	PABPC4 *	rs7539279	39584896	A	G	0.1192680	0.0664680	0.0094053	9.40E-13
1	PABPC4 *	rs61781371	39586436	G	C	0.1114350	0.0678725	0.0096920	1.30E-12
1	PABPC4 *	rs9729677	39587137	T	G	0.1187870	0.0651533	0.0094325	2.90E-12
1	PABPC4 *	rs11206387	39587326	A	G	0.1187460	0.0648517	0.0094328	3.60E-12
1	PABPC4 *	rs61781373	39587421	C	A	0.1044340	0.0675319	0.0100534	2.10E-11
1	PABPC4 *	rs2695324	39587969	A	G	0.1187590	0.0651295	0.0094331	2.90E-12
1	PABPC4 *	rs11206390	39588827	G	A	0.1187530	0.0650550	0.0094336	3.10E-12
1	PABPC4 *	rs2695319	39591028	C	G	0.1175610	0.0672669	0.0094831	9.30E-13
1	PABPC4 *	rs113825410	39591871	G	A	0.1114360	0.0678218	0.0096930	1.50E-12
1	PABPC4 *	rs76841360	39594353	A	G	0.1114340	0.0678677	0.0096933	1.50E-12
1	PABPC4 *	rs4660303	39594801	A	G	0.1114290	0.0679221	0.0096939	1.50E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	PABPC4 *	rs12037222	39599289	A	G	0.1089350	0.0647315	0.0097800	3.10E-11
1	PABPC4 *	rs74504886	39599944	A	G	0.1083540	0.0665801	0.0098033	9.10E-12
1	HEYL *	rs149794918	39600183	G	GT	0.1070510	0.0657878	0.0098685	1.60E-11
1	HEYL *	rs3916164	39604267	A	G	0.1090320	0.0660206	0.0097707	1.00E-11
1	HEYL *	rs113879410	39607339	C	G	0.1083890	0.0654930	0.0098010	1.60E-11
1	HEYL *	rs61781377	39609786	T	C	0.1119760	0.0652102	0.0096712	1.10E-11
1	HEYL *	rs61781390	39610222	A	G	0.1120330	0.0651064	0.0096660	1.20E-11
1	HEYL *	rs61781391	39611865	A	G	0.1120750	0.0648550	0.0096699	1.50E-11
1	HEYL *	rs61781392	39617969	A	C	0.1133600	0.0640075	0.0096227	2.10E-11
1	HEYL *	chr1:39618218_C_CTT	39618218	CTT	C	0.1329730	0.0568336	0.0090955	3.20E-10
1	HEYL *	rs61232586	39620685	T	G	0.1129000	0.0643314	0.0096505	2.10E-11
1	HEYL *	rs61781393	39622092	A	G	0.1122670	0.0636834	0.0096762	3.70E-11
1	HEYL *	rs17343290	39622371	A	G	0.1127210	0.0648607	0.0096525	1.50E-11
1	HEYL	rs72663570	39629862	T	C	0.0996090	0.0577672	0.0103568	3.40E-08
1	USP1 *	rs12025429	62430113	T	C	0.3344260	-0.0332567	0.0064579	4.40E-08
1	USP1 *	rs10493324	62432471	T	C	0.3243060	-0.0367374	0.0065742	2.80E-09
1	USP1 *	rs60500353	62433313	T	C	0.2115720	-0.0605420	0.0075965	1.40E-16
1	USP1 *	rs624698	62435140	G	A	0.2603390	-0.0662180	0.0069796	1.80E-23
1	USP1 *	rs624700	62435141	C	G	0.2603390	-0.0662180	0.0069796	1.80E-23
1	USP1 *	rs626787	62435572	G	C	0.2598970	-0.0664963	0.0069543	1.20E-23
1	USP1 *	rs631106	62436136	A	C	0.2597530	-0.0664425	0.0069548	1.20E-23
1	USP1	rs646179	62437203	G	A	0.3831420	-0.0419503	0.0063003	8.30E-13
1	USP1	rs9436221	62437688	C	T	0.2543310	-0.0662206	0.0070012	4.00E-23
1	USP1	rs9436222	62437692	G	C	0.2543310	-0.0662206	0.0070012	4.00E-23
1	USP1	rs9436223	62437876	T	C	0.2543270	-0.0662164	0.0069997	4.00E-23
1	USP1	rs12029068	62438624	T	C	0.2543270	-0.0662164	0.0069997	4.00E-23
1	USP1	rs9436661	62438904	G	T	0.2543230	-0.0662676	0.0069999	3.60E-23
1	USP1	rs11588261	62439265	A	G	0.2543250	-0.0662691	0.0069999	3.60E-23
1	USP1	rs10493322	62440222	T	C	0.2126110	-0.0692665	0.0074413	1.60E-22
1	USP1	rs60688353	62440418	CAA	C	0.2126080	-0.0692926	0.0074412	1.80E-22
1	USP1	rs638714	62440818	T	G	0.2538950	-0.0663709	0.0070044	3.50E-23
1	USP1	rs638305	62440866	T	G	0.2544850	-0.0663970	0.0069965	3.00E-23
1	USP1	chr1:62441011_A_AT	62441011	AT	A	0.2398330	-0.0667434	0.0072194	4.00E-22
1	USP1	rs637723	62441057	T	C	0.2517600	-0.0668681	0.0070408	3.10E-23
1	USP1	rs656297	62441924	G	A	0.2544850	-0.0663970	0.0069965	3.00E-23
1	USP1	rs642845	62442564	C	T	0.2618750	-0.0628282	0.0069576	3.00E-21
1	USP1	rs641540	62442867	G	A	0.2544850	-0.0663970	0.0069965	3.00E-23
1	USP1	rs527281380	62444278	A	AAAG	0.2261360	-0.0673372	0.0073622	8.30E-22
1	USP1	rs1553145497	62445632	GTGTA	G	0.2545260	-0.0660308	0.0070008	5.40E-23
1	USP1	rs10647753	62445634	GTA	G	0.2548310	-0.0661030	0.0070027	5.00E-23
1	USP1	rs598253	62445670	C	T	0.2544690	-0.0663984	0.0069968	3.00E-23
1	USP1	rs11207969	62446080	G	A	0.2544690	-0.0663984	0.0069968	3.00E-23
1	USP1	rs659656	62446449	G	C	0.2544690	-0.0663984	0.0069968	3.00E-23
1	USP1	rs10158897	62447248	T	C	0.2126270	-0.0694112	0.0074434	1.60E-22
1	USP1	rs783291	62449307	A	G	0.2544870	-0.0665267	0.0069967	2.50E-23
1	USP1	rs11207970	62449802	T	C	0.2115830	-0.0700217	0.0074632	1.10E-22
1	USP1	rs583609	62451125	C	T	0.2544980	-0.0665058	0.0069967	2.50E-23
1	USP1 *	rs597470	62452125	G	T	0.2544870	-0.0665255	0.0069967	2.50E-23
1	USP1 *	rs597078	62452186	A	G	0.2540320	-0.0668254	0.0070048	1.90E-23
1	USP1 *	rs597076	62452194	A	T	0.2540320	-0.0668254	0.0070048	1.90E-23
1	USP1 *	rs630144	62453193	G	A	0.2544910	-0.0664919	0.0069968	2.60E-23
1	DOCK7 *	chr1:62453356_GT_G	62453356	G	GT	0.2517280	-0.0688945	0.0070844	2.70E-24
1	DOCK7 *	rs79346928	62454307	CAT	C	0.2126390	-0.0693145	0.0074411	1.60E-22
1	DOCK7 *	rs636523	62454337	G	A	0.2123810	-0.0680331	0.0074464	6.50E-22
1	DOCK7 *	rs636497	62454358	G	A	0.2545090	-0.0663335	0.0069964	3.10E-23
1	DOCK7 *	rs624660	62454717	A	C	0.2550990	-0.0666484	0.0069994	2.20E-23
1	DOCK7	rs634341	62455751	C	T	0.2515930	-0.0656733	0.0070429	1.60E-22
1	DOCK7	rs3913007	62455915	C	T	0.2126400	-0.0693010	0.0074413	1.70E-22
1	DOCK7	rs4350231	62456989	A	G	0.2105310	-0.0705547	0.0074714	6.00E-23
1	DOCK7	rs12023489	62458187	A	G	0.2539810	-0.0662820	0.0070058	4.50E-23
1	DOCK7	rs12037659	62458192	T	C	0.2120670	-0.0693531	0.0074539	2.20E-22
1	DOCK7	rs62932760	62458534	TG	T	0.2372230	-0.0657547	0.0072447	8.40E-21
1	DOCK7	rs9988450	62458777	T	C	0.2545150	-0.0663035	0.0069967	3.30E-23
1	DOCK7	rs77064258	62460056	T	C	0.1769800	-0.0666521	0.0080305	1.40E-18
1	DOCK7	rs1305520	62460386	A	T	0.2547060	-0.0661899	0.0070004	4.30E-23
1	DOCK7	rs7547965	62460700	G	A	0.2547630	-0.0663162	0.0070004	3.50E-23
1	DOCK7	chr1:62462070_CA_C	62462070	C	CA	0.2324230	-0.0682218	0.0073617	3.60E-22
1	DOCK7	rs1167996	62462126	T	G	0.2521250	-0.0672590	0.0070237	1.10E-23
1	DOCK7	rs998403	62462878	A	G	0.2107980	-0.0705384	0.0074647	4.30E-23
1	DOCK7	rs11356503	62463707	T	TA	0.2107980	-0.0705384	0.0074647	4.30E-23
1	DOCK7	rs1177541	62464221	G	A	0.2531500	-0.0673533	0.0070135	8.80E-24
1	DOCK7	rs77083979	62464435	A	G	0.2024740	-0.0692642	0.0075776	8.50E-22

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs11207972	62464553	G	A	0.2531680	-0.0673305	0.0070131	9.10E-24
1	DOCK7	rs1167998	62465961	C	A	0.2598240	-0.0655600	0.0069495	2.80E-23
1	DOCK7	rs77907749	62466449	T	C	0.2025070	-0.0688821	0.0075763	1.30E-21
1	DOCK7	rs1168001	62468087	G	A	0.2531870	-0.0671539	0.0070126	1.10E-23
1	DOCK7	rs12124284	62468356	A	G	0.2110660	-0.0705511	0.0074619	3.70E-23
1	DOCK7	rs1168002	62468637	A	G	0.2540580	-0.0675262	0.0070183	6.60E-24
1	DOCK7	rs1168003	62469175	G	A	0.2531870	-0.0671539	0.0070126	1.10E-23
1	DOCK7	rs12043877	62469328	T	C	0.2025080	-0.0689966	0.0075765	1.10E-21
1	DOCK7	rs1007205	62471241	T	C	0.2531130	-0.0673011	0.0070157	9.10E-24
1	DOCK7	rs10889330	62473795	C	G	0.2531860	-0.0671213	0.0070127	1.20E-23
1	DOCK7	rs1979722	62474426	A	G	0.2108410	-0.0702830	0.0074635	5.70E-23
1	DOCK7	rs11442941	62474595	T	TG	0.2530930	-0.0669517	0.0070157	1.70E-23
1	DOCK7	chr1:62475497_GA_G	62475497	GA	G	0.2565190	-0.0677336	0.0070405	2.20E-23
1	DOCK7	rs10889331	62477336	G	T	0.2531860	-0.0670751	0.0070128	1.20E-23
1	DOCK7	rs1168009	62478283	G	A	0.2533940	-0.0671633	0.0070164	1.10E-23
1	DOCK7	rs1168010	62478308	G	A	0.2534690	-0.0669735	0.0070167	1.50E-23
1	DOCK7	rs35913674	62479276	CA	C	0.2537440	-0.0673930	0.0070130	9.60E-24
1	DOCK7	rs1183260	62479747	A	G	0.2529370	-0.0670706	0.0070142	1.30E-23
1	DOCK7	rs6587976	62479960	T	C	0.2529370	-0.0670706	0.0070142	1.30E-23
1	DOCK7	rs1305521	62483363	A	G	0.2541790	-0.0668559	0.0070126	1.90E-23
1	DOCK7	rs11207974	62484289	C	T	0.2528970	-0.0670533	0.0070145	1.40E-23
1	DOCK7	rs10889332	62485187	T	C	0.2528570	-0.0673085	0.0070190	1.00E-23
1	DOCK7	rs2489835	62489300	T	C	0.2528420	-0.0671365	0.0070153	1.20E-23
1	DOCK7	rs1690761	62490191	C	T	0.2528340	-0.0670554	0.0070156	1.30E-23
1	DOCK7	rs10889333	62491359	A	G	0.2107870	-0.0708372	0.0074646	2.70E-23
1	DOCK7	rs10889334	62491528	G	C	0.2107770	-0.0707599	0.0074648	2.90E-23
1	DOCK7	rs10789112	62492087	C	T	0.2107790	-0.0707488	0.0074657	3.00E-23
1	DOCK7	rs1183851	62492987	T	C	0.3784710	-0.0430165	0.0063114	1.90E-13
1	DOCK7	rs10889335	62494430	G	A	0.2028390	-0.0692704	0.0076150	1.40E-21
1	DOCK7	rs1168041	62494579	T	C	0.2175510	-0.0644282	0.0073849	2.30E-20
1	DOCK7	chr1:62494664_T_TG	62494664	TG	T	0.1562840	-0.0709831	0.0085753	3.20E-18
1	DOCK7	rs1168040	62494904	T	C	0.2527260	-0.0681617	0.0070174	2.30E-24
1	DOCK7	rs1168036	62497063	A	G	0.2513920	-0.0678960	0.0070236	5.90E-24
1	DOCK7	rs1002687	62498066	G	A	0.2529530	-0.0668669	0.0070199	1.90E-23
1	DOCK7	chr1:62498080_A_AT	62498080	A	AT	0.2609770	-0.0660259	0.0070776	2.70E-22
1	DOCK7	rs1168034	62498243	G	C	0.2515770	-0.0679456	0.0070210	4.80E-24
1	DOCK7	chr1:62499937_GA_G	62499937	GA	G	0.2522740	-0.0681900	0.0070301	3.90E-24
1	DOCK7	rs35529421	62499950	A	T	0.2050420	-0.0729206	0.0075805	8.50E-24
1	DOCK7	rs1168032	62502076	A	G	0.2513900	-0.0680294	0.0070237	4.30E-24
1	DOCK7	rs1168031	62502316	C	T	0.2515770	-0.0679456	0.0070210	4.80E-24
1	DOCK7	chr1:62502762_A_AT	62502762	AT	A	0.2094520	-0.0709028	0.0074806	3.90E-23
1	DOCK7	rs1168030	62502820	C	T	0.2517320	-0.0684129	0.0070229	2.60E-24
1	DOCK7	rs56342264	62503238	T	TA	0.2095840	-0.0712833	0.0074782	2.30E-23
1	DOCK7	rs1168029	62503731	G	A	0.2525220	-0.0671929	0.0070190	1.30E-23
1	DOCK7	rs1168028	62503760	G	A	0.2515750	-0.0679377	0.0070210	4.80E-24
1	DOCK7	rs1168027	62504513	T	C	0.2513850	-0.0679539	0.0070237	5.50E-24
1	DOCK7	rs1168026	62505325	T	C	0.2515750	-0.0679377	0.0070210	4.80E-24
1	DOCK7	chr1:62506471_CT_C	62506471	CT	C	0.2542490	-0.0665302	0.0070305	4.50E-23
1	DOCK7	rs7527004	62506557	G	A	0.2516190	-0.0680414	0.0070233	4.50E-24
1	DOCK7	rs12027778	62507642	G	C	0.1927400	-0.0707277	0.0077162	1.00E-21
1	DOCK7	rs1184865	62508124	A	G	0.2515660	-0.0680009	0.0070212	4.50E-24
1	DOCK7	rs1168042	62508479	A	T	0.2513810	-0.0680031	0.0070237	5.20E-24
1	DOCK7	rs35836805	62508787	T	TTTAC	0.2092030	-0.0716075	0.0074861	1.80E-23
1	DOCK7	rs11207976	62511080	A	G	0.2513790	-0.0679928	0.0070237	5.30E-24
1	DOCK7	rs11207977	62511636	T	C	0.2097900	-0.0705823	0.0074833	6.90E-23
1	DOCK7	rs1781212	62511748	G	A	0.2536580	-0.0663199	0.0070490	6.10E-23
1	DOCK7	rs1168044	62511887	A	C	0.2546540	-0.0673081	0.0070291	1.40E-23
1	DOCK7	rs1690755	62514490	A	G	0.2516620	-0.0681331	0.0070209	3.60E-24
1	DOCK7	rs10557760	62514728	CACA	C	0.2517260	-0.0680068	0.0070233	5.10E-24
1	DOCK7	rs10889336	62514739	C	T	0.2097290	-0.0712664	0.0074800	2.60E-23
1	DOCK7	rs10889337	62514936	A	G	0.2515660	-0.0680009	0.0070212	4.50E-24
1	DOCK7	rs12090886	62515769	G	A	0.2515660	-0.0680009	0.0070212	4.50E-24
1	DOCK7	rs11207979	62517323	A	G	0.2513850	-0.0677184	0.0070236	7.80E-24
1	DOCK7	rs1168046	62518022	A	C	0.2512800	-0.0679165	0.0070242	5.90E-24
1	DOCK7	rs1168047	62518080	C	T	0.2513850	-0.0677184	0.0070236	7.80E-24
1	DOCK7	rs10889338	62519226	T	C	0.2093980	-0.0710613	0.0074813	3.50E-23
1	DOCK7	rs1168050	62521284	C	T	0.2514250	-0.0676255	0.0070239	9.00E-24
1	DOCK7	rs1690766	62521618	T	C	0.2513900	-0.0676550	0.0070234	8.70E-24
1	DOCK7	rs1781195	62523301	T	C	0.2519530	-0.0677180	0.0070185	9.10E-24
1	DOCK7	rs1627591	62524136	C	T	0.2513880	-0.0676702	0.0070234	8.60E-24
1	DOCK7	rs11577840	62525698	T	C	0.2513880	-0.0676702	0.0070234	8.60E-24
1	DOCK7	rs12062275	62526234	T	C	0.2513880	-0.0676702	0.0070234	8.60E-24

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs11207980	62527078	C	T	0.2096920	-0.0714277	0.0074844	2.10E-23
1	DOCK7	rs4915838	62527397	G	A	0.2513870	-0.0676556	0.0070234	8.70E-24
1	DOCK7	rs12403207	62527949	T	C	0.2520370	-0.0683441	0.0070346	4.30E-24
1	DOCK7	rs12039115	62529592	T	C	0.2010480	-0.0695917	0.0075955	8.80E-22
1	DOCK7	rs1168015	62530375	C	G	0.2513830	-0.0676465	0.0070233	8.80E-24
1	DOCK7	rs1168013	62531167	C	G	0.2513680	-0.0675078	0.0070229	1.00E-23
1	DOCK7	rs10458569	62531930	A	C	0.1817680	-0.0691504	0.0078974	4.40E-20
1	DOCK7	rs35664253	62532065	C	CAG	0.2513880	-0.0675990	0.0070232	9.00E-24
1	DOCK7	chr1:62533439_A_AT	62533439	A	AT	0.2515000	-0.0678858	0.0070245	6.40E-24
1	DOCK7	rs4915840	62533924	C	G	0.2515660	-0.0679742	0.0070261	5.50E-24
1	DOCK7	rs61393465	62535060	G	GC	0.2094040	-0.0709555	0.0074809	4.00E-23
1	DOCK7	rs1168018	62535449	A	C	0.2513700	-0.0677365	0.0070233	7.60E-24
1	DOCK7	rs1168017	62536880	A	G	0.2513880	-0.0675990	0.0070232	9.00E-24
1	DOCK7	rs76176236	62538722	C	T	0.1212770	-0.0659750	0.0093707	5.80E-14
1	DOCK7	rs56115463	62540080	A	C	0.2001510	-0.0691645	0.0076175	1.90E-21
1	DOCK7	rs7548877	62540279	T	C	0.2514070	-0.0674917	0.0070238	1.10E-23
1	DOCK7	rs11207981	62540416	C	A	0.2516190	-0.0675560	0.0070272	1.10E-23
1	DOCK7	rs1168023	62540924	A	T	0.2514090	-0.0674915	0.0070239	1.00E-23
1	DOCK7	rs66827188	62541132	TATAG	T	0.2519230	-0.0676232	0.0070294	8.40E-24
1	DOCK7	rs1781221	62541171	A	C	0.2514430	-0.0675798	0.0070244	9.00E-24
1	DOCK7	rs11207982	62541511	T	C	0.2094210	-0.0708894	0.0074817	4.30E-23
1	DOCK7	rs1184547	62541557	G	A	0.2514090	-0.0674915	0.0070239	1.00E-23
1	DOCK7	rs1168022	62542050	A	T	0.2514010	-0.0675114	0.0070240	1.00E-23
1	DOCK7	rs1168021	62544229	A	G	0.2522950	-0.0670027	0.0070212	2.10E-23
1	DOCK7	rs1168020	62544285	C	T	0.2524940	-0.0670337	0.0070275	2.20E-23
1	DOCK7	rs1179765	62544439	G	C	0.2514090	-0.0675712	0.0070239	9.10E-24
1	DOCK7	rs12074528	62545200	T	C	0.2514090	-0.0675712	0.0070239	9.10E-24
1	DOCK7	rs10889339	62546385	A	G	0.2516370	-0.0675874	0.0070259	7.90E-24
1	DOCK7	rs10889340	62546400	A	C	0.2515270	-0.0674817	0.0070250	9.90E-24
1	DOCK7	rs11207983	62546436	C	T	0.2514090	-0.0675712	0.0070239	9.10E-24
1	DOCK7	rs2029763	62547463	G	A	0.2094210	-0.0709801	0.0074817	3.70E-23
1	DOCK7	rs11207984	62547725	C	T	0.2514090	-0.0675712	0.0070239	9.10E-24
1	DOCK7	rs11207985	62548115	A	G	0.2514560	-0.0675513	0.0070239	9.50E-24
1	DOCK7	rs10789113	62549528	T	A	0.2094380	-0.0710038	0.0074819	3.70E-23
1	DOCK7	chr1:62550719_AT_A	62550719	AT	A	0.2630100	-0.0646764	0.0070775	1.00E-21
1	DOCK7	rs11207986	62552499	T	C	0.2514230	-0.0676232	0.0070242	8.60E-24
1	DOCK7	rs10889342	62553181	T	C	0.2072790	-0.0719606	0.0075213	1.50E-23
1	DOCK7	rs11207988	62553316	T	A	0.1889690	-0.0668161	0.0078984	9.00E-19
1	DOCK7	rs7519785	62554248	G	A	0.2514470	-0.0675055	0.0070236	1.10E-23
1	DOCK7	rs10159255	62555145	A	C	0.2094680	-0.0708914	0.0074811	4.40E-23
1	DOCK7	rs2131925	62560271	G	T	0.2525900	-0.0675218	0.0070178	8.60E-24
1	DOCK7	rs2131926	62560340	C	T	0.2516160	-0.0677162	0.0070204	7.70E-24
1	DOCK7	rs10889343	62560758	T	G	0.2516160	-0.0677162	0.0070204	7.70E-24
1	DOCK7	rs4329540	62561353	C	T	0.2522460	-0.0672736	0.0070162	1.40E-23
1	DOCK7	chr1:62562233_CTTT_C	62562233	C	CTTT	0.2096290	-0.0710327	0.0074775	3.60E-23
1	DOCK7	rs4915621	62563762	A	G	0.2515670	-0.0676515	0.0070214	8.40E-24
1	DOCK7	rs12025714	62565940	A	C	0.1972050	-0.0673781	0.0076711	5.50E-20
1	DOCK7	rs6693353	62565945	A	C	0.2515570	-0.0677049	0.0070217	7.90E-24
1	DOCK7	rs139360475	62566892	AACAG	A	0.4577580	-0.0345224	0.0061754	2.00E-09
1	DOCK7	rs10889344	62568270	T	C	0.2515550	-0.0677179	0.0070217	7.70E-24
1	DOCK7	rs10789114	62568551	C	T	0.2082260	-0.0707447	0.0075071	7.10E-23
1	DOCK7	rs7555577	62568692	A	C	0.2514050	-0.0675864	0.0070371	9.90E-24
1	DOCK7	rs10789115	62570458	A	G	0.2515490	-0.0677190	0.0070219	7.60E-24
1	DOCK7	rs12735272	62571136	G	A	0.2515490	-0.0677190	0.0070219	7.60E-24
1	DOCK7	rs12116574	62572166	T	C	0.2058180	-0.0691645	0.0075470	1.60E-21
1	DOCK7	rs142666378	62572632	T	TGG	0.2515490	-0.0677190	0.0070219	7.60E-24
1	DOCK7	rs6696502	62573862	C	T	0.2515440	-0.0678473	0.0070220	6.50E-24
1	DOCK7	rs12038768	62575057	T	G	0.2096270	-0.0710780	0.0074777	3.40E-23
1	DOCK7	rs11207990	62575415	T	C	0.2515390	-0.0678658	0.0070221	6.40E-24
1	DOCK7	rs11207992	62576129	G	T	0.2096270	-0.0710780	0.0074777	3.40E-23
1	DOCK7	rs1472257	62576455	A	G	0.2515330	-0.0678597	0.0070222	6.40E-24
1	DOCK7	rs10789116	62577067	G	A	0.2096270	-0.0710780	0.0074777	3.40E-23
1	DOCK7	rs1748201	62579835	A	C	0.2503420	-0.0681385	0.0070389	5.50E-24
1	DOCK7	rs1748200	62580368	T	C	0.2517060	-0.0678487	0.0070218	7.20E-24
1	DOCK7	rs1629122	62580907	C	A	0.2518170	-0.0676446	0.0070222	7.90E-24
1	DOCK7	chr1:62582603_C_CCCCA	62582603	CCCCA	C	0.2068110	-0.0698533	0.0076571	5.70E-21
1	DOCK7	rs9436224	62582604	C	A	0.2297620	-0.0653693	0.0074048	9.20E-20
1	DOCK7	rs34465969	62582605	C	A	0.2273130	-0.0649131	0.0074100	1.30E-19
1	DOCK7	rs35194512	62582606	C	A	0.1860600	-0.0691254	0.0079652	3.40E-19
1	DOCK7	rs11207995	62583880	C	A	0.2120090	-0.0704966	0.0074715	4.50E-23
1	DOCK7	rs1748195	62583922	G	C	0.2439990	-0.0668758	0.0070965	1.40E-22
1	DOCK7	rs12042319	62584148	A	G	0.2096090	-0.0708747	0.0074786	4.20E-23

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs3850634	62584927	G	T	0.2096860	-0.0706313	0.0074764	6.00E-23
1	DOCK7	rs12030293	62586017	T	C	0.2012220	-0.0696839	0.0075927	7.40E-22
1	DOCK7	rs12048208	62589609	A	G	0.1998040	-0.0697514	0.0076241	8.80E-22
1	DOCK7	rs11207996	62589799	A	G	0.2099380	-0.0710756	0.0074835	4.10E-23
1	DOCK7	rs1748197	62590441	A	G	0.2218110	-0.0703936	0.0073231	2.80E-23
1	DOCK7	rs2366636	62590999	A	G	0.2218110	-0.0703936	0.0073231	2.80E-23
1	DOCK7	rs1748199	62591465	C	T	0.2218110	-0.0703936	0.0073231	2.80E-23
1	DOCK7	rs79439217	62594366	TAAGA	T	0.2514850	-0.0685137	0.0070277	3.20E-24
1	DOCK7	rs6690733	62594640	C	A	0.2514500	-0.0678840	0.0070235	6.10E-24
1	DOCK7	rs11207997	62596235	T	C	0.2514860	-0.0679825	0.0070230	5.40E-24
1	ANGPTL3, 1	rs34483103	62604866	A	TTAATC	0.2092850	-0.0708328	0.0074900	4.70E-23
1	DOCK7	rs10789117	62606594	C	A	0.2533480	-0.0666324	0.0070106	2.30E-23
1	DOCK7	rs59952505	62607196	C	CA	0.2533690	-0.0669755	0.0070079	1.20E-23
1	DOCK7	rs6675401	62608304	T	C	0.2530900	-0.0670063	0.0070075	1.40E-23
1	DOCK7	rs6678483	62608771	A	C	0.2530920	-0.0670126	0.0070075	1.40E-23
1	DOCK7	rs71776858	62608856	C	CTCAT	0.2095130	-0.0706811	0.0074840	5.70E-23
1	DOCK7	rs10889347	62610155	A	G	0.2530860	-0.0670646	0.0070077	1.30E-23
1	DOCK7	rs10889348	62612551	T	A	0.2096170	-0.0706006	0.0074850	6.10E-23
1	DOCK7	rs10889349	62616248	G	A	0.2465370	-0.0681478	0.0070956	2.40E-23
1	DOCK7	rs2031373	62617618	A	C	0.3858700	-0.0427568	0.0062790	1.80E-13
1	DOCK7	rs61471917	62618359	A	G	0.2530880	-0.0670385	0.0070076	1.40E-23
1	DOCK7	rs10889350	62619595	T	C	0.2533540	-0.0667077	0.0070106	2.10E-23
1	DOCK7	chr1:62619812_T_TA	62619812	TA	T	0.3767980	-0.0402676	0.0063828	7.20E-12
1	DOCK7	rs12239736	62620326	A	T	0.2086170	-0.0708483	0.0075086	5.20E-23
1	DOCK7	rs12239737	62620330	A	T	0.1536290	-0.0684407	0.0086229	1.90E-16
1	DOCK7	rs6587980	62625187	T	C	0.2514170	-0.0676539	0.0070263	6.70E-24
1	DOCK7	rs11207998	62625800	C	G	0.2010260	-0.0695799	0.0075971	9.10E-22
1	DOCK7	rs10157265	62627946	T	C	0.2530630	-0.0669694	0.0070084	1.50E-23
1	DOCK7	rs34211669	62627990	G	GT	0.2094080	-0.0709927	0.0074827	3.90E-23
1	DOCK7	rs11485618	62628536	G	A	0.2093860	-0.0709715	0.0074823	4.00E-23
1	DOCK7	rs10789118	62629021	G	A	0.2093800	-0.0708990	0.0074823	4.20E-23
1	DOCK7	rs7520810	62630040	T	C	0.2529700	-0.0668271	0.0070105	1.80E-23
1	DOCK7	rs12025800	62631110	G	C	0.2530670	-0.0669832	0.0070085	1.50E-23
1	DOCK7	rs141409973	62631753	AG	A	0.2530670	-0.0669832	0.0070085	1.50E-23
1	DOCK7	rs10789119	62632564	A	G	0.2093980	-0.0709571	0.0074821	3.90E-23
1	DOCK7	rs11207999	62632970	C	A	0.2530670	-0.0669832	0.0070085	1.50E-23
1	DOCK7	rs10889352	62633352	C	T	0.2093800	-0.0708990	0.0074823	4.20E-23
1	DOCK7	rs2366638	62633906	A	G	0.2530670	-0.0669732	0.0070085	1.50E-23
1	DOCK7	rs377031118	62634374	GA	G	0.2525760	-0.0667732	0.0070177	2.20E-23
1	DOCK7	rs10789120	62635452	A	G	0.2088140	-0.0708068	0.0074924	4.60E-23
1	DOCK7	rs1570694	62637546	G	A	0.2093610	-0.0707916	0.0074824	4.90E-23
1	DOCK7	rs6657050	62639582	G	A	0.2521830	-0.0669450	0.0070209	1.70E-23
1	DOCK7	rs12047226	62639867	C	T	0.2093540	-0.0708367	0.0074824	4.50E-23
1	DOCK7	rs113795489	62640503	A	AAAGC	0.2093520	-0.0708332	0.0074824	4.50E-23
1	DOCK7	rs7538689	62640577	A	G	0.3862350	-0.0423932	0.0062664	3.00E-13
1	DOCK7	rs7539035	62641096	A	C	0.2530470	-0.0670237	0.0070086	1.40E-23
1	DOCK7	rs995000	62641855	T	C	0.2084380	-0.0701281	0.0074952	1.30E-22
1	DOCK7	rs10789121	62642348	C	T	0.3861380	-0.0425639	0.0062672	2.50E-13
1	DOCK7	rs11208000	62642703	G	A	0.2496910	-0.0684834	0.0070595	3.00E-24
1	DOCK7	rs66531495	62643009	G	AGCCAC	0.2499820	-0.0680155	0.0070651	9.70E-24
1	DOCK7	rs993013	62645398	G	T	0.2543420	-0.0673410	0.0070020	7.30E-24
1	DOCK7	rs1168085	62646649	C	G	0.2530610	-0.0670624	0.0070086	1.30E-23
1	DOCK7	rs1168086	62646718	A	G	0.2530610	-0.0670624	0.0070086	1.30E-23
1	DOCK7	rs746735	62647840	C	A	0.2533560	-0.0669719	0.0070130	1.40E-23
1	DOCK7	rs1168089	62648048	T	C	0.2519740	-0.0662190	0.0070195	4.40E-23
1	DOCK7	rs33999917	62650370	GA	G	0.2520070	-0.0664268	0.0070169	3.40E-23
1	DOCK7	rs1168093	62650556	G	A	0.2520140	-0.0664126	0.0070167	3.40E-23
1	DOCK7	rs112957492	62651339	C	T	0.2083020	-0.0702988	0.0074941	9.70E-23
1	DOCK7	rs35107877	62651507	A	AG	0.2520250	-0.0664481	0.0070165	3.20E-23
1	DOCK7	rs10889353	62652525	C	A	0.2090270	-0.0691761	0.0074894	4.30E-22
1	DOCK7	rs1168097	62654700	C	T	0.2564690	-0.0658102	0.0070020	1.00E-22
1	DOCK7	rs60286666	62655430	T	TC	0.2532580	-0.0675467	0.0070106	6.90E-24
1	DOCK7	rs1168098	62655623	G	A	0.2529620	-0.0676924	0.0070153	6.10E-24
1	DOCK7	rs1168099	62657188	C	A	0.2532890	-0.0673150	0.0070093	9.30E-24
1	DOCK7	rs4495740	62658794	G	T	0.2083270	-0.0704381	0.0074940	8.30E-23
1	DOCK7	rs1168100	62658871	T	C	0.4519940	-0.0342025	0.0061734	3.40E-09
1	DOCK7	rs1168102	62662034	C	T	0.2520220	-0.0664436	0.0070167	3.50E-23
1	DOCK7	rs1168103	62662410	C	T	0.2521150	-0.0662416	0.0070174	4.90E-23
1	DOCK7	rs1168104	62662654	A	G	0.2520160	-0.0664068	0.0070169	3.80E-23
1	DOCK7	rs10889354	62663411	C	T	0.2083810	-0.0706370	0.0074966	6.50E-23
1	DOCK7	rs11208001	62664760	T	C	0.2512710	-0.0641811	0.0070699	3.40E-21
1	DOCK7	rs12024419	62664854	A	G	0.1810360	-0.0692005	0.0079211	5.80E-20

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs2479464	62665320	G	A	0.2520310	-0.0660461	0.0070204	7.00E-23
1	DOCK7	rs1168132	62667797	T	A	0.2519890	-0.0661077	0.0070206	6.70E-23
1	DOCK7	rs4587594	62668259	A	G	0.2083130	-0.0699999	0.0074961	1.60E-22
1	DOCK7	rs28399032	62669953	C	G	0.2082630	-0.0701272	0.0074978	1.50E-22
1	DOCK7	rs1168128	62670175	C	G	0.2520630	-0.0664671	0.0070260	4.20E-23
1	DOCK7	rs181835401	62670284	A	G	0.2506740	-0.0663531	0.0070447	6.10E-23
1	DOCK7	rs1168124	62674059	C	T	0.2518560	-0.0663075	0.0070226	5.00E-23
1	DOCK7	rs11208004	62679768	A	G	0.2085790	-0.0690845	0.0075017	6.10E-22
1	DOCK7	rs4459145	62680578	A	C	0.2468500	-0.0651668	0.0071032	7.10E-22
1	DOCK7	rs7531579	62681369	C	A	0.2080600	-0.0706581	0.0075042	7.80E-23
1	DOCK7	chr1:62686882_G_GA	62686882	GA	G	0.1954700	-0.0691783	0.0077679	7.40E-21
1	DOCK7	rs56280080	62687528	T	TCAGA/	0.2075650	-0.0700995	0.0075356	1.70E-22
1	DOCK7	rs4344355	62688282	T	C	0.2082400	-0.0709686	0.0075365	7.20E-23
1	DOCK7 *	rs10889356	62689678	A	G	0.2077340	-0.0701818	0.0075311	2.10E-22
1	DOCK7 *	rs1168114	62690372	A	G	0.2162400	-0.0681634	0.0074373	2.70E-21
1	DOCK7 *	rs1168113	62690427	T	C	0.2359050	-0.0627418	0.0072030	2.70E-19
1	DOCK7 *	rs35834397	62693541	TA	T	0.2264800	-0.0609850	0.0072979	1.50E-17
1	DOCK7 *	rs10889357	62694611	T	C	0.1937240	-0.0665452	0.0077312	3.80E-19
1	DOCK7 *	rs1168107	62695502	A	T	0.2265080	-0.0607113	0.0072981	2.00E-17
1	DOCK7 *	rs12136083	62697402	C	T	0.1937920	-0.0665557	0.0077289	3.50E-19
1	DOCK7 *	rs9659790	62700090	G	A	0.2265080	-0.0609039	0.0072956	1.50E-17
1	DOCK7 *	rs11208006	62704195	T	C	0.2265140	-0.0607386	0.0072961	1.80E-17
1	DOCK7 *	rs12041843	62704478	G	T	0.1781380	-0.0634404	0.0080267	1.70E-16
1	DOCK7 *	rs6682423	62705392	C	T	0.2264740	-0.0609311	0.0072955	1.50E-17
1	DOCK7 *	rs6666816	62705528	C	T	0.2264750	-0.0609094	0.0072955	1.50E-17
1	DOCK7 *	rs880694	62707613	C	T	0.2265620	-0.0608435	0.0072940	1.60E-17
1	DOCK7 *	rs10889360	62708247	T	C	0.1937760	-0.0667379	0.0077280	2.80E-19
1	DOCK7 *	rs11208007	62710412	T	A	0.1938260	-0.0666766	0.0077269	2.90E-19
1	DOCK7 *	rs4409689	62711694	C	T	0.2265030	-0.0611364	0.0072954	1.20E-17
1	DOCK7 *	rs60152331	62711868	G	T	0.3710520	-0.0372912	0.0063832	5.20E-10
1	DOCK7 *	rs7518497	62712025	C	A	0.1937680	-0.0668857	0.0077282	2.20E-19
1	DOCK7 *	rs9787151	62713467	C	T	0.2265780	-0.0611162	0.0072934	1.10E-17
1	DOCK7 *	rs9787156	62713541	G	A	0.2265850	-0.0611187	0.0072932	1.10E-17
1	DOCK7 *	rs12043910	62715877	A	G	0.1854620	-0.0657938	0.0078603	2.60E-18
1	DOCK7 *	rs6686331	62716464	C	T	0.2265320	-0.0612448	0.0072968	1.00E-17
1	DOCK7 *	rs75650238	62717743	C	CCA	0.1849140	-0.0658977	0.0078759	3.00E-18
1	DOCK7 *	rs6661669	62720298	T	C	0.2268180	-0.0614759	0.0072963	7.80E-18
1	DOCK7 *	rs76609868	62720544	C	A	0.1832710	-0.0661770	0.0079100	2.30E-18
1	DOCK7 *	rs12031537	62722415	A	C	0.1837710	-0.0652953	0.0078843	6.90E-18
1	DOCK7 *	rs7517372	62723893	G	A	0.2124090	-0.0567123	0.0074802	7.40E-15
1	DOCK7 *	rs4915624	62725847	G	A	0.2159690	-0.0583554	0.0074161	7.50E-16
1	DOCK7 *	rs76794398	62725894	A	G	0.1839130	-0.0641469	0.0078762	1.80E-17
1	DOCK7 *	rs4915853	62725906	C	A	0.2248200	-0.0597677	0.0073087	5.70E-17
1	DOCK7 *	rs199747920	62727151	ATTTC	A	0.2164140	-0.0582057	0.0074105	8.00E-16
1	DOCK7 *	rs149188767	62727166	TTTTC	C	0.2247890	-0.0564124	0.0074043	5.40E-15
1	DOCK7 *	chr1:62727171_CT_C	62727171	C	CT	0.2143900	-0.0579466	0.0074509	1.50E-15
1	DOCK7 *	rs12029452	62727599	C	A	0.1839090	-0.0641649	0.0078762	1.80E-17
1	DOCK7 *	rs12026283	62728242	A	T	0.1839090	-0.0641649	0.0078762	1.80E-17
1	DOCK7 *	rs2149116	62728301	G	A	0.3749870	-0.0355661	0.0063925	3.40E-09
1	DOCK7 *	rs12023282	62728306	A	G	0.1839460	-0.0640564	0.0078767	1.90E-17
1	DOCK7 *	rs6664692	62729989	C	T	0.2128810	-0.0582853	0.0074598	9.60E-16
1	DOCK7 *	rs11208009	62730021	C	T	0.2212890	-0.0598166	0.0073549	7.20E-17
1	DOCK7 *	rs10889364	62731143	T	C	0.1840230	-0.0641789	0.0078734	1.70E-17
1	DOCK7 *	rs12049254	62731481	C	G	0.1840470	-0.0642076	0.0078729	1.70E-17
1	DOCK7 *	rs76753312	62733237	C	G	0.1840440	-0.0636055	0.0078683	2.70E-17
1	DOCK7 *	chr1:62733488_GA_G	62733488	GA	G	0.1851130	-0.0639446	0.0078688	2.90E-17
1	DOCK7 *	rs4630152	62733601	C	T	0.2135070	-0.0580758	0.0074411	1.10E-15
1	DOCK7 *	rs150990100	62733676	TG	T	0.2229560	-0.0597529	0.0073638	9.30E-17
1	DOCK7 *	rs61775961	62733677	G	T	0.2225820	-0.0594008	0.0073714	1.50E-16
1	DOCK7 *	rs61775962	62733679	A	G	0.2225820	-0.0594008	0.0073714	1.50E-16
1	DOCK7 *	rs6679002	62734265	G	T	0.2220950	-0.0594370	0.0073331	9.30E-17
1	DOCK7 *	rs12024044	62734645	A	G	0.1846140	-0.0639270	0.0078561	2.30E-17
1	DOCK7 *	rs12025111	62735769	A	G	0.1845170	-0.0638216	0.0078582	2.70E-17
1	DOCK7 *	rs12028944	62735867	A	T	0.1845900	-0.0636797	0.0078568	3.00E-17
1	ATG4C *	chr1:62736501_AT_A	62736501	AT	A	0.1953530	-0.0622238	0.0078613	2.20E-16
1	ATG4C *	rs12121288	62736790	G	A	0.2130690	-0.0584244	0.0074587	8.30E-16
1	ATG4C *	rs72915166	62736922	A	G	0.2127260	-0.0589836	0.0074703	4.70E-16
1	ATG4C *	rs78731792	62736973	A	G	0.1839140	-0.0639087	0.0078944	2.50E-17
1	ATG4C *	rs66676942	62737728	A	AT	0.1812830	-0.0638139	0.0080007	8.10E-17
1	ATG4C *	rs10789123	62737950	T	A	0.2096010	-0.0586662	0.0076029	2.00E-15
1	ATG4C *	rs12027341	62738235	A	G	0.1795110	-0.0641247	0.0080532	1.00E-16
1	ATG4C *	rs77870744	62738693	C	T	0.1812730	-0.0626779	0.0080386	3.70E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	MTF2 *	rs7532549	93074099	G	T	0.3513460	-0.0342261	0.0063989	4.70E-08
1	MTF2 *	rs1856027	93078574	T	C	0.3480460	-0.0344793	0.0064113	3.60E-08
1	MTF2	rs12128131	93080742	T	G	0.3458440	-0.0344812	0.0064151	4.10E-08
1	MTF2	rs11164870	93086630	C	G	0.3478970	-0.0342810	0.0064008	4.10E-08
1	MTF2	rs11164871	93090125	C	T	0.3478960	-0.0343573	0.0064020	4.00E-08
1	MTF2	rs12038699	93093261	A	G	0.3468460	-0.0347106	0.0064209	3.20E-08
1	MTF2	rs1474927	93104811	G	A	0.3470860	-0.0346178	0.0064057	3.00E-08
1	MTF2	rs12139009	93107936	A	G	0.3471150	-0.0345687	0.0064056	3.20E-08
1	MTF2	rs4847398	93112845	C	T	0.3477010	-0.0344121	0.0064031	3.70E-08
1	MTF2	rs2295424	93115322	T	C	0.3465300	-0.0348945	0.0064093	2.30E-08
1	MTF2	rs2295423	93115467	T	C	0.3465120	-0.0341086	0.0064136	4.50E-08
1	MTF2	rs4847399	93119049	G	A	0.3471340	-0.0346995	0.0064050	2.70E-08
1	MTF2	rs2208044	93121878	C	T	0.3480210	-0.0352971	0.0064144	1.70E-08
1	TMED5	rs1572343	93150645	T	C	0.3452000	-0.0355624	0.0064237	1.50E-08
1	TMED5	rs7532195	93151846	T	G	0.3378560	-0.0346984	0.0064574	4.10E-08
1	TMED5	rs1060622	93154836	G	A	0.3447840	-0.0355115	0.0064355	1.80E-08
1	TMED5	rs1057257	93155926	A	G	0.3438160	-0.0350903	0.0064301	2.50E-08
1	TMED5	rs12130734	93158817	T	C	0.3384770	-0.0352363	0.0064527	2.30E-08
1	TMED5	chr1:93159677_T_TA	93159677	T	TA	0.3421850	-0.0356316	0.0064704	3.00E-08
1	TMED5	rs2783489	93161427	T	C	0.3384090	-0.0352077	0.0064531	2.50E-08
1	TMED5	rs4847235	93162170	T	C	0.3387010	-0.0352767	0.0064523	2.20E-08
1	TMED5	rs4847401	93162456	C	G	0.3389730	-0.0349870	0.0064486	2.90E-08
1	TMED5	rs4847402	93162505	G	A	0.3441840	-0.0350296	0.0064258	2.40E-08
1	TMED5	rs71728015	93163153	TACTC	T	0.3443460	-0.0349603	0.0064277	2.60E-08
1	TMED5	rs10874759	93164615	G	A	0.3443260	-0.0350450	0.0064259	2.30E-08
1	TMED5	rs11164876	93164953	T	C	0.3389860	-0.0349663	0.0064486	2.90E-08
1	TMED5	rs2152358	93168452	G	A	0.3441990	-0.0350123	0.0064259	2.50E-08
1	TMED5	rs6685271	93169033	C	A	0.3389910	-0.0349776	0.0064487	2.90E-08
1	TMED5	rs6697683	93169034	A	G	0.3389910	-0.0349776	0.0064487	2.90E-08
1	TMED5	rs1932314	93172843	G	A	0.3442020	-0.0350156	0.0064259	2.50E-08
1	TMED5	rs34206647	93173286	C	CAT	0.3064460	-0.0365214	0.0066295	3.50E-08
1	TMED5	rs10874762	93173544	T	G	0.3442100	-0.0350344	0.0064260	2.50E-08
1	TMED5	rs12044657	93174039	T	C	0.3396530	-0.0352301	0.0064478	2.30E-08
1	TMED5	rs6688230	93175567	C	T	0.3444750	-0.0348534	0.0064409	2.90E-08
1	TMED5	rs7553465	93178853	C	T	0.3442000	-0.0350479	0.0064285	2.40E-08
1	TMED5	rs7553916	93179286	C	G	0.3471390	-0.0343387	0.0064267	4.00E-08
1	TMED5	rs1335679	93179625	C	T	0.3442060	-0.0350554	0.0064284	2.40E-08
1	TMED5	rs2297707	93180650	T	C	0.3444160	-0.0351204	0.0064309	2.20E-08
1	CCDC18	rs7535628	93183171	T	C	0.3389290	-0.0345775	0.0064684	4.90E-08
1	CCDC18	rs6682670	93184175	A	G	0.3441840	-0.0354193	0.0064282	1.70E-08
1	CCDC18	rs10601381	93184605	ACT	A	0.3441840	-0.0354193	0.0064282	1.70E-08
1	CCDC18	rs12118230	93185904	T	G	0.3441860	-0.0354350	0.0064282	1.70E-08
1	CCDC18	rs12118262	93185990	T	C	0.3439960	-0.0355515	0.0064298	1.60E-08
1	CCDC18	rs12124011	93186987	C	A	0.3436320	-0.0354408	0.0064330	1.80E-08
1	CCDC18	rs7539307	93187146	G	A	0.3394940	-0.0358718	0.0064567	1.40E-08
1	CCDC18	rs7517363	93187228	C	T	0.3441860	-0.0354350	0.0064282	1.70E-08
1	CCDC18	rs11164879	93189965	G	A	0.3442520	-0.0355100	0.0064285	1.60E-08
1	CCDC18	rs7541687	93191031	A	G	0.3438770	-0.0352635	0.0064310	2.10E-08
1	CCDC18	rs11164880	93192539	A	C	0.3389860	-0.0354311	0.0064511	1.90E-08
1	CCDC18	rs11164881	93193432	C	A	0.3450330	-0.0352111	0.0064293	1.90E-08
1	CCDC18	rs10782955	93194205	A	G	0.3451040	-0.0352069	0.0064300	1.90E-08
1	CCDC18	rs10874764	93195785	C	A	0.3441980	-0.0354935	0.0064282	1.60E-08
1	CCDC18	rs67544684	93196366	TACTC	T	0.3448450	-0.0352796	0.0064327	2.10E-08
1	CCDC18	rs61799471	93197901	A	G	0.3451750	-0.0357353	0.0064266	1.20E-08
1	CCDC18	rs1537758	93199594	A	G	0.3389250	-0.0353727	0.0064519	2.20E-08
1	CCDC18	rs7513705	93200792	T	C	0.3389960	-0.0353799	0.0064509	2.10E-08
1	CCDC18	rs12030549	93203661	T	C	0.3446710	-0.0360627	0.0064331	1.10E-08
1	CCDC18	rs5776173	93206124	AC	A	0.3447280	-0.0365337	0.0064156	5.80E-09
1	CCDC18	rs2783499	93207131	T	C	0.3074860	-0.0384073	0.0066113	5.80E-09
1	CCDC18	rs71586782	93208037	AT	A	0.3447180	-0.0365139	0.0064159	5.80E-09
1	CCDC18	rs2783500	93208050	A	T	0.3074680	-0.0383884	0.0066117	5.90E-09
1	CCDC18	rs2783501	93208079	T	C	0.3074680	-0.0383884	0.0066117	5.90E-09
1	CCDC18	rs797675	93208669	A	T	0.3447180	-0.0365139	0.0064159	5.80E-09
1	CCDC18	rs2783504	93209856	A	G	0.3075190	-0.0384661	0.0066118	5.60E-09
1	CCDC18	rs531358	93210454	C	T	0.3467150	-0.0366041	0.0064218	5.20E-09
1	CCDC18	rs555161	93210757	A	G	0.3447340	-0.0365314	0.0064156	5.70E-09
1	CCDC18	rs797676	93211021	A	G	0.3447730	-0.0364381	0.0064160	6.30E-09
1	CCDC18	rs2765545	93211712	G	A	0.3453180	-0.0362150	0.0064162	7.60E-09
1	CCDC18	rs661126	93213411	T	G	0.3485510	-0.0363029	0.0064995	1.40E-08
1	CCDC18	rs2815415	93214283	A	G	0.3074860	-0.0384073	0.0066113	5.80E-09
1	CCDC18	rs612037	93217321	A	G	0.3449850	-0.0364757	0.0064159	6.30E-09
1	CCDC18	rs624131	93217653	G	A	0.3447320	-0.0365259	0.0064156	5.80E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	CCDC18	rs627779	93218532	C	T	0.3434570	-0.0366022	0.0064287	6.30E-09
1	CCDC18	rs34507895	93221289	CTGTT	C	0.3447320	-0.0365259	0.0064156	5.80E-09
1	CCDC18	rs797661	93221534	T	G	0.3447320	-0.0365259	0.0064156	5.80E-09
1	CCDC18	rs61799496	93226177	G	A	0.3074860	-0.0384073	0.0066113	5.80E-09
1	CCDC18	rs797668	93229232	G	C	0.3447380	-0.0365478	0.0064155	5.60E-09
1	CCDC18	rs4484937	93233968	T	C	0.3074930	-0.0384468	0.0066113	5.60E-09
1	CCDC18	rs531514	93234655	T	C	0.3447350	-0.0365115	0.0064156	5.80E-09
1	CCDC18	rs112240098	93234783	CGTTT	C	0.3122490	-0.0384235	0.0065867	4.90E-09
1	CCDC18	rs797671	93234806	A	C	0.3438000	-0.0360345	0.0064280	8.90E-09
1	CCDC18	rs797672	93236562	T	A	0.3443310	-0.0362100	0.0064201	8.50E-09
1	CCDC18	rs12048219	93238362	T	C	0.3070660	-0.0381057	0.0066167	8.50E-09
1	CCDC18	rs5776175	93239169	TA	T	0.3073200	-0.0382871	0.0066142	6.80E-09
1	CCDC18	rs5776176	93239236	C	CT	0.3449330	-0.0363050	0.0064174	7.00E-09
1	CCDC18	rs565919	93241156	T	C	0.3443310	-0.0362100	0.0064201	8.50E-09
1	CCDC18	rs3754186	93246225	T	A	0.3462750	-0.0367586	0.0064144	5.50E-09
1	CCDC18	rs12044557	93247207	A	G	0.3076140	-0.0384073	0.0066118	6.00E-09
1	CCDC18	rs72959220	93248125	G	C	0.3073850	-0.0383485	0.0066125	5.80E-09
1	CCDC18	rs58354545	93248305	T	C	0.3074940	-0.0383984	0.0066114	5.80E-09
1	CCDC18	rs687394	93248360	A	G	0.3447430	-0.0365257	0.0064157	5.70E-09
1	CCDC18	rs3904665	93248546	A	G	0.3074940	-0.0383984	0.0066114	5.80E-09
1	CCDC18	rs11164885	93249138	T	C	0.3074940	-0.0383984	0.0066114	5.80E-09
1	CCDC18	rs622608	93249662	A	G	0.3447430	-0.0365257	0.0064157	5.70E-09
1	CCDC18	rs7512911	93250261	G	C	0.3447430	-0.0365257	0.0064157	5.70E-09
1	CCDC18	rs637646	93250826	C	A	0.3447450	-0.0365312	0.0064157	5.70E-09
1	CCDC18	rs797680	93251417	T	G	0.3456180	-0.0366863	0.0064106	4.30E-09
1	CCDC18	rs797681	93252189	C	T	0.3447460	-0.0365365	0.0064157	5.70E-09
1	CCDC18	rs61799500	93253573	T	G	0.3074960	-0.0384053	0.0066114	5.80E-09
1	CCDC18	rs682514	93253873	C	A	0.3447440	-0.0365306	0.0064156	5.70E-09
1	CCDC18	rs12030843	93254513	G	C	0.3075210	-0.0382648	0.0066117	6.40E-09
1	CCDC18	rs12031765	93255040	T	C	0.3059370	-0.0379716	0.0066404	9.80E-09
1	CCDC18	rs693737	93259367	A	G	0.3447200	-0.0365898	0.0064162	5.60E-09
1	CCDC18	rs547866	93259496	T	C	0.3457690	-0.0369436	0.0064144	3.50E-09
1	CCDC18	rs602204	93262022	G	A	0.3447380	-0.0365367	0.0064159	5.80E-09
1	CCDC18	rs535760	93263201	A	T	0.3447380	-0.0365367	0.0064159	5.80E-09
1	CCDC18	rs10714121	93264112	C	CA	0.3447380	-0.0365367	0.0064159	5.80E-09
1	CCDC18	rs797666	93266338	A	G	0.3447370	-0.0365534	0.0064158	5.70E-09
1	CCDC18	rs2296558	93270998	T	C	0.3445120	-0.0367993	0.0064164	4.40E-09
1	CCDC18	rs1553191144	93272955	TAA	T	0.3446350	-0.0365208	0.0064170	6.00E-09
1	CCDC18	rs35797862	93272958	AAG	A	0.3451160	-0.0369559	0.0064153	3.60E-09
1	CCDC18	rs6541401	93273391	A	G	0.3448790	-0.0364650	0.0064170	5.80E-09
1	CCDC18	rs6541404	93277877	T	A	0.3447790	-0.0364695	0.0064166	6.00E-09
1	CCDC18 *	rs144112978	93279699	T	ACCTCA	0.3326760	-0.0381840	0.0066325	4.50E-09
1	CCDC18 *	rs9660390	93279978	T	C	0.3447160	-0.0366149	0.0064160	5.40E-09
1	CCDC18 *	rs7526112	93282126	G	T	0.3447130	-0.0366022	0.0064160	5.50E-09
1	CCDC18 *	rs12405487	93283515	G	A	0.3074770	-0.0384341	0.0066115	5.70E-09
1	CCDC18 *	rs2391251	93285014	T	C	0.3074560	-0.0384700	0.0066113	5.50E-09
1	CCDC18 *	rs7551485	93285723	A	G	0.3446990	-0.0365759	0.0064158	5.60E-09
1	CCDC18 *	rs61799516	93287425	T	C	0.3074790	-0.0384592	0.0066116	5.40E-09
1	CCDC18 *	rs6684908	93288375	T	C	0.3074860	-0.0384128	0.0066116	5.60E-09
1	CCDC18 *	rs7418101	93290635	A	G	0.3447990	-0.0365207	0.0064165	5.70E-09
1	CCDC18 *	rs6676902	93291329	T	C	0.3074890	-0.0384767	0.0066117	5.30E-09
1	CCDC18 *	rs111969858	93292230	CCCAT	G	0.3431550	-0.0361819	0.0064282	6.50E-09
1	CCDC18 *	rs7541304	93292281	A	T	0.3447320	-0.0365837	0.0064163	5.30E-09
1	CCDC18 *	rs4847406	93292893	C	T	0.3461150	-0.0367665	0.0064158	5.20E-09
1	CCDC18 *	rs7540025	93293671	T	C	0.3444880	-0.0364138	0.0064188	6.30E-09
1	CCDC18 *	rs9432681	93296339	G	A	0.3448510	-0.0368087	0.0064174	4.20E-09
1	CCDC18 *	rs10782957	93298339	C	T	0.3451910	-0.0365959	0.0064158	4.90E-09
1	CCDC18 *	rs35042495	93299394	CTT	C	0.3447400	-0.0365406	0.0064191	5.50E-09
1	CCDC18 *	rs12139633	93303770	A	G	0.3436070	-0.0363528	0.0064369	6.00E-09
1	CCDC18 *	rs6680107	93305323	G	A	0.3450420	-0.0363215	0.0064181	7.20E-09
1	CCDC18 *	rs9432453	93306072	G	A	0.3441260	-0.0367292	0.0064242	5.50E-09
1	CCDC18 *	rs1000607	93306444	T	C	0.3447220	-0.0365292	0.0064199	5.90E-09
1	CCDC18 *	rs4240966	93309255	C	A	0.3446330	-0.0363279	0.0064190	7.00E-09
1	LOC100131:rs7537403	93312167	T	C	0.3446440	-0.0363642	0.0064191	6.90E-09	
1	LOC100131:rs9432459	93313106	G	A	0.3446560	-0.0363760	0.0064191	6.80E-09	
1	LOC100131:rs11164902	93313237	A	G	0.3446440	-0.0363642	0.0064191	6.90E-09	
1	LOC100131:rs4000699	93314248	C	T	0.3450740	-0.0357009	0.0064189	1.20E-08	
1	LOC100131:rs9432465	93315034	G	A	0.3446450	-0.0363690	0.0064191	6.80E-09	
1	LOC100131:rs12031709	93315061	T	C	0.3074220	-0.0382907	0.0066142	6.60E-09	
1	LOC100131:rs11164904	93315185	G	A	0.3459900	-0.0365373	0.0064185	6.70E-09	
1	LOC100131:rs7547244	93316211	A	G	0.3447650	-0.0364723	0.0064192	6.20E-09	
1	LOC100131:rs2031225	93321157	G	A	0.3446450	-0.0363343	0.0064190	7.00E-09	

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	LOC100131:rs2031226		93321207	G	T	0.3446560	-0.0364412	0.0064195	6.20E-09
1	LOC100131:rs10874772		93322213	G	A	0.3445850	-0.0363438	0.0064201	7.20E-09
1	LOC100131:rs6541349		93322310	C	T	0.3126370	-0.0382036	0.0065835	5.70E-09
1	LOC100131:rs6703310		93323183	T	G	0.3445810	-0.0363353	0.0064202	7.20E-09
1	LOC100131:rs12563120		93325088	C	T	0.3074420	-0.0382945	0.0066142	6.60E-09
1	LOC100131:rs4847408		93325880	G	C	0.3445810	-0.0363353	0.0064202	7.20E-09
1	LOC100131:rs2391254		93329609	A	T	0.3445810	-0.0363319	0.0064204	7.20E-09
1	LOC100131:rs11164908		93332834	A	C	0.3061370	-0.0384832	0.0066324	5.90E-09
1	LOC100131:rs10874773		93332939	T	G	0.3445820	-0.0363477	0.0064202	7.10E-09
1	LOC100131:rs12124771		93333682	A	G	0.3445760	-0.0363664	0.0064205	7.00E-09
1	LOC100131:rs12566752		93334087	T	C	0.3070160	-0.0382451	0.0066192	6.20E-09
1	LOC100131:rs7524964		93335535	C	T	0.3445760	-0.0363340	0.0064205	7.30E-09
1	LOC100131:rs942196		93336707	T	A	0.3445280	-0.0365007	0.0064197	6.20E-09
1	LOC100131:rs4847410		93337224	G	A	0.3445700	-0.0364746	0.0064184	6.20E-09
1	LOC100131:rs1535699		93339395	G	A	0.3445750	-0.0364792	0.0064185	6.20E-09
1	LOC100131:rs1535701		93339644	T	G	0.3445730	-0.0364900	0.0064186	6.10E-09
1	LOC100131:rs34317538		93341705	T	TC	0.3073490	-0.0384364	0.0066136	5.60E-09
1	LOC100131:rs60230322		93341858	A	ATTGT	0.3073840	-0.0384390	0.0066142	5.50E-09
1	LOC100131:rs61266405		93344153	T	C	0.3068160	-0.0390017	0.0066207	3.20E-09
1	DR1 rs3767962		93348854	A	G	0.3477590	-0.0373314	0.0064010	1.90E-09
1	DR1 rs771462		93349268	A	T	0.3087260	-0.0384546	0.0066052	5.00E-09
1	DR1 rs3767964		93349933	T	C	0.3475370	-0.0370675	0.0064042	2.50E-09
1	DR1 rs12133576		93350843	A	G	0.3477980	-0.0373632	0.0064013	1.70E-09
1	DR1 rs4847240		93352389	A	G	0.3477790	-0.0373791	0.0064009	1.80E-09
1	DR1 rs12044883		93355018	G	A	0.3478200	-0.0369954	0.0064020	2.60E-09
1	DR1 rs6658257		93355127	A	G	0.3477580	-0.0373217	0.0064011	1.90E-09
1	DR1 chr1:93356723_AT_A		93356723	AT	A	0.3592290	-0.0382408	0.0064228	9.40E-10
1	DR1 rs771458		93356792	C	G	0.3077530	-0.0387262	0.0066201	4.00E-09
1	DR1 rs1559828		93360081	T	A	0.3477570	-0.0373203	0.0064011	1.90E-09
1	DR1 * rs7525248		93362966	T	A	0.3477690	-0.0373322	0.0064011	1.90E-09
1	DR1 * rs4847412		93363691	C	G	0.3477570	-0.0373203	0.0064011	1.90E-09
1	DR1 * rs34055819		93364853	T	TTC	0.3498240	-0.0376450	0.0064584	1.60E-09
1	DR1 * rs7535214		93367008	A	T	0.3135190	-0.0384483	0.0065811	4.10E-09
1	DR1 * chr1:93367149_CAAAAAA_C		93367149	AAAAA	C	0.3296230	-0.0372288	0.0066313	4.90E-09
1	DR1 * rs6680022		93367980	C	T	0.3477570	-0.0373203	0.0064011	1.90E-09
1	DR1 * rs11576494		93371409	G	A	0.3478000	-0.0374705	0.0064014	1.70E-09
1	DR1 * rs12752223		93371576	T	C	0.3482880	-0.0377350	0.0064046	1.20E-09
1	DR1 * chr1:93371642_C_CT		93371642	CT	C	0.3051810	-0.0390700	0.0066618	5.00E-09
1	DR1 * rs35915989		93373345	C	A	0.3087290	-0.0384402	0.0066052	4.90E-09
1	DR1 * rs35910103		93373473	G	A	0.3087290	-0.0384402	0.0066052	4.90E-09
1	DR1 * rs35628716		93374051	T	G	0.3087300	-0.0384480	0.0066052	4.90E-09
1	DR1 * rs6694508		93376466	A	C	0.3477570	-0.0373203	0.0064011	1.90E-09
1	DR1 * rs1081522		93378341	A	G	0.3087350	-0.0384600	0.0066051	4.90E-09
1	DR1 * rs4847419		93380098	T	A	0.3460870	-0.0376490	0.0064155	1.60E-09
1	DR1 * rs4847420		93380117	A	C	0.3460870	-0.0376490	0.0064155	1.60E-09
1	DR1 * rs771481		93381096	A	T	0.3087350	-0.0384600	0.0066051	4.90E-09
1	DR1 * rs1426318		93381863	A	G	0.3477080	-0.0373106	0.0064020	2.00E-09
1	DR1 * rs59417472		93382956	T	C	0.3477080	-0.0373106	0.0064020	2.00E-09
1	DR1 * rs771478		93383243	T	C	0.3067770	-0.0386870	0.0066167	4.20E-09
1	DR1 * rs12133907		93384726	C	A	0.3477200	-0.0373085	0.0064019	2.00E-09
1	DR1 * rs11164916		93387458	G	C	0.3428030	-0.0365169	0.0064359	3.90E-09
1	DR1 * rs7417952		93388629	C	G	0.3473120	-0.0371776	0.0064060	2.10E-09
1	DR1 * rs2114273		93388960	T	C	0.3473120	-0.0371776	0.0064060	2.10E-09
1	DR1 * rs4847423		93389437	G	A	0.3473120	-0.0371776	0.0064060	2.10E-09
1	DR1 * rs1365298		93392732	A	G	0.3113830	-0.0387016	0.0065941	3.10E-09
1	DR1 * rs1365297		93392735	G	A	0.3065890	-0.0388499	0.0066199	3.70E-09
1	DR1 * rs1593512		93392817	G	A	0.3453490	-0.0373323	0.0064143	1.90E-09
1	DR1 * rs35386534		93393294	T	TA	0.3058820	-0.0386473	0.0066274	4.20E-09
1	DR1 * rs12406245		93395068	G	A	0.3473120	-0.0371776	0.0064060	2.10E-09
1	DR1 * rs812214		93395503	A	G	0.3080650	-0.0385064	0.0066193	4.50E-09
1	DR1 * rs144955708		93396025	T	TTG	0.2925830	-0.0378474	0.0068679	2.10E-08
1	DR1 * rs398103026		93396026	T	TG	0.2998550	-0.0389853	0.0067690	9.30E-09
1	DR1 * rs12565182		93396032	T	G	0.3371670	-0.0371897	0.0065795	6.20E-09
1	DR1 * rs10874777		93396463	T	C	0.3462430	-0.0365226	0.0064938	8.60E-09
1	MARC1 rs2642438		220796686	A	G	0.2010340	0.0403730	0.0076268	6.40E-09
1	MARC1 rs2642439		220797157	A	G	0.1942620	0.0391338	0.0077354	4.90E-08
1	MARC1 rs2807834		220797251	T	G	0.1950730	0.0397719	0.0077437	3.70E-08
1	GALNT2 rs11122400		230144512	G	C	0.1187700	-0.0503012	0.0094712	3.50E-08
1	GALNT2 rs11122401		230145321	A	G	0.1187710	-0.0501755	0.0094712	3.70E-08
1	GALNT2 rs4846908		230149309	A	G	0.1187330	-0.0498885	0.0094727	4.60E-08
1	GALNT2 rs10864722		230154507	A	G	0.1169410	-0.0501245	0.0095653	4.60E-08
1	GALNT2 rs4631704		230157783	T	C	0.1997240	-0.0596563	0.0076653	2.90E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	GALNT2	rs11122446	230158030	G	A	0.2376120	-0.0423790	0.0072746	1.00E-09
1	GALNT2	rs4846913	230158968	A	C	0.1909880	-0.0623378	0.0077914	7.30E-17
1	GALNT2	rs2144300	230159169	T	C	0.1914780	-0.0626404	0.0077675	4.80E-17
1	GALNT2	rs6143660	230159329	T	IGTTCA	0.1933210	-0.0619773	0.0077536	6.20E-17
1	GALNT2	rs17315646	230159560	G	C	0.2196520	-0.0497325	0.0074032	2.70E-12
1	GALNT2	rs4846914	230159944	A	G	0.2200960	-0.0497506	0.0073943	2.30E-12
1	GALNT2	rs10864726	230160406	T	C	0.2199750	-0.0502759	0.0073954	1.40E-12
1	GALNT2	rs2281721	230161390	T	C	0.2171920	-0.0502751	0.0074468	1.70E-12
1	GALNT2	rs2281719	230161913	T	C	0.2341670	-0.0446319	0.0072365	1.00E-10
1	GALNT2	rs2281718	230162032	T	A	0.2341720	-0.0447300	0.0072367	9.00E-11
1	GALNT2	rs10864727	230162193	G	A	0.2341730	-0.0447604	0.0072352	9.40E-11
1	GALNT2	rs4846917	230163476	C	T	0.2797800	-0.0416787	0.0068717	3.90E-10
1	GALNT2	rs10779835	230164203	C	T	0.2344360	-0.0449796	0.0072304	7.70E-11
1	GALNT2	rs11122449	230164735	T	C	0.2753040	-0.0423251	0.0068979	3.00E-10
1	GALNT2	rs11122450	230166065	G	T	0.2366210	-0.0444601	0.0072039	9.60E-11
1	GALNT2	rs4846840	230166775	G	T	0.2802240	-0.0424965	0.0068638	1.80E-10
1	GALNT2	rs4846841	230166915	G	A	0.2823930	-0.0424595	0.0068474	1.40E-10
1	GALNT2	rs6672758	230167766	T	C	0.2799240	-0.0425289	0.0068663	1.90E-10
1	GALNT2	rs11122453	230167865	A	C	0.2343240	-0.0445919	0.0072244	1.20E-10
1	GALNT2	rs1546954	230168102	G	T	0.2350100	-0.0442966	0.0072131	1.30E-10
1	GALNT2	rs34966440	230168184	G	GGC	0.2344980	-0.0444209	0.0072166	1.30E-10
1	GALNT2	rs11122454	230168305	T	C	0.2345810	-0.0441895	0.0072182	1.50E-10
1	GALNT2	rs4846921	230168606	A	G	0.2351210	-0.0438737	0.0072095	2.10E-10
1	GALNT2	rs10864728	230169168	G	A	0.2374100	-0.0437890	0.0071813	1.60E-10
1	GALNT2	rs11122455	230169184	G	C	0.2374060	-0.0437767	0.0071813	1.60E-10
1	GALNT2	rs10489615	230169242	G	A	0.2374060	-0.0437767	0.0071813	1.60E-10
1	GALNT2	rs1321257	230169566	A	G	0.2374060	-0.0437767	0.0071813	1.60E-10
1	GALNT2	rs11122456	230170220	G	A	0.2358390	-0.0431689	0.0072408	4.40E-10
2	C2orf43 *	rs6732741	20894274	A	T	0.1588400	-0.0432850	0.0084202	3.70E-08
2	C2orf43 *	rs60220193	20894620	A	G	0.1587860	-0.0434700	0.0084202	3.30E-08
2	C2orf43 *	rs13008369	20900678	T	G	0.1505430	-0.0471736	0.0085459	2.90E-09
2	C2orf43 *	rs7583126	20901107	G	A	0.1504360	-0.0488299	0.0085537	9.80E-10
2	C2orf43 *	rs13015995	20901187	T	C	0.1504300	-0.0488259	0.0085540	9.80E-10
2	C2orf43 *	rs6722139	20901622	A	C	0.1502510	-0.0489677	0.0085599	8.90E-10
2	APOB *	rs113780557	20920505	C	T	0.1417220	-0.0460651	0.0089052	7.60E-09
2	APOB *	rs114851711	20921082	A	C	0.1398560	-0.0463115	0.0089635	1.00E-08
2	APOB *	rs7580543	20921560	A	G	0.1423030	-0.0472475	0.0088787	3.20E-09
2	APOB *	chr2:20921764_C_CA	20921764	CA	C	0.1420570	-0.0465573	0.0088917	5.40E-09
2	APOB *	rs7588415	20923901	A	G	0.1423570	-0.0476318	0.0088796	3.00E-09
2	APOB *	rs7586740	20925873	C	T	0.1423450	-0.0477367	0.0088795	2.90E-09
2	APOB *	rs7596102	20926088	A	G	0.1423190	-0.0476470	0.0088805	3.00E-09
2	APOB *	rs7594084	20927845	C	T	0.1433490	-0.0471905	0.0088534	3.60E-09
2	APOB *	rs4479392	20928382	T	C	0.1434860	-0.0468615	0.0088578	4.60E-09
2	APOB *	rs111471227	20929266	T	C	0.1437270	-0.0465356	0.0088470	6.00E-09
2	APOB *	rs6731905	20929669	C	T	0.1437860	-0.0465333	0.0088461	6.20E-09
2	APOB *	rs6732027	20929774	G	T	0.1437860	-0.0465333	0.0088461	6.20E-09
2	APOB *	rs7565511	20930030	G	C	0.1427240	-0.0471800	0.0088778	4.40E-09
2	APOB *	rs72888845	20931957	A	C	0.1385680	-0.0464389	0.0089946	1.40E-08
2	APOB *	rs76203970	20937176	A	C	0.1497100	-0.0466252	0.0086931	8.80E-10
2	APOB *	rs9306897	20938306	T	C	0.0815497	0.0923313	0.0112748	2.40E-17
2	APOB *	rs72888868	20938435	A	G	0.1508710	-0.0458185	0.0086675	1.50E-09
2	APOB *	rs75509845	20940759	A	G	0.1511190	-0.0465960	0.0086589	9.00E-10
2	APOB *	rs11096689	20940780	C	T	0.0796802	0.0963426	0.0113732	3.30E-18
2	APOB *	rs13414987	20942072	A	C	0.1466690	-0.0475116	0.0087831	1.50E-09
2	APOB *	rs4072815	20942098	T	G	0.1466310	-0.0475190	0.0087846	1.40E-09
2	APOB *	rs4296389	20943234	C	T	0.0955700	0.0931748	0.0104912	3.90E-20
2	APOB *	rs4507059	20943569	G	A	0.0836438	0.0868040	0.0110802	1.00E-15
2	APOB *	rs10201379	20943917	C	A	0.1301180	0.0858409	0.0091654	8.40E-23
2	APOB *	rs4426495	20944222	C	T	0.1301510	0.0859905	0.0091624	6.80E-23
2	APOB *	rs10180633	20945069	G	T	0.1268560	0.0864336	0.0092742	2.10E-22
2	APOB *	rs13020417	20945074	T	G	0.0492305	0.1066950	0.0141512	5.40E-14
2	APOB *	rs10183548	20945739	G	A	0.1254550	0.0873410	0.0092900	6.30E-23
2	APOB *	rs5829761	20946172	AC	A	0.1254640	0.0873658	0.0092898	6.50E-23
2	APOB *	rs6732011	20946761	G	T	0.1254290	0.0878840	0.0092934	2.90E-23
2	APOB *	rs35424228	20947933	T	C	0.0489607	0.1065070	0.0141860	8.00E-14
2	APOB *	rs3923037	20948514	A	C	0.1234610	0.0865178	0.0093533	2.10E-22
2	APOB *	rs149034253	20951648	A	G	0.0493259	0.1064430	0.0141316	5.10E-14
2	APOB *	rs141074569	20952398	C	G	0.0363889	0.0866740	0.0163930	1.60E-08
2	APOB *	rs1477526787	20953510	T	TTATG	0.0459542	0.1125820	0.0146103	1.60E-14
2	APOB *	rs1323575780	20954023	T	IGTGTG	0.0391302	0.0891811	0.0158303	2.00E-09
2	APOB *	chr2:20954030_TGTG_T	20954030	T	TGTG	0.0391970	0.0890609	0.0158126	1.90E-09
2	APOB *	chr2:20954889_AGT_A	20954889	AGT	A	0.0406978	0.0895421	0.0155222	9.90E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs148458076	20955854	C	T	0.1229950	0.0945828	0.0093356	6.30E-26
2	APOB *	rs36145916	20956506	T	C	0.1223430	0.0954360	0.0093572	2.90E-26
2	APOB *	rs143375141	20956554	T	C	0.1617240	-0.0464710	0.0083604	1.80E-10
2	APOB *	rs36187918	20958070	G	A	0.1225210	0.0949128	0.0093468	3.60E-26
2	APOB *	rs141232528	20958693	T	C	0.0409318	0.0878959	0.0154433	1.80E-09
2	APOB *	rs36190370	20958814	A	C	0.0459894	0.1123400	0.0145885	1.90E-14
2	APOB *	rs199556826	20958937	C	CT	0.0410089	0.0879096	0.0154252	1.70E-09
2	APOB *	rs147436013	20959450	T	G	0.1628630	-0.0456566	0.0083143	2.70E-10
2	APOB *	rs36191919	20960266	G	A	0.0418646	0.0879806	0.0152632	1.00E-09
2	APOB *	rs1344063	20961673	T	C	0.1259460	0.0927082	0.0092207	1.10E-25
2	APOB *	rs2337382	20961892	A	G	0.0890792	0.1045220	0.0107217	2.60E-23
2	APOB *	rs17397667	20961975	A	G	0.0419355	0.0878815	0.0152470	9.00E-10
2	APOB *	rs12999441	20963235	C	T	0.0443937	0.1229880	0.0148095	1.60E-16
2	APOB *	rs2337381	20963249	A	C	0.0419413	0.0877109	0.0152459	9.50E-10
2	APOB *	rs4665639	20964019	A	G	0.1223940	0.0971067	0.0093164	1.80E-27
2	APOB *	rs62120837	20964499	A	G	0.0420028	0.0880099	0.0152411	8.60E-10
2	APOB *	rs62120838	20964641	C	T	0.0423266	0.0913033	0.0151864	2.10E-10
2	APOB *	rs17393586	20964727	A	G	0.0443937	0.1229880	0.0148095	1.60E-16
2	APOB *	rs6707950	20964769	T	C	0.0869180	0.1099980	0.0108405	4.70E-25
2	APOB *	rs4665788	20965616	T	C	0.0419413	0.0877109	0.0152459	9.50E-10
2	APOB *	rs4665790	20965698	T	A	0.1228990	0.0975156	0.0092965	1.00E-27
2	APOB *	rs17041662	20966196	C	T	0.1228400	0.0975727	0.0092984	1.10E-27
2	APOB *	rs17397826	20966219	T	C	0.0443937	0.1229880	0.0148095	1.60E-16
2	APOB *	rs56142315	20966511	A	C	0.0419413	0.0877109	0.0152459	9.50E-10
2	APOB *	rs68093099	20967235	T	G	0.0419413	0.0877109	0.0152459	9.50E-10
2	APOB *	rs17041663	20967366	G	T	0.1222990	0.0968014	0.0093167	2.50E-27
2	APOB *	rs35695820	20967415	G	GCGCC	0.1325020	0.0851069	0.0090564	4.10E-23
2	APOB *	rs79490663	20968191	G	A	0.1600110	-0.0460574	0.0083440	2.50E-10
2	APOB *	rs6706783	20968537	A	T	0.0868364	0.1097040	0.0108417	6.00E-25
2	APOB *	rs1320144	20969240	A	C	0.1222100	0.0969457	0.0093200	2.10E-27
2	APOB *	rs1320145	20969490	G	A	0.1226720	0.0979559	0.0093070	6.00E-28
2	APOB *	rs35893087	20969651	A	G	0.1222470	0.0968235	0.0093201	2.20E-27
2	APOB *	rs72788558	20971996	C	T	0.1595990	-0.0464464	0.0083559	2.10E-10
2	APOB *	rs17041679	20972540	T	C	0.1227800	0.0957719	0.0092985	8.50E-27
2	APOB *	rs72788559	20972650	T	G	0.1589390	-0.0465681	0.0083691	2.10E-10
2	APOB *	rs10495712	20973240	A	G	0.0421459	0.0872048	0.0152047	1.20E-09
2	APOB *	rs34335269	20973378	A	G	0.1218430	0.0976986	0.0093290	7.60E-28
2	APOB *	rs62120842	20973575	A	G	0.0421459	0.0872048	0.0152047	1.20E-09
2	APOB *	rs62120843	20973812	G	T	0.0421545	0.0875480	0.0152048	1.00E-09
2	APOB *	rs938848	20973975	G	C	0.0424697	0.0904787	0.0151504	2.90E-10
2	APOB *	rs201349382	20974609	T	TC	0.1524630	-0.0556724	0.0085018	3.90E-13
2	APOB *	rs6733447	20975264	G	A	0.1230200	0.0991646	0.0092904	9.90E-29
2	APOB *	rs55664492	20975554	T	C	0.0446836	0.1242610	0.0147668	5.10E-17
2	APOB *	rs10495713	20977647	A	G	0.1213220	0.0991674	0.0093477	2.70E-28
2	APOB *	rs7608123	20980007	T	G	0.1213060	0.0992178	0.0093473	2.60E-28
2	APOB *	rs112097204	20980087	A	C	0.0421522	0.0877690	0.0152023	9.80E-10
2	APOB *	rs62120845	20981558	C	G	0.0453665	0.0770486	0.0147043	2.60E-08
2	APOB *	rs7571469	20981609	G	C	0.1213160	0.0993584	0.0093445	2.30E-28
2	APOB *	rs10172650	20982585	A	G	0.1571360	-0.0520843	0.0083878	3.00E-12
2	APOB *	rs10164442	20982691	G	A	0.1568560	-0.0521365	0.0083924	2.90E-12
2	APOB *	rs35131127	20983042	C	T	0.0873752	0.1108790	0.0108076	2.00E-25
2	APOB *	rs62120847	20983048	C	T	0.0424774	0.0907130	0.0151449	2.80E-10
2	APOB *	rs9789416	20983180	A	G	0.1212400	0.0991434	0.0093462	3.40E-28
2	APOB *	rs11124924	20983403	C	G	0.1739040	-0.0477682	0.0080618	1.60E-11
2	APOB *	rs56327713	20983964	T	G	0.0874279	0.1111440	0.0108156	1.40E-25
2	APOB *	rs56403064	20984034	C	T	0.1218240	0.1003700	0.0093267	6.70E-29
2	APOB *	rs56213756	20984123	G	C	0.1214650	0.1010290	0.0093407	3.00E-29
2	APOB *	rs67212568	20985612	G	T	0.0443302	0.1236260	0.0148169	1.10E-16
2	APOB *	rs55938327	20986670	C	T	0.0425059	0.0895311	0.0151445	4.70E-10
2	APOB *	rs34059329	20986894	T	C	0.0874679	0.1106400	0.0108122	2.00E-25
2	APOB *	chr2:20986987_TG_T	20986987	TG	T	0.1722740	0.0773907	0.0082864	3.30E-22
2	APOB *	rs1320143	20989476	G	A	0.1202560	0.1012270	0.0094060	4.30E-29
2	APOB *	rs6721844	20989699	T	G	0.0869774	0.1088920	0.0108538	1.50E-24
2	APOB *	rs6722374	20990190	T	G	0.1196380	0.1017430	0.0094301	3.30E-29
2	APOB *	rs13014683	20990254	T	C	0.0493317	0.1117230	0.0140936	1.30E-15
2	APOB *	rs4665642	20990313	G	A	0.1196490	0.1017370	0.0094305	3.20E-29
2	APOB *	rs62120852	20990672	T	C	0.0422186	0.0849842	0.0151899	3.10E-09
2	APOB *	rs1318006	20991280	G	A	0.1203680	0.1025920	0.0094152	1.30E-29
2	APOB *	rs1318005	20991336	G	A	0.1200720	0.1016240	0.0094284	4.60E-29
2	APOB *	rs1318004	20991337	C	T	0.1200720	0.1016240	0.0094284	4.60E-29
2	APOB *	rs72780134	20991960	A	G	0.1680890	-0.0511267	0.0082071	3.30E-12
2	APOB *	rs12992267	20992773	T	C	0.0712830	0.1066930	0.0118920	1.90E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs34776010	20993375	G	C	0.0712872	0.1068080	0.0118915	1.80E-19
2	APOB *	rs79823619	20993415	C	G	0.1645810	-0.0497714	0.0082867	1.10E-11
2	APOB *	rs62122481	20993943	A	C	0.0422902	0.0841359	0.0151705	4.90E-09
2	APOB *	rs57947200	20994357	A	T	0.0691881	0.1113490	0.0121272	6.20E-20
2	APOB *	rs56984418	20994358	G	A	0.0712690	0.1080230	0.0118957	5.20E-20
2	APOB *	rs74580781	20994558	A	G	0.0381101	0.0892206	0.0159725	5.70E-09
2	APOB *	rs13392272	20994618	T	C	0.0447777	0.0826058	0.0147529	3.60E-09
2	APOB *	rs6756501	20995933	T	C	0.0666365	0.1050050	0.0122820	7.40E-18
2	APOB *	rs6725189	20996129	T	G	0.0669362	0.1057700	0.0122590	3.30E-18
2	APOB *	rs4665709	20998083	A	G	0.0713641	0.1071160	0.0118896	1.00E-19
2	APOB *	rs4371387	20998261	A	G	0.0712821	0.1072900	0.0118939	8.40E-20
2	APOB *	rs952274	20998485	T	G	0.0669551	0.1053200	0.0122560	4.20E-18
2	APOB *	rs952275	20998527	G	T	0.0432709	0.0906758	0.0150083	2.40E-10
2	APOB *	rs62122484	21000700	A	G	0.0393323	0.1240040	0.0157210	7.20E-15
2	APOB *	rs369226260	21001217	A	T	0.0363022	0.1218820	0.0164789	2.20E-13
2	APOB *	rs371445178	21001218	T	A	0.0363069	0.1218000	0.0164781	2.30E-13
2	APOB *	rs551038752	21001219	A	T	0.0363022	0.1218820	0.0164789	2.20E-13
2	APOB	rs1042031	21002881	T	C	0.0443811	0.1211790	0.0148138	6.00E-16
2	APOB	rs1800479	21004511	G	C	0.0429298	0.1247280	0.0150806	2.60E-16
2	APOB	rs693	21009323	A	G	0.0486360	0.0946680	0.0141937	2.60E-12
2	APOB	rs1041968	21009932	A	G	0.0481916	0.0918147	0.0142424	1.00E-11
2	APOB	rs3749054	21014366	T	A	0.0444764	0.1211220	0.0148023	5.40E-16
2	APOB	rs2854725	21014914	G	T	0.1555940	-0.0524498	0.0084435	3.00E-12
2	APOB	rs76622701	21017012	T	A	0.0424768	0.1005070	0.0152284	2.90E-12
2	APOB	rs13003321	21017014	C	T	0.0383220	0.1196030	0.0160351	8.50E-14
2	APOB	rs12720828	21018872	T	C	0.0432089	0.1241960	0.0150182	2.10E-16
2	APOB	rs10199768	21021128	T	G	0.0478045	0.0979196	0.0143038	3.40E-13
2	APOB	rs57825321	21024193	A	T	0.1470360	-0.0676935	0.0086603	8.90E-18
2	APOB	rs679899	21028042	G	A	0.1486120	0.0438062	0.0085928	4.40E-08
2	APOB	rs13306194	21029662	A	G	0.1432680	-0.0720027	0.0087893	4.00E-19
2	APOB	rs520354	21036740	A	G	0.1480550	0.0448746	0.0085864	1.30E-08
2	APOB	rs597331	21039555	G	A	0.1461300	0.0449811	0.0087176	2.90E-08
2	APOB *	rs11893021	21050706	G	T	0.1776740	-0.0519890	0.0081423	3.10E-12
2	APOB *	rs58612563	21051291	G	A	0.1780270	-0.0517328	0.0081273	3.10E-12
2	APOB *	rs75022238	21052006	C	T	0.1781050	-0.0519249	0.0081236	2.40E-12
2	APOB *	rs111397565	21052832	CA	C	0.1781760	-0.0518822	0.0081189	2.30E-12
2	APOB *	chr2:21054688_TTTG_T	21054688	T	TTTG	0.1773950	-0.0509034	0.0081714	7.30E-12
2	APOB *	rs57922105	21055341	T	C	0.1729490	-0.0512717	0.0081923	7.80E-12
2	APOB *	rs75565290	21055810	G	A	0.1729370	-0.0515347	0.0081886	6.10E-12
2	APOB *	rs1003177	21057947	A	G	0.0766170	-0.0509052	0.0117150	4.10E-08
2	APOB *	rs35750610	21059021	C	T	0.0417097	0.0996246	0.0153768	1.10E-10
2	APOB *	rs75208098	21060292	C	T	0.1736150	-0.0514009	0.0081712	5.60E-12
2	APOB *	rs60857806	21061227	G	T	0.1733170	-0.0513146	0.0081782	6.10E-12
2	APOB *	rs56885855	21061405	T	C	0.1733290	-0.0513334	0.0081785	6.00E-12
2	APOB *	rs75953246	21061841	A	G	0.1733250	-0.0513501	0.0081779	5.90E-12
2	APOB *	rs77257367	21062230	T	C	0.1723860	-0.0515789	0.0082001	5.70E-12
2	APOB *	rs11894096	21062695	G	A	0.1711630	-0.0521300	0.0082294	4.20E-12
2	APOB *	chr2:21062703_C_CA	21062703	CA	C	0.1736040	-0.0515735	0.0081709	5.00E-12
2	APOB *	rs11894310	21063145	G	A	0.1740030	-0.0513327	0.0081607	6.00E-12
2	APOB *	rs57024468	21064771	C	T	0.1740280	-0.0514025	0.0081590	5.70E-12
2	APOB *	rs67608778	21067028	A	AAG	0.1719410	-0.0495568	0.0082128	3.10E-11
2	APOB *	rs75207863	21068360	A	G	0.1742670	-0.0506355	0.0081567	9.40E-12
2	APOB *	rs79662771	21068361	G	A	0.1742670	-0.0506355	0.0081567	9.40E-12
2	APOB *	rs113414662	21068827	T	TAAG	0.1742710	-0.0506683	0.0081563	9.10E-12
2	APOB *	rs17041755	21069695	A	G	0.1742790	-0.0506628	0.0081561	9.10E-12
2	APOB *	rs1897084	21074114	G	A	0.1737760	-0.0507865	0.0081314	9.60E-12
2	APOB *	rs7422168	21074322	C	G	0.1737770	-0.0508670	0.0081312	8.90E-12
2	APOB *	rs58420813	21077134	C	T	0.1740770	-0.0511809	0.0081202	7.30E-12
2	APOB *	rs80196520	21078435	A	C	0.1742870	-0.0510963	0.0081137	6.40E-12
2	APOB *	rs59263713	21079390	T	G	0.1743220	-0.0507239	0.0081120	8.40E-12
2	APOB *	rs11886946	21082715	C	A	0.1747240	-0.0513391	0.0080989	5.10E-12
2	APOB *	rs79721590	21083359	C	G	0.1747040	-0.0508898	0.0080986	7.00E-12
2	APOB *	rs112680646	21084238	A	G	0.1747450	-0.0504989	0.0080955	9.20E-12
2	APOB *	rs138654155	21091983	A	ATATC1	0.1762850	-0.0475646	0.0080321	7.00E-11
2	APOB *	rs57666320	21093675	T	C	0.1756550	-0.0483236	0.0080314	3.70E-11
2	APOB *	rs11899839	21095586	A	T	0.1765440	-0.0468679	0.0080034	1.10E-10
2	APOB *	rs1544977	21097940	G	C	0.1765670	-0.0467423	0.0079991	1.10E-10
2	APOB *	rs76234631	21101118	A	C	0.1767160	-0.0463813	0.0079953	1.50E-10
2	APOB *	rs77449706	21104188	T	C	0.1767170	-0.0465654	0.0079999	1.30E-10
2	APOB *	rs77809614	21105146	A	C	0.1765430	-0.0464822	0.0079982	1.40E-10
2	APOB *	rs57334943	21105494	GCTTC	G	0.1763360	-0.0465558	0.0080067	1.40E-10
2	APOB *	rs6757883	21107738	G	A	0.1766510	-0.0467665	0.0079967	1.10E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs2337384	21110978	G	A	0.1766640	-0.0467136	0.0079965	1.20E-10
2	APOB *	rs78943787	21111867	A	T	0.1766640	-0.0467136	0.0079965	1.20E-10
2	APOB *	rs74367604	21112857	C	T	0.1766640	-0.0467136	0.0079965	1.20E-10
2	APOB *	rs112223447	21113105	CACTG	C	0.1766640	-0.0467136	0.0079965	1.20E-10
2	APOB *	rs61086479	21114871	T	C	0.1766070	-0.0464924	0.0079969	1.30E-10
2	APOB *	rs12172886	21116332	G	C	0.1766050	-0.0464745	0.0079970	1.30E-10
2	APOB *	rs11892905	21116651	G	A	0.1766240	-0.0464769	0.0079973	1.40E-10
2	APOB *	rs74957119	21118017	C	T	0.1766240	-0.0465275	0.0079975	1.30E-10
2	APOB *	rs72207140	21118375	T	TA	0.1766050	-0.0465250	0.0079972	1.30E-10
2	APOB *	rs312955	21119021	G	A	0.2724370	0.0401906	0.0068723	2.80E-10
2	APOB *	rs79542263	21121389	G	A	0.1766620	-0.0467462	0.0079967	1.10E-10
2	APOB *	rs76885666	21121682	C	A	0.1766620	-0.0467462	0.0079967	1.10E-10
2	APOB *	rs78051902	21122133	A	C	0.1715560	-0.0463852	0.0081079	3.20E-10
2	APOB *	rs61517696	21126306	C	T	0.1766960	-0.0464179	0.0079956	1.40E-10
2	APOB *	rs113135613	21126367	C	CT	0.1718700	-0.0465295	0.0081270	3.50E-10
2	APOB *	rs74582026	21127869	C	T	0.1767960	-0.0466927	0.0079963	1.10E-10
2	APOB *	rs61142046	21129214	C	T	0.1761300	-0.0461973	0.0080102	1.90E-10
2	APOB *	rs77258720	21129410	A	G	0.1766910	-0.0463867	0.0079955	1.40E-10
2	APOB *	rs79909173	21129857	C	T	0.1766910	-0.0463867	0.0079955	1.40E-10
2	APOB *	rs61437001	21131249	A	G	0.1767930	-0.0460485	0.0079938	1.80E-10
2	APOB *	rs11903814	21133608	C	T	0.1763520	-0.0459851	0.0080051	2.30E-10
2	APOB *	rs59537367	21134007	A	T	0.1760510	-0.0465157	0.0080091	1.40E-10
2	APOB *	rs79538365	21136575	G	C	0.1764980	-0.0466192	0.0080008	1.30E-10
2	APOB *	rs312966	21137711	A	G	0.2837520	0.0378882	0.0068029	8.60E-10
2	APOB *	rs79783818	21147375	A	T	0.1713590	-0.0463249	0.0081470	2.70E-10
2	APOB *	rs78059021	21148150	T	C	0.1764660	-0.0467243	0.0080019	1.20E-10
2	APOB *	rs11685909	21149673	T	C	0.0428265	0.0878507	0.0151371	9.00E-09
2	APOB *	rs11689541	21149675	C	T	0.0427397	0.0881997	0.0151519	8.30E-09
2	APOB *	rs140043113	21149823	T	G	0.1765020	-0.0467602	0.0080023	1.10E-10
2	APOB *	rs11900335	21150887	C	T	0.1764770	-0.0466634	0.0080024	1.20E-10
2	APOB *	rs113725991	21151946	T	C	0.1749640	-0.0451479	0.0080393	4.50E-10
2	APOB *	rs35112647	21152185	A	G	0.0446363	0.0842559	0.0148227	1.40E-08
2	APOB *	rs11893753	21152259	G	A	0.1764570	-0.0466483	0.0080021	1.20E-10
2	APOB *	rs60403956	21153184	G	A	0.1760730	-0.0461641	0.0080118	1.90E-10
2	APOB *	rs58658975	21153912	T	C	0.1758980	-0.0466023	0.0080137	1.40E-10
2	APOB *	rs60132502	21153937	A	G	0.1758980	-0.0466023	0.0080137	1.40E-10
2	APOB *	rs74369686	21154770	G	T	0.1767620	-0.0463458	0.0079988	1.50E-10
2	APOB *	rs12997242	21158305	A	G	0.2720630	0.0384136	0.0068780	1.50E-09
2	APOB *	rs34468875	21160481	T	C	0.2729850	0.0388780	0.0068784	9.30E-10
2	APOB *	rs114624425	21162078	G	A	0.1764870	-0.0469894	0.0080067	1.10E-10
2	APOB *	rs117023568	21163502	T	C	0.1563710	-0.0434987	0.0084598	3.60E-08
2	APOB *	rs61407223	21164291	G	A	0.1585730	-0.0426609	0.0084001	3.90E-08
2	APOB *	rs34054060	21164823	G	A	0.0444474	0.0828992	0.0148618	2.90E-08
2	APOB *	rs36068322	21167459	C	T	0.0443951	0.0839173	0.0148800	1.70E-08
2	APOB *	rs75249613	21191561	G	T	0.1562090	-0.0432685	0.0085046	3.00E-08
2	ABHD1	rs4665946	27125063	A	C	0.2997380	0.0485229	0.0067075	2.30E-13
2	ABHD1	rs4665947	27125161	C	T	0.3008590	0.0480748	0.0067197	8.50E-13
2	ABHD1	rs6741646	27125330	T	C	0.3074420	0.0472554	0.0066342	7.40E-13
2	ABHD1	rs12467319	27125819	C	T	0.2993610	0.0443862	0.0066672	2.20E-11
2	ABHD1	rs1866561	27128411	G	A	0.2994510	0.0462454	0.0066581	2.80E-12
2	ABHD1	rs2304678	27130639	C	G	0.1630800	0.0488723	0.0082948	2.80E-09
2	PREB	rs71401560	27131111	TA	T	0.1631880	0.0490358	0.0082988	2.40E-09
2	PREB	rs11695930	27132103	T	C	0.1620620	0.0477082	0.0083268	1.00E-08
2	PREB	rs2289358	27133123	T	G	0.1625240	0.0480385	0.0083292	6.50E-09
2	PREB	rs2289359	27133410	C	T	0.1625920	0.0479224	0.0083296	6.80E-09
2	PREB *	rs11678061	27134751	T	C	0.1625810	0.0478371	0.0083346	8.20E-09
2	PRR30	rs11121	27137019	C	T	0.2942700	0.0437154	0.0067620	8.20E-11
2	PRR30	rs2304680	27138378	T	C	0.1575850	0.0484594	0.0084391	7.10E-09
2	PRR30	rs3795961	27139079	A	G	0.1577260	0.0484510	0.0084405	7.10E-09
2	PRR30 *	rs11691585	27139503	G	A	0.1599430	0.0493767	0.0083961	2.80E-09
2	PRR30 *	rs7574004	27140243	C	T	0.2950730	0.0445312	0.0067644	3.70E-11
2	PRR30 *	chr2:27141287_CT_C	27141287	C	CT	0.2913350	0.0484960	0.0068370	1.20E-12
2	PRR30 *	rs2439076	27142694	T	C	0.2946080	0.0447864	0.0067548	3.00E-11
2	PRR30 *	rs1659677	27142747	A	G	0.2946630	0.0448291	0.0067552	2.90E-11
2	PRR30 *	rs1659711	27143540	C	A	0.2986700	0.0447184	0.0067350	2.20E-11
2	TCF23 *	rs1298360	27144930	T	C	0.1576600	0.0488907	0.0084420	5.50E-09
2	TCF23 *	rs44665950	27145435	A	G	0.1576570	0.0488548	0.0084422	5.60E-09
2	TCF23 *	rs1275518	27145623	G	A	0.1600060	0.0498181	0.0083978	2.10E-09
2	TCF23 *	rs1275515	27147364	C	T	0.1599940	0.0500641	0.0083986	1.70E-09
2	TCF23 *	rs1275514	27147662	C	T	0.1586080	0.0506120	0.0084684	1.20E-09
2	TCF23 *	rs7606672	27147737	C	G	0.1599910	0.0500119	0.0083996	1.90E-09
2	TCF23 *	rs1275513	27148102	T	C	0.2957270	0.0470755	0.0067571	2.30E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	TCF23	rs1275511	27150802	T	C	0.3056480	0.0409322	0.0067232	1.10E-09
2	TCF23	rs1275510	27150871	A	G	0.1568570	0.0488583	0.0084790	7.20E-09
2	TCF23	rs1275509	27151141	G	A	0.3070030	0.0395420	0.0067115	4.20E-09
2	TCF23	rs1275508	27151551	C	A	0.1566000	0.0490801	0.0084813	6.00E-09
2	SLC5A6 *	rs74684611	27191771	C	T	0.1046950	-0.0735042	0.0101884	1.30E-13
2	CAD *	rs118130043	27245399	G	A	0.0438472	0.0987861	0.0151621	1.10E-11
2	TRIM54	rs76147177	27286115	C	T	0.0428587	0.0830669	0.0152361	4.50E-08
2	TRIM54	rs189387480	27292538	T	A	0.0254170	-0.0974949	0.0195293	3.50E-08
2	MPV17	rs146502189	27322314	T	G	0.0319517	-0.1061190	0.0173703	3.20E-10
2	GTF3C2	rs201232671	27348271	G	A	0.0404195	0.1054380	0.0157884	1.10E-11
2	PPM1G	rs140391935	27387603	T	C	0.0447905	0.1006250	0.0149604	2.30E-12
2	PPM1G	rs79803862	27399271	A	T	0.0666574	-0.0999124	0.0124548	5.80E-17
2	PPM1G *	rs1728918	27412596	A	G	0.2086320	0.0696343	0.0075087	4.20E-21
2	NRBP1 *	rs147530299	27419228	A	AGTGGC	0.1578780	0.0688379	0.0084322	2.00E-16
2	IFT172	rs117414910	27455222	T	C	0.0472505	0.1024790	0.0145571	2.10E-13
2	IFT172	rs140257887	27456289	T	C	0.0272474	-0.1017170	0.0187891	6.20E-09
2	GCKR	rs201393954	27500983	T	TC	0.0255130	-0.1015520	0.0194230	7.20E-09
2	GCKR	rs1260326	27508073	T	C	0.4922090	0.1477180	0.0061040	7.40E-140
2	GCKR	rs3817588	27508345	C	T	0.3579840	-0.1380880	0.0063651	1.10E-111
2	GCKR	rs146716184	27508726	C	T	0.0698004	0.0732745	0.0121003	1.80E-10
2	GCKR	rs148527487	27509703	AT	A	0.3535400	-0.1365590	0.0064263	9.00E-107
2	GCKR	rs6547692	27512105	G	A	0.4909900	0.1448670	0.0061189	2.00E-133
2	GCKR	rs780096	27518205	C	G	0.4902730	0.1444120	0.0061069	1.00E-132
2	GCKR	rs780095	27518238	A	G	0.4889590	0.1446040	0.0061121	6.60E-133
2	GCKR	rs780094	27518370	T	C	0.4799680	0.1421110	0.0061063	1.70E-128
2	GCKR	rs780093	27519736	T	C	0.4826180	0.1403120	0.0061075	2.00E-125
2	GCKR	rs780092	27520287	G	A	0.3603390	-0.1357570	0.0063519	5.60E-108
2	GCKR	rs814295	27520348	G	A	0.3621280	-0.1353360	0.0063440	1.60E-107
2	GCKR	rs74928908	27521222	G	A	0.3592480	-0.1350660	0.0063601	1.30E-106
2	GCKR *	rs1260334	27525730	C	A	0.4860330	0.1416440	0.0061365	4.00E-126
2	GCKR *	rs1260333	27525757	A	G	0.4852640	0.1398100	0.0060970	1.30E-124
2	GCKR *	rs1313566	27526037	G	A	0.4829020	0.1400840	0.0061434	9.40E-124
2	GCKR *	rs11336847	27526125	AT	A	0.4831870	0.1403920	0.0061632	5.80E-123
2	GCKR *	rs6744393	27527272	T	C	0.3596310	-0.1336230	0.0064338	6.90E-102
2	GCKR *	rs2950835	27527678	A	G	0.4845080	0.1377530	0.0061897	5.20E-118
2	GCKR *	rs2911711	27527679	T	A	0.4845120	0.1377250	0.0061897	5.70E-118
2	GCKR *	rs78680773	27528695	C	A	0.3577280	-0.1321650	0.0064353	1.40E-99
2	GCKR *	rs6753534	27530004	C	T	0.4853930	0.1224930	0.0062041	4.90E-93
2	GCKR *	rs74450311	27531758	C	CAT	0.3755370	-0.0957818	0.0063105	1.30E-54
2	GCKR *	rs62131879	27532245	G	T	0.3762590	-0.0962151	0.0063075	3.90E-55
2	GCKR *	rs7606605	27532849	T	A	0.2106220	0.0613824	0.0076024	2.70E-17
2	GCKR *	rs4665987	27532958	A	G	0.4720990	0.1078190	0.0061214	3.50E-73
2	GCKR *	rs10181342	27534476	G	A	0.3761490	-0.0962067	0.0063073	4.30E-55
2	GCKR *	rs149454845	27536953	C	T	0.0217345	-0.1196530	0.0210120	6.40E-09
2	GCKR *	rs4665988	27538569	A	C	0.4722640	0.1078290	0.0061200	3.00E-73
2	GCKR *	rs116443177	27541255	T	C	0.3779280	-0.0956803	0.0063027	1.20E-54
2	GCKR *	rs62131881	27541914	T	G	0.3760190	-0.0962119	0.0063061	4.20E-55
2	GCKR *	rs62131882	27542613	C	T	0.3776180	-0.0956785	0.0062985	1.20E-54
2	GCKR *	rs12473139	27542720	C	T	0.4731600	0.1086600	0.0061168	2.20E-74
2	GCKR *	rs4665991	27543417	A	G	0.4727350	0.1084560	0.0061221	5.40E-74
2	GCKR *	rs67080990	27544621	G	GC	0.4732970	0.1084400	0.0061183	4.70E-74
2	GCKR *	rs62141278	27545514	T	C	0.3783720	-0.0950563	0.0063005	5.90E-54
2	GCKR *	rs59210625	27546607	C	A	0.2108310	0.0613997	0.0075985	2.20E-17
2	GCKR *	rs62141279	27548548	T	C	0.3770350	-0.0957769	0.0063050	1.10E-54
2	C2orf16 *	chr2:27550224_C_CT	27550224	CT	C	0.3728720	-0.0952324	0.0063588	7.80E-53
2	C2orf16 *	rs2384627	27551582	A	G	0.3762180	-0.0950896	0.0063039	9.60E-54
2	C2orf16 *	rs202103665	27553764	A	AT	0.4713270	0.1082020	0.0061170	1.20E-73
2	C2orf16 *	rs62141281	27554784	T	G	0.3770090	-0.0950350	0.0062965	6.10E-54
2	C2orf16 *	rs6751087	27555149	C	T	0.3770100	-0.0950363	0.0062965	6.10E-54
2	C2orf16 *	rs12995461	27555300	C	A	0.4716630	0.1078680	0.0061137	3.70E-73
2	C2orf16 *	rs10169065	27555693	G	A	0.4716620	0.1078680	0.0061137	3.70E-73
2	C2orf16 *	rs10179872	27555705	A	G	0.4704520	0.1070910	0.0061176	3.50E-72
2	C2orf16 *	rs79414972	27558930	G	A	0.3645130	-0.0920511	0.0064109	5.40E-49
2	C2orf16 *	rs62141288	27560331	A	G	0.3551170	-0.0900582	0.0064559	6.60E-46
2	C2orf16 *	rs200969564	27560335	GAC	G	0.3551170	-0.0900582	0.0064559	6.60E-46
2	C2orf16 *	rs62141290	27560525	C	T	0.3752760	-0.0951760	0.0063126	1.10E-53
2	C2orf16 *	rs4665382	27560934	C	T	0.4716740	0.1078760	0.0061147	3.90E-73
2	C2orf16 *	rs62141291	27561167	T	C	0.3770250	-0.0949189	0.0062955	9.40E-54
2	C2orf16 *	rs62141292	27561433	C	A	0.3770190	-0.0949350	0.0062955	9.10E-54
2	C2orf16 *	rs7570476	27561791	T	C	0.4716000	0.1078990	0.0061144	4.10E-73
2	C2orf16 *	rs10208529	27563321	T	A	0.4716080	0.1078740	0.0061143	4.40E-73
2	C2orf16 *	rs60854669	27564062	C	T	0.3769980	-0.0949204	0.0062958	9.00E-54

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	C2orf16 *	rs965813	27566994	A	T	0.3769740	-0.0948327	0.0062962	1.10E-53
2	C2orf16 *	rs4665383	27568688	G	C	0.4716120	0.1078740	0.0061143	4.40E-73
2	C2orf16 *	rs59876138	27569456	C	A	0.3769840	-0.0948599	0.0062963	1.00E-53
2	C2orf16 *	rs7577311	27571054	T	G	0.4718220	0.1077490	0.0061168	6.40E-73
2	C2orf16 *	rs6704596	27574060	G	A	0.3769920	-0.0948705	0.0062963	9.90E-54
2	C2orf16	rs1919127	27578626	C	T	0.4715930	0.1077410	0.0061122	6.30E-73
2	C2orf16	rs1919128	27578892	G	A	0.4716380	0.1076260	0.0061116	8.70E-73
2	C2orf16	rs3811644	27579938	G	A	0.3769680	-0.0949469	0.0062956	8.00E-54
2	ZNF512	rs6734059	27585287	C	T	0.3770710	-0.0950129	0.0062954	7.00E-54
2	ZNF512	rs12478841	27588855	G	A	0.4724310	0.1081230	0.0061120	1.80E-73
2	ZNF512	rs6760250	27589385	A	G	0.4724310	0.1081230	0.0061120	1.80E-73
2	ZNF512	rs62138963	27591507	T	C	0.3769530	-0.0949703	0.0062953	7.70E-54
2	ZNF512	rs62138964	27591571	T	C	0.3769530	-0.0949703	0.0062953	7.70E-54
2	ZNF512	rs145275920	27591660	T	C	0.0580091	-0.0982583	0.0131291	7.90E-16
2	ZNF512	rs13022873	27592643	C	A	0.4723650	0.1078300	0.0061145	5.00E-73
2	ZNF512	rs76013440	27593448	A	G	0.3759260	-0.0950714	0.0063071	1.80E-53
2	ZNF512	rs62138965	27593726	C	T	0.3761260	-0.0944725	0.0063043	3.80E-53
2	ZNF512	rs13010586	27594950	A	G	0.4724430	0.1080920	0.0061119	2.00E-73
2	ZNF512	rs1919129	27595854	G	C	0.3769500	-0.0949627	0.0062952	8.00E-54
2	ZNF512	rs62138966	27596305	A	G	0.3766930	-0.0951924	0.0062968	5.70E-54
2	ZNF512	rs12989678	27598615	T	C	0.4718700	0.1095830	0.0061315	1.10E-74
2	ZNF512	rs78378018	27599416	GAC	G	0.3770600	-0.0949081	0.0062965	1.00E-53
2	ZNF512	rs117655217	27600099	C	T	0.0577708	-0.0988218	0.0131371	6.30E-16
2	ZNF512	rs56725354	27601301	C	G	0.3769490	-0.0949705	0.0062952	7.90E-54
2	ZNF512	rs62138968	27601618	G	C	0.3769470	-0.0949824	0.0062952	7.70E-54
2	ZNF512	rs112927528	27601644	TTTTTG	T	0.3757650	-0.0957237	0.0063065	2.50E-54
2	ZNF512	rs12467476	27602848	C	T	0.4710980	0.1077250	0.0061162	6.00E-73
2	ZNF512	rs12464616	27604225	T	C	0.4723880	0.1080390	0.0061124	2.10E-73
2	ZNF512	rs2141372	27604329	T	G	0.3769720	-0.0949303	0.0062959	9.30E-54
2	ZNF512	rs66497975	27604459	T	TCATG	0.4709920	0.1085580	0.0061232	1.30E-73
2	ZNF512	rs6719960	27607200	G	A	0.3769360	-0.0950319	0.0062957	7.00E-54
2	ZNF512	rs6547735	27608740	C	T	0.3769320	-0.0950957	0.0062960	6.10E-54
2	ZNF512	rs2384656	27609188	G	A	0.4723990	0.1081280	0.0061125	1.60E-73
2	ZNF512	rs1881397	27609418	G	A	0.3773670	-0.0952150	0.0062992	5.90E-54
2	ZNF512	chr2:27609869_CA_C	27609869	C	CA	0.3962200	-0.0896828	0.0063641	5.80E-47
2	ZNF512	rs112427483	27610460	T	ATATA	0.3323540	-0.1000670	0.0066070	2.10E-53
2	ZNF512	rs74175068	27610635	C	T	0.4589020	0.1072760	0.0062448	1.70E-69
2	ZNF512	rs34016998	27610820	T	C	0.4717600	0.1080750	0.0061123	2.10E-73
2	ZNF512	rs12987055	27611285	C	T	0.4720770	0.1076020	0.0061124	9.40E-73
2	ZNF512	rs13405762	27611748	C	A	0.3746080	-0.0941345	0.0063188	1.10E-52
2	ZNF512	rs78170284	27612215	A	G	0.3772620	-0.0941801	0.0062966	5.20E-53
2	ZNF512	rs13020949	27613738	T	C	0.4718790	0.1076620	0.0061155	9.20E-73
2	ZNF512	chr2:27614806_CT_C	27614806	C	CT	0.3769500	-0.0943387	0.0063032	4.70E-53
2	ZNF512	rs1881395	27615682	A	G	0.3768880	-0.0943375	0.0063040	5.20E-53
2	ZNF512	rs4666000	27616502	C	T	0.4717460	0.1074930	0.0061179	1.30E-72
2	ZNF512	rs2068834	27616672	C	T	0.4713930	0.1077360	0.0061187	7.40E-73
2	ZNF512	rs7571558	27616965	G	C	0.3769650	-0.0943084	0.0063043	5.10E-53
2	ZNF512	rs4666001	27617672	G	A	0.1564050	0.0568057	0.0084128	8.60E-12
2	ZNF512	rs4666002	27617773	C	G	0.4711670	0.1081270	0.0061242	3.60E-73
2	ZNF512	rs62138971	27617887	A	G	0.3758040	-0.0955889	0.0063362	4.30E-54
2	ZNF512	rs1881396	27621734	G	T	0.3718300	-0.0955165	0.0063484	1.70E-53
2	GPN1	rs3749147	27629051	A	G	0.3135180	0.0878652	0.0065860	8.00E-43
2	GPN1	rs146892484	27629283	C	CG	0.4172200	0.0681334	0.0062119	2.50E-29
2	GPN1	rs34502053	27631657	A	G	0.3161420	0.0894212	0.0065744	1.60E-44
2	GPN1	rs10173720	27632530	A	T	0.4186210	0.0678953	0.0061968	3.60E-29
2	GPN1	rs6719175	27636484	A	T	0.3146950	0.0899054	0.0066073	1.50E-44
2	GPN1	rs77350364	27643272	A	G	0.4181040	0.0673703	0.0062150	1.40E-28
2	GPN1	rs12474585	27648726	C	T	0.4181220	0.0680009	0.0062117	2.90E-29
2	GPN1	rs35605899	27649445	AATAT		0.3350330	0.0793731	0.0064902	1.20E-36
2	GPN1	rs8731	27650459	C	G	0.4176810	0.0682392	0.0062123	2.30E-29
2	SUPT7L	chr2:27652149_AAAAT_A	27652149	AAAAT	A	0.4169210	0.0681822	0.0062259	3.00E-29
2	SUPT7L	rs67775899	27652169	TAAA	T	0.4175530	0.0674763	0.0062322	1.10E-28
2	SUPT7L	rs10202364	27652175	T	A	0.4180690	0.0674229	0.0062240	1.00E-28
2	SUPT7L	rs4666010	27655819	T	C	0.4175950	0.0683442	0.0062121	1.70E-29
2	SLC4A1AP	rs2272406	27669156	T	A	0.3349810	0.0793557	0.0064863	1.20E-36
2	SLC4A1AP	rs76586169	27674968	G	A	0.4172870	0.0681135	0.0062113	2.60E-29
2	SLC4A1AP	rs13021208	27678861	T	C	0.3350550	0.0804489	0.0064886	2.00E-37
2	SLC4A1AP	rs72613829	27680120	C	T	0.4164440	0.0685767	0.0062155	1.40E-29
2	SLC4A1AP	rs13023094	27687839	C	A	0.3351230	0.0793300	0.0064836	1.10E-36
2	SLC4A1AP	rs12998770	27690321	C	T	0.3353360	0.0793292	0.0064842	1.10E-36
2	SLC4A1AP	rs80322731	27697569	G	A	0.2080810	0.0600652	0.0076377	1.70E-16
2	SLC4A1AP	rs13030973	27705930	C	T	0.3322600	0.0791413	0.0064852	2.20E-36

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	SLC4A1AP	rs4665385	27707970	C	T	0.4129380	0.0677717	0.0062091	5.50E-29
2	SLC4A1AP	rs6727388	27709720	G	A	0.3315100	0.0795771	0.0064905	1.20E-36
2	SLC4A1AP	rs4616435	27710775	T	C	0.3322200	0.0791728	0.0064861	2.10E-36
2	SLC4A1AP	rs58199976	27711657	T	C	0.4120470	0.0683800	0.0062111	2.00E-29
2	SLC4A1AP	rs6727215	27711864	A	G	0.3314760	0.0796828	0.0064908	9.70E-37
2	SLC4A1AP	rs4665386	27712485	C	A	0.4135160	0.0687223	0.0062080	1.10E-29
2	SLC4A1AP	rs6742571	27719021	G	A	0.4192200	0.0679510	0.0062111	2.70E-29
2	SLC4A1AP	chr2:27724905_CT_C	27724905	C	CT	0.4116120	0.0658816	0.0063002	9.70E-27
2	SLC4A1AP	rs1881394	27726185	G	A	0.4152850	0.0678179	0.0062623	1.10E-28
2	SLC4A1AP	rs10432705	27727970	A	G	0.3313350	0.0816819	0.0065583	1.80E-37
2	SLC4A1AP	rs867282	27728791	C	T	0.4151080	0.0676506	0.0062578	1.60E-28
2	SLC4A1AP	rs2384655	27729368	T	A	0.4151550	0.0675081	0.0062577	2.20E-28
2	SLC4A1AP	rs12994085	27729539	T	C	0.4151640	0.0674972	0.0062578	2.20E-28
2	SLC4A1AP	rs12993377	27729900	C	G	0.4151590	0.0674875	0.0062580	2.30E-28
2	MRPL33 *	rs12624148	27733614	C	T	0.4153540	0.0671951	0.0062688	6.30E-28
2	MRPL33 *	rs6753736	27735988	G	C	0.4205460	0.0645603	0.0062538	3.10E-26
2	MRPL33 *	rs75429814	27738747	T	C	0.4109680	0.0630773	0.0063019	1.10E-24
2	MRPL33 *	rs111938697	27740266	C	T	0.4151020	0.0628134	0.0062798	1.40E-24
2	MRPL33 *	rs12714223	27740463	A	G	0.4141020	0.0617927	0.0062787	7.50E-24
2	MRPL33 *	rs36017854	27740804	AAT	A	0.4132270	0.0618771	0.0062881	7.70E-24
2	MRPL33 *	rs9678824	27741461	G	C	0.4143150	0.0614547	0.0062749	1.30E-23
2	MRPL33 *	rs13023194	27744393	C	G	0.3333270	0.0700629	0.0065427	9.90E-28
2	MRPL33 *	rs9967838	27745587	C	A	0.4143010	0.0612628	0.0062363	1.20E-23
2	MRPL33 *	chr2:27747209_A_AT	27747209	AT	A	0.4026180	0.0600782	0.0062746	1.60E-22
2	MRPL33 *	rs9677663	27749578	A	G	0.4095350	0.0623266	0.0062174	1.10E-24
2	MRPL33 *	rs57238885	27751393	C	G	0.4096230	0.0628070	0.0062143	5.90E-25
2	MRPL33 *	rs10201247	27752104	G	A	0.4096230	0.0628070	0.0062143	5.90E-25
2	MRPL33 *	rs6547796	27752527	C	T	0.4099160	0.0626545	0.0062151	7.60E-25
2	MRPL33 *	rs4666011	27758045	G	C	0.4096510	0.0627658	0.0062132	5.50E-25
2	MRPL33 *	rs10209020	27758077	T	C	0.4098950	0.0625444	0.0062150	8.40E-25
2	MRPL33 *	rs12471347	27758788	G	C	0.4097410	0.0627229	0.0062111	5.40E-25
2	MRPL33 *	rs77154381	27759252	A	G	0.4079660	0.0633708	0.0062213	1.90E-25
2	MRPL33 *	rs12477908	27764179	C	A	0.4108110	0.0621610	0.0062094	1.30E-24
2	MRPL33 *	rs13006480	27764354	G	C	0.3260460	0.0693410	0.0065697	5.10E-27
2	MRPL33 *	rs140124512	27764951	T	A	0.0428284	-0.1022600	0.0154215	6.70E-11
2	MRPL33 *	rs13013484	27765954	A	G	0.4097810	0.0627559	0.0062113	5.10E-25
2	MRPL33 *	rs146796793	27766610	G	A	0.0531723	-0.0831315	0.0137890	5.20E-11
2	MRPL33 *	rs4665390	27767042	C	T	0.4108220	0.0620455	0.0062129	1.70E-24
2	MRPL33 *	rs74429612	27770976	C	T	0.4109140	0.0619881	0.0062092	1.70E-24
2	MRPL33	rs3736594	27772914	C	A	0.4109200	0.0622768	0.0062091	1.00E-24
2	MRPL33	rs3792252	27773064	A	G	0.4097450	0.0626661	0.0062109	5.80E-25
2	MRPL33	rs35463245	27777857	C	G	0.4078480	0.0617343	0.0062285	3.20E-24
2	MRPL33	rs17006242	27778184	C	A	0.4107610	0.0622174	0.0062097	1.10E-24
2	MRPL33	rs3792253	27779135	T	C	0.4096460	0.0626994	0.0062123	5.70E-25
2	MRPL33 *	rs13030345	27780307	T	G	0.3063810	0.0669158	0.0066787	2.10E-24
2	RBKS	rs74327441	27784205	G	A	0.4036660	0.0622555	0.0063082	5.10E-24
2	RBKS	rs7596967	27789917	T	G	0.3896730	0.0569321	0.0063270	3.60E-20
2	RBKS	rs7593136	27794925	A	G	0.4110950	0.0605065	0.0062088	1.20E-23
2	RBKS	rs6744348	27795158	A	C	0.4111070	0.0604539	0.0062082	1.40E-23
2	RBKS	rs36035825	27795264	T	G	0.4111050	0.0604624	0.0062082	1.30E-23
2	RBKS	rs4666012	27795426	A	G	0.4111020	0.0604758	0.0062081	1.30E-23
2	RBKS	rs11322614	27796225	AT	A	0.4098130	0.0603846	0.0062241	1.30E-23
2	RBKS	rs4666013	27796239	C	T	0.4111050	0.0604611	0.0062080	1.30E-23
2	RBKS	rs4666014	27796308	G	A	0.4111950	0.0602303	0.0062079	1.80E-23
2	RBKS	rs4666015	27796500	G	A	0.4111240	0.0604017	0.0062078	1.40E-23
2	RBKS	rs34181670	27796989	T	C	0.4111250	0.0604261	0.0062078	1.30E-23
2	RBKS	rs35679500	27797099	T	C	0.4111250	0.0604261	0.0062078	1.30E-23
2	RBKS	rs12623170	27797290	C	T	0.4115290	0.0594668	0.0062061	8.60E-23
2	RBKS	rs3935148	27798099	T	A	0.4082530	0.0610060	0.0062183	6.70E-24
2	RBKS	rs13027427	27798176	G	T	0.3796790	0.0541848	0.0063064	4.20E-19
2	RBKS	rs6745545	27798978	C	G	0.3796110	0.0541667	0.0063072	4.30E-19
2	RBKS	rs7570730	27799808	G	A	0.3795500	0.0543494	0.0063131	3.70E-19
2	RBKS	rs11127125	27800253	T	C	0.3788200	0.0543241	0.0063182	3.90E-19
2	RBKS	rs11127126	27800417	C	T	0.3795740	0.0541545	0.0063146	4.60E-19
2	RBKS	rs12473340	27800930	G	A	0.3795050	0.0540339	0.0063158	5.20E-19
2	RBKS	rs12473400	27801157	G	T	0.3803540	0.0535314	0.0063168	1.10E-18
2	RBKS	rs4630723	27801464	T	C	0.3896250	0.0516838	0.0063660	2.70E-17
2	RBKS	rs13019037	27801775	C	T	0.3796250	0.0535463	0.0063213	1.10E-18
2	RBKS	rs4632296	27802117	T	C	0.3808090	0.0534013	0.0063401	1.60E-18
2	RBKS	rs13001060	27802194	T	C	0.3824550	0.0525357	0.0063353	4.70E-18
2	RBKS	rs12995865	27802199	A	C	0.3824540	0.0525405	0.0063353	4.70E-18
2	RBKS	rs11891769	27802713	G	C	0.3797060	0.0532691	0.0063208	1.70E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	RBKS	rs12465012	27805324	C	T	0.3589760	0.0474121	0.0063935	1.10E-14
2	RBKS	rs4665392	27806782	A	G	0.3587960	0.0470485	0.0063937	1.50E-14
2	RBKS	rs12986980	27807570	A	G	0.3580170	0.0476750	0.0063937	7.50E-15
2	RBKS	rs13023003	27809270	G	C	0.3584120	0.0473965	0.0063873	1.00E-14
2	RBKS	rs4233716	27811517	C	T	0.3790480	0.0426227	0.0063213	2.00E-12
2	RBKS	rs4233717	27811813	A	T	0.3790480	0.0426227	0.0063213	2.00E-12
2	RBKS	chr2:27813039_TAA_T	27813039	TAA	T	0.3786790	0.0427056	0.0063223	1.70E-12
2	RBKS	rs4666016	27814273	T	A	0.3774430	0.0434449	0.0063243	8.00E-13
2	RBKS	rs4464229	27815213	C	T	0.3791320	0.0427932	0.0063291	1.60E-12
2	RBKS	rs12617171	27815932	C	T	0.3780840	0.0427530	0.0063224	1.60E-12
2	RBKS	rs4420671	27816433	G	C	0.3781670	0.0429928	0.0063208	1.30E-12
2	RBKS	rs4493211	27816605	G	T	0.3786280	0.0429670	0.0063233	1.50E-12
2	RBKS	rs4665393	27817409	G	A	0.3781770	0.0429702	0.0063208	1.30E-12
2	RBKS	rs4666017	27817658	C	A	0.3781770	0.0429702	0.0063208	1.30E-12
2	RBKS	rs12478766	27818333	T	C	0.3781400	0.0428650	0.0063216	1.50E-12
2	RBKS	rs13026758	27818406	A	G	0.3781550	0.0429286	0.0063216	1.40E-12
2	RBKS	rs4666018	27819192	C	T	0.3832180	0.0423889	0.0063170	3.10E-12
2	RBKS	rs66523005	27822746	TAGAA	T	0.3869390	0.0429611	0.0063104	2.10E-12
2	RBKS	rs4666020	27823161	G	A	0.3869120	0.0432989	0.0063088	1.50E-12
2	RBKS	chr2:27825136_CA_C	27825136	CA	C	0.3882760	0.0417729	0.0063227	1.10E-11
2	RBKS	rs9679543	27828084	C	T	0.3817690	0.0426638	0.0062922	2.50E-12
2	RBKS	rs10531773	27831894	GAA	G	0.3819750	0.0427698	0.0062938	2.20E-12
2	RBKS	rs4666021	27833014	A	G	0.3812530	0.0420727	0.0062938	5.00E-12
2	RBKS	rs9678430	27834262	G	C	0.3812570	0.0421582	0.0062951	4.50E-12
2	RBKS	rs12463914	27834492	C	T	0.3813280	0.0420937	0.0062936	5.00E-12
2	RBKS	rs7560060	27834657	T	C	0.3812530	0.0420727	0.0062938	5.00E-12
2	RBKS	rs4666022	27834956	T	C	0.3811740	0.0423394	0.0062941	3.70E-12
2	RBKS	rs12464988	27835359	C	T	0.3795700	0.0411883	0.0063239	1.50E-11
2	RBKS	rs13027666	27835566	T	C	0.3801200	0.0413931	0.0063134	1.20E-11
2	RBKS	rs11885959	27836033	C	G	0.3811740	0.0423394	0.0062941	3.70E-12
2	RBKS	rs4665394	27836155	T	C	0.3811050	0.0422175	0.0062945	4.30E-12
2	RBKS	rs12617110	27837044	A	G	0.3812320	0.0424344	0.0062947	3.20E-12
2	RBKS	rs12617113	27837070	A	G	0.3812320	0.0424344	0.0062947	3.20E-12
2	RBKS	rs12992890	27837964	T	C	0.3811740	0.0423394	0.0062941	3.70E-12
2	RBKS	rs34096628	27838123	A	C	0.3811740	0.0423394	0.0062941	3.70E-12
2	RBKS	rs4275987	27840089	A	G	0.3859830	0.0432644	0.0063186	1.30E-12
2	RBKS	rs4462754	27841127	C	T	0.3817550	0.0427726	0.0062918	2.20E-12
2	RBKS	rs9678336	27842537	A	G	0.3812130	0.0422847	0.0062942	4.00E-12
2	RBKS	rs74446114	27843255	C	T	0.2999200	0.0512115	0.0067089	4.30E-15
2	RBKS	rs4233718	27843493	A	G	0.3812680	0.0422398	0.0062942	4.00E-12
2	RBKS	rs11127127	27844037	G	T	0.3818660	0.0426671	0.0062920	2.40E-12
2	RBKS	rs11127128	27844103	T	A	0.3812680	0.0422398	0.0062942	4.00E-12
2	RBKS	rs77853892	27844692	A	C	0.1653380	0.0522368	0.0083667	1.00E-10
2	RBKS	rs4564736	27846676	A	T	0.3811750	0.0423348	0.0062941	3.70E-12
2	RBKS	rs11901133	27846846	T	G	0.3812020	0.0423618	0.0062944	3.60E-12
2	RBKS	rs4555299	27848323	A	G	0.3811750	0.0423348	0.0062941	3.70E-12
2	RBKS	rs35841453	27849835	T	C	0.3812540	0.0422729	0.0062941	3.90E-12
2	RBKS	rs4666024	27850112	C	G	0.3789110	0.0425403	0.0063061	2.90E-12
2	RBKS	rs4666025	27851027	C	T	0.3812540	0.0422729	0.0062941	3.90E-12
2	RBKS	rs4313931	27851834	C	T	0.3812540	0.0422729	0.0062941	3.90E-12
2	RBKS	rs4583413	27851957	C	T	0.3811750	0.0423348	0.0062941	3.70E-12
2	RBKS	rs4419196	27852431	A	G	0.3811750	0.0423348	0.0062941	3.70E-12
2	RBKS	rs4447576	27853381	T	C	0.3848130	0.0421589	0.0063212	4.40E-12
2	RBKS	rs11127129	27853841	C	G	0.3815430	0.0431573	0.0063061	1.50E-12
2	RBKS	rs7426295	27856127	G	A	0.3758630	0.0422843	0.0063149	7.10E-12
2	RBKS	rs4233719	27856477	C	A	0.3758630	0.0422843	0.0063149	7.10E-12
2	RBKS	rs4233720	27856908	A	G	0.3759530	0.0419825	0.0063147	9.90E-12
2	RBKS	rs13025314	27857347	G	A	0.3759530	0.0419825	0.0063147	9.90E-12
2	RBKS	rs4578808	27858763	G	T	0.3759530	0.0419825	0.0063147	9.90E-12
2	RBKS	rs4578809	27859627	G	A	0.3759530	0.0419825	0.0063147	9.90E-12
2	RBKS	chr2:27860975_C_CT	27860975	C	CT	0.3759460	0.0420256	0.0063147	9.60E-12
2	RBKS	rs6714106	27860977	C	T	0.3785680	0.0427304	0.0063224	5.90E-12
2	RBKS	rs7595986	27862444	A	G	0.3758000	0.0423859	0.0063141	6.30E-12
2	RBKS	rs13021285	27862480	T	C	0.3758900	0.0420842	0.0063139	8.80E-12
2	RBKS	rs77353560	27862677	A	C	0.2846930	0.0487584	0.0068279	3.90E-13
2	RBKS	rs11902158	27863898	A	G	0.3758900	0.0420842	0.0063139	8.80E-12
2	RBKS	rs13004096	27864338	C	T	0.3758900	0.0420842	0.0063139	8.80E-12
2	RBKS	rs1973116	27865051	C	T	0.3749300	0.0434525	0.0063295	2.60E-12
2	RBKS	rs4666028	27865713	T	A	0.3770110	0.0420179	0.0063130	9.80E-12
2	RBKS	rs71441095	27866981	A	G	0.4718960	-0.0620695	0.0061851	1.10E-24
2	RBKS	rs10171517	27867192	T	C	0.4720530	-0.0621928	0.0061842	9.00E-25
2	RBKS	rs898034	27867953	T	C	0.4721620	-0.0622042	0.0061833	8.30E-25

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	RBKS	rs2337373	27870055	C	T	0.3758660	0.0422395	0.0063151	7.40E-12
2	RBKS	rs13016573	27871403	C	G	0.3771610	0.0425428	0.0063244	6.10E-12
2	RBKS	rs4665398	27871903	A	T	0.3759500	0.0420008	0.0063146	9.70E-12
2	RBKS	rs12466687	27873840	C	A	0.3768880	0.0425775	0.0063219	5.80E-12
2	RBKS	rs12466717	27873925	G	A	0.3757910	0.0424388	0.0063142	5.90E-12
2	RBKS	rs4666030	27874355	C	T	0.3757890	0.0424383	0.0063142	5.90E-12
2	RBKS	rs13411592	27875857	A	G	0.3757950	0.0425080	0.0063140	5.40E-12
2	RBKS	rs35445284	27878028	A	AT	0.3765030	0.0426951	0.0063201	5.20E-12
2	RBKS	rs6706209	27879071	T	C	0.3757380	0.0431271	0.0063132	2.70E-12
2	RBKS	rs12620151	27879837	T	A	0.3758170	0.0431060	0.0063130	2.80E-12
2	RBKS	rs6547814	27880131	G	A	0.3757390	0.0431230	0.0063131	2.70E-12
2	RBKS	rs11886463	27881670	C	T	0.3758240	0.0428343	0.0063130	3.70E-12
2	RBKS	rs13413962	27881699	A	G	0.3757370	0.0431412	0.0063131	2.60E-12
2	RBKS	rs6708889	27884825	T	C	0.3757290	0.0430015	0.0063124	3.00E-12
2	RBKS	chr2:27888789_TA_T	27888789	T	TA	0.3754390	0.0430395	0.0063150	2.80E-12
2	BRE	rs7607546	27895795	A	G	0.3755670	0.0424833	0.0063020	4.60E-12
2	BRE	rs141361525	27896053	G	C	0.0556880	-0.0767132	0.0135141	1.00E-09
2	BRE	rs7592580	27898323	C	T	0.3765020	0.0422437	0.0063002	7.20E-12
2	BRE	rs17006365	27900507	G	T	0.3764410	0.0428456	0.0063036	3.10E-12
2	BRE	rs6709765	27900893	T	A	0.3757000	0.0424891	0.0063000	4.40E-12
2	BRE	rs10177845	27901304	A	G	0.3757750	0.0423573	0.0062995	5.10E-12
2	BRE	rs34483784	27906524	G	A	0.3896020	0.0382344	0.0062705	5.90E-10
2	BRE	rs10201105	27908366	C	G	0.3896100	0.0381944	0.0062707	6.10E-10
2	BRE	rs10190494	27908376	G	A	0.3898450	0.0377764	0.0062696	9.30E-10
2	BRE	rs10204488	27909383	A	G	0.3866670	0.0389573	0.0062703	2.30E-10
2	BRE	rs2016616	27911170	G	A	0.3906650	0.0389022	0.0062796	3.20E-10
2	BRE	rs1458396	27913484	G	A	0.3895500	0.0383849	0.0062700	5.20E-10
2	BRE	rs35177396	27916281	TA	T	0.3934640	0.0379372	0.0062788	1.10E-09
2	BRE	rs2337372	27917482	G	A	0.3895820	0.0383192	0.0062707	5.70E-10
2	BRE	rs10173848	27920150	T	G	0.3864540	0.0391828	0.0062707	1.70E-10
2	BRE	rs1870325	27921200	A	G	0.3864880	0.0390710	0.0062695	1.90E-10
2	BRE	rs6745379	27924674	C	T	0.3874060	0.0398178	0.0062683	9.10E-11
2	BRE	rs13026003	27927931	C	T	0.3899320	0.0385192	0.0062733	4.70E-10
2	BRE	rs111357701	27928463	TTTCTC	T	0.3878470	0.0384786	0.0062893	4.90E-10
2	BRE	rs10185472	27928487	A	G	0.3890620	0.0385986	0.0062755	4.20E-10
2	BRE	rs6547815	27932328	A	T	0.3872350	0.0380899	0.0062720	5.70E-10
2	BRE	rs11886375	27932881	A	C	0.3871050	0.0380274	0.0062694	6.20E-10
2	BRE	rs10174070	27933753	G	A	0.3882700	0.0371519	0.0063123	2.80E-09
2	BRE	rs10194283	27936212	A	G	0.3872250	0.0385871	0.0062627	3.40E-10
2	BRE	rs10184052	27936777	G	A	0.3873260	0.0384913	0.0062624	3.60E-10
2	BRE	rs13400398	27939242	T	C	0.3869980	0.0386833	0.0062627	3.40E-10
2	BRE	rs13416434	27939407	C	T	0.3869990	0.0386811	0.0062627	3.40E-10
2	BRE	rs4390729	27939994	C	T	0.3903280	0.0378983	0.0062622	9.00E-10
2	BRE	rs11274834	27940623	3CTAAC	C	0.3836670	0.0378497	0.0062987	1.10E-09
2	BRE	rs10170872	27941686	T	C	0.3869450	0.0388625	0.0062632	2.90E-10
2	BRE	rs57403744	27942131	A	G	0.1581700	0.0486474	0.0084540	4.90E-09
2	BRE	rs13399709	27944583	T	C	0.3871090	0.0385361	0.0062618	3.90E-10
2	BRE	rs7577437	27945548	G	A	0.3872950	0.0385054	0.0062618	3.70E-10
2	BRE	rs6547816	27946730	C	T	0.3886600	0.0377806	0.0062795	1.00E-09
2	BRE	rs12165240	27949258	T	A	0.3892370	0.0379590	0.0062729	8.70E-10
2	BRE	rs13382482	27949426	C	T	0.3896200	0.0384777	0.0062681	5.00E-10
2	BRE	rs7595847	27950176	A	T	0.3897890	0.0383789	0.0062685	5.00E-10
2	BRE	rs1506535	27951214	G	A	0.3899070	0.0382716	0.0062674	5.60E-10
2	BRE	rs13008539	27951540	A	C	0.3899070	0.0382716	0.0062674	5.60E-10
2	BRE	rs7584462	27953189	T	A	0.3903410	0.0380653	0.0062672	7.30E-10
2	BRE	rs7587180	27953242	G	A	0.3907330	0.0376696	0.0062659	9.80E-10
2	BRE	rs10205313	27953660	C	A	0.3890890	0.0367481	0.0062839	2.70E-09
2	BRE	chr2:27955981_G_GT	27955981	GT	G	0.3882820	0.0376282	0.0062927	1.30E-09
2	BRE	rs10559599	27958465	TTA	T	0.3904890	0.0378457	0.0062670	9.10E-10
2	BRE	rs1506537	27959034	C	G	0.3874090	0.0384351	0.0062659	4.50E-10
2	BRE	rs1506536	27959139	C	T	0.3900440	0.0378321	0.0062699	9.40E-10
2	BRE	rs2012704	27961899	A	T	0.3870470	0.0379800	0.0062709	6.40E-10
2	BRE	rs1350481	27962941	C	G	0.3866750	0.0373878	0.0062687	1.20E-09
2	BRE	rs3056502	27966214	T	TTTC	0.3842550	0.0381242	0.0062795	6.40E-10
2	BRE	rs1902966	27966413	A	G	0.3842550	0.0381242	0.0062795	6.40E-10
2	BRE	rs1841068	27968762	T	C	0.3870080	0.0387175	0.0062625	3.30E-10
2	BRE	rs10188108	27969688	G	C	0.3874470	0.0380253	0.0062605	5.80E-10
2	BRE	rs10198257	27973444	C	T	0.3758660	0.0367457	0.0063906	5.60E-09
2	BRE	rs12465000	27976557	A	G	0.3872660	0.0385999	0.0062619	3.30E-10
2	BRE	rs12465103	27976869	C	G	0.3872910	0.0384653	0.0062618	3.80E-10
2	BRE	rs2337374	27977285	A	G	0.3872900	0.0384597	0.0062618	3.80E-10
2	BRE	rs898032	27980069	G	C	0.3878200	0.0380418	0.0062611	6.30E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	BRE	rs7577342	27982714	T	C	0.3880420	0.0383530	0.0062643	4.60E-10
2	BRE	rs28662360	27986053	G	A	0.3872860	0.0384036	0.0062618	4.10E-10
2	BRE	rs10209126	27986416	T	C	0.3869980	0.0386084	0.0062625	3.60E-10
2	BRE	rs13029008	27990023	A	G	0.3867690	0.0381163	0.0062633	5.70E-10
2	BRE	rs10175508	27990557	T	C	0.3868750	0.0384967	0.0062642	4.20E-10
2	BRE	rs12470614	27994460	C	T	0.3878170	0.0380219	0.0062610	6.40E-10
2	BRE	rs1458397	27996741	C	T	0.3890470	0.0374942	0.0062620	1.10E-09
2	BRE	rs1458398	27997074	G	A	0.3884780	0.0379875	0.0062579	6.80E-10
2	BRE	rs10204513	27998058	C	G	0.3886230	0.0374654	0.0062565	1.10E-09
2	BRE	rs10196483	27998315	T	A	0.3886230	0.0374654	0.0062565	1.10E-09
2	BRE	rs10204832	28005541	A	T	0.3886250	0.0374536	0.0062565	1.10E-09
2	BRE	rs10168171	28009220	G	A	0.3886310	0.0375009	0.0062564	1.10E-09
2	BRE	rs2839791	28009412	C	A	0.3882000	0.0382305	0.0062586	5.80E-10
2	BRE	rs58258810	28011829	GA	G	0.3871980	0.0368018	0.0062836	2.60E-09
2	BRE	rs56046821	28011834	A	T	0.3886270	0.0375336	0.0062565	1.00E-09
2	BRE	rs7602328	28012317	A	G	0.3884830	0.0380524	0.0062579	6.40E-10
2	BRE	rs13003383	28012896	C	T	0.3884330	0.0374994	0.0062586	1.20E-09
2	BRE	rs10495761	28013088	T	C	0.3880950	0.0377495	0.0062579	9.30E-10
2	BRE	rs11127132	28013253	C	T	0.3883640	0.0377269	0.0062575	9.50E-10
2	BRE	rs6547817	28015118	T	C	0.3881990	0.0382480	0.0062587	5.80E-10
2	BRE	rs35526001	28017352	A	ATGT	0.3860960	0.0381069	0.0062727	8.00E-10
2	BRE	rs10180107	28017658	C	T	0.3875260	0.0383098	0.0062589	5.40E-10
2	BRE	rs4616436	28019441	A	G	0.3873790	0.0387980	0.0062603	3.40E-10
2	BRE	rs6725627	28019585	G	T	0.3875450	0.0382818	0.0062591	5.60E-10
2	BRE	rs12997202	28027522	A	G	0.3867530	0.0383763	0.0062611	5.00E-10
2	BRE	rs6727432	28028123	G	T	0.3875850	0.0380640	0.0062601	6.70E-10
2	BRE	rs937812	28032435	T	C	0.3873050	0.0387382	0.0062617	3.60E-10
2	BRE	rs9309658	28033964	G	A	0.3872900	0.0387589	0.0062615	3.50E-10
2	BRE	rs7593127	28035160	A	G	0.3872900	0.0387589	0.0062615	3.50E-10
2	BRE	rs6731650	28038296	A	C	0.3869550	0.0389593	0.0062643	3.10E-10
2	BRE	rs10175826	28038517	A	G	0.3862820	0.0384092	0.0062687	4.50E-10
2	BRE	rs6547819	28043177	G	A	0.3840870	0.0370679	0.0063209	2.50E-09
2	BRE	rs7580274	28043202	T	C	0.3842530	0.0386007	0.0062995	4.20E-10
2	BRE	rs6738887	28045600	T	C	0.3877710	0.0379211	0.0062599	8.10E-10
2	BRE	rs12614744	28046835	T	A	0.3882410	0.0376770	0.0062664	1.00E-09
2	BRE	rs13402420	28048568	G	T	0.4018800	0.0349133	0.0062227	1.20E-08
2	BRE	rs1395324	28053776	G	C	0.3872180	0.0388595	0.0062615	3.10E-10
2	BRE	rs1911128	28056782	G	T	0.4020060	0.0349524	0.0062205	1.10E-08
2	BRE	rs1911127	28056826	A	G	0.4020100	0.0349166	0.0062204	1.10E-08
2	BRE	rs6547820	28058678	A	G	0.3871570	0.0390630	0.0062601	2.50E-10
2	BRE	rs6758799	28061766	C	T	0.3868900	0.0382984	0.0062652	4.80E-10
2	BRE	rs13414801	28067480	C	T	0.4017820	0.0350649	0.0062234	1.00E-08
2	BRE	rs13409819	28070432	A	C	0.3859210	0.0399720	0.0063700	1.90E-10
2	BRE	rs11691385	28076117	G	A	0.4699930	0.0444492	0.0062395	3.00E-13
2	BRE	rs6737313	28076400	G	A	0.4708150	0.0452433	0.0062404	1.20E-13
2	BRE	rs11363251	28078343	G	GC	0.4420160	0.0441749	0.0061523	1.80E-13
2	BRE	rs2337699	28080846	T	C	0.4449030	0.0445147	0.0061380	9.60E-14
2	BRE	rs11682011	28081194	A	G	0.2932950	0.0398290	0.0067446	2.50E-09
2	BRE	chr2:28082112_GA_G	28082112	G	GA	0.2930000	0.0405307	0.0067544	1.50E-09
2	BRE	rs13415164	28082796	T	C	0.2938620	0.0392835	0.0067408	4.10E-09
2	BRE	rs2337700	28084076	G	A	0.4615850	0.0399493	0.0061099	1.70E-11
2	BRE	rs12614949	28084924	A	G	0.4426910	0.0440281	0.0061398	2.40E-13
2	BRE	rs13402525	28091991	T	G	0.2956580	0.0391349	0.0067194	3.80E-09
2	BRE	rs13405377	28092277	T	G	0.2945270	0.0407204	0.0067353	9.40E-10
2	BRE	rs13431542	28092278	T	C	0.2945270	0.0407204	0.0067353	9.40E-10
2	BRE	rs6710214	28094574	G	A	0.3215470	0.0360931	0.0065750	3.00E-08
2	BRE	rs10182585	28094942	G	A	0.3189200	0.0378057	0.0066053	1.10E-08
2	BRE	rs7578052	28096012	G	A	0.3043210	0.0406761	0.0066574	8.60E-10
2	BRE	rs6757405	28096049	T	C	0.3032400	0.0410766	0.0066698	6.40E-10
2	BRE	rs3863	28096267	G	A	0.3028720	0.0409843	0.0066714	6.60E-10
2	BRE	rs13395259	28096429	T	C	0.4521300	0.0459201	0.0061465	2.80E-14
2	BRE	rs11679638	28096872	T	C	0.3047970	0.0408675	0.0066439	5.70E-10
2	BRE	rs7581813	28097094	G	T	0.4513960	0.0452191	0.0061226	4.60E-14
2	BRE	rs7572644	28097166	T	C	0.4512010	0.0450004	0.0061234	5.90E-14
2	BRE	rs7558946	28097314	T	C	0.4503690	0.0455087	0.0061281	2.90E-14
2	BRE	rs10209559	28099593	A	G	0.2939370	0.0408734	0.0067199	9.40E-10
2	BRE	rs10187665	28101263	G	A	0.3189990	0.0373784	0.0065835	1.20E-08
2	BRE	rs77252308	28101842	T	TC	0.2935330	0.0405934	0.0067330	1.30E-09
2	BRE	rs6705961	28102334	T	C	0.4413350	0.0447081	0.0061578	1.10E-13
2	BRE	rs9309659	28103391	C	G	0.4519710	0.0466640	0.0061618	1.20E-14
2	BRE	rs10186196	28104963	G	C	0.2934650	0.0385134	0.0067670	7.30E-09
2	BRE	rs55796876	28107028	G	A	0.4591250	0.0391599	0.0062258	8.30E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	BRE	rs13000292	28112486	C	T	0.4509960	0.0375951	0.0062109	4.50E-10
2	BRE	rs1948922	28119286	A	G	0.4416070	0.0349446	0.0062147	5.60E-09
2	BRE	rs141106979	28145437	A	T	0.0206137	-0.1198130	0.0215676	1.70E-08
2	INHBB *	rs7578604	120551084	T	G	0.2999120	0.0370135	0.0067579	1.10E-08
2	INHBB *	rs954244	120551655	G	C	0.3012760	0.0368095	0.0067353	8.80E-09
2	GRB14 *	rs12692735	164648055	T	G	0.1025770	-0.0650442	0.0100519	3.00E-10
2	GRB14 *	rs10930133	164650214	A	T	0.1061400	-0.0617144	0.0099122	1.40E-09
2	COBLL1 *	rs6754919	164651333	T	C	0.1028640	-0.0656068	0.0100371	1.70E-10
2	COBLL1 *	rs6713419	164651790	C	T	0.1028740	-0.0655593	0.0100368	1.70E-10
2	COBLL1 *	rs10184004	164651879	T	C	0.1027640	-0.0652502	0.0100380	2.40E-10
2	COBLL1 *	rs10179126	164655284	G	C	0.1028500	-0.0651319	0.0100334	2.50E-10
2	COBLL1 *	rs34271465	164656555	C	CA	0.1033280	-0.0644459	0.0100236	3.40E-10
2	COBLL1 *	rs10195252	164656581	C	T	0.1029980	-0.0643170	0.0100293	4.80E-10
2	COBLL1 *	rs36105243	164668241	G	C	0.1028450	-0.0655128	0.0100334	2.00E-10
2	COBLL1 *	rs7592412	164669828	C	T	0.1028350	-0.0655468	0.0100336	2.00E-10
2	COBLL1 *	rs13432797	164670077	C	G	0.0803062	-0.0694314	0.0112164	3.40E-09
2	COBLL1 *	rs1128249	164672114	T	G	0.1029880	-0.0652379	0.0100284	2.30E-10
2	COBLL1 *	rs13389219	164672366	T	C	0.1030900	-0.0665187	0.0100343	1.10E-10
2	COBLL1 *	rs10187501	164675944	G	A	0.0800146	-0.0693740	0.0112403	3.60E-09
2	COBLL1	rs6717858	164683151	C	T	0.1035650	-0.0652538	0.0100109	2.20E-10
2	COBLL1	rs6753142	164687561	C	T	0.1032610	-0.0651141	0.0100207	2.40E-10
2	COBLL1	rs6738627	164687940	A	G	0.1035260	-0.0655171	0.0100088	1.80E-10
2	COBLL1	rs10601676	164688063	G	GAA	0.1025910	-0.0665446	0.0100535	1.20E-10
2	COBLL1	rs10630427	164688863	CAA	C	0.1030160	-0.0658170	0.0100368	1.80E-10
2	COBLL1	rs10649609	164696196	AAAAA	A	0.1133250	-0.0549160	0.0096892	3.50E-08
2	COBLL1	rs12692737	164697799	A	C	0.0780691	-0.0658085	0.0113620	2.70E-08
2	COBLL1	rs9653282	164698148	T	A	0.0778549	-0.0652195	0.0113772	3.50E-08
2	COBLL1	chr2:164698386_T_TTA	164698386	TTA	T	0.0778518	-0.0652512	0.0113774	3.40E-08
2	COBLL1	rs7609045	164698697	A	G	0.0778518	-0.0652512	0.0113774	3.40E-08
2	COBLL1	rs34704590	164699087	A	AT	0.0777765	-0.0656145	0.0113849	2.90E-08
2	COBLL1	rs2198550	164700250	C	A	0.0777253	-0.0653139	0.0113922	3.40E-08
2	COBLL1	rs6712203	164700808	T	C	0.1139770	-0.0545514	0.0096168	3.30E-08
2	CPS1	chr2:210482676_AAG_A	210482676	AAG	A	0.3948990	-0.0332403	0.0063229	1.90E-08
2	CPS1	rs10932337	210496251	G	T	0.4012620	-0.0336079	0.0062584	1.40E-08
2	CPS1	rs11696008	210505420	G	C	0.4017490	-0.0331907	0.0062405	1.80E-08
2	CPS1	rs10176675	210507361	A	G	0.4017790	-0.0328704	0.0062395	2.30E-08
2	CPS1	rs10200303	210507444	C	T	0.4017850	-0.0328856	0.0062393	2.30E-08
2	CPS1	rs4673537	210508922	C	A	0.4018340	-0.0327809	0.0062374	2.40E-08
2	CPS1	rs4414620	210510423	C	A	0.4018650	-0.0330015	0.0062313	1.80E-08
2	CPS1	rs918233	210511692	C	T	0.4018260	-0.0330259	0.0062310	1.80E-08
2	CPS1	rs918232	210511877	A	G	0.4018240	-0.0330378	0.0062311	1.80E-08
2	CPS1	rs115945693	210513104	G	A	0.4059880	-0.0327593	0.0062489	2.20E-08
2	CPS1	rs113151386	210513123	T	C	0.4059880	-0.0327593	0.0062489	2.20E-08
2	CPS1	rs62203707	210513171	T	G	0.4035780	-0.0340126	0.0062424	6.00E-09
2	CPS1	rs2370963	210514182	A	T	0.4017930	-0.0330113	0.0062312	1.80E-08
2	CPS1	rs1588365	210514530	A	G	0.4017880	-0.0329986	0.0062312	1.90E-08
2	CPS1	rs13399079	210515609	G	A	0.4017820	-0.0329297	0.0062314	2.00E-08
2	CPS1	rs1544717	210517737	T	A	0.4001550	-0.0324589	0.0062354	3.20E-08
2	CPS1	rs3915695	210517860	C	T	0.4001550	-0.0324589	0.0062354	3.20E-08
2	CPS1	rs3915694	210519402	A	G	0.4001140	-0.0322429	0.0062362	3.80E-08
2	CPS1	rs3915693	210519498	C	T	0.4001810	-0.0324670	0.0062359	3.20E-08
2	CPS1	rs1509819	210521813	A	G	0.4001630	-0.0323602	0.0062364	3.40E-08
2	CPS1	rs59337803	210522233	T	C	0.4002170	-0.0324696	0.0062367	3.10E-08
2	CPS1	rs13405091	210522479	G	A	0.4006990	-0.0326080	0.0062429	2.80E-08
2	CPS1	rs10165084	210523441	A	C	0.4001860	-0.0323544	0.0062368	3.50E-08
2	CPS1	rs2664238	210524698	T	C	0.4026930	-0.0327357	0.0062421	2.30E-08
3	SYN2 *	chr3:11987206_CAAA_C	11987206	CAAA	C	0.1681780	-0.0421859	0.0081882	4.80E-08
3	SYN2 *	rs2600262	11988560	C	T	0.1673500	-0.0424867	0.0082050	4.70E-08
3	SYN2 *	rs10560475	11995300	TCA	T	0.0346629	-0.0871474	0.0166898	4.50E-08
3	SYN2 *	rs2618403	11997989	C	T	0.0346425	-0.0876868	0.0166903	3.80E-08
3	SYN2	rs2923857	12004864	G	C	0.0344140	-0.0880915	0.0167454	3.40E-08
3	SYN2	rs2600235	12004945	T	G	0.0344140	-0.0880915	0.0167454	3.40E-08
3	SYN2	rs2623879	12004946	T	C	0.0344305	-0.0883743	0.0167423	3.20E-08
3	SYN2	rs2618389	12007234	C	T	0.0344039	-0.0877788	0.0167478	3.80E-08
3	SYN2	rs2618387	12007963	T	A	0.0335456	-0.0939213	0.0169624	7.10E-09
3	SYN2	rs217049	12019417	C	T	0.0343681	-0.0875051	0.0167566	4.30E-08
3	SYN2	rs59306735	12020503	C	T	0.0343681	-0.0875051	0.0167566	4.30E-08
3	SYN2	rs307611	12021844	G	C	0.0343681	-0.0875051	0.0167566	4.30E-08
3	SYN2	rs394945	12033617	T	C	0.0343705	-0.0875625	0.0167558	4.20E-08
3	SYN2	rs402149	12033844	G	A	0.0343705	-0.0875625	0.0167558	4.20E-08
3	SYN2	rs373827	12034975	G	A	0.0343705	-0.0875625	0.0167558	4.20E-08
3	SYN2	rs6767059	12035062	G	A	0.0343705	-0.0875625	0.0167558	4.20E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	SYN2	rs454615	12035510	T	C	0.0343705	-0.0875625	0.0167558	4.20E-08
3	SYN2	rs10510409	12041804	T	C	0.0343355	-0.0877246	0.0167670	4.00E-08
3	SYN2	rs167408	12046948	A	G	0.0343700	-0.0875448	0.0167558	4.20E-08
3	SYN2	rs2030150	12050190	T	C	0.0343697	-0.0875392	0.0167558	4.20E-08
3	SYN2	rs307560	12051905	T	C	0.0343697	-0.0875392	0.0167558	4.20E-08
3	SYN2	rs71304084	12077400	T	C	0.1152470	-0.0526918	0.0096035	6.80E-09
3	SYN2	rs148566174	12078193	C	CTT	0.1149890	-0.0517463	0.0096146	1.40E-08
3	SYN2	rs147433183	12078502	G	A	0.0343463	-0.0874247	0.0167571	4.30E-08
3	SYN2	rs1587385	12087736	G	C	0.0343394	-0.0876496	0.0167586	4.00E-08
3	SYN2	rs35416561	12088199	T	TCAAA	0.0343394	-0.0876496	0.0167586	4.00E-08
3	SYN2	rs61156889	12088662	TAA	T	0.0343394	-0.0876496	0.0167586	4.00E-08
3	SYN2	rs2119812	12090187	T	C	0.0343178	-0.0875476	0.0167642	4.30E-08
3	SYN2	rs34389637	12090516	CT	C	0.0343178	-0.0875476	0.0167642	4.30E-08
3	SYN2	rs184262	12093240	A	G	0.0343170	-0.0875453	0.0167642	4.30E-08
3	SYN2	rs13061425	12095404	G	T	0.0343168	-0.0875378	0.0167641	4.30E-08
3	SYN2	rs143095555	12095450	A	AGG	0.0351395	-0.0901025	0.0166208	1.30E-08
3	SYN2	rs6798755	12097592	T	C	0.0329775	-0.0934849	0.0170987	1.80E-08
3	SYN2	rs58683249	12098765	C	T	0.0343165	-0.0875292	0.0167641	4.30E-08
3	SYN2	rs453131	12099453	C	G	0.0343158	-0.0875042	0.0167641	4.30E-08
3	SYN2	rs6442307	12101855	C	A	0.0343158	-0.0875042	0.0167641	4.30E-08
3	SYN2	rs160113	12103739	T	C	0.1155140	-0.0524316	0.0095887	7.50E-09
3	SYN2	rs34206487	12103849	G	A	0.0343153	-0.0875252	0.0167641	4.30E-08
3	SYN2	rs11715886	12105736	G	C	0.0343150	-0.0875374	0.0167641	4.30E-08
3	SYN2	rs73813125	12106763	C	T	0.0343150	-0.0875374	0.0167641	4.30E-08
3	SYN2	rs13079332	12107348	A	G	0.0343150	-0.0875374	0.0167641	4.30E-08
3	SYN2	rs35544543	12112767	CA	C	0.1199930	-0.0488862	0.0094595	4.60E-08
3	SYN2	rs71628735	12113377	AG	A	0.0343258	-0.0875290	0.0167609	4.30E-08
3	SYN2	rs35814004	12114537	C	CTA	0.0343346	-0.0877622	0.0167602	4.00E-08
3	SYN2	rs11720130	12114816	A	G	0.1158590	-0.0520338	0.0095723	8.40E-09
3	SYN2	rs71628736	12115035	A	C	0.0343258	-0.0875290	0.0167609	4.30E-08
3	SYN2	rs66822996	12115142	C	CAT	0.0343494	-0.0877331	0.0167579	4.10E-08
3	SYN2	rs13064956	12128751	C	T	0.1157970	-0.0517161	0.0095771	7.40E-09
3	SYN2	rs34831171	12132155	C	T	0.1159570	-0.0532247	0.0095690	3.80E-09
3	SYN2	rs7621569	12143057	G	A	0.1151970	-0.0533620	0.0096023	2.80E-09
3	SYN2	rs1867012	12146743	C	T	0.0341685	-0.0873809	0.0168033	4.60E-08
3	SYN2	rs11708978	12146995	G	A	0.0341685	-0.0873809	0.0168033	4.60E-08
3	SYN2	rs35522627	12147066	A	C	0.0341685	-0.0873809	0.0168033	4.60E-08
3	SYN2	chr3:12147956_C_CA	12147956	CA	C	0.1117760	-0.0535711	0.0097453	5.70E-09
3	SYN2	rs7629805	12150894	G	A	0.0341353	-0.0893429	0.0168113	2.40E-08
3	SYN2	rs7652520	12151127	C	G	0.0341353	-0.0893429	0.0168113	2.40E-08
3	SYN2, TIMF	rs17035945	12153128	T	C	0.1147280	-0.0526109	0.0096280	5.90E-09
3	SYN2, TIMF	rs71304089	12155463	T	C	0.0341356	-0.0891048	0.0168095	2.60E-08
3	SYN2, TIMF	rs71304090	12155999	G	A	0.0341320	-0.0890920	0.0168103	2.60E-08
3	SYN2, TIMF	rs10433537	12156985	T	A	0.0341315	-0.0890805	0.0168103	2.60E-08
3	SYN2	rs146888519	12163301	ATTAT	A	0.0339448	-0.0891720	0.0168558	3.60E-08
3	SYN2	rs78518024	12165961	C	T	0.0345829	-0.0884582	0.0167017	2.70E-08
3	SYN2	chr3:12168855_AT_A	12168855	AT	A	0.1164080	-0.0536065	0.0095630	3.30E-09
3	SYN2	rs13064273	12174631	A	G	0.0345853	-0.0883212	0.0167009	2.90E-08
3	SYN2	rs6781687	12174760	G	A	0.0507453	-0.0830071	0.0140044	1.10E-10
3	SYN2	rs34189310	12175017	A	AT	0.0346027	-0.0885531	0.0167021	2.60E-08
3	SYN2	rs13070993	12176297	T	C	0.0348658	-0.0882258	0.0166388	2.70E-08
3	SYN2	rs6805092	12179924	T	C	0.0447335	-0.0908197	0.0147818	8.80E-11
3	SYN2	rs34646613	12187872	A	AC	0.0345647	-0.0874001	0.0167080	3.50E-08
3	SYN2	rs310763	12189204	T	C	0.1164990	-0.0519198	0.0095535	7.80E-09
3	SYN2 *	rs71304092	12195065	A	G	0.0447535	-0.0899230	0.0147832	1.20E-10
3	SYN2 *	rs13077227	12200266	G	A	0.0447578	-0.0898350	0.0147827	1.20E-10
3	SYN2 *	rs7637403	12200988	A	G	0.1162820	-0.0532763	0.0095607	3.50E-09
3	SYN2 *	rs13079837	12209346	A	T	0.1173290	-0.0511989	0.0095195	1.00E-08
3	SYN2 *	rs13099882	12209388	G	A	0.1174210	-0.0514675	0.0095156	8.60E-09
3	SYN2 *	rs35000292	12213022	C	CAA	0.0343354	-0.0888338	0.0167690	1.90E-08
3	SYN2 *	rs11718525	12213765	T	C	0.0339242	-0.0903399	0.0168799	1.50E-08
3	SYN2 *	rs34733382	12214747	T	TA	0.0333212	-0.0919627	0.0170303	8.60E-09
3	SYN2 *	rs34562457	12214750	C	T	0.0333212	-0.0919627	0.0170303	8.60E-09
3	SYN2 *	rs74280642	12221434	A	G	0.0332337	-0.0944971	0.0170558	2.90E-09
3	SYN2 *	rs6786675	12223962	C	G	0.0333570	-0.0956844	0.0170173	1.80E-09
3	SYN2 *	rs35355828	12225005	A	G	0.0461882	-0.0925235	0.0145898	6.40E-12
3	SYN2 *	rs11720578	12225584	T	G	0.0462275	-0.0913431	0.0145874	1.10E-11
3	SYN2 *	rs35146940	12229787	T	A	0.0332364	-0.0945490	0.0170447	3.30E-09
3	SYN2 *	rs310749	12232268	G	T	0.1366900	-0.0488527	0.0089462	1.00E-08
3	SYN2 *	rs13065423	12233092	A	G	0.0342540	-0.0903775	0.0167814	7.30E-09
3	SYN2 *	rs13088452	12233461	C	T	0.0342573	-0.0904953	0.0167806	7.10E-09
3	SYN2 *	rs13066157	12233494	A	G	0.0342607	-0.0904485	0.0167798	7.20E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	SYN2 *	rs171304093	12233820	T	C	0.0342634	-0.0905926	0.0167790	6.60E-09
3	SYN2 *	rs13071168	12233947	A	G	0.0342657	-0.0905669	0.0167782	6.80E-09
3	SYN2 *	rs11709119	12234993	T	G	0.0343718	-0.0900026	0.0167478	7.50E-09
3	SYN2 *	rs36086545	12235690	A	G	0.0344160	-0.0902254	0.0167298	6.80E-09
3	SYN2 *	rs112560967	12236156	A	C	0.0344764	-0.0884746	0.0167142	1.10E-08
3	SYN2 *	rs113205156	12236157	C	T	0.0343828	-0.0875183	0.0167404	1.70E-08
3	SYN2 *	rs17036101	12236345	A	G	0.0348149	-0.0903486	0.0166456	4.60E-09
3	SYN2 *	rs34780220	12236613	G	A	0.0344730	-0.0888122	0.0167150	9.70E-09
3	SYN2 *	rs11715362	12236964	G	T	0.0344276	-0.0885539	0.0167296	1.10E-08
3	SYN2 *	rs11719082	12237028	G	A	0.0344281	-0.0885602	0.0167296	1.10E-08
3	SYN2 *	rs35551471	12237709	A	G	0.0344364	-0.0887140	0.0167262	1.10E-08
3	SYN2 *	rs67201468	12238506	G	GT	0.0344366	-0.0887248	0.0167262	1.10E-08
3	PPARG *	rs35220653	12242071	G	C	0.0344602	-0.0885262	0.0167172	1.10E-08
3	PPARG *	rs1562040	12243905	A	G	0.0344682	-0.0886795	0.0167157	1.00E-08
3	PPARG *	rs7616902	12245546	G	T	0.3831070	0.0329232	0.0063864	4.10E-08
3	PPARG *	rs7651874	12245673	T	C	0.3831050	0.0329204	0.0063864	4.00E-08
3	PPARG *	rs17036130	12246788	A	G	0.0345162	-0.0888210	0.0167039	1.00E-08
3	PPARG *	rs13081389	12248301	G	A	0.0349920	-0.0840110	0.0166014	4.00E-08
3	PPARG *	rs7628899	12249014	A	T	0.0345229	-0.0889163	0.0167024	9.90E-09
3	PPARG *	rs34835192	12249293	C	CA	0.0345229	-0.0889163	0.0167024	9.90E-09
3	PPARG *	rs1596417	12249399	T	A	0.0345971	-0.0874022	0.0166864	1.70E-08
3	PPARG *	rs34881099	12250003	A	C	0.0345229	-0.0889163	0.0167024	9.90E-09
3	PPARG *	rs35577339	12254847	A	G	0.0344456	-0.0887650	0.0167300	1.10E-08
3	PPARG *	rs71304095	12255014	A	G	0.0344461	-0.0887794	0.0167300	1.10E-08
3	PPARG *	rs35252428	12255654	T	C	0.0344496	-0.0887752	0.0167301	1.00E-08
3	PPARG *	rs773846047	12256287	G	A	0.0344050	-0.0853257	0.0167650	3.20E-08
3	PPARG *	rs35316189	12257068	A	G	0.0344401	-0.0883121	0.0167333	1.20E-08
3	PPARG *	rs35099296	12257139	C	CATA	0.0344392	-0.0882201	0.0167341	1.20E-08
3	PPARG *	rs71304096	12257866	G	A	0.0344361	-0.0883730	0.0167349	1.10E-08
3	PPARG *	rs71304097	12258116	A	C	0.0344358	-0.0883676	0.0167349	1.10E-08
3	PPARG *	rs35877199	12258161	A	G	0.0344358	-0.0883676	0.0167349	1.10E-08
3	PPARG *	rs35057507	12258223	A	G	0.0347672	-0.0879852	0.0166825	1.20E-08
3	PPARG *	rs13067702	12258446	C	G	0.0344298	-0.0883616	0.0167365	1.10E-08
3	PPARG *	rs34685612	12258484	A	G	0.0344298	-0.0883616	0.0167365	1.10E-08
3	PPARG *	rs71304098	12258559	A	G	0.0344303	-0.0883372	0.0167365	1.10E-08
3	PPARG *	rs13088598	12259564	T	C	0.0343455	-0.0878337	0.0167630	1.50E-08
3	PPARG *	rs13088608	12259617	G	A	0.0343455	-0.0878337	0.0167630	1.50E-08
3	PPARG *	rs13089415	12259861	T	G	0.0343410	-0.0882346	0.0167646	1.30E-08
3	PPARG *	rs6771792	12259973	T	C	0.0343412	-0.0882367	0.0167646	1.30E-08
3	PPARG *	rs34430055	12260072	C	T	0.0343412	-0.0882367	0.0167646	1.30E-08
3	PPARG *	rs35541642	12260763	T	C	0.0343422	-0.0882669	0.0167647	1.20E-08
3	PPARG *	rs113764196	12271009	T	C	0.3903730	0.0336454	0.0062793	1.10E-08
3	PPARG *	rs11715261	12275733	C	G	0.0356796	-0.0833248	0.0164429	3.20E-08
3	PPARG *	rs11715234	12275811	A	C	0.0356809	-0.0833250	0.0164429	3.20E-08
3	PPARG *	rs80182988	12281910	T	C	0.3826570	0.0343315	0.0063426	4.80E-09
3	PPARG *	rs79310821	12285066	A	G	0.3840640	0.0338456	0.0063403	8.10E-09
3	PPARG *	rs73021485	12285888	T	G	0.3835620	0.0349303	0.0063422	3.10E-09
3	PPARG *	rs2920502	12287696	G	C	0.2192080	-0.0429491	0.0075034	2.90E-09
3	PPARG	rs17036188	12299426	C	T	0.3772630	0.0335748	0.0063461	1.90E-08
3	PPARG	rs60943442	12300202	C	CAG	0.3749350	0.0328746	0.0063513	3.00E-08
3	PPARG	rs12631819	12301362	T	G	0.3777010	0.0337309	0.0063400	1.60E-08
3	PPARG	rs74833298	12302050	A	C	0.3777080	0.0337559	0.0063399	1.60E-08
3	PPARG	rs78846589	12304609	T	A	0.3366470	0.0391854	0.0065068	3.30E-10
3	PPARG	rs12485478	12309724	G	A	0.3212740	0.0403853	0.0065378	1.60E-10
3	PPARG	chr3:12318858_G_GT	12318858	GT	G	0.0386047	-0.0835576	0.0158743	1.90E-08
3	PPARG	rs12633551	12318995	T	C	0.3220620	0.0405519	0.0065285	1.20E-10
3	PPARG	rs117350179	12332833	G	C	0.3216460	0.0406071	0.0065416	1.30E-10
3	PPARG	chr3:12333144_A_AAAAC	12333144	AAAAC	A	0.3216870	0.0406892	0.0065415	1.20E-10
3	PPARG	rs76608844	12334081	T	C	0.3215860	0.0405566	0.0065426	1.30E-10
3	PPARG	rs79644791	12334928	G	A	0.3215830	0.0405743	0.0065427	1.30E-10
3	PPARG	rs138502109	12341816	G	GA	0.3195780	0.0396374	0.0065947	3.70E-10
3	PPARG	rs73134740	12342767	T	C	0.3196850	0.0414914	0.0066101	4.10E-11
3	PPARG	rs4684847	12344838	T	C	0.0392700	-0.0799507	0.0157029	4.70E-08
3	PPARG	rs12497191	12348636	G	A	0.3232300	0.0401753	0.0065796	1.40E-10
3	PPARG	rs4135249	12355280	T	C	0.3186280	0.0405505	0.0066397	1.80E-10
3	KBTBD8 *	rs9813067	66812220	T	C	0.4704260	-0.0349748	0.0061635	3.20E-09
3	KBTBD8 *	rs7638057	66812294	C	T	0.4709140	-0.0350112	0.0061633	3.00E-09
3	KBTBD8 *	rs7645370	66812469	T	G	0.4704660	-0.0351244	0.0061625	2.50E-09
3	KBTBD8 *	rs7642618	66812578	A	G	0.4703020	-0.0347726	0.0061643	3.60E-09
3	KBTBD8 *	rs7629637	66812641	G	C	0.4749870	-0.0352809	0.0061756	1.80E-09
3	KBTBD8 *	rs34113192	66813244	A	G	0.4701820	-0.0353278	0.0061685	2.10E-09
3	KBTBD8 *	rs11342763	66814250	GA	G	0.4661400	-0.0339112	0.0061876	8.40E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	KBTBD8 *	rs4856967	66814463	T	C	0.4677680	-0.0335484	0.0061810	1.00E-08
3	KBTBD8 *	rs4856968	66814508	A	G	0.4682160	-0.0330063	0.0061871	1.60E-08
3	KBTBD8 *	rs9682765	66815451	C	T	0.4742330	-0.0346054	0.0061924	3.30E-09
3	KBTBD8 *	rs6549423	66816248	G	A	0.4727800	-0.0347887	0.0061659	2.70E-09
3	KBTBD8 *	rs6549424	66816324	T	C	0.4731030	-0.0348185	0.0061719	2.50E-09
3	KBTBD8 *	rs6549425	66816387	T	A	0.4728340	-0.0343647	0.0061631	3.70E-09
3	KBTBD8 *	rs4856827	66817179	A	G	0.4721740	-0.0349640	0.0061786	2.50E-09
4	HTT	rs10015979	3107715	G	A	0.4494710	0.0345889	0.0062339	3.60E-08
4	MSANTD1	rs10937921	3274764	C	T	0.3978380	-0.0346165	0.0062532	3.80E-08
4	MSANTD1	rs6446731	3283024	G	A	0.4174140	-0.0395118	0.0062638	5.50E-10
4	MSANTD1	rs3135064	3283662	T	C	0.3923110	-0.0355478	0.0063161	1.90E-08
4	RGS12 *	rs3129316	3286179	A	G	0.3795060	-0.0375225	0.0063458	2.40E-09
4	RGS12 *	rs2071666	3288676	A	G	0.3783690	-0.0373429	0.0063471	2.70E-09
4	RGS12 *	rs3129314	3291312	G	T	0.3785560	-0.0366625	0.0063540	5.50E-09
4	RGS12 *	rs3135145	3297777	T	C	0.3446710	-0.0368034	0.0064712	8.20E-09
4	RGS12 *	rs73193354	3298808	G	T	0.3363480	0.0436185	0.0065137	2.60E-11
4	RGS12 *	rs3129310	3299661	T	G	0.3773980	-0.0386774	0.0063296	4.70E-10
4	RGS12 *	rs2239725	3304012	C	T	0.3481220	-0.0362529	0.0064278	1.00E-08
4	RGS12 *	rs910568	3305646	A	G	0.3464980	-0.0365101	0.0064324	8.80E-09
4	RGS12 *	rs76334211	3305705	G	GC	0.3342690	0.0412900	0.0064882	2.60E-10
4	RGS12 *	rs3135146	3305911	C	G	0.3478140	-0.0367455	0.0064253	7.50E-09
4	RGS12 *	rs73193357	3306228	G	C	0.3338340	0.0415390	0.0064891	2.00E-10
4	RGS12 *	rs3129308	3307545	G	A	0.3816790	-0.0377806	0.0062952	9.60E-10
4	RGS12 *	rs2749786	3313239	C	T	0.3360870	0.0426563	0.0064654	6.70E-11
4	RGS12	rs2236052	3316686	A	G	0.3486960	-0.0382747	0.0064044	1.60E-09
4	RGS12	rs2281470	3317826	T	C	0.3336770	0.0418794	0.0064734	1.30E-10
4	RGS12	rs12643903	3319967	A	G	0.3361280	0.0422154	0.0064671	6.80E-11
4	RGS12	rs2857859	3320413	T	C	0.3348790	0.0424309	0.0064711	7.50E-11
4	RGS12	rs2857861	3322040	C	T	0.4410590	-0.0382520	0.0061715	5.40E-10
4	RGS12	rs2051558	3323159	G	A	0.4084890	-0.0414057	0.0062142	2.50E-11
4	RGS12	rs2749785	3323452	G	C	0.3497080	-0.0380778	0.0064061	1.60E-09
4	RGS12	rs2749783	3324371	A	C	0.3823450	-0.0400735	0.0062852	1.00E-10
4	RGS12	rs2857860	3328062	G	A	0.3285850	0.0431958	0.0065318	5.60E-11
4	RGS12	rs3129336	3333174	T	C	0.3259300	0.0425691	0.0065622	1.00E-10
4	RGS12	rs2748447	3336104	G	A	0.3519460	-0.0381173	0.0064172	1.40E-09
4	RGS12	rs12640526	3338001	T	C	0.3339190	0.0426162	0.0064804	6.50E-11
4	RGS12	rs2749782	3338034	T	C	0.3507720	-0.0377209	0.0064251	2.20E-09
4	RGS12	chr4:3340762_A_AGGTGCAGGCC	3340762	A	TTGCAG	0.3816660	-0.0401323	0.0062952	9.20E-11
4	RGS12	rs2073286	3343164	C	T	0.3370190	0.0424682	0.0064646	8.90E-11
4	RGS12	rs2749781	3344890	T	C	0.3513000	-0.0375305	0.0064257	2.70E-09
4	RGS12	rs2749780	3347365	T	A	0.3811490	-0.0395713	0.0063007	2.10E-10
4	RGS12	rs2749779	3348521	G	A	0.3368490	0.0428031	0.0064638	6.40E-11
4	RGS12	rs76078669	3349544	A	ACT	0.3347680	0.0427273	0.0064804	5.90E-11
4	RGS12	rs2749778	3349978	T	C	0.3497490	-0.0377853	0.0064195	1.90E-09
4	RGS12	rs2749776	3353308	G	A	0.3347560	0.0426468	0.0064782	7.40E-11
4	RGS12	rs2749775	3353811	T	C	0.3347150	0.0425320	0.0064788	7.20E-11
4	RGS12	rs2857982	3356938	G	A	0.3577690	-0.0379209	0.0063826	1.30E-09
4	RGS12	rs149402347	3362478	G	GTGTA	0.3126890	0.0433682	0.0067222	1.20E-10
4	RGS12	rs60181496	3362661	C	G	0.3625420	-0.0358312	0.0064347	1.30E-08
4	RGS12	rs60208975	3362803	A	G	0.3934640	-0.0373680	0.0063339	1.70E-09
4	RGS12	rs881816	3363639	A	G	0.3479770	-0.0352354	0.0065065	2.70E-08
4	RGS12	rs881817	3363654	A	G	0.3887680	-0.0384508	0.0063163	7.10E-10
4	RGS12	rs881818	3363680	C	G	0.3228240	0.0416721	0.0065882	3.40E-10
4	RGS12	rs16844197	3364833	G	T	0.3249250	0.0414622	0.0065735	4.50E-10
4	RGS12	rs62274923	3365109	G	A	0.3256210	0.0405439	0.0065681	8.30E-10
4	RGS12	rs16844201	3365141	C	G	0.3256200	0.0405436	0.0065681	8.30E-10
4	RGS12	rs13104157	3365223	T	C	0.3559710	-0.0358029	0.0064314	1.50E-08
4	RGS12	rs13150241	3365554	A	G	0.3553150	-0.0364031	0.0064219	7.50E-09
4	RGS12	rs6819202	3366537	G	A	0.3563510	-0.0365135	0.0064275	5.70E-09
4	RGS12	rs3129334	3366799	T	C	0.3549720	-0.0361860	0.0064289	8.50E-09
4	RGS12	rs10155132	3367773	A	G	0.3530900	-0.0380695	0.0064420	1.80E-09
4	RGS12	rs7435601	3367918	T	C	0.3521190	-0.0377260	0.0064500	2.80E-09
4	RGS12	rs112257814	3368451	G	T	0.3265700	0.0405258	0.0065559	9.20E-10
4	RGS12	rs58949283	3368639	G	T	0.3265300	0.0405180	0.0065567	9.10E-10
4	RGS12	rs62274924	3369138	A	G	0.3264940	0.0406037	0.0065574	8.40E-10
4	RGS12	rs73193369	3369182	A	C	0.3267180	0.0403038	0.0065545	1.10E-09
4	RGS12	rs73193371	3369183	G	C	0.3267180	0.0403038	0.0065545	1.10E-09
4	RGS12	rs12640721	3372448	G	A	0.3370680	0.0425059	0.0065064	1.30E-10
4	RGS12	rs12640186	3372812	T	C	0.3340680	0.0414689	0.0065204	3.90E-10
4	RGS12	rs10937924	3373171	T	C	0.3737670	-0.0424588	0.0063832	2.10E-11
4	RGS12	rs73193372	3373261	T	C	0.3334150	0.0416063	0.0065253	3.30E-10
4	RGS12	rs3129333	3373271	A	G	0.3339400	0.0413916	0.0065251	4.20E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
4	RGS12	rs3129332	3374041	A	G	0.3361100	0.0420207	0.0065222	2.80E-10
4	RGS12	rs2343799	3375007	C	T	0.3340030	0.0414931	0.0065535	4.70E-10
4	RGS12	rs138391629	3375752	GC	G	0.3338400	0.0414159	0.0065753	5.80E-10
4	RGS12	rs3129331	3375947	A	G	0.3330660	0.0418932	0.0065754	3.20E-10
4	RGS12	rs3129330	3377653	T	C	0.3318630	0.0421328	0.0066132	3.50E-10
4	RGS12	rs1894442	3384588	T	C	0.4597760	-0.0622179	0.0061798	5.70E-22
4	RGS12	rs1264442	3385844	A	G	0.4951400	0.0619890	0.0062047	4.70E-22
4	RGS12	rs4690090	3387800	T	C	0.4419820	-0.0597093	0.0062369	6.20E-20
4	RGS12	rs6828057	3388084	A	G	0.4445360	-0.0595598	0.0062381	1.10E-19
4	RGS12	rs2269496	3388419	C	T	0.2871580	0.0509588	0.0069042	2.40E-12
4	RGS12	rs13127597	3388545	C	A	0.4644970	-0.0620035	0.0061441	3.60E-22
4	RGS12	rs73193383	3390547	T	C	0.2760490	0.0576115	0.0069621	2.30E-15
4	RGS12	rs17797467	3390588	G	C	0.4671040	-0.0597073	0.0061863	1.50E-20
4	RGS12	rs13152128	3390623	A	C	0.4609460	-0.0605424	0.0061735	6.90E-21
4	RGS12	rs12510769	3392647	C	T	0.2822010	0.0567868	0.0068853	4.60E-15
4	RGS12	rs9995777	3403748	T	C	0.4476310	0.0564239	0.0062901	2.50E-18
4	RGS12	rs10027926	3412927	A	G	0.2623320	0.0584772	0.0071129	2.60E-15
4	RGS12	rs62274930	3413609	T	C	0.4734280	-0.0616537	0.0062214	9.00E-22
4	RGS12	rs16844301	3413651	A	G	0.4986430	0.0577076	0.0062110	2.60E-19
4	RGS12	rs3213506	3415757	A	G	0.4729010	-0.0623968	0.0062298	3.00E-22
4	RGS12	rs3213507	3416118	C	G	0.4990950	-0.0587602	0.0062217	5.40E-20
4	RGS12	rs17190954	3416357	G	A	0.2655330	0.0586986	0.0070716	1.30E-15
4	RGS12	rs16844307	3416438	T	C	0.4735780	-0.0627466	0.0062329	2.20E-22
4	RGS12	rs16844309	3416539	A	G	0.4731520	-0.0633002	0.0062326	8.10E-23
4	RGS12	rs12641989	3418113	A	G	0.2650810	0.0579688	0.0070780	3.80E-15
4	RGS12	rs3748037	3418544	A	G	0.2651290	0.0582397	0.0070760	2.60E-15
4	RGS12	rs3748036	3418644	T	C	0.4734110	-0.0627152	0.0062405	1.90E-22
4	RGS12	rs4690095	3419582	C	T	0.4871580	0.0600841	0.0062574	2.20E-20
4	RGS12	rs3088231	3420484	A	G	0.2637410	0.0573370	0.0071073	7.10E-15
4	RGS12	rs3789739	3421715	T	C	0.4756510	-0.0621369	0.0062603	9.40E-22
4	RGS12	rs58143210	3423303	T	C	0.4721840	-0.0624700	0.0062682	4.70E-22
4	HGFAC *	rs28766336	3452024	T	G	0.4740650	-0.0564928	0.0062478	5.80E-19
4	HGFAC *	rs4690099	3452727	T	C	0.4647320	-0.0542569	0.0062515	1.20E-17
4	DOK7 *	rs2091626	3460173	T	G	0.4666020	-0.0549394	0.0062544	5.20E-18
4	DOK7 *	rs1076903	3460467	G	A	0.4666370	-0.0551835	0.0062551	3.70E-18
4	DOK7 *	rs28478452	3461750	A	G	0.4654360	-0.0554445	0.0062653	2.90E-18
4	DOK7	rs56738936	3468759	TGTGA	T	0.3400650	0.0394907	0.0065416	1.50E-09
4	DOK7	rs36205397	3468877	G	A	0.3804920	0.0427317	0.0063275	1.30E-11
4	DOK7	chr4:3469063_A_AGT	3469063	AGT	A	0.3789370	0.0416977	0.0063361	4.90E-11
4	DOK7	rs10007119	3471339	G	A	0.3815450	0.0423181	0.0062976	1.70E-11
4	DOK7	rs6831256	3471412	G	A	0.3819870	0.0419167	0.0062916	2.40E-11
4	NCAPG	rs11941723	17810905	G	A	0.1431180	0.0486499	0.0087377	1.60E-08
4	NCAPG	rs16895796	17811596	A	T	0.1424440	0.0479529	0.0087548	2.60E-08
4	NCAPG	rs16895802	17814266	G	C	0.1431120	0.0479272	0.0087258	2.70E-08
4	NCAPG	rs139724825	17822441	T	C	0.1417160	0.0485017	0.0087714	1.80E-08
4	LCORL, NC	rs59037741	17843847	T	C	0.1413430	0.0474914	0.0087769	4.60E-08
4	LCORL	rs16895882	17847141	G	T	0.1429270	0.0469650	0.0087410	4.90E-08
4	C4orf36	rs72613147	86887867	G	C	0.2267460	-0.0428237	0.0073804	2.40E-08
4	AFF1 *	rs2705619	86915499	G	A	0.3626450	-0.0428618	0.0064394	2.50E-11
4	AFF1 *	rs2442078	86915702	A	G	0.3620860	-0.0428485	0.0064457	2.80E-11
4	AFF1 *	rs72613148	86916198	C	T	0.2212600	-0.0450838	0.0074236	1.70E-09
4	AFF1 *	chr4:86917330_T_TGAAG	86917330	T	TGAAG	0.3650020	-0.0445762	0.0064610	4.60E-12
4	AFF1 *	rs137974793	86917870	AATG	A	0.3620110	-0.0429906	0.0064612	2.70E-11
4	LOC100506	rs1868246	86927930	C	T	0.2213730	-0.0457836	0.0074336	1.10E-09
4	LOC100506	rs72613149	86928070	A	G	0.2213750	-0.0457623	0.0074335	1.10E-09
4	AFF1	rs10558187	86935801	G	GACTTA	0.2219390	-0.0457594	0.0074254	1.10E-09
4	AFF1	rs1447993	86936439	A	T	0.2218780	-0.0458559	0.0074270	1.00E-09
4	AFF1	rs6419117	86937756	T	A	0.2215960	-0.0452039	0.0074323	1.50E-09
4	AFF1	rs12506662	86940324	G	A	0.2222250	-0.0456739	0.0074198	1.00E-09
4	AFF1	rs9996533	86941327	A	G	0.2221990	-0.0458222	0.0074201	9.10E-10
4	AFF1	rs7671931	86941491	C	T	0.2222100	-0.0458740	0.0074203	8.70E-10
4	AFF1	rs6836128	86942618	C	T	0.2222190	-0.0461247	0.0074193	6.70E-10
4	AFF1	rs17012186	86947701	T	C	0.2218800	-0.0434209	0.0074033	7.40E-09
4	AFF1	rs1992876	86952012	G	A	0.2207890	-0.0426726	0.0074097	8.30E-09
4	AFF1	rs67773101	86955236	A	C	0.2225390	-0.0425366	0.0073875	1.20E-08
4	AFF1	rs725030	86956139	G	A	0.2210680	-0.0429250	0.0074048	9.60E-09
4	AFF1	rs61586576	86960226	A	G	0.2213670	-0.0435448	0.0073950	3.40E-09
4	AFF1	rs7693889	86964249	A	G	0.2158220	-0.0439352	0.0075016	3.80E-09
4	AFF1	rs7693780	86964364	T	C	0.2184140	-0.0431283	0.0074424	5.80E-09
4	AFF1	rs2869632	86967298	T	C	0.2200870	-0.0438889	0.0074065	2.90E-09
4	AFF1	rs2904151	86967515	T	C	0.2201370	-0.0438604	0.0074046	2.80E-09
4	AFF1	chr4:86969153_AT_A	86969153	A	AT	0.2224610	-0.0426802	0.0073639	6.10E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
4	AFF1	rs28522052	86970635	T	A	0.2226410	-0.0423227	0.0073586	8.30E-09
4	AFF1	rs28396892	87016728	T	C	0.2202390	-0.0415365	0.0073748	1.80E-08
4	AFF1	rs3775230	87051057	C	G	0.2203290	-0.0408137	0.0073776	3.10E-08
4	AFF1	rs386485	87051896	C	T	0.2203170	-0.0407566	0.0073776	3.20E-08
4	AFF1	rs7660883	87061724	G	C	0.4070940	-0.0427497	0.0062103	6.60E-13
4	AFF1	rs10597574	87061855	A	ATG	0.4071360	-0.0431755	0.0062112	3.90E-13
4	AFF1	rs3035539	87062748	C	CAT	0.4071450	-0.0435027	0.0062116	2.70E-13
4	AFF1	rs28432336	87063179	G	A	0.4075330	-0.0435780	0.0062155	2.50E-13
4	AFF1	rs11946481	87063458	T	C	0.4073670	-0.0431920	0.0062134	3.90E-13
4	AFF1	rs3775228	87064014	T	C	0.4043740	0.0420568	0.0062468	1.50E-12
4	AFF1	rs17668131	87064378	T	G	0.4059650	0.0424634	0.0062393	9.60E-13
4	AFF1	rs72877984	87064569	A	G	0.4071420	-0.0433386	0.0062123	3.30E-13
4	AFF1	rs10018904	87065054	C	G	0.4060890	0.0422605	0.0062406	1.20E-12
4	AFF1	rs28677145	87065229	A	G	0.4070720	-0.0439798	0.0062279	1.50E-13
4	AFF1	rs13120301	87065243	T	C	0.4059980	0.0425163	0.0062419	9.00E-13
4	AFF1	rs236679	87065449	C	A	0.4057900	0.0414969	0.0062469	3.50E-12
4	AFF1	rs236681	87067356	G	T	0.4077020	0.0431249	0.0062333	5.10E-13
4	AFF1	rs2280952	87067388	C	T	0.4058700	0.0427585	0.0062332	6.90E-13
4	AFF1	rs2280953	87067438	T	C	0.4054210	0.0427164	0.0062348	7.50E-13
4	AFF1	rs2280954	87067710	G	A	0.4054940	0.0424583	0.0062354	1.00E-12
4	AFF1	rs3775226	87068313	A	G	0.4028840	0.0420880	0.0062535	1.50E-12
4	AFF1	rs11097127	87069182	T	G	0.4071290	-0.0439161	0.0062296	1.80E-13
4	AFF1	rs11461770	87069713	CA	C	0.4091170	-0.0438070	0.0062280	1.80E-13
4	AFF1	rs3736668	87071058	C	T	0.4038210	0.0423020	0.0062438	1.20E-12
4	AFF1	rs3736669	87071601	A	G	0.4132980	-0.0459333	0.0062238	1.50E-14
4	AFF1	rs17012368	87074967	G	T	0.4151380	-0.0462579	0.0062206	1.40E-14
4	AFF1	rs2125787	87075471	G	A	0.4157020	-0.0461679	0.0062093	1.30E-14
4	AFF1	rs17605615	87075593	A	G	0.3960070	0.0449168	0.0062536	6.20E-14
4	AFF1	rs11408312	87076256	CT	C	0.4162570	-0.0460753	0.0061935	1.30E-14
4	AFF1	rs9998251	87077903	A	G	0.4145590	-0.0467762	0.0062003	5.40E-15
4	AFF1	rs236995	87079271	G	C	0.4158420	-0.0464523	0.0061923	7.20E-15
4	AFF1	rs3775223	87079294	T	A	0.4145650	-0.0467928	0.0062002	5.30E-15
4	AFF1	rs3836602	87083662	ATT	A	0.4150510	-0.0465188	0.0061998	7.80E-15
4	AFF1	rs236996	87084051	A	G	0.4163760	-0.0463830	0.0061901	8.90E-15
4	AFF1	rs151451	87085215	T	C	0.3954310	0.0442345	0.0062523	1.40E-13
4	AFF1	rs4693156	87086075	C	T	0.4150500	-0.0464178	0.0062000	8.70E-15
4	AFF1	rs236984	87087462	A	G	0.4163150	-0.0460480	0.0061924	1.20E-14
4	AFF1	rs236985	87087630	A	G	0.4162910	-0.0460680	0.0061927	1.10E-14
4	AFF1	rs3836601	87087885	C	CATT	0.4150230	-0.0464197	0.0062006	8.30E-15
4	AFF1	rs236676	87088468	A	G	0.3955600	0.0443130	0.0062510	1.30E-13
4	AFF1	chr4:87088605_AT_A	87088605	A	AT	0.4132850	-0.0466911	0.0062116	1.00E-14
4	AFF1	rs236987	87088627	T	C	0.4157510	-0.0460214	0.0061985	1.30E-14
4	AFF1	rs3775221	87090641	G	T	0.4150530	-0.0464188	0.0062009	8.20E-15
4	AFF1	rs2045592	87093194	G	C	0.4145830	-0.0463890	0.0062052	8.60E-15
4	AFF1	rs3775220	87093601	G	A	0.4147710	-0.0461575	0.0062029	1.10E-14
4	AFF1	rs151450	87095362	A	G	0.3964530	0.0447821	0.0062484	6.20E-14
4	AFF1	rs236992	87095587	A	G	0.4156510	-0.0459714	0.0061956	1.20E-14
4	AFF1	rs236993	87095722	G	T	0.4155640	-0.0460608	0.0061953	1.10E-14
4	AFF1	rs342452	87097256	A	G	0.4155370	-0.0462584	0.0061948	8.20E-15
4	AFF1	rs342453	87097337	C	G	0.4156220	-0.0461643	0.0061953	9.60E-15
4	AFF1	rs2035403	87097839	G	A	0.3966710	0.0450024	0.0062487	4.40E-14
4	AFF1	rs3775217	87098315	G	A	0.4143510	-0.0465967	0.0062039	6.20E-15
4	AFF1	rs342454	87100348	T	A	0.4155320	-0.0461931	0.0061987	9.30E-15
4	AFF1	rs60695258	87101557	T	C	0.3970880	0.0445375	0.0062913	9.10E-14
4	AFF1	rs3836600	87102076	A	AT	0.4153250	-0.0462321	0.0061989	8.40E-15
4	AFF1	rs3775214	87102147	G	A	0.4153220	-0.0462349	0.0061989	8.30E-15
4	AFF1	rs342456	87102718	T	C	0.4135000	-0.0460499	0.0062023	1.10E-14
4	AFF1	rs3755985	87103586	G	A	0.3994420	0.0447309	0.0062444	4.60E-14
4	AFF1	rs1674999	87106498	G	A	0.4137840	-0.0464436	0.0061999	6.70E-15
4	AFF1	rs3841987	87107093	A	AG	0.4138360	-0.0464162	0.0061993	6.90E-15
4	AFF1	rs3733377	87108330	G	C	0.3991100	0.0444890	0.0062453	7.10E-14
4	AFF1	rs442177	87109109	G	T	0.4139100	-0.0472712	0.0061953	2.00E-15
4	AFF1	rs75921854	87110944	A	T	0.3998420	0.0438269	0.0062561	2.30E-13
4	AFF1	rs7440770	87111645	A	C	0.1940100	-0.0419387	0.0077418	3.50E-08
4	AFF1	rs3755983	87116640	A	G	0.3988900	0.0458986	0.0062760	2.20E-14
4	AFF1	rs3836599	87117848	T	TC	0.4154090	-0.0483058	0.0062037	8.40E-16
4	AFF1	rs3775211	87117939	C	T	0.3989360	0.0458379	0.0062763	2.30E-14
4	AFF1	rs2307789	87118309	C	CAT	0.4154040	-0.0482916	0.0062036	8.40E-16
4	AFF1	rs11280827	87119033	T	CCAGC	0.4159960	-0.0482195	0.0062094	1.10E-15
4	AFF1	rs342438	87119254	A	G	0.4153860	-0.0482466	0.0062013	8.90E-16
4	AFF1	rs342437	87119757	A	G	0.4151120	-0.0481259	0.0061999	9.70E-16
4	AFF1	rs2307788	87121026	CAG	C	0.4151040	-0.0482326	0.0062051	8.80E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
4	AFF1	rs3755980	87121099	T	C	0.3980350	0.0458740	0.0062846	2.60E-14
4	AFF1	rs342435	87122054	G	A	0.4157350	-0.0480260	0.0062006	1.30E-15
4	AFF1	rs16930	87122793	G	A	0.4170900	-0.0472845	0.0062133	3.40E-15
4	AFF1	rs3775209	87125794	A	G	0.3986780	0.0457876	0.0062700	2.00E-14
4	AFF1	rs1037814	87128698	T	C	0.4142970	-0.0488221	0.0061945	3.40E-16
4	AFF1	rs342469	87129402	G	A	0.4142340	-0.0488734	0.0061959	3.50E-16
4	AFF1	rs342468	87130756	G	A	0.4142680	-0.0486089	0.0061962	4.80E-16
4	AFF1	rs342467	87131067	T	C	0.4142680	-0.0486089	0.0061962	4.80E-16
4	AFF1	rs342466	87131933	C	T	0.4142550	-0.0486315	0.0061970	4.70E-16
4	AFF1	chr4:87135567_GT_G	87135567	GT	G	0.4140610	-0.0490707	0.0061993	2.80E-16
4	AFF1	rs1408	87136201	G	A	0.4140820	-0.0487505	0.0062004	5.20E-16
4	AFF1	rs3755979	87137188	G	C	0.1937210	-0.0430984	0.0077309	2.00E-08
4	AFF1	rs3841986	87137491	CT	C	0.4020930	0.0473785	0.0062718	4.80E-15
4	AFF1	rs10029915	87138465	C	G	0.4020830	0.0476086	0.0062749	3.60E-15
4	AFF1	rs1842685	87139680	C	T	0.4038920	0.0468681	0.0062892	1.10E-14
4	AFF1	chr4:87140472_ATATAT_A	87140472	ATATAA	A	0.4145480	-0.0511148	0.0062391	2.90E-17
4	AFF1 *	rs2926511	87141459	A	G	0.4122070	-0.0502805	0.0062222	9.60E-17
4	AFF1 *	rs66477840	87142207	A	G	0.4011450	0.0478648	0.0062895	3.30E-15
4	AFF1 *	rs10023050	87143279	G	A	0.4107570	-0.0511025	0.0062338	3.80E-17
4	AFF1 *	rs10023056	87143314	G	A	0.4030690	0.0481456	0.0062846	1.80E-15
4	AFF1 *	rs10032710	87145107	A	G	0.3873100	0.0478109	0.0063548	7.80E-15
4	AFF1 *	rs17012512	87146352	C	T	0.3895340	0.0468240	0.0063554	4.10E-14
4	AFF1 *	rs17012517	87149332	G	A	0.4551580	0.0413890	0.0062578	2.70E-12
4	KLHL8 *	rs28734493	87151541	T	A	0.4518200	0.0414144	0.0062587	2.40E-12
4	KLHL8 *	chr4:87152570_C_CA	87152570	CA	C	0.4517650	0.0417487	0.0062586	1.80E-12
4	KLHL8 *	rs6841004	87154409	C	T	0.3909520	-0.0342002	0.0063295	5.20E-09
4	KLHL8 *	rs28882732	87154824	G	A	0.4492790	0.0412681	0.0062829	3.10E-12
4	KLHL8 *	rs55747890	87155474	G	A	0.3620290	0.0459194	0.0064729	9.30E-14
4	KLHL8 *	rs7437661	87156860	C	A	0.4518720	0.0410148	0.0062573	3.80E-12
4	KLHL8 *	rs1021104	87157017	A	G	0.4518750	0.0410309	0.0062572	3.70E-12
4	KLHL8 *	rs28670747	87157327	G	C	0.4518580	0.0409938	0.0062572	3.80E-12
4	KLHL8 *	rs111686783	87158018	A	G	0.4508140	0.0410221	0.0062673	4.70E-12
4	KLHL8 *	rs1481947	87159990	T	C	0.4509590	0.0409120	0.0062573	4.60E-12
4	KLHL8	rs3209390	87161300	C	T	0.4689410	0.0416767	0.0062405	1.30E-12
4	KLHL8	rs3193672	87161955	C	T	0.4509590	0.0405272	0.0062510	6.10E-12
4	KLHL8	rs10000784	87166331	G	A	0.4678100	0.0381511	0.0062367	6.70E-11
4	KLHL8	rs28505236	87172309	G	C	0.4499890	0.0365867	0.0062556	3.70E-10
4	KLHL8	rs1552144	87173498	T	C	0.4503790	0.0364211	0.0062534	4.90E-10
4	KLHL8	rs7698284	87181456	C	T	0.3873810	-0.0324584	0.0063027	1.80E-08
4	KLHL8	rs7698923	87181815	C	T	0.3873770	-0.0324623	0.0063026	1.80E-08
4	KLHL8	rs66527077	87188846	A	G	0.4675830	0.0376651	0.0062438	1.10E-10
4	KLHL8	rs11946293	87191788	A	C	0.4678970	0.0380636	0.0062350	7.30E-11
4	KLHL8	rs4577539	87202806	G	T	0.4680140	0.0385316	0.0062334	4.80E-11
4	KLHL8	rs10025704	87207192	A	G	0.4681500	0.0386197	0.0062331	4.40E-11
4	KLHL8	rs12649293	87207953	T	C	0.3871950	-0.0326993	0.0063006	1.60E-08
4	KLHL8 *	rs35624376	87237936	C	T	0.4495510	0.0346267	0.0062057	6.80E-09
4	KLHL8 *	rs35844368	87238219	T	C	0.4479800	0.0348440	0.0062073	7.00E-09
4	KLHL8 *	rs13137873	87238277	T	C	0.4483580	0.0344907	0.0062013	8.90E-09
4	KLHL8 *	rs13113529	87238292	C	T	0.4483580	0.0344889	0.0062013	9.00E-09
4	KLHL8 *	rs10006766	87238866	G	A	0.4484340	0.0344624	0.0061999	9.60E-09
4	KLHL8 *	rs10029254	87238988	T	C	0.4484530	0.0344329	0.0061998	9.90E-09
4	KLHL8 *	rs71660125	87246258	G	GTTT	0.4403070	0.0350282	0.0062575	7.00E-09
4	KLHL8 *	rs35469118	87247026	T	C	0.3556450	0.0395106	0.0065024	5.20E-10
4	KLHL8 *	rs7656630	87252540	C	T	0.4509500	0.0342474	0.0061880	9.80E-09
4	KLHL8 *	rs9997582	87260377	G	A	0.3908050	0.0327236	0.0062642	4.60E-08
4	MIR5705 *	rs28419230	87275167	T	G	0.3853760	0.0332213	0.0062942	4.00E-08
5	ANKRD55 *	rs16885581	56500345	G	A	0.1354930	-0.0494280	0.0089727	9.40E-09
5	ANKRD55 *	rs6881312	56500733	T	G	0.2873790	0.0385112	0.0067612	4.50E-09
5	ANKRD55 *	rs73132727	56502276	G	C	0.2896060	0.0395817	0.0067328	1.40E-09
5	ANKRD55 *	rs73132728	56504012	G	A	0.2907050	0.0392538	0.0067188	1.60E-09
5	ANKRD55 *	rs60762814	56504882	T	C	0.2896130	0.0395558	0.0067325	1.40E-09
5	ANKRD55 *	rs73132731	56505331	G	A	0.2907170	0.0391861	0.0067187	1.60E-09
5	ANKRD55 *	rs73132735	56505759	T	A	0.2899830	0.0393244	0.0067372	1.80E-09
5	ANKRD55 *	rs56198135	56507151	A	G	0.2847000	0.0362466	0.0067736	2.50E-08
5	ANKRD55 *	rs16885608	56510081	T	G	0.2903670	0.0393987	0.0067187	1.40E-09
5	ANKRD55 *	rs459193	56510924	A	G	0.4700660	-0.0563254	0.0061153	3.10E-21
5	LOC101928 *	rs464605	56511543	C	T	0.4703400	-0.0567644	0.0061186	1.50E-21
5	LOC101928 *	rs157507	56512451	T	C	0.3304820	-0.0379348	0.0064946	2.70E-09
5	LOC101928 *	rs392794	56512515	C	T	0.4702220	-0.0569062	0.0061201	1.10E-21
5	LOC101928 *	rs465002	56512648	C	T	0.4702200	-0.0569378	0.0061202	1.00E-21
5	LOC101928 *	rs157510	56513139	C	A	0.3304220	-0.0378718	0.0064936	2.90E-09
5	LOC101928 *	rs157512	56513300	C	T	0.4354450	-0.0514200	0.0061686	5.20E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	LOC101928	rs256903	56513311	C	A	0.4695110	-0.0570983	0.0061259	8.90E-22
5	LOC101928	rs173964	56513638	A	G	0.4692570	-0.0571918	0.0061272	8.20E-22
5	LOC101928	rs256904	56514478	A	T	0.4698010	-0.0568587	0.0061276	1.60E-21
5	LOC101928	rs245142	56514622	A	G	0.3301230	-0.0377437	0.0064938	3.50E-09
5	LOC101928	rs456867	56515265	T	C	0.3302240	-0.0376542	0.0064904	3.90E-09
5	LOC101928	rs459447	56515514	A	G	0.3289700	-0.0371360	0.0065016	6.30E-09
5	LOC101928	rs465983	56516303	G	A	0.4385550	-0.0505653	0.0061726	2.20E-17
5	LOC101928	rs61142999	56516795	A	G	0.2830220	0.0380131	0.0067975	4.40E-09
5	LOC101928	rs405176	56517885	G	A	0.3691960	-0.0387578	0.0063481	6.10E-10
5	LOC101928	rs60202005	56518728	T	C	0.2847520	0.0380299	0.0067822	4.40E-09
5	LOC101928	rs56411612	56519256	T	G	0.2847910	0.0380903	0.0067829	4.20E-09
5	LOC101928	rs455660	56521061	T	C	0.3811160	-0.0405551	0.0062877	3.10E-11
5	LOC101928	rs76721602	56522121	A	C	0.2822680	0.0381921	0.0068974	5.00E-09
5	LOC101928	rs76878791	56522574	G	A	0.2825340	0.0379882	0.0069249	8.10E-09
5	TNFAIP8	rs5870855	119377761	AT	A	0.1586610	-0.0504033	0.0083988	1.30E-09
5	TNFAIP8	rs59406275	119379517	A	G	0.0382019	-0.0920108	0.0159892	1.80E-08
5	TNFAIP8	rs140403040	119381339	G	A	0.0378878	-0.0895340	0.0160428	3.70E-08
5	TNFAIP8	rs12332329	119385999	A	G	0.1446020	-0.0491202	0.0086970	6.00E-09
5	TNFAIP8	rs6595187	119387914	G	A	0.1597430	-0.0491957	0.0083522	2.30E-09
5	TNFAIP8	rs9764678	119390967	C	T	0.1589430	-0.0489676	0.0083660	2.90E-09
5	TNFAIP8	rs7720409	119392561	A	G	0.1575000	-0.0488061	0.0083820	3.70E-09
5	TNFAIP8	rs3203922	119393258	C	G	0.1575100	-0.0487134	0.0083815	3.90E-09
5	TNFAIP8	rs1045241	119393591	T	C	0.1576250	-0.0490377	0.0083769	3.50E-09
5	TNFAIP8	rs1045242	119393632	G	A	0.1576770	-0.0489642	0.0083847	3.30E-09
5	TNFAIP8 *	rs7703744	119396492	G	C	0.1525460	-0.0474189	0.0085224	1.20E-08
5	TNFAIP8 *	rs56017758	119404998	A	G	0.1485430	-0.0469749	0.0086565	3.10E-08
5	TIMD4 *	rs6882076	156963286	T	C	0.2719570	-0.0423813	0.0068811	1.10E-10
5	TIMD4 *	rs6874202	156964617	T	C	0.2718760	-0.0422743	0.0068838	1.30E-10
5	TIMD4 *	rs4704826	156965071	C	A	0.2719470	-0.0422539	0.0068841	1.30E-10
5	TIMD4 *	rs4704827	156965078	T	C	0.2718740	-0.0422780	0.0068838	1.30E-10
5	TIMD4 *	rs12517431	156965237	C	T	0.2718600	-0.0423621	0.0068841	1.20E-10
5	TIMD4 *	rs28735189	156967082	C	T	0.2712150	-0.0426302	0.0069090	1.10E-10
5	TIMD4 *	rs9715911	156967430	G	A	0.2711700	-0.0427093	0.0069109	1.00E-10
5	TIMD4 *	rs11745603	156967507	C	T	0.2711620	-0.0427448	0.0069111	1.00E-10
5	TIMD4 *	rs12657266	156968992	C	T	0.2708550	-0.0425644	0.0069235	1.30E-10
5	TIMD4 *	rs1393207	156970529	T	A	0.2706940	-0.0430673	0.0069289	8.00E-11
5	TIMD4 *	rs6882345	156970662	G	A	0.2706920	-0.0430102	0.0069287	8.60E-11
5	TIMD4 *	rs58198139	156972028	C	T	0.2706720	-0.0431463	0.0069318	7.90E-11
5	TIMD4 *	rs11134475	156972939	A	G	0.2706460	-0.0431082	0.0069342	8.20E-11
5	TIMD4 *	rs28722027	156973514	T	C	0.2642390	-0.0425908	0.0069889	2.50E-10
5	TIMD4 *	rs6891318	156973733	C	A	0.2643350	-0.0425547	0.0069892	2.60E-10
5	TIMD4 *	rs55776147	156973797	A	G	0.2710460	-0.0426200	0.0069357	1.40E-10
5	TIMD4 *	rs7702004	156974719	C	T	0.2625870	-0.0423114	0.0070133	4.00E-10
5	TIMD4 *	rs10055656	156977360	C	T	0.2591530	-0.0415422	0.0070395	9.80E-10
5	TIMD4 *	rs28575973	156977576	A	C	0.2590130	-0.0414133	0.0070417	1.10E-09
5	HAVCR1 *	rs4704834	157016055	A	G	0.2623740	-0.0406440	0.0069626	7.10E-10
5	HAVCR1 *	rs6866758	157028101	T	C	0.2556410	-0.0401524	0.0070229	2.10E-09
5	HAVCR1	rs3842063	157033162	T	TA	0.2561280	-0.0401129	0.0070203	2.60E-09
6	GABBR1	rs150971595	29632584	T	C	0.0955067	-0.0608703	0.0110861	2.90E-08
6	MOG *	rs9380134	29653999	C	G	0.1121420	-0.0615152	0.0102876	1.70E-09
6	HLA-F *	rs75791723	29756751	T	C	0.1093050	-0.0666765	0.0104346	1.60E-10
6	HCG4 *	rs9368611	29772040	C	A	0.1055950	-0.0663635	0.0106225	2.20E-10
6	ZNRD1-AS1	rs9380151	30052051	C	T	0.1108570	-0.0668487	0.0103521	7.90E-11
6	TRIM40 *	rs9393991	30134864	A	G	0.1122430	-0.0689366	0.0103012	3.70E-11
6	TRIM26	rs117565607	30204594	A	T	0.1113180	-0.0698998	0.0103706	4.10E-11
6	HCG17	rs62407543	30243396	A	G	0.3442650	-0.0375691	0.0069213	2.20E-08
6	HCG17	rs72841870	30246234	C	G	0.3343580	-0.0383729	0.0069706	1.90E-08
6	HCG17	rs9391803	30247600	A	T	0.3349360	-0.0384423	0.0069577	1.70E-08
6	HCG17	rs77916299	30253390	A	AT	0.3342980	-0.0393024	0.0069746	8.60E-09
6	HCG17	rs9405046	30254114	C	G	0.3361730	-0.0384947	0.0069690	2.10E-08
6	HCG17	rs2516715	30258388	C	G	0.4791130	-0.0366834	0.0066380	3.70E-08
6	HCG17	rs2516714	30258527	G	A	0.4791360	-0.0366946	0.0066385	3.80E-08
6	HCG17, HL	rs2516708	30260944	A	G	0.4791260	-0.0367486	0.0066376	3.60E-08
6	HCG17, HL	rs2428507	30261529	G	A	0.4791150	-0.0365520	0.0066420	4.50E-08
6	HCG17, HL	rs2428506	30261991	C	A	0.4791470	-0.0366709	0.0066377	3.90E-08
6	HCG17, HL	rs2844766	30262884	C	T	0.4791800	-0.0365236	0.0066379	4.40E-08
6	HCG17, HL	rs2844764	30266891	A	T	0.4772710	-0.0362648	0.0066161	4.70E-08
6	HCG17	rs2516696	30267269	T	G	0.4790420	-0.0363117	0.0066377	4.90E-08
6	HCG17	rs2844762	30268977	C	T	0.4790350	-0.0363098	0.0066377	4.90E-08
6	HCG17	rs2844760	30270084	C	T	0.4789050	-0.0364343	0.0066386	4.40E-08
6	HCG17	rs28751303	30270674	CA	C	0.4789840	-0.0364574	0.0066381	4.30E-08
6	HCG17	rs2844759	30271107	G	A	0.4788800	-0.0363593	0.0066398	4.90E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	HCG17	rs968909	30276802	T	C	0.4789590	-0.0363363	0.0066383	4.60E-08
6	HCG17	rs2097574	30276934	A	C	0.4789920	-0.0364023	0.0066381	4.50E-08
6	HCG17	rs2844755	30277724	A	T	0.4785350	-0.0370300	0.0066429	2.70E-08
6	HCG17	rs28751305	30278729	TTTTC	T	0.4786290	-0.0362969	0.0066386	4.70E-08
6	HCG17	rs1075105	30283609	G	C	0.4789980	-0.0364141	0.0066382	4.50E-08
6	HCG17	rs1264626	30285234	C	T	0.4789820	-0.0364100	0.0066384	4.50E-08
6	HCG17, HCG17	rs117416277	30288213	C	T	0.1117760	-0.0687409	0.0103722	9.40E-11
6	HCG17, HCG17	rs28383816	30291527	TCAAA	T	0.4793060	-0.0377114	0.0066500	1.50E-08
6	HCG17, HCG17	rs28360018	30291528	C	T	0.4788490	-0.0364875	0.0066401	4.00E-08
6	HCG17, HCG17	rs1264619	30292242	C	G	0.4813530	-0.0372440	0.0066383	2.30E-08
6	HCG17, HCG17	rs3214075	30294198	AC	A	0.4790220	-0.0363928	0.0066387	4.30E-08
6	HCG17, HCG17	rs1264618	30295292	G	C	0.4790180	-0.0363889	0.0066387	4.40E-08
6	HCG17, HCG17	rs1264617	30295353	G	A	0.4790180	-0.0363889	0.0066387	4.40E-08
6	HCG17, HCG17	rs9357097	30317344	T	C	0.4031040	-0.0357666	0.0067334	3.70E-08
6	RPP21 *	rs9391681	30383227	C	T	0.1095530	-0.0660962	0.0105116	5.40E-10
6	ABCF1 *	rs9380181	30595202	T	A	0.1165200	-0.0594432	0.0101879	1.40E-08
6	PPP1R10	rs9348841	30610096	C	T	0.1140000	-0.0569751	0.0102342	4.00E-08
6	ATAT1	rs143128695	30635406	G	A	0.1152230	-0.0609955	0.0102491	7.00E-09
6	DHX16 *	rs151195028	30673581	C	G	0.1153270	-0.0589007	0.0102401	2.20E-08
6	FLOT1	rs9380182	30735848	C	A	0.1136090	-0.0577907	0.0102823	2.50E-08
6	IER3 *	rs9391634	30807802	G	C	0.1104370	-0.0628530	0.0104430	3.50E-09
6	DDR1 *	rs9391636	30904155	A	T	0.3422060	-0.0370200	0.0068224	3.90E-08
6	MUC21	chr6:30984996_CAATAA_C	30984996	C	CAATAA/	0.4034100	-0.0378736	0.0065917	1.30E-08
6	MUC22	rs6457300	31030965	G	T	0.3268840	0.0460153	0.0067564	6.50E-12
6	MUC22	rs6457301	31031102	C	T	0.3267070	0.0460979	0.0067562	5.70E-12
6	MUC22	rs11330895	31031830	C	CA	0.2816340	0.0422513	0.0070611	2.50E-09
6	MUC22	rs10807077	31033690	G	A	0.3270250	0.0467072	0.0067572	3.40E-12
6	MUC22	rs10947124	31033719	T	G	0.3269450	0.0465541	0.0067566	3.90E-12
6	MUC22	rs11969581	31033729	T	A	0.2632990	0.0416627	0.0070647	3.00E-09
6	MUC22	rs11964623	31033742	T	C	0.2632990	0.0416627	0.0070647	3.00E-09
6	MUC22	rs10947125	31033856	G	A	0.3269600	0.0465743	0.0067564	3.80E-12
6	MUC22	rs10947126	31033891	A	G	0.3283420	0.0466162	0.0067178	3.20E-12
6	MUC22	rs28360042	31034004	T	C	0.3728190	0.0422591	0.0071246	1.20E-09
6	C6orf15 *	rs1265051	31112927	G	T	0.2844910	-0.0403721	0.0073398	2.30E-08
6	C6orf15 *	rs4486065	31112956	G	C	0.2841740	-0.0407153	0.0073420	1.90E-08
6	C6orf15 *	rs2233967	31113051	G	C	0.2828320	-0.0423580	0.0073590	4.90E-09
6	C6orf15 *	rs2233965	31113122	G	T	0.2826690	-0.0422870	0.0073595	5.50E-09
6	C6orf15 *	rs2233964	31113142	G	A	0.2841670	-0.0406842	0.0073404	2.10E-08
6	C6orf15 *	rs2233962	31113204	C	T	0.2841070	-0.0413173	0.0073510	1.40E-08
6	C6orf15 *	rs1265047	31113687	G	A	0.3979520	-0.0406659	0.0069736	1.50E-08
6	HLA-C *	rs2524096	31268690	T	G	0.4338230	-0.0368595	0.0067313	2.40E-09
6	HLA-C	rs2074493	31271999	C	A	0.3392880	0.0459562	0.0074442	2.10E-11
6	HLA-C *	rs2074489	31272351	T	C	0.3292300	0.0456384	0.0075860	4.20E-11
6	HLA-B *	rs9265525	31330131	T	C	0.2619350	0.0405430	0.0083355	4.80E-08
6	HLA-B *	rs9265552	31330519	G	C	0.2626380	0.0410919	0.0083011	3.40E-08
6	VEGFA *	rs117828773	43767240	T	C	0.0601868	-0.0716361	0.0131230	2.20E-08
6	VEGFA *	rs79469752	43770044	T	C	0.0591733	-0.0770211	0.0132349	2.60E-09
6	VEGFA *	rs3025053	43785588	A	G	0.1482260	-0.0508171	0.0087257	3.30E-09
6	VEGFA *	rs4711750	43789345	T	A	0.4371240	-0.0658674	0.0061517	1.50E-28
6	VEGFA *	rs998584	43790159	C	A	0.4436550	-0.0655152	0.0061494	3.50E-28
6	VEGFA *	rs6905288	43791136	G	A	0.2989990	-0.0689801	0.0066777	1.60E-25
6	VEGFA *	rs6458349	43792052	G	A	0.2140500	-0.0695762	0.0075488	1.90E-20
6	VEGFA *	rs11967262	43792590	C	G	0.4313330	-0.0660154	0.0061814	1.00E-28
6	VEGFA *	rs12204488	43796622	T	C	0.2604570	-0.0370007	0.0069843	9.60E-09
6	VEGFA *	rs1358980	43796814	C	T	0.4490970	-0.0634019	0.0061414	3.90E-27
6	VEGFA *	rs1885658	43797617	C	A	0.2653110	-0.0362071	0.0070631	2.50E-08
6	VEGFA *	rs1885659	43797796	A	G	0.1599440	-0.0609813	0.0085691	1.20E-13
6	VEGFA *	rs9349263	43819696	T	C	0.1982170	-0.0557319	0.0076400	2.00E-13
6	VEGFA *	rs9381252	43819948	T	C	0.1985070	-0.0552991	0.0076340	2.80E-13
6	VEGFA *	rs9367175	43820018	A	G	0.1978420	-0.0550964	0.0076463	3.40E-13
6	VEGFA *	rs10046267	43820246	A	G	0.1987370	-0.0547181	0.0076287	4.70E-13
6	VEGFA *	rs10046366	43820459	C	T	0.1981840	-0.0550695	0.0076408	3.30E-13
6	VEGFA *	rs12662985	43820460	A	G	0.1982050	-0.0547487	0.0076402	4.50E-13
6	VEGFA *	rs10046368	43820678	C	T	0.1989930	-0.0544043	0.0076248	5.60E-13
6	VEGFA *	rs57690032	43820817	A	G	0.1987350	-0.0548538	0.0076287	4.10E-13
6	VEGFA *	rs59297936	43820965	A	AG	0.1987350	-0.0548538	0.0076287	4.10E-13
6	VEGFA *	rs9381253	43821283	T	C	0.1779400	-0.0557711	0.0081023	3.20E-12
6	VEGFA *	rs9381254	43821523	T	C	0.1988990	-0.0549221	0.0076357	4.60E-13
6	VEGFA *	rs6458350	43821879	G	A	0.2016750	-0.0569979	0.0076043	3.90E-14
6	VEGFA *	rs10948098	43821944	G	T	0.2014870	-0.0566479	0.0076091	5.30E-14
6	VEGFA *	rs6910726	43822176	G	A	0.2001240	-0.0571251	0.0076475	3.10E-14
6	VEGFA *	rs2396083	43837071	G	C	0.2193260	-0.0489671	0.0073946	1.50E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	VEGFA *	rs2396084	43837088	A	G	0.2194120	-0.0494705	0.0073931	1.00E-11
6	VEGFA *	rs744103	43837625	T	A	0.2194640	-0.0487256	0.0073964	2.00E-11
6	VEGFA *	rs10223666	43837765	G	C	0.2197410	-0.0487361	0.0073862	1.60E-11
6	VEGFA *	rs3081073	43838578	C	CTAAG	0.2192210	-0.0484945	0.0073916	1.90E-11
6	VEGFA *	rs1317983	43838598	T	C	0.2190950	-0.0482676	0.0073899	2.40E-11
6	VEGFA *	rs881858	43838872	G	A	0.2202840	-0.0474652	0.0073748	3.80E-11
6	MCM9	rs141536065	118874622	A	G	0.2691220	0.0371879	0.0068995	4.30E-08
6	MCM9	rs199795700	118882830	TA	T	0.2736360	0.0380882	0.0068902	1.80E-08
6	LPA	rs9355291	160568256	C	T	0.4989080	-0.0385447	0.0062137	5.10E-11
6	LPA	rs13198987	160593075	C	T	0.4993950	-0.0386105	0.0061236	1.50E-11
6	LPA	rs34747443	160595634	C	CTT	0.4676460	0.0383626	0.0061562	1.80E-11
6	LPA	rs9355296	160596961	A	G	0.4690440	0.0390477	0.0061257	8.40E-12
6	LPA	rs35499210	160602459	T	G	0.4689610	0.0389392	0.0061247	9.00E-12
6	LPA	rs4063600	160658867	TAGG	T	0.4637100	-0.0328312	0.0061705	1.20E-08
6	LPA	rs1652507	160661429	C	T	0.4687740	0.0384359	0.0061310	1.60E-11
6	LPA	rs2315129	160664088	A	T	0.4722210	0.0377612	0.0061486	6.70E-11
6	LPA *	rs783149	160667886	A	C	0.4619460	0.0379042	0.0061598	7.10E-11
6	LPA *	rs1084651	160668785	A	G	0.4605540	0.0330185	0.0061194	7.10E-09
7	POM121	rs117135057	72938316	T	G	0.0119616	-0.1400060	0.0283134	4.00E-08
7	NSUN5	rs3750074	73308628	T	C	0.0159878	-0.1949590	0.0244827	5.40E-18
7	FKBP6 *	rs200456061	73371588	T	C	0.0159487	-0.1938770	0.0245092	7.00E-18
7	FKBP6 *	rs186391487	73384030	A	G	0.0158958	-0.1973920	0.0245583	2.60E-18
7	FZD9 *	rs42123	73425622	G	T	0.1094680	-0.1344770	0.0099233	8.70E-47
7	FZD9 *	rs42122	73427493	A	G	0.0923507	-0.1546720	0.0106060	5.60E-53
7	FZD9 *	chr7:73428127_GAC_G	73428127	G	GAC	0.0866614	-0.1558560	0.0109619	1.00E-50
7	FZD9 *	rs140439318	73428135	C	CAT	0.0872411	-0.1609010	0.0109372	1.10E-53
7	FZD9 *	chr7:73428147_GAC_G	73428147	G	GAC	0.0897899	-0.1588780	0.0107988	1.10E-53
7	FZD9 *	chr7:73428394_GAC_G	73428394	G	GAC	0.0926273	-0.1463900	0.0107930	2.60E-46
7	FZD9 *	rs200948285	73429969	AC	A	0.0118678	-0.1883340	0.0282848	3.60E-13
7	FZD9 *	rs200392099	73432411	CTTT	C	0.0866010	-0.1555260	0.0109077	5.60E-51
7	FZD9 *	rs868953856	73432413	T	A	0.0747612	-0.1620340	0.0117799	8.90E-47
7	FZD9 *	rs782289776	73432414	T	C	0.0747612	-0.1620340	0.0117799	8.90E-47
7	FZD9	rs138414411	73434563	T	C	0.0208891	-0.1556030	0.0214457	2.40E-13
7	FZD9	rs1178947	73435848	C	T	0.0905244	-0.1565730	0.0106763	6.60E-54
7	BAZ1B	rs2240466	73441939	A	G	0.0918021	-0.1552370	0.0105884	1.10E-53
7	BAZ1B	rs1178979	73442100	C	T	0.0912489	-0.1557540	0.0106189	8.30E-54
7	BAZ1B	rs1178977	73442719	G	A	0.0911918	-0.1555960	0.0106217	1.00E-53
7	BAZ1B	rs34604283	73443383	C	CA	0.0911937	-0.1559540	0.0106216	6.20E-54
7	BAZ1B	rs113452856	73444805	A	G	0.0212088	-0.1504760	0.0212931	8.20E-13
7	BAZ1B	rs2237280	73447452	T	C	0.3755640	0.0356987	0.0063108	2.00E-08
7	BAZ1B	rs146626977	73448166	C	T	0.0118921	-0.1866280	0.0282554	4.80E-13
7	BAZ1B	rs13231516	73448919	G	T	0.0960064	-0.1503080	0.0103768	1.10E-52
7	BAZ1B	rs2074756	73449425	C	T	0.0118991	-0.1848520	0.0282472	7.40E-13
7	BAZ1B	rs714052	73450539	G	A	0.0964079	-0.1484620	0.0103624	1.20E-51
7	BAZ1B	rs34763247	73452286	T	A	0.0959407	-0.1504890	0.0103800	9.20E-53
7	BAZ1B	rs1306476	73454192	G	A	0.0959430	-0.1504440	0.0103806	1.10E-52
7	BAZ1B	rs71071936	73455536	CT	C	0.0919121	-0.1549770	0.0105936	2.30E-53
7	BAZ1B	rs35330527	73455877	G	A	0.0974364	-0.1484580	0.0103258	1.00E-51
7	BAZ1B	rs60982449	73459090	G	A	0.0899536	-0.1573040	0.0106973	4.10E-54
7	BAZ1B	rs2074755	73462836	C	T	0.0952047	-0.1511650	0.0104179	6.20E-53
7	BAZ1B	rs35797675	73463714	G	T	0.0973973	-0.1487860	0.0103253	2.70E-52
7	BAZ1B	rs12056034	73464315	G	A	0.0965532	-0.1484050	0.0103573	1.30E-51
7	BAZ1B	rs71556715	73467477	T	C	0.0951887	-0.1515100	0.0104186	3.60E-53
7	BAZ1B	rs62465144	73468776	C	T	0.0958359	-0.1511710	0.0103881	4.00E-53
7	BAZ1B	rs6976930	73471480	A	G	0.0905663	-0.1572200	0.0106588	1.60E-54
7	BAZ1B	rs141027825	73471893	C	G	0.0138791	-0.1675410	0.0262963	2.60E-12
7	BAZ1B	rs73362331	73473247	G	A	0.3828310	0.0351786	0.0062903	3.30E-08
7	BAZ1B	rs139267697	73475356	A	G	0.0119036	-0.1849770	0.0282430	7.10E-13
7	BAZ1B	rs35695283	73479073	G	A	0.0910817	-0.1563000	0.0106294	4.60E-54
7	BAZ1B	rs75229905	73481616	C	T	0.0958362	-0.1507150	0.0103869	7.90E-53
7	BAZ1B	rs7797566	73482065	C	A	0.0958362	-0.1507150	0.0103869	7.90E-53
7	BAZ1B	rs17145713	73490480	T	C	0.0952329	-0.1513650	0.0104169	4.20E-53
7	BAZ1B	rs111837003	73493129	T	C	0.0904203	-0.1579080	0.0106664	7.30E-55
7	BAZ1B	rs118023175	73494447	G	C	0.0119361	-0.1844190	0.0282057	7.70E-13
7	BAZ1B	rs117830225	73494457	C	G	0.0119036	-0.1849800	0.0282430	7.10E-13
7	BAZ1B	rs13244268	73497513	C	T	0.0958675	-0.1509020	0.0104083	1.40E-52
7	BAZ1B	rs67243124	73497702	A	AAAAA	0.0948905	-0.1517840	0.0104359	2.90E-53
7	BAZ1B	rs201533187	73497710	A	AAAAG	0.0866181	-0.1459820	0.0109419	8.00E-45
7	BAZ1B	rs34482346	73501191	C	G	0.0951823	-0.1519230	0.0104192	2.00E-53
7	BAZ1B	chr7:73505631_GA_G	73505631	G	GA	0.0896774	-0.1523820	0.0108022	4.30E-50
7	BAZ1B	rs79862839	73507279	C	T	0.0951858	-0.1519550	0.0104192	2.00E-53
7	BAZ1B	rs13221253	73507903	G	A	0.0950761	-0.1514580	0.0104256	4.30E-53

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	BAZ1B	rs34437827	73509008	G	A	0.0951758	-0.1518950	0.0104199	2.10E-53
7	BAZ1B	rs7811265	73520180	G	A	0.0866574	-0.1549580	0.0109137	2.40E-50
7	BAZ1B *	rs62466264	73524388	C	T	0.0954151	-0.1516350	0.0104139	3.20E-53
7	BAZ1B *	rs11983997	73524914	C	G	0.0950717	-0.1516180	0.0104256	3.50E-53
7	BAZ1B *	rs80189144	73525609	C	T	0.0950717	-0.1516180	0.0104256	3.50E-53
7	BCL7B *	rs143934761	73533607	G	A	0.0208702	-0.1519710	0.0214378	5.80E-13
7	BCL7B *	rs4717094	73535752	T	C	0.4365580	0.0351508	0.0062056	9.30E-09
7	BCL7B	rs142030730	73542085	T	C	0.0129503	-0.1722710	0.0270856	1.40E-12
7	BCL7B	rs17145732	73555938	G	T	0.0992299	-0.1580860	0.0102346	9.30E-60
7	BCL7B	rs13233571	73556901	T	C	0.0952257	-0.1642270	0.0104135	5.00E-62
7	BCL7B	rs7793710	73557201	G	C	0.0951728	-0.1644970	0.0104182	3.60E-62
7	BCL7B	rs13234157	73557398	A	C	0.0942183	-0.1634690	0.0104983	1.50E-60
7	BCL7B *	rs13244614	73559524	A	C	0.0951556	-0.1645270	0.0104203	3.50E-62
7	BCL7B *	rs140173690	73560328	A	C	0.0171272	-0.1862640	0.0235755	1.90E-17
7	BCL7B *	rs111269058	73561372	T	C	0.0951639	-0.1645520	0.0104204	3.40E-62
7	BCL7B *	rs13225333	73561688	T	C	0.0951367	-0.1646610	0.0104212	3.00E-62
7	BCL7B *	rs13225347	73561718	T	C	0.0951610	-0.1645920	0.0104206	3.20E-62
7	BCL7B *	rs13225450	73561793	T	C	0.0950374	-0.1643370	0.0104278	4.40E-62
7	BCL7B *	rs34594435	73562919	T	C	0.0951646	-0.1645980	0.0104204	3.20E-62
7	BCL7B *	rs6946689	73563307	A	T	0.0952328	-0.1644830	0.0104205	4.00E-62
7	TBL2 *	rs12539316	73563568	G	A	0.0962465	-0.1628470	0.0103819	5.20E-61
7	TBL2 *	rs12539351	73563782	G	A	0.0903784	-0.1710940	0.0106690	6.70E-64
7	TBL2 *	rs147472118	73563984	T	C	0.0191380	-0.1836170	0.0222749	3.90E-16
7	TBL2 *	rs17145738	73568544	T	C	0.0953089	-0.1644760	0.0104113	3.50E-62
7	TBL2	rs13232120	73568980	T	A	0.0953194	-0.1644350	0.0104120	3.70E-62
7	TBL2	rs14415	73570450	C	T	0.0953194	-0.1644350	0.0104120	3.70E-62
7	TBL2	rs190174185	73572316	C	G	0.0114836	-0.1966160	0.0286869	4.50E-12
7	TBL2	rs2286276	73573024	T	C	0.0954318	-0.1638350	0.0104056	8.40E-62
7	TBL2	rs35659126	73573739	T	C	0.0950562	-0.1648950	0.0104252	2.30E-62
7	TBL2	chr7:73574811_C_CA	73574811	CA	C	0.0958121	-0.1652580	0.0104034	1.10E-62
7	TBL2	rs11974409	73575060	G	A	0.0951275	-0.1649010	0.0104243	2.10E-62
7	TBL2	rs12540011	73577374	A	G	0.0951950	-0.1652380	0.0104205	1.40E-62
7	TBL2	rs4717779	73577795	T	A	0.4361380	0.0367637	0.0062469	3.00E-09
7	TBL2	rs13246490	73578020	T	C	0.0951782	-0.1652430	0.0104213	1.40E-62
7	TBL2 *	rs66553475	73579219	TGCTG	T	0.0945522	-0.1649990	0.0104582	5.30E-62
7	TBL2 *	chr7:73581580_C_CA	73581580	CA	C	0.0833532	-0.1637430	0.0112181	9.80E-54
7	TBL2 *	rs66506038	73581613	C	T	0.0952092	-0.1649380	0.0104197	2.10E-62
7	TBL2 *	rs67644909	73581624	T	C	0.0938072	-0.1649620	0.0105027	1.60E-61
7	TBL2 *	rs9638180	73584622	G	A	0.0952452	-0.1653540	0.0104201	1.20E-62
7	TBL2 *	rs9638181	73584713	G	A	0.0952452	-0.1653540	0.0104201	1.20E-62
7	TBL2 *	rs9638182	73584775	G	T	0.0952452	-0.1653540	0.0104201	1.20E-62
7	MLXIPL *	rs35173225	73586691	T	C	0.0952828	-0.1652250	0.0104223	1.60E-62
7	MLXIPL *	rs187404224	73588697	G	A	0.0951811	-0.1652280	0.0104212	1.50E-62
7	MLXIPL *	rs185081604	73588973	C	A	0.0951811	-0.1652280	0.0104212	1.50E-62
7	MLXIPL *	rs145099458	73589985	T	C	0.0906915	-0.1632700	0.0106998	4.90E-58
7	MLXIPL *	rs35866503	73591446	T	C	0.0951804	-0.1652380	0.0104212	1.40E-62
7	MLXIPL *	rs13225660	73592058	T	C	0.0951804	-0.1652380	0.0104212	1.40E-62
7	MLXIPL *	chr7:73592757_C_CA	73592757	CA	C	0.0883063	-0.1661940	0.0108654	8.30E-59
7	MLXIPL	rs1051921	73593613	A	G	0.0951804	-0.1652330	0.0104212	1.40E-62
7	MLXIPL	rs13247874	73596112	T	C	0.0970791	-0.1666660	0.0103371	1.90E-64
7	MLXIPL	rs35332062	73597712	A	G	0.0978721	-0.1674580	0.0102929	1.30E-65
7	MLXIPL	rs79624003	73598455	G	A	0.0977861	-0.1684300	0.0103004	3.20E-66
7	MLXIPL	rs35732917	73598939	C	T	0.0976836	-0.1690680	0.0103073	1.30E-66
7	MLXIPL	rs13235543	73599571	T	C	0.0976132	-0.1689360	0.0103097	1.80E-66
7	MLXIPL	rs13240065	73601039	A	G	0.0965814	-0.1683120	0.0103766	3.80E-65
7	MLXIPL	rs34346326	73601851	C	T	0.0974302	-0.1687050	0.0103224	3.40E-66
7	MLXIPL	rs879969597	73602094	G	GCCTT	0.0105450	-0.1977600	0.0305103	6.20E-11
7	MLXIPL	rs13240994	73602532	C	T	0.0881399	-0.1825260	0.0108456	1.20E-69
7	MLXIPL	rs13226650	73602675	G	A	0.0975521	-0.1679940	0.0103230	1.20E-65
7	MLXIPL	rs35368205	73603327	T	C	0.0884161	-0.1824570	0.0107731	1.10E-70
7	MLXIPL	rs34166762	73604194	C	T	0.0889194	-0.1896170	0.0107690	1.10E-75
7	MLXIPL	rs61010704	73605645	G	A	0.0862610	-0.1942970	0.0108899	1.10E-77
7	MLXIPL	rs3812316	73606007	G	C	0.0862707	-0.1948320	0.0108875	4.30E-78
7	MLXIPL	rs6968170	73606346	A	G	0.0863087	-0.1944960	0.0108849	7.30E-78
7	MLXIPL	rs77048596	73607881	A	G	0.0862974	-0.1946790	0.0108866	5.70E-78
7	MLXIPL	rs13246993	73608416	A	G	0.0862982	-0.1946800	0.0108868	5.70E-78
7	MLXIPL	rs141854486	73608603	A	AAG	0.0780702	-0.1929120	0.0114728	4.50E-70
7	MLXIPL	rs12531645	73609551	A	G	0.0862235	-0.1945780	0.0108912	7.40E-78
7	MLXIPL	rs35512732	73610432	T	TC	0.0862989	-0.1946930	0.0108870	5.50E-78
7	MLXIPL	rs13234131	73611645	G	A	0.0994143	-0.1776540	0.0101974	6.00E-73
7	MLXIPL	rs13234378	73611821	T	A	0.0998899	-0.1771550	0.0101859	7.80E-73
7	MLXIPL	rs17145750	73612048	T	C	0.0997845	-0.1780870	0.0101808	1.70E-73

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	MLXIPL	rs7808877	73613120	G	C	0.0996159	-0.1776120	0.0101902	5.60E-73
7	MLXIPL	rs139002804	73613553	A	G	0.0116548	-0.1852260	0.0285805	1.10E-12
7	MLXIPL	rs33951980	73615107	T	C	0.0996174	-0.1776060	0.0101902	5.70E-73
7	MLXIPL	rs2074768	73615773	C	A	0.0996101	-0.1775440	0.0101909	5.90E-73
7	MLXIPL	rs13229619	73615845	A	G	0.0996101	-0.1775440	0.0101909	5.90E-73
7	MLXIPL	rs7798357	73617935	C	G	0.0995572	-0.1777780	0.0101949	4.10E-73
7	MLXIPL	rs7785479	73618505	C	T	0.0995565	-0.1778330	0.0101950	3.70E-73
7	MLXIPL	rs34062580	73619229	A	G	0.0995564	-0.1778340	0.0101952	3.70E-73
7	MLXIPL	rs6975495	73619700	G	A	0.0995564	-0.1778950	0.0101955	3.40E-73
7	MLXIPL	rs71556736	73620599	T	C	0.0996238	-0.1780920	0.0101920	2.60E-73
7	MLXIPL	rs7800944	73621527	C	T	0.0999739	-0.1757960	0.0101810	1.30E-71
7	MLXIPL	rs1207541622	73621799	C	T	0.0120313	-0.2044690	0.0283966	2.80E-14
7	MLXIPL	rs2736909	73621803	G	C	0.0120313	-0.2044690	0.0283966	2.80E-14
7	MLXIPL	rs55747707	73623036	A	G	0.0995221	-0.1784390	0.0102009	1.50E-73
7	MLXIPL	rs34060476	73623626	G	A	0.0994966	-0.1783000	0.0102027	1.70E-73
7	MLXIPL *	rs35493868	73625076	G	C	0.0994995	-0.1784870	0.0102035	1.20E-73
7	MLXIPL *	rs34121855	73626484	G	T	0.0974460	-0.1784600	0.0103175	1.70E-72
7	MLXIPL *	rs62466318	73627755	T	C	0.1078720	-0.1636290	0.0098451	1.40E-66
7	MLXIPL *	chr7:73627972_GCTTT_G	73627972	G	GCTTT	0.1081470	-0.1623620	0.0098411	1.30E-65
7	MLXIPL *	rs117739002	73628073	T	C	0.0177306	-0.1775010	0.0231589	5.00E-14
7	MLXIPL *	rs6460047	73628113	C	T	0.1093710	-0.1609840	0.0097982	8.40E-65
7	MLXIPL *	rs7805504	73628255	C	T	0.1092620	-0.1609720	0.0098016	9.40E-65
7	MLXIPL *	rs7786376	73628284	G	A	0.1105800	-0.1602160	0.0097556	8.90E-65
7	MLXIPL *	rs35340690	73628738	C	G	0.1520990	-0.1126070	0.0085971	9.90E-42
7	MLXIPL *	rs34958196	73628771	A	G	0.1396310	-0.1307540	0.0088862	1.10E-52
7	MLXIPL *	rs34430945	73629335	C	T	0.1391430	-0.1295740	0.0088946	9.20E-52
7	MLXIPL *	rs34321592	73630874	A	G	0.1671730	-0.1129310	0.0082582	2.20E-45
7	MLXIPL *	rs7784668	73631153	C	T	0.1386450	-0.1299840	0.0089165	7.50E-52
7	MLXIPL *	rs78815801	73631608	C	T	0.1293130	-0.1326180	0.0092777	7.60E-50
7	MLXIPL *	rs1412452301	73631935	TTCTT	C	0.1657000	-0.1130800	0.0083115	8.00E-45
7	MLXIPL *	rs17145813	73632428	A	C	0.1653710	-0.1119490	0.0083268	9.50E-44
7	MLXIPL *	rs17145817	73632449	G	A	0.1653720	-0.1119240	0.0083269	1.00E-43
7	MLXIPL *	rs36091304	73633181	C	T	0.1636460	-0.1130930	0.0083822	5.80E-44
7	MLXIPL *	rs34899589	73633190	C	T	0.1621840	-0.1111950	0.0084309	4.60E-42
7	MLXIPL *	rs35855035	73633221	T	C	0.1620180	-0.1105130	0.0084319	1.60E-41
7	MLXIPL *	rs35703204	73633518	T	C	0.1651170	-0.1130750	0.0083450	2.30E-44
7	MLXIPL *	rs13230514	73633765	G	A	0.1649050	-0.1126300	0.0083468	4.50E-44
7	MLXIPL *	rs62466323	73634348	A	G	0.1648890	-0.1113340	0.0083504	3.60E-43
7	MLXIPL *	rs13234805	73634852	A	G	0.1348330	-0.1292760	0.0090852	1.60E-49
7	MLXIPL *	rs13222090	73635057	C	T	0.1650970	-0.1109610	0.0083440	5.30E-43
7	VPS37D *	rs371515311	73660465	A	G	0.0172601	-0.1745720	0.0235032	8.30E-16
7	ABHD11	rs1136954	73736364	A	C	0.4734820	0.0325887	0.0062461	4.00E-08
7	ABHD11	rs6460052	73737314	A	G	0.4731080	0.0324998	0.0062437	4.00E-08
7	ABHD11 *	chr7:73740250_AT_A	73740250	AT	A	0.4730870	0.0323492	0.0062355	4.30E-08
7	ABHD11 *	rs10266412	73741881	A	G	0.4732770	0.0330301	0.0062304	2.70E-08
7	ABHD11 *	rs10278588	73743151	C	A	0.4732810	0.0326694	0.0062278	3.80E-08
7	ABHD11 *	rs1880954	73743556	A	G	0.4733970	0.0327361	0.0062259	3.60E-08
7	ABHD11 *	rs6460053	73744089	C	T	0.4769860	0.0332380	0.0062058	1.80E-08
7	ABHD11 *	rs4717105	73746297	T	C	0.4729840	0.0328214	0.0062219	2.80E-08
7	ABHD11 *	rs10226706	73751424	A	C	0.4766050	0.0334837	0.0061881	1.10E-08
7	CLDN3 *	rs140600045	73762740	C	CCTTT	0.4821450	0.0322309	0.0062051	3.80E-08
7	CLDN3 *	rs11764572	73764105	G	A	0.4751950	0.0327841	0.0061375	1.40E-08
7	CLDN3 *	rs11979807	73768611	G	T	0.4757510	0.0328805	0.0061380	1.10E-08
7	CLDN3	rs7084	73770105	G	C	0.4761570	0.0326896	0.0061429	1.30E-08
7	CLDN3	rs6460054	73770204	T	C	0.4753410	0.0328698	0.0061392	1.30E-08
7	CLDN3 *	rs28408072	73771842	G	A	0.4757550	0.0328979	0.0061379	1.10E-08
7	CLDN3 *	rs10558095	73772006	CTT	C	0.4756810	0.0329574	0.0061377	1.10E-08
7	CLDN3 *	rs4484568	73773321	A	G	0.4756570	0.0329431	0.0061374	1.10E-08
7	CLDN3 *	rs4131376	73773988	T	C	0.4750910	0.0328601	0.0061368	1.20E-08
7	WBSCR28 *	rs1435702538	73892484	T	TTTCT	0.0121398	-0.1642050	0.0280098	3.50E-11
7	WBSCR28 *	rs6964590	73894020	A	G	0.0318332	-0.0975150	0.0175037	1.00E-09
7	WBSCR28 *	rs13241670	73903956	C	T	0.0322075	-0.0948009	0.0173973	2.20E-09
7	WBSCR28 *	rs73144858	73922565	G	C	0.0199152	-0.1478150	0.0219736	1.20E-13
7	ELN *	rs188072556	73999294	T	C	0.0167747	-0.1730090	0.0238401	2.30E-15
7	ELN *	rs576957617	74071436	T	TAA	0.0122277	-0.1603930	0.0279258	7.30E-11
7	RFC2	rs148741166	74252973	A	C	0.0128645	-0.1666110	0.0272758	3.60E-12
7	CLIP2	rs151126504	74392493	T	C	0.0207136	-0.1406420	0.0216302	1.40E-12
7	GTF2IRD1 *	rs145049525	74440602	G	C	0.0159589	-0.1346820	0.0246453	8.20E-10
7	GNAI1 *	rs373885367	80225192	C	T	0.0150083	-0.1390280	0.0251725	1.50E-08
7	GNAI1 *	rs147070009	80226706	C	A	0.0150086	-0.1390520	0.0251725	1.50E-08
7	GNAI1 *	rs544068653	80297253	A	G	0.0135310	-0.1601440	0.0265501	2.60E-10
7	LOC101927:rs188315921		80374323	A	C	0.0169265	-0.1467270	0.0237374	7.60E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	GNAT3 *	rs186731157	80389221	G	A	0.0197436	-0.1176840	0.0220763	2.00E-08
7	GNAT3 *	rs142895840	80521969	T	C	0.0199352	-0.1772400	0.0219455	4.40E-17
7	GNAT3 *	rs145638771	80550968	G	A	0.0206281	-0.1785700	0.0215413	1.10E-17
7	GNAT3 *	rs140363762	80554248	C	T	0.0351064	-0.1060260	0.0166033	4.70E-11
7	CD36 *	rs182480663	80567623	G	A	0.0206247	-0.1783990	0.0215429	1.30E-17
7	CD36 *	rs531971155	80601582	T	G	0.0200745	-0.1861250	0.0218346	2.50E-18
7	CD36	rs577611417	80651863	A	C	0.0199108	-0.1835960	0.0219377	4.20E-18
7	CD36	rs572295823	80661109	A	AAC	0.0198403	-0.1862640	0.0219794	1.60E-18
7	CD36 *	rs147949209	80688152	C	T	0.0308584	-0.1361260	0.0176699	1.40E-15
7	SEMA3C *	rs186972232	80740942	G	C	0.0341250	-0.1146840	0.0170375	3.40E-12
7	SEMA3C	rs185193868	80760615	G	A	0.0117511	-0.1799150	0.0283959	1.20E-10
7	CDK6	rs56353205	92667354	C	T	0.3557920	0.0358872	0.0065095	3.30E-08
7	CDK6	rs2301557	92671549	T	C	0.3548230	0.0356389	0.0064959	2.80E-08
7	CDK6	rs75882441	92676131	A	T	0.3526080	0.0358622	0.0064949	2.60E-08
7	CDK6	rs2282987	92683489	C	G	0.3538640	0.0370313	0.0064331	1.10E-08
7	CDK6	rs6964803	92686016	T	C	0.3505850	0.0353442	0.0064140	3.10E-08
7	CDK6	rs11981340	92686346	C	T	0.3515210	0.0356848	0.0064022	2.20E-08
7	CDK6	rs11981374	92686460	C	T	0.3515210	0.0356848	0.0064022	2.20E-08
7	CDK6	rs13437843	92686930	T	C	0.3510260	0.0360027	0.0064095	1.70E-08
7	CDK6	rs60726864	92686968	A	T	0.3510260	0.0360027	0.0064095	1.70E-08
7	CDK6	rs2282988	92688060	C	T	0.3515230	0.0356795	0.0064022	2.30E-08
7	CDK6	rs11533993	92690158	C	T	0.3514560	0.0349005	0.0064017	4.20E-08
7	CDK6	rs10225660	92695041	C	T	0.3519990	0.0352922	0.0063979	3.00E-08
7	CDK6	rs17164721	92695105	T	G	0.3517540	0.0351569	0.0063983	3.30E-08
7	CDK6	chr7:92695282_A_AAAAG	92695282	AAAAG	A	0.3367260	0.0359019	0.0065845	3.70E-08
7	KLF14 *	rs6973807	130739211	G	A	0.3088270	-0.0537584	0.0067385	1.30E-15
7	KLF14 *	rs6974400	130739314	A	G	0.3088190	-0.0536628	0.0067361	1.30E-15
7	KLF14 *	rs6974288	130739451	G	A	0.3089420	-0.0536809	0.0067318	1.10E-15
7	KLF14 *	rs11762784	130739885	A	G	0.3090260	-0.0536089	0.0067233	1.20E-15
7	KLF14 *	rs3996350	130742296	C	G	0.3100180	-0.0543502	0.0066817	2.60E-16
7	KLF14 *	rs13234269	130744427	A	T	0.3109860	-0.0556120	0.0066500	4.10E-17
7	KLF14 *	rs4731701	130746171	T	C	0.3098130	-0.0547224	0.0066781	2.20E-16
7	KLF14 *	rs10260148	130746210	T	C	0.3991890	0.0478472	0.0063533	4.40E-14
7	KLF14 *	rs34072724	130747710	A	G	0.3117120	-0.0544963	0.0066139	1.10E-16
7	KLF14 *	rs6971365	130747722	C	T	0.4015400	0.0475357	0.0063289	5.70E-14
7	KLF14 *	rs13241165	130747779	T	A	0.3117640	-0.0544924	0.0066137	1.10E-16
7	KLF14 *	rs4731702	130748625	T	C	0.3115590	-0.0550236	0.0066083	5.10E-17
7	KLF14 *	rs11976955	130748835	G	C	0.4030270	0.0461145	0.0063310	3.40E-13
7	KLF14 *	rs6961342	130749185	A	C	0.4029980	0.0462257	0.0063285	2.90E-13
7	KLF14 *	rs35722851	130749741	C	T	0.3106530	-0.0551264	0.0066371	6.70E-17
7	KLF14 *	rs35057928	130749767	C	T	0.3102760	-0.0554448	0.0066394	4.50E-17
7	KLF14 *	rs34282904	130749770	A	G	0.3105220	-0.0550943	0.0066376	6.80E-17
7	KLF14 *	rs287621	130750422	T	C	0.4015180	0.0470450	0.0063261	1.00E-13
7	KLF14 *	chr7:130751316_A_AAT	130751316	AAT	A	0.3113020	-0.0552720	0.0066263	4.80E-17
7	KLF14 *	rs34084575	130751643	TA	T	0.3121690	-0.0554081	0.0066182	3.70E-17
7	KLF14 *	rs11979110	130751700	T	C	0.3120890	-0.0552160	0.0066184	4.60E-17
7	KLF14 *	rs13230111	130752365	G	A	0.3114180	-0.0551938	0.0066197	4.80E-17
7	KLF14 *	rs7810507	130752717	A	G	0.4021050	0.0469314	0.0063195	1.00E-13
7	KLF14 *	rs13233731	130752930	A	G	0.3113660	-0.0549833	0.0066190	5.90E-17
7	KLF14 *	rs13234407	130753455	A	G	0.3113740	-0.0549532	0.0066189	6.20E-17
7	KLF14 *	rs7783857	130754299	G	C	0.4215250	0.0495680	0.0062222	1.80E-15
7	KLF14 *	rs13241538	130755103	C	G	0.3121570	-0.0552309	0.0066075	4.30E-17
7	KLF14 *	rs13228906	130757125	A	G	0.3118160	-0.0546239	0.0066170	9.40E-17
7	KLF14 *	rs6467314	130757382	G	C	0.4204020	0.0494019	0.0062157	1.70E-15
7	KLF14 *	rs17185445	130757868	T	C	0.3121140	-0.0550965	0.0066212	5.90E-17
7	KLF14 *	rs3996352	130760175	G	A	0.3098030	-0.0546992	0.0066427	1.20E-16
7	KLF14 *	rs13240528	130760369	A	C	0.3097070	-0.0550511	0.0066446	7.60E-17
7	KLF14 *	chr7:130760669_C_CT	130760669	CT	C	0.3019640	-0.0534984	0.0067568	2.50E-15
7	KLF14 *	rs17789506	130760815	A	G	0.3101280	-0.0545759	0.0066439	1.40E-16
7	KLF14 *	rs35712907	130761088	T	TA	0.3101010	-0.0545883	0.0066457	1.50E-16
7	KLF14 *	rs11765979	130761118	C	A	0.3101050	-0.0546073	0.0066459	1.40E-16
7	KLF14 *	rs1364422	130761222	T	C	0.4220510	0.0488053	0.0061911	3.40E-15
7	KLF14 *	rs59326756	130762371	G	A	0.4239640	0.0481525	0.0062007	1.20E-14
7	KLF14 *	rs12667251	130764699	G	A	0.3442350	-0.0481129	0.0065255	1.60E-13
7	KLF14 *	rs185963	130765392	C	T	0.3424130	-0.0463250	0.0065302	1.30E-12
7	KLF14 *	rs288484	130765438	A	G	0.3423460	-0.0463996	0.0065304	1.30E-12
7	KLF14 *	rs172306	130765628	G	A	0.3442680	-0.0474371	0.0065232	3.60E-13
7	KLF14 *	rs577195	130765902	C	G	0.3423600	-0.0462478	0.0065299	1.40E-12
7	KLF14 *	rs1665759	130766738	T	C	0.3424080	-0.0464589	0.0065287	1.10E-12
7	KLF14 *	rs1646629	130766864	C	T	0.3422420	-0.0464475	0.0065300	1.10E-12
7	KLF14 *	rs1646631	130766912	G	A	0.3423540	-0.0465789	0.0065279	9.80E-13
7	KLF14 *	rs56258902	130767225	C	CTTTA	0.3147400	-0.0457806	0.0066787	9.40E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	KLF14 *	rs10238574	130767468	T	C	0.3423450	-0.0464808	0.0065269	1.10E-12
7	KLF14 *	rs1596972	130768623	A	G	0.3424720	-0.0462603	0.0065234	1.40E-12
7	KLF14 *	rs1562398	130773172	C	G	0.3400990	-0.0459050	0.0065510	2.60E-12
7	KLF14 *	rs34748838	130774483	T	C	0.3162290	-0.0448062	0.0066443	1.70E-11
7	KLF14 *	rs6968740	130775517	G	T	0.3430300	-0.0458388	0.0065078	2.00E-12
7	KLF14 *	rs6951054	130775721	T	G	0.3430300	-0.0458162	0.0065077	2.00E-12
7	KLF14 *	rs35964477	130777099	A	AT	0.3165030	-0.0446968	0.0066411	1.90E-11
7	KLF14 *	rs4425698	130777483	T	C	0.3430830	-0.0455215	0.0065039	2.60E-12
7	KLF14 *	rs1596973	130777524	G	A	0.3430870	-0.0454191	0.0065036	3.00E-12
7	KLF14 *	rs6467315	130778433	C	G	0.3189210	-0.0442975	0.0066640	3.30E-11
7	KLF14 *	rs6949956	130778566	T	G	0.3426030	-0.0449754	0.0064946	4.40E-12
7	KLF14 *	rs6968233	130778697	G	A	0.3427390	-0.0447958	0.0064926	4.80E-12
7	KLF14 *	rs10954284	130778999	A	T	0.3161760	-0.0438301	0.0066276	4.30E-11
7	KLF14 *	rs10245520	130779072	T	C	0.3426700	-0.0447709	0.0064898	5.50E-12
7	KLF14 *	rs6972634	130779366	A	G	0.3429450	-0.0445651	0.0064886	6.90E-12
7	KLF14 *	rs6467316	130779837	C	T	0.3426240	-0.0441198	0.0064909	1.10E-11
7	KLF14 *	rs6467317	130779901	A	G	0.3435940	-0.0446610	0.0064888	7.10E-12
7	KLF14 *	rs9641894	130780295	T	G	0.3428840	-0.0444175	0.0064837	7.80E-12
7	KLF14 *	rs34188023	130780856	G	GT	0.3436130	-0.0441470	0.0064801	9.20E-12
7	KLF14 *	rs1447059	130780895	A	G	0.3431380	-0.0439938	0.0064800	1.20E-11
7	KLF14 *	rs1447060	130781332	A	G	0.3407940	-0.0438344	0.0064817	1.60E-11
7	KLF14 *	rs972283	130782095	A	G	0.3142560	-0.0438239	0.0065869	3.90E-11
7	KLF14 *	rs972284	130782207	C	T	0.3419480	-0.0442184	0.0064661	7.80E-12
8	NAT2 *	rs35548819	18371107	C	T	0.4724340	0.0373830	0.0061659	1.20E-09
8	NAT2 *	rs2172426	18371511	C	T	0.4419020	-0.0397242	0.0061691	5.30E-11
8	NAT2 *	rs1845736	18372655	T	C	0.4392840	-0.0388441	0.0061659	1.50E-10
8	NAT2 *	rs13267304	18374424	T	C	0.4904680	0.0364880	0.0060987	1.30E-09
8	NAT2 *	rs7835476	18375604	A	C	0.4905580	0.0361363	0.0060978	1.90E-09
8	NAT2 *	rs7006687	18376073	C	T	0.4632510	-0.0394221	0.0061152	3.30E-11
8	NAT2 *	rs4481648	18378050	G	T	0.4620010	-0.0386846	0.0061519	1.10E-10
8	NAT2 *	rs2047252	18380477	T	C	0.4868860	0.0369114	0.0062068	2.20E-09
8	NAT2 *	rs13266992	18382187	C	T	0.4768450	0.0363119	0.0062027	3.40E-09
8	NAT2 *	rs59416053	18383290	C	G	0.4745530	0.0354643	0.0061723	7.20E-09
8	NAT2 *	rs35354956	18383809	C	T	0.4766920	0.0362772	0.0061528	3.10E-09
8	NAT2 *	rs13277738	18383997	T	C	0.4738620	0.0353612	0.0061572	7.30E-09
8	NAT2 *	rs13262341	18385587	G	A	0.4781890	0.0354450	0.0061468	6.80E-09
8	NAT2 *	rs10109286	18386093	C	T	0.4754570	0.0357250	0.0061466	4.60E-09
8	NAT2 *	rs10095072	18387152	T	G	0.4992590	0.0352401	0.0061335	8.00E-09
8	NAT2 *	rs10095159	18387174	G	A	0.5004970	-0.0350869	0.0061444	1.00E-08
8	NAT2 *	rs75501607	18387243	T	C	0.4989150	0.0342823	0.0061290	1.60E-08
8	NAT2 *	rs13282367	18387476	G	T	0.4799790	0.0347870	0.0061428	1.20E-08
8	NAT2 *	rs10085931	18387939	A	G	0.5004920	-0.0384191	0.0061564	3.90E-10
8	NAT2 *	rs11780884	18388543	A	G	0.4912680	0.0361247	0.0061530	3.10E-09
8	NAT2 *	rs4646243	18390099	C	T	0.4753850	0.0394888	0.0061112	5.80E-11
8	NAT2 *	rs4646267	18390403	G	A	0.4753700	0.0393220	0.0061106	6.50E-11
8	NAT2 *	rs4646246	18391151	G	A	0.4732600	0.0389801	0.0061173	8.50E-11
8	NAT2 *	rs55686478	18392865	A	G	0.4719410	0.0384104	0.0061292	1.50E-10
8	NAT2 *	rs35583283	18396999	C	G	0.4778270	0.0386979	0.0061335	1.40E-10
8	NAT2 *	rs1041983	18400285	T	C	0.4323920	-0.0419513	0.0061494	2.60E-12
8	NAT2 *	rs4646254	18404549	G	A	0.4804660	0.0376787	0.0061212	3.30E-10
8	NAT2 *	rs4646257	18405036	T	C	0.4797430	0.0379338	0.0061190	3.00E-10
8	NAT2 *	rs12674710	18406153	C	A	0.4802550	0.0379153	0.0061216	2.80E-10
8	NAT2 *	rs12676857	18409062	C	T	0.4729170	0.0381556	0.0061404	2.60E-10
8	NAT2 *	rs2898475	18409186	C	T	0.4290170	-0.0325701	0.0061982	2.60E-08
8	NAT2 *	rs2410561	18409264	A	G	0.4728680	0.0383268	0.0061403	2.10E-10
8	NAT2 *	rs2410562	18409322	C	T	0.4290150	-0.0325630	0.0061982	2.70E-08
8	NAT2 *	rs7837608	18409337	A	G	0.4290150	-0.0325630	0.0061982	2.70E-08
8	NAT2 *	rs2898476	18409414	A	G	0.4723470	0.0384413	0.0061426	2.00E-10
8	NAT2 *	rs7460653	18409473	C	G	0.4741320	0.0380739	0.0061444	2.90E-10
8	NAT2 *	rs10103029	18409828	G	A	0.4747280	0.0380980	0.0061404	2.90E-10
8	NAT2 *	rs10103148	18409919	C	A	0.4761300	0.0376944	0.0061411	4.50E-10
8	NAT2 *	rs10087857	18409951	C	G	0.4747010	0.0380054	0.0061407	3.20E-10
8	NAT2 *	rs10103281	18410032	A	G	0.4267260	-0.0323867	0.0062020	3.60E-08
8	NAT2 *	rs10088333	18410368	A	G	0.4746820	0.0379716	0.0061407	3.30E-10
8	NAT2 *	rs1603290	18411760	G	A	0.4245900	-0.0330721	0.0062055	2.10E-08
8	NAT2 *	rs10089958	18411833	G	A	0.4772000	0.0382022	0.0061400	2.70E-10
8	NAT2 *	rs57180587	18412071	T	A	0.4767470	0.0385087	0.0061411	2.10E-10
8	NAT2 *	chr8:18414568_A_AT	18414568	AT	A	0.3811950	-0.0336625	0.0063372	4.10E-08
8	NAT2 *	rs4921911	18414597	T	C	0.3880100	-0.0344966	0.0062594	1.10E-08
8	NAT2 *	rs4921912	18414623	G	A	0.3883550	-0.0342775	0.0062554	1.20E-08
8	NAT2 *	rs4921913	18414867	T	C	0.4808320	-0.0369052	0.0060942	8.80E-10
8	NAT2 *	rs4921914	18414928	T	C	0.4848480	-0.0378984	0.0061127	4.50E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	NAT2 *	rs4921915	18414956	A	G	0.4820320	-0.0385448	0.0060946	2.30E-10
8	NAT2 *	rs11267998	18414993	GAGCTC	C	0.4849450	-0.0384598	0.0060967	2.40E-10
8	NAT2 *	rs35246381	18415025	T	C	0.4848810	-0.0380590	0.0060937	3.50E-10
8	NAT2 *	rs35570672	18415125	C	T	0.4845630	-0.0383167	0.0060950	2.70E-10
8	NAT2 *	rs1495741	18415371	A	G	0.4837210	-0.0382061	0.0060931	2.80E-10
8	NAT2 *	rs13254811	18415508	G	A	0.4685750	0.0357703	0.0061381	3.10E-09
8	NAT2 *	rs1495743	18415790	C	G	0.4844910	-0.0372589	0.0061012	7.30E-10
8	NAT2 *	rs35942058	18416888	A	G	0.4690280	0.0360743	0.0061439	3.00E-09
8	NAT2 *	rs34987019	18416933	C	T	0.4690520	0.0360578	0.0061440	3.00E-09
8	NAT2 *	rs7812546	18417104	A	T	0.4683480	0.0352881	0.0061562	7.60E-09
8	NAT2 *	rs34537991	18417174	C	G	0.4701460	0.0361206	0.0061520	3.70E-09
8	NAT2 *	rs7828489	18417249	G	T	0.4785920	0.0365515	0.0061559	2.60E-09
8	NAT2 *	rs7816847	18417679	C	A	0.4706210	0.0360098	0.0061422	2.70E-09
8	NAT2 *	rs4560828	18418784	T	A	0.4706090	0.0361807	0.0061613	3.80E-09
8	NAT2 *	rs13255048	18419130	A	G	0.4685750	0.0367343	0.0061560	1.90E-09
8	NAT2 *	chr8:18419370_AAACAAC_A	18419370	AACAA	A	0.4664910	0.0347194	0.0061660	1.80E-08
8	NAT2 *	rs7005648	18420698	T	A	0.4730680	0.0359440	0.0061529	3.00E-09
8	CSGALNAC	rs147413778	19411544	T	G	0.0238281	0.1197660	0.0202455	4.20E-10
8	CSGALNAC	rs116960282	19461352	G	C	0.0279089	0.1039980	0.0187000	1.20E-09
8	INTS10 *	rs142950473	19771660	C	T	0.0119511	-0.1564680	0.0282258	2.30E-09
8	INTS10 *	rs189872709	19786981	C	T	0.0199116	0.1244650	0.0222080	2.10E-08
8	INTS10 *	rs4922099	19790975	C	T	0.4443670	0.0333820	0.0061495	4.10E-08
8	INTS10 *	rs4398935	19791976	C	T	0.4453350	0.0338828	0.0061485	2.30E-08
8	INTS10 *	rs6995371	19792757	G	A	0.4458670	0.0334153	0.0061436	3.30E-08
8	INTS10 *	rs67391684	19797131	T	A	0.4461820	0.0349026	0.0061407	8.60E-09
8	INTS10 *	rs11777075	19798155	A	G	0.4445540	0.0361482	0.0061492	2.60E-09
8	INTS10 *	rs3907477	19800233	T	C	0.4432370	0.0342476	0.0061699	1.40E-08
8	INTS10 *	rs3907478	19800242	T	G	0.4432370	0.0342476	0.0061699	1.40E-08
8	INTS10 *	rs75939150	19809564	A	T	0.1569300	-0.0504209	0.0085264	1.60E-09
8	INTS10 *	rs6586871	19856595	A	T	0.2134110	-0.0434594	0.0075728	1.20E-08
8	INTS10 *	rs4922110	19857369	T	C	0.1449730	-0.0483604	0.0086767	1.90E-08
8	INTS10 *	rs6586874	19859580	A	G	0.1479010	-0.0487648	0.0085826	1.30E-08
8	INTS10 *	rs2119693	19862884	G	T	0.1488960	-0.0489085	0.0085482	1.20E-08
8	INTS10 *	rs10096561	19863322	T	C	0.1476250	-0.0489048	0.0085766	1.10E-08
8	INTS10 *	rs11204079	19865044	A	G	0.1479420	-0.0475091	0.0085770	3.40E-08
8	INTS10 *	rs11998681	19865049	G	T	0.2204290	-0.0425043	0.0074438	2.50E-08
8	INTS10 *	rs74549553	19874863	C	G	0.0758568	-0.0886893	0.0116772	8.30E-14
8	INTS10 *	rs28625109	19875076	C	T	0.1569510	-0.0479782	0.0083878	5.10E-10
8	INTS10 *	rs10098182	19875595	C	T	0.1523290	-0.0478915	0.0085122	6.80E-10
8	INTS10 *	rs1561747	19876057	C	A	0.1550620	-0.0463854	0.0084453	1.40E-09
8	INTS10 *	rs7818070	19877405	A	G	0.1534050	-0.0489847	0.0084962	3.60E-10
8	INTS10 *	rs4922113	19877440	A	G	0.1204580	-0.0839050	0.0095166	5.30E-18
8	INTS10 *	rs2197088	19879646	G	A	0.1621780	-0.0423431	0.0083415	1.50E-08
8	INTS10 *	rs1441767	19879768	C	A	0.1619560	-0.0428949	0.0083447	9.90E-09
8	INTS10 *	rs75070501	19880081	G	A	0.1180370	-0.0945535	0.0095722	2.30E-22
8	INTS10 *	rs6586875	19880591	T	G	0.1581970	-0.0486656	0.0084912	1.80E-10
8	INTS10 *	rs7830586	19881367	G	A	0.1607040	-0.0414519	0.0083806	3.60E-08
8	INTS10 *	rs17410407	19881732	T	G	0.1162210	-0.0944865	0.0096156	3.60E-22
8	INTS10 *	rs77829308	19883675	T	C	0.1141370	-0.0939990	0.0096976	1.10E-21
8	INTS10 *	chr8:19884251_C_CA	19884251	CA	C	0.1117930	-0.0987372	0.0098227	2.90E-23
8	INTS10 *	rs73607783	19884693	A	T	0.1234390	-0.0928456	0.0094148	7.50E-23
8	INTS10 *	rs79341217	19885706	T	C	0.1007140	-0.1075540	0.0102245	9.90E-26
8	INTS10 *	rs74974359	19885743	C	T	0.0688355	-0.1030710	0.0121755	4.40E-17
8	INTS10 *	rs10503666	19887085	C	G	0.0868391	-0.1254310	0.0108498	4.60E-31
8	INTS10 *	rs35550741	19889296	C	G	0.4800600	0.0343336	0.0061513	2.20E-08
8	INTS10 *	rs17482310	19889365	T	G	0.0966302	-0.1085250	0.0103568	1.10E-25
8	INTS10 *	rs34955499	19889987	A	G	0.4772530	0.0336238	0.0061430	4.80E-08
8	INTS10 *	rs79396901	19890937	C	T	0.0871847	-0.1252120	0.0108207	4.00E-31
8	INTS10 *	rs7844579	19891092	C	T	0.4858380	0.0357809	0.0061167	5.20E-09
8	INTS10 *	rs7822518	19891345	C	T	0.4899060	0.0375261	0.0061272	9.80E-10
8	INTS10 *	rs138094414	19892729	C	G	0.0837656	-0.1289640	0.0110093	2.70E-32
8	INTS10 *	rs112861901	19893440	C	T	0.0870100	-0.1260030	0.0108264	1.10E-31
8	INTS10 *	rs12550077	19893888	A	G	0.0824875	-0.1282000	0.0110866	1.30E-31
8	INTS10 *	rs1441776	19894049	G	C	0.4809690	0.0383055	0.0061755	5.20E-10
8	INTS10 *	rs1441775	19894140	A	G	0.4844840	0.0363003	0.0061537	3.50E-09
8	INTS10 *	rs11995314	19894696	A	G	0.4951740	-0.0357590	0.0060845	6.10E-09
8	LPL *	rs17482386	19896010	G	A	0.0984648	-0.1117650	0.0102792	1.50E-27
8	LPL *	chr8:19896793_C_CT	19896793	CT	C	0.1037000	-0.1131560	0.0100884	4.50E-30
8	LPL *	rs1919482	19897207	T	A	0.0997034	-0.1096610	0.0102299	5.60E-28
8	LPL *	rs76085257	19897616	A	C	0.0825600	-0.1298090	0.0110705	1.80E-32
8	LPL *	rs73597688	19897664	A	C	0.0967176	-0.1179560	0.0103659	3.80E-31
8	LPL *	rs73597690	19898115	A	C	0.0885275	-0.1256950	0.0107722	9.60E-33

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs12543154	19898466	T	G	0.0875581	-0.1261630	0.0108164	1.60E-32
8	LPL *	rs10091649	19898910	G	T	0.0919334	-0.1294620	0.0106327	4.40E-36
8	LPL *	rs73597699	19899081	T	C	0.0785723	-0.1282980	0.0114242	5.30E-30
8	LPL *	rs10102717	19899302	T	C	0.0895288	-0.1301320	0.0107541	1.10E-35
8	LPL *	rs1441771	19899789	T	C	0.0892832	-0.1344030	0.0107761	8.70E-38
8	LPL *	rs1441770	19899808	A	G	0.0894392	-0.1325890	0.0107657	6.50E-37
8	LPL *	rs183801835	19904479	C	T	0.0202635	-0.2046310	0.0217080	5.20E-24
8	LPL *	rs77032723	19906481	T	C	0.1285710	-0.1316350	0.0092214	3.30E-49
8	LPL *	rs192423215	19907403	C	G	0.0193961	-0.2124750	0.0221605	9.80E-25
8	LPL *	rs60526148	19909692	T	C	0.1531990	-0.1463050	0.0085267	1.10E-69
8	LPL *	rs3988301	19912868	G	T	0.1577820	-0.1464010	0.0084338	2.10E-71
8	LPL *	rs28834434	19917379	A	C	0.1508790	-0.1500350	0.0085124	6.50E-74
8	LPL *	rs4466415	19919470	C	A	0.1621530	-0.1455650	0.0083091	2.60E-72
8	LPL *	rs77899453	19922799	A	G	0.1504490	-0.1515200	0.0085378	1.10E-74
8	LPL *	rs2119692	19922946	C	G	0.1515010	-0.1493560	0.0085161	3.40E-73
8	LPL *	rs3866470	19927611	A	G	0.0164067	-0.2220050	0.0240295	3.40E-23
8	LPL *	rs7816032	19929380	T	C	0.1567540	-0.1466210	0.0083765	5.30E-73
8	LPL *	rs139001474	19931094	A	T	0.1606410	-0.1463370	0.0083226	5.50E-73
8	LPL *	rs149764042	19931164	C	G	0.0679134	-0.2202310	0.0122170	2.30E-77
8	LPL *	rs4592053	19931255	G	A	0.1610370	-0.1461690	0.0083167	5.90E-73
8	LPL *	rs528397993	19932174	A	G	0.0206631	0.1131350	0.0218323	2.30E-08
8	LPL *	rs150331294	19932487	A	T	0.1561790	-0.1469570	0.0084023	6.50E-73
8	LPL *	rs182893294	19933207	C	T	0.0134501	-0.2468120	0.0265456	3.40E-22
8	LPL *	rs9694336	19933560	T	C	0.1494170	-0.1517910	0.0085765	7.20E-75
8	LPL *	rs145353248	19933835	T	C	0.1493390	-0.1520800	0.0085770	3.70E-75
8	LPL	rs3779787	19940405	T	G	0.1568560	-0.1443320	0.0084155	2.10E-70
8	LPL	rs1534649	19942130	T	G	0.1568490	-0.1477120	0.0084084	8.20E-74
8	LPL	rs112127208	19944019	G	T	0.1554630	-0.1484960	0.0084283	4.20E-74
8	LPL	rs10104051	19944891	T	C	0.1556460	-0.1483370	0.0084261	5.50E-74
8	LPL	rs3779788	19945582	T	C	0.1547480	-0.1496510	0.0084450	9.40E-75
8	LPL	rs56321069	19946485	A	T	0.1541040	-0.1513170	0.0084813	7.20E-76
8	LPL	rs8176337	19949160	G	C	0.1534620	-0.1544180	0.0085380	8.30E-78
8	LPL	rs74304285	19950519	A	G	0.1520350	-0.1571510	0.0086314	2.70E-79
8	LPL	rs113023641	19950620	A	G	0.1519670	-0.1573460	0.0086358	2.00E-79
8	LPL	rs73667472	19952184	C	T	0.0597645	-0.2372900	0.0129958	5.50E-80
8	LPL	rs343	19953276	A	C	0.1502270	-0.0705979	0.0086916	8.50E-17
8	LPL	rs249	19953495	C	T	0.0602499	-0.2485480	0.0129307	1.70E-87
8	LPL	rs250	19953512	ATG	A	0.1536990	-0.0675167	0.0086167	4.80E-16
8	LPL	rs254	19954386	G	C	0.2180970	-0.1382180	0.0074775	3.80E-81
8	LPL	rs255	19954390	C	T	0.2181010	-0.1382550	0.0074778	3.60E-81
8	LPL	rs256	19954456	T	C	0.2186690	-0.1391760	0.0074612	1.40E-82
8	LPL	rs263	19955301	T	C	0.2201330	-0.1402220	0.0073870	4.10E-85
8	LPL	rs264	19955669	A	G	0.2100170	-0.1280710	0.0074912	1.90E-68
8	LPL	rs269	19956156	G	T	0.2194250	-0.1418000	0.0074359	7.80E-86
8	LPL	rs271	19956191	A	G	0.2187780	-0.1415970	0.0074426	1.60E-85
8	LPL	chr8:19956458_G_GT	19956458	GT	G	0.2154180	-0.1431020	0.0075276	1.00E-84
8	LPL	rs285	19957678	T	C	0.3523280	-0.1238180	0.0065229	2.30E-86
8	LPL	rs287	19958045	G	A	0.2038670	-0.1836770	0.0075746	1.20E-137
8	LPL	rs289	19958108	C	T	0.2037110	-0.1842500	0.0075695	9.20E-139
8	LPL	rs291	19958341	C	T	0.2046090	-0.1837980	0.0075564	4.90E-139
8	LPL	chr8:19958567_T_TA	19958567	TA	T	0.2037940	-0.1826930	0.0075754	1.30E-136
8	LPL	rs294	19958614	C	T	0.1004430	-0.0577455	0.0101440	1.90E-08
8	LPL	rs295	19958727	C	A	0.2048910	-0.1833890	0.0075495	9.80E-139
8	LPL	rs297	19958860	C	T	0.2037060	-0.1844340	0.0075688	5.50E-139
8	LPL	rs301	19959423	C	T	0.2035060	-0.1856310	0.0075775	2.30E-140
8	LPL	rs303	19959768	C	G	0.0999551	-0.0592410	0.0101660	9.60E-09
8	LPL	rs304	19959850	G	T	0.1981170	-0.1846740	0.0077045	3.50E-134
8	LPL	rs305	19959890	G	A	0.2027450	-0.1851770	0.0075925	5.30E-139
8	LPL	rs308	19959965	G	T	0.0797457	-0.2577070	0.0112794	5.80E-125
8	LPL	rs310	19960035	T	C	0.0999609	-0.0592367	0.0101657	9.50E-09
8	LPL	rs312	19960486	C	G	0.1003790	-0.0593574	0.0101523	8.30E-09
8	LPL	rs314	19960531	A	G	0.2036290	-0.1850020	0.0075770	2.20E-139
8	LPL	rs316	19960925	A	C	0.0999906	-0.0595735	0.0101634	8.00E-09
8	LPL	rs117026536	19961262	T	G	0.1037960	-0.2651710	0.0100127	7.70E-167
8	LPL	rs320	19961566	G	T	0.2040320	-0.1856260	0.0075633	1.20E-140
8	LPL	rs322	19961706	C	A	0.2042920	-0.1855540	0.0075742	4.50E-140
8	LPL	rs325	19961817	C	T	0.1031680	-0.2687930	0.0100238	1.40E-170
8	LPL	rs326	19961928	G	A	0.2041060	-0.1866630	0.0075598	3.30E-142
8	LPL	rs327	19962025	G	T	0.2043470	-0.1863900	0.0075641	1.90E-141
8	LPL	rs328	19962213	G	C	0.1031580	-0.2685190	0.0100246	3.40E-170
8	LPL	rs330	19962885	A	G	0.0997128	-0.0598025	0.0101666	8.70E-09
8	LPL	rs331	19962894	A	G	0.2025390	-0.1866450	0.0075790	2.20E-141

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL	rs12679834	19962922	C	T	0.1031270	-0.2691430	0.0100265	6.30E-171
8	LPL	rs117199990	19963405	T	C	0.1009120	-0.2700110	0.0101415	2.50E-168
8	LPL	rs145391587	19963422	C	A	0.0999695	-0.2711900	0.0101881	1.50E-168
8	LPL	rs75278536	19963914	G	T	0.1028340	-0.2690420	0.0100392	1.40E-170
8	LPL	rs146265243	19963956	G	GT	0.1028550	-0.2691890	0.0100407	1.10E-170
8	LPL	rs77069344	19964271	G	T	0.1028330	-0.2690350	0.0100392	1.40E-170
8	LPL	rs11570891	19965299	T	C	0.1030460	-0.2689590	0.0100300	1.60E-170
8	LPL	rs4922115	19965319	A	G	0.0969434	-0.0595655	0.0102900	1.60E-08
8	LPL	rs11570892	19966106	G	A	0.0956695	-0.0594133	0.0103622	2.20E-08
8	LPL	rs3208305	19966137	T	A	0.1966260	-0.1876880	0.0076864	3.40E-139
8	LPL	rs1803924	19966163	T	C	0.1030480	-0.2689680	0.0100299	1.50E-170
8	LPL	rs1059507	19966452	T	C	0.0969537	-0.0595339	0.0102868	1.70E-08
8	LPL	rs3735964	19966534	A	C	0.1030950	-0.2687450	0.0100265	1.80E-170
8	LPL	rs13702	19966981	C	T	0.2005560	-0.1873890	0.0076095	1.80E-141
8	LPL	rs1059611	19967052	C	T	0.1031250	-0.2684420	0.0100252	4.10E-170
8	LPL	rs10645926	19967115	CTT	C	0.1030840	-0.2688090	0.0100271	1.50E-170
8	LPL	rs15285	19967156	T	C	0.2000720	-0.1878910	0.0076137	9.40E-142
8	LPL	rs3866471	19967158	A	C	0.0969891	-0.0597648	0.0102836	1.50E-08
8	LPL *	rs3916027	19967357	A	G	0.2000020	-0.1877320	0.0076162	1.80E-141
8	LPL *	rs4921683	19967557	A	T	0.0969816	-0.0597223	0.0102858	1.50E-08
8	LPL *	rs4921684	19967617	T	C	0.0969787	-0.0596900	0.0102860	1.50E-08
8	LPL *	rs77150190	19968791	C	G	0.0944784	-0.2653710	0.0104278	1.50E-153
8	LPL *	rs77729186	19968807	G	A	0.0944784	-0.2653710	0.0104278	1.50E-153
8	LPL *	rs2197089	19968862	A	G	0.3457810	-0.1215890	0.0064105	1.50E-85
8	LPL *	rs79108221	19969190	T	C	0.0944338	-0.2653220	0.0104293	1.70E-153
8	LPL *	rs1563590475	19969589	A	ACTT	0.0801138	-0.2578910	0.0113493	1.10E-123
8	LPL *	rs10105606	19970337	A	C	0.1997250	-0.1879990	0.0076191	8.80E-142
8	LPL *	rs2410616	19971168	T	C	0.0971284	-0.0628146	0.0102763	1.90E-09
8	LPL *	rs2410617	19971382	A	T	0.0971501	-0.0628462	0.0102751	1.90E-09
8	LPL *	rs76270802	19971644	T	A	0.0902722	-0.0593715	0.0106421	2.10E-08
8	LPL *	rs1569209	19972659	G	T	0.0215686	-0.2590220	0.0209933	3.30E-37
8	LPL *	rs1561750	19973255	C	T	0.0970194	-0.0614144	0.0103006	4.50E-09
8	LPL *	rs1011685	19973258	T	C	0.1021650	-0.2680790	0.0100672	3.80E-168
8	LPL *	rs10096633	19973410	T	C	0.1022860	-0.2678150	0.0100620	5.10E-168
8	LPL *	rs1372339	19974287	G	A	0.0968366	-0.0618327	0.0103135	3.60E-09
8	LPL *	rs17091872	19974466	A	G	0.0968351	-0.0618316	0.0103137	3.60E-09
8	LPL *	rs17482753	19975135	T	G	0.1016930	-0.2683370	0.0100880	1.30E-167
8	LPL *	rs4922116	19975267	A	G	0.0967803	-0.0613842	0.0103175	5.00E-09
8	LPL *	rs1441777	19976060	C	T	0.0968829	-0.0606386	0.0103147	7.80E-09
8	LPL *	rs1837845	19976649	C	T	0.0968800	-0.0605728	0.0103148	8.00E-09
8	LPL *	chr8:19977329_T_TA	19977329	TA	T	0.0969272	-0.0607249	0.0103152	7.30E-09
8	LPL *	rs2165557	19977539	T	A	0.0968066	-0.0613764	0.0103183	5.00E-09
8	LPL *	rs78963197	19979135	C	T	0.0985786	-0.2637920	0.0102688	5.80E-157
8	LPL *	rs74855321	19979473	T	C	0.1007530	-0.2676990	0.0101358	7.90E-166
8	LPL *	rs34406568	19980876	CA	C	0.0942415	-0.0589784	0.0104424	2.50E-08
8	LPL *	rs4464984	19980958	T	C	0.1957260	-0.1872500	0.0077036	4.40E-138
8	LPL *	rs58946909	19982830	A	G	0.1015540	-0.2667820	0.0101032	3.20E-165
8	LPL *	rs75551077	19982897	C	G	0.1015990	-0.2666790	0.0101010	3.80E-165
8	LPL *	rs1554519534	19985625	CA	C	0.0560316	-0.2665720	0.0135391	8.50E-92
8	LPL *	rs17091891	19985660	C	T	0.0918766	-0.2670470	0.0106336	8.30E-150
8	LPL *	rs17410914	19985951	A	C	0.0988572	-0.2719110	0.0102253	1.20E-167
8	LPL *	rs117227752	19986350	A	G	0.1017180	-0.2683620	0.0100882	9.50E-168
8	LPL *	rs59147390	19986368	C	T	0.1017140	-0.2683670	0.0100882	9.20E-168
8	LPL *	rs184371102	19986419	T	G	0.0782927	-0.2571020	0.0113687	3.60E-122
8	LPL *	rs12678919	19986711	G	A	0.1019970	-0.2673640	0.0100742	5.90E-167
8	LPL *	rs34770253	19986717	C	T	0.0976411	-0.0599411	0.0102760	9.80E-09
8	LPL *	rs7819706	19986904	G	A	0.1015510	-0.2684120	0.0100988	1.80E-167
8	LPL *	rs115129770	19986928	G	C	0.1015510	-0.2684120	0.0100988	1.80E-167
8	LPL *	rs149670831	19986936	C	CT	0.1015510	-0.2684120	0.0100988	1.80E-167
8	LPL *	rs7841189	19987865	T	C	0.1020120	-0.2677910	0.0100832	4.70E-167
8	LPL *	rs78458743	19988803	G	T	0.1016540	-0.2689580	0.0100940	2.60E-168
8	LPL *	rs114566157	19988978	G	C	0.1016540	-0.2689580	0.0100940	2.60E-168
8	LPL *	rs139894713	19989069	A	C	0.0215568	-0.2597360	0.0209965	2.20E-37
8	LPL *	rs12682115	19989549	A	G	0.1016540	-0.2689580	0.0100940	2.60E-168
8	LPL *	rs78013771	19989712	C	T	0.1016530	-0.2689470	0.0100939	2.60E-168
8	LPL *	rs12545984	19989748	T	C	0.0976182	-0.0592497	0.0102767	1.40E-08
8	LPL *	rs76496571	19989930	A	C	0.1017020	-0.2687390	0.0100911	4.80E-168
8	LPL *	rs10503669	19990179	A	C	0.1017980	-0.2680730	0.0100764	1.20E-167
8	LPL *	rs17410962	19990569	A	G	0.1017220	-0.2687240	0.0100891	4.80E-168
8	LPL *	rs117604010	19990885	A	G	0.0786660	-0.2580570	0.0113404	1.10E-123
8	LPL *	rs17489185	19990988	C	G	0.1017230	-0.2687330	0.0100891	4.70E-168
8	LPL *	rs17410983	19991182	T	C	0.1017240	-0.2687300	0.0100891	4.80E-168

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs17489226	19991367	T	A	0.1017250	-0.2687300	0.0100892	4.80E-168
8	LPL *	rs17410996	19991761	G	T	0.1016490	-0.2684730	0.0100925	1.70E-167
8	LPL *	rs75801420	19992159	G	T	0.1017250	-0.2678910	0.0100933	7.90E-167
8	LPL *	rs17091905	19992246	A	G	0.1017480	-0.2688400	0.0100879	4.20E-168
8	LPL *	rs114964604	19992478	G	A	0.1008850	-0.2681770	0.0101377	8.60E-166
8	LPL *	rs73600084	19992481	C	T	0.1008850	-0.2681770	0.0101377	8.60E-166
8	LPL *	rs76975037	19993997	A	C	0.1016810	-0.2691100	0.0100929	1.90E-168
8	LPL *	rs17489268	19994534	A	T	0.1995610	-0.1864280	0.0076372	4.50E-139
8	LPL *	rs17411024	19994623	A	G	0.1014900	-0.2691240	0.0101016	2.50E-168
8	LPL *	rs17091909	19994645	T	G	0.1016550	-0.2691490	0.0100950	1.80E-168
8	LPL *	rs147729680	19994665	T	TTC	0.1996780	-0.1865550	0.0076351	3.10E-139
8	LPL *	rs17411031	19994799	G	C	0.1996030	-0.1865600	0.0076353	2.70E-139
8	LPL *	rs17411045	19994851	C	T	0.1994670	-0.1865750	0.0076407	4.00E-139
8	LPL *	rs17489282	19995007	T	C	0.1996430	-0.1866220	0.0076364	2.60E-139
8	LPL *	rs4922117	19995075	C	T	0.1996000	-0.1865650	0.0076353	2.70E-139
8	LPL *	rs1822200	19995318	T	G	0.1996000	-0.1865650	0.0076353	2.70E-139
8	LPL *	rs1372344	19995428	T	A	0.1996000	-0.1865650	0.0076353	2.70E-139
8	LPL *	rs1372345	19995437	A	C	0.0977961	-0.0588306	0.0102643	1.60E-08
8	LPL *	rs1992442	19995878	C	A	0.1997540	-0.1859840	0.0076371	1.90E-138
8	LPL *	rs2410618	19995989	A	G	0.1996080	-0.1866660	0.0076355	2.10E-139
8	LPL *	rs1992443	19996076	A	G	0.1996080	-0.1866660	0.0076355	2.10E-139
8	LPL *	rs920588	19996756	T	C	0.1996350	-0.1865570	0.0076353	3.20E-139
8	LPL *	rs920589	19996850	T	G	0.1996080	-0.1866750	0.0076355	2.00E-139
8	LPL *	rs4425772	19996989	T	C	0.1990940	-0.1866840	0.0076447	3.90E-139
8	LPL *	rs4628269	19996998	T	C	0.1990940	-0.1866840	0.0076447	3.90E-139
8	LPL *	rs2410619	19997042	A	C	0.1996080	-0.1866750	0.0076355	2.00E-139
8	LPL *	rs4320561	19997126	A	C	0.1994380	-0.1863510	0.0076395	7.80E-139
8	LPL *	rs2410620	19997149	T	C	0.1994380	-0.1863510	0.0076395	7.80E-139
8	LPL *	rs2410621	19997171	C	T	0.1994380	-0.1863510	0.0076395	7.80E-139
8	LPL *	rs2410623	19997378	G	A	0.1996190	-0.1866660	0.0076353	2.10E-139
8	LPL *	rs17411113	19997495	G	C	0.1017280	-0.2689480	0.0100949	3.20E-168
8	LPL *	rs79734126	19997519	T	C	0.0780950	-0.2574900	0.0113823	2.40E-122
8	LPL *	rs34564316	19997710	T	C	0.1996930	-0.1864220	0.0076419	5.50E-139
8	LPL *	rs17411126	19997761	C	T	0.1996250	-0.1867190	0.0076349	1.70E-139
8	LPL *	rs17411133	19997820	A	T	0.1996530	-0.1866090	0.0076342	2.40E-139
8	LPL *	rs17489373	19997833	A	G	0.1996590	-0.1866190	0.0076341	2.50E-139
8	LPL *	rs17411168	19998089	C	T	0.1998900	-0.1862230	0.0076260	3.80E-139
8	LPL *	rs34932218	19998150	G	A	0.1999490	-0.1861500	0.0076244	3.80E-139
8	LPL *	rs140426714	19998333	G	ATTATT	0.1983430	-0.1849220	0.0076640	4.80E-136
8	LPL *	rs34716293	19998568	T	C	0.0982600	-0.0584977	0.0102325	1.60E-08
8	LPL *	rs2165558	19998749	G	T	0.2197460	-0.1683250	0.0074767	5.80E-118
8	LPL *	rs4523270	19999028	C	T	0.2000000	-0.1859390	0.0076220	5.40E-139
8	LPL *	rs2103325	20000832	T	C	0.1996900	-0.1865820	0.0076246	5.20E-140
8	LPL *	rs1581675	20000988	A	T	0.1996960	-0.1865980	0.0076245	5.00E-140
8	LPL *	rs4490856	20001609	C	T	0.3534940	-0.1312060	0.0064220	1.90E-99
8	LPL *	rs79347507	20001937	A	T	0.0974837	-0.0591075	0.0102734	1.50E-08
8	LPL *	rs2119690	20002028	A	G	0.1997790	-0.1866430	0.0076227	3.60E-140
8	LPL *	rs2165556	20002116	T	C	0.1997780	-0.1866100	0.0076229	4.30E-140
8	LPL *	rs12541912	20002280	C	G	0.2001590	-0.1859530	0.0076172	2.70E-139
8	LPL *	rs74869266	20002686	C	A	0.0216709	-0.2620520	0.0209388	2.90E-38
8	LPL *	rs79236614	20002949	G	C	0.1015280	-0.2690500	0.0100983	1.90E-168
8	LPL *	rs34818360	20003236	A	G	0.1995080	-0.1864850	0.0076267	1.00E-139
8	LPL *	rs4083261	20003715	C	T	0.2001690	-0.1861900	0.0076171	1.20E-139
8	LPL *	rs3844510	20003850	C	A	0.1998440	-0.1869870	0.0076216	1.30E-140
8	LPL *	rs2410625	20004709	T	C	0.1998250	-0.1869410	0.0076218	1.40E-140
8	LPL *	rs4644277	20005059	C	T	0.1998250	-0.1869410	0.0076218	1.40E-140
8	LPL *	rs4389957	20005235	A	G	0.3541470	-0.1284920	0.0064126	8.00E-96
8	LPL *	rs1441766	20005277	T	A	0.2015940	-0.1854510	0.0076134	9.50E-139
8	LPL *	rs1441765	20005362	T	C	0.0981371	-0.0595942	0.0102336	8.70E-09
8	LPL *	rs1441764	20005513	T	C	0.2001740	-0.1862000	0.0076169	1.20E-139
8	LPL *	rs6586884	20005847	C	T	0.1016630	-0.2694620	0.0100928	4.90E-169
8	LPL *	rs6999813	20005960	A	T	0.1016630	-0.2694620	0.0100928	4.90E-169
8	LPL *	rs2119689	20005996	T	C	0.1998250	-0.1869410	0.0076218	1.40E-140
8	LPL *	chr8:20006328_G_GA	20006328	GA	G	0.1973280	-0.1892780	0.0076763	4.70E-142
8	LPL *	rs1596102	20006362	C	T	0.0981371	-0.0595942	0.0102336	8.70E-09
8	LPL *	rs1441763	20007045	C	T	0.1998310	-0.1869840	0.0076216	1.10E-140
8	LPL *	rs1441762	20007176	A	G	0.1999870	-0.1872800	0.0076244	5.70E-141
8	LPL *	rs1441761	20007237	C	G	0.1991850	-0.1862640	0.0076337	4.60E-139
8	LPL *	rs1441760	20007238	T	C	0.1991850	-0.1862640	0.0076337	4.60E-139
8	LPL *	chr8:20007371_T_TAAA	20007371	TAAA	T	0.1928160	-0.1868280	0.0077786	5.00E-136
8	LPL *	rs2083637	20007664	G	A	0.1997930	-0.1866440	0.0076211	3.20E-140
8	LPL *	rs2083636	20007752	G	T	0.2002590	-0.1862270	0.0076148	9.50E-140

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs77237194	20007944	T	A	0.1017040	-0.2693920	0.0100907	5.20E-169
8	LPL *	rs35495249	20007998	A	C	0.1986900	-0.1875570	0.0076448	9.90E-141
8	LPL *	rs894211	20008236	T	C	0.1987610	-0.1876050	0.0076433	8.50E-141
8	LPL *	rs894210	20008332	A	G	0.3554310	-0.1305260	0.0064030	5.80E-99
8	LPL *	rs765547	20008763	A	G	0.1999000	-0.1869420	0.0076197	1.30E-140
8	LPL *	rs765548	20009083	T	C	0.1998890	-0.1869460	0.0076198	1.30E-140
8	LPL *	rs765549	20009120	G	A	0.2002030	-0.1861630	0.0076163	1.30E-139
8	LPL *	rs1441758	20009367	T	A	0.1998890	-0.1869460	0.0076198	1.30E-140
8	LPL *	rs139547332	20009665	CT	C	0.0786055	-0.2582940	0.0113448	7.00E-124
8	LPL *	rs9644637	20009709	C	T	0.1998890	-0.1869460	0.0076198	1.30E-140
8	LPL *	rs9644638	20009889	T	C	0.1994700	-0.1862580	0.0076289	2.60E-139
8	LPL *	rs11986942	20009934	G	C	0.2002030	-0.1861630	0.0076163	1.30E-139
8	LPL *	rs34327087	20009983	T	G	0.1998220	-0.1867930	0.0076212	2.10E-140
8	LPL *	rs34345068	20010025	T	G	0.1998230	-0.1866380	0.0076211	3.70E-140
8	LPL *	rs2009493	20010342	A	G	0.1998910	-0.1869350	0.0076199	1.40E-140
8	LPL *	rs1837843	20010591	T	C	0.1960370	-0.1842890	0.0076805	8.70E-135
8	LPL *	rs1837842	20010779	C	T	0.1998910	-0.1869350	0.0076199	1.40E-140
8	LPL *	rs1441757	20010866	C	G	0.1998910	-0.1869350	0.0076199	1.40E-140
8	LPL *	rs1441755	20011377	C	T	0.1998910	-0.1869350	0.0076199	1.40E-140
8	LPL *	rs1441754	20011428	A	G	0.1991090	-0.1877100	0.0076371	3.60E-141
8	LPL *	rs4406409	20011460	C	T	0.1989220	-0.1859120	0.0076477	3.30E-138
8	LPL *	rs1441753	20011553	A	G	0.1998910	-0.1869350	0.0076199	1.40E-140
8	LPL *	rs4126104	20011855	T	G	0.1998910	-0.1869350	0.0076199	1.40E-140
8	LPL *	rs1919484	20012165	A	G	0.1998750	-0.1868860	0.0076200	1.60E-140
8	LPL *	rs35687633	20012476	G	A	0.1994830	-0.1867050	0.0076363	1.30E-139
8	LPL *	rs34942551	20012504	G	T	0.1994910	-0.1866810	0.0076364	1.50E-139
8	LPL *	rs34499461	20012516	C	G	0.1993710	-0.1867890	0.0076397	1.20E-139
8	LPL *	rs35369244	20012533	C	G	0.1993710	-0.1868300	0.0076398	1.10E-139
8	LPL *	rs35739466	20012576	A	G	0.1963590	-0.1825040	0.0076928	4.80E-132
8	LPL *	rs35617716	20012752	A	T	0.1969190	-0.1825960	0.0076691	2.00E-132
8	LPL *	rs35237252	20012760	A	C	0.1969610	-0.1823450	0.0076679	5.70E-132
8	LPL *	rs1569213	20013224	A	G	0.1774370	-0.1674470	0.0081340	9.50E-100
8	LPL *	rs78810414	20013602	T	C	0.0841407	-0.2577250	0.0110158	3.30E-132
8	LPL *	rs1372343	20013809	T	C	0.1848500	-0.1737650	0.0078777	4.10E-114
8	LPL *	rs1372342	20013820	A	T	0.1848550	-0.1737900	0.0078776	3.80E-114
8	LPL *	rs1372341	20013821	A	T	0.1848550	-0.1737900	0.0078776	3.80E-114
8	LPL *	rs1372340	20013861	A	G	0.1816720	-0.1700760	0.0079340	2.60E-108
8	LPL *	rs2410626	20013976	G	C	0.0965129	-0.0597742	0.0103294	1.70E-08
8	LPL *	rs2410627	20014002	C	T	0.1852430	-0.1731040	0.0078683	1.00E-113
8	LPL *	rs7461115	20014029	G	C	0.1852440	-0.1730670	0.0078682	1.20E-113
8	LPL *	rs2898494	20014069	G	C	0.0965298	-0.0595697	0.0103286	1.90E-08
8	LPL *	rs2410628	20014118	T	C	0.1852390	-0.1729370	0.0078681	1.70E-113
8	LPL *	rs2410629	20014126	C	T	0.1853220	-0.1730810	0.0078655	9.70E-114
8	LPL *	rs2898495	20014381	G	A	0.1853210	-0.1729190	0.0078655	1.50E-113
8	LPL *	rs4593558	20014497	G	A	0.1853310	-0.1729160	0.0078651	1.50E-113
8	LPL *	rs17489518	20014668	A	G	0.0965944	-0.0598023	0.0103242	1.60E-08
8	LPL *	rs17411294	20014675	T	C	0.0965944	-0.0598023	0.0103242	1.60E-08
8	LPL *	rs6986010	20015269	C	T	0.1853200	-0.1729120	0.0078654	1.60E-113
8	LPL *	rs35465966	20016045	A	C	0.1849700	-0.1728870	0.0078726	2.40E-113
8	LPL *	rs34693282	20016055	G	A	0.1852300	-0.1728400	0.0078675	2.30E-113
8	LPL *	rs17489539	20016071	A	T	0.1850600	-0.1728480	0.0078719	3.70E-113
8	LPL *	rs146562051	20016513	C	CTG	0.0966157	-0.0598086	0.0103241	1.60E-08
8	LPL *	rs4922118	20016634	T	C	0.1850230	-0.1730610	0.0078838	3.50E-113
8	LPL *	rs4922119	20016642	T	C	0.1850230	-0.1730610	0.0078838	3.50E-113
8	LPL *	rs4375019	20016987	A	T	0.1814050	-0.1700470	0.0079350	2.50E-108
8	LPL *	rs141287949	20017421	A	AAGAC	0.0845690	-0.2578400	0.0109766	3.10E-133
8	LPL *	rs4333617	20017493	G	A	0.1819870	-0.1689010	0.0079255	3.20E-107
8	LPL *	rs2410630	20017589	T	C	0.1820440	-0.1686710	0.0079250	6.40E-107
8	LPL *	rs6586886	20017897	A	G	0.1821510	-0.1686880	0.0079192	5.20E-107
8	LPL *	rs4403423	20018043	G	A	0.0967099	-0.0578845	0.0103244	4.20E-08
8	LPL *	rs73208815	20018604	C	G	0.1819620	-0.1692330	0.0079211	1.30E-107
8	LPL *	rs28675909	20018723	T	A	0.0845091	-0.2581030	0.0109789	5.50E-133
8	LPL *	rs79198716	20018753	T	C	0.0847077	-0.2579910	0.0109653	1.90E-133
8	LPL *	chr8:20018790_G_GA	20018790	GA	G	0.1832920	-0.1690320	0.0079213	3.10E-107
8	LPL *	rs78300069	20019013	T	C	0.0851818	-0.2576690	0.0109336	7.30E-134
8	LPL *	rs76737188	20019083	C	G	0.0888500	-0.2584700	0.0107188	1.20E-139
8	LPL *	rs7016880	20019235	C	G	0.0889135	-0.2579670	0.0107142	2.70E-139
8	LPL *	rs7007609	20019286	C	T	0.0888500	-0.2584700	0.0107188	1.20E-139
8	LPL *	rs7007797	20019459	G	T	0.0888506	-0.2584700	0.0107188	1.20E-139
8	LPL *	rs7004149	20019697	G	A	0.0888506	-0.2584700	0.0107188	1.20E-139
8	LPL *	rs7004158	20019722	G	A	0.0888506	-0.2584700	0.0107188	1.20E-139
8	LPL *	rs6983430	20019742	C	G	0.0888506	-0.2584700	0.0107188	1.20E-139

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs77219697	20019950	C	T	0.0888557	-0.2583730	0.0107198	1.60E-139
8	LPL *	rs12678603	20020221	T	C	0.0851981	-0.2575230	0.0109367	9.40E-134
8	LPL *	rs12678604	20020262	G	C	0.0851666	-0.2578680	0.0109363	4.80E-134
8	LPL *	rs1534650	20020643	C	T	0.3499780	-0.1247600	0.0064406	1.00E-90
8	LPL *	rs7013777	20020845	C	T	0.1865020	-0.1714080	0.0078493	2.80E-112
8	LPL *	rs4922120	20021087	G	A	0.3493740	-0.1229950	0.0064372	2.20E-88
8	LPL *	rs112994260	20021193	A	T	0.0888095	-0.2586770	0.0107240	9.30E-140
8	LPL *	rs142117848	20021359	A	C	0.0888120	-0.2587110	0.0107240	8.60E-140
8	LPL *	rs4335137	20021363	T	A	0.1874990	-0.1709900	0.0078327	5.80E-112
8	LPL *	rs1819092	20021566	C	T	0.1864880	-0.1717600	0.0078498	9.30E-113
8	LPL *	rs1819094	20021804	G	C	0.1831340	-0.1684810	0.0079085	2.60E-107
8	LPL *	rs4406410	20022163	C	T	0.0972604	-0.0582728	0.0103034	2.90E-08
8	LPL *	rs75082673	20022298	A	G	0.0851104	-0.2580740	0.0109401	4.10E-134
8	LPL *	rs7814717	20022339	T	C	0.0968313	-0.0584515	0.0103205	2.80E-08
8	LPL *	rs11989309	20022819	T	C	0.0887586	-0.2587540	0.0107266	8.40E-140
8	LPL *	rs34211025	20022868	A	G	0.0968343	-0.0584672	0.0103204	2.80E-08
8	LPL *	rs75675187	20023215	T	C	0.0887429	-0.2587920	0.0107278	8.20E-140
8	LPL *	rs74511360	20023529	A	G	0.0850852	-0.2579790	0.0109417	4.70E-134
8	LPL *	rs78404258	20023547	G	A	0.0888098	-0.2585610	0.0107248	1.00E-139
8	LPL *	rs74615535	20023725	A	G	0.0887344	-0.2589700	0.0107281	5.10E-140
8	LPL *	rs60223219	20024290	G	A	0.0887768	-0.2587870	0.0107264	7.10E-140
8	LPL *	rs35048052	20024541	AT	A	0.3505470	-0.1236430	0.0064256	1.80E-89
8	LPL *	rs1919485	20025210	G	T	0.0969376	-0.0585010	0.0103165	2.80E-08
8	LPL *	rs7816447	20025439	C	T	0.0874450	-0.2589680	0.0108175	5.30E-138
8	LPL *	rs1919486	20025776	T	A	0.0969824	-0.0588087	0.0103136	2.30E-08
8	LPL *	rs1919487	20026019	A	T	0.1825390	-0.1694190	0.0079141	2.90E-108
8	LPL *	rs73208819	20026413	C	T	0.2237300	0.0570988	0.0073332	2.10E-16
8	LPL *	rs114650503	20026746	A	G	0.0850643	-0.2579290	0.0109433	4.60E-134
8	LPL *	rs9644639	20027436	G	C	0.0850343	-0.2587010	0.0109476	9.30E-135
8	LPL *	rs140500946	20027919	T	TG	0.0976316	-0.0598890	0.0102712	9.60E-09
8	LPL *	rs2410631	20028057	T	A	0.1839080	-0.1684290	0.0078878	1.10E-107
8	LPL *	rs2410632	20028146	A	G	0.1837710	-0.1687260	0.0078915	6.00E-108
8	LPL *	rs11984636	20028215	C	T	0.0856145	-0.2571030	0.0109221	2.00E-133
8	LPL *	rs11984698	20028423	C	T	0.0855848	-0.2571740	0.0109257	1.90E-133
8	LPL *	rs35147888	20028593	T	TG	0.1838650	-0.1685550	0.0078890	7.60E-108
8	LPL *	rs11995475	20029177	T	C	0.0855591	-0.2572040	0.0109262	1.90E-133
8	LPL *	rs75469215	20029651	T	A	0.0850196	-0.2567240	0.0109802	1.00E-131
8	LPL *	rs4543558	20030818	G	C	0.1838190	-0.1690590	0.0078975	1.80E-108
8	LPL *	rs2178296	20031614	T	G	0.1669730	-0.1701770	0.0081765	7.10E-103
8	LPL *	rs78358410	20031888	G	T	0.0991816	-0.2510600	0.0102984	1.20E-142
8	LPL *	rs10103634	20033101	A	G	0.2498960	-0.1200230	0.0070679	2.50E-71
8	LPL *	rs139315015	20035786	G	A	0.1133420	-0.2050950	0.0096509	2.40E-110
8	LPL *	rs28841897	20036993	C	T	0.3380300	-0.1225900	0.0064934	4.20E-86
8	LPL *	rs149001621	20039893	T	C	0.0108691	0.2809730	0.0296865	1.10E-23
8	LPL *	rs4244457	20041535	T	C	0.3277590	-0.1237660	0.0064920	1.70E-87
8	LPL *	rs76259755	20041650	C	T	0.1128980	-0.2044990	0.0096523	3.20E-110
8	LPL *	rs7826306	20043160	C	G	0.3301150	-0.1205940	0.0064891	1.90E-83
8	LPL *	rs6993414	20045407	G	A	0.1137620	-0.2069310	0.0096201	2.70E-113
8	LPL *	rs74983646	20045739	A	G	0.0976184	-0.1950730	0.0103177	2.10E-88
8	LPL *	rs78299715	20048393	G	C	0.0488047	-0.1167590	0.0141786	1.10E-18
8	LPL *	rs118099376	20048449	A	G	0.0167437	-0.2624500	0.0238278	9.40E-30
8	LPL *	rs11991231	20050401	C	T	0.1135910	-0.2066650	0.0096309	8.90E-113
8	LPL *	rs66462329	20054549	A	G	0.2421710	-0.1262980	0.0071440	3.30E-77
8	LPL *	rs115849089	20054859	A	G	0.1101680	-0.2023800	0.0097580	1.50E-105
8	LPL *	rs4585763	20055743	T	A	0.3275730	-0.1240820	0.0065272	1.30E-87
8	SLC18A1 *	rs6586891	20057087	A	C	0.3233580	-0.1216510	0.0065522	4.70E-83
8	SLC18A1 *	rs10104610	20058043	C	G	0.2425600	-0.1261840	0.0071409	2.80E-77
8	SLC18A1 *	rs66778572	20058609	A	G	0.2415980	-0.1263070	0.0071553	4.40E-77
8	SLC18A1 *	rs10086580	20061975	G	A	0.2324670	-0.0450778	0.0072808	3.80E-10
8	SLC18A1 *	rs4128744	20062144	T	C	0.1113640	-0.2001670	0.0097178	3.20E-104
8	SLC18A1 *	rs4637851	20065099	A	G	0.3425920	-0.1242690	0.0065227	1.50E-87
8	SLC18A1 *	rs6999158	20070502	A	T	0.2645870	-0.1282800	0.0070153	3.00E-82
8	SLC18A1 *	rs10106652	20070649	A	G	0.2631010	-0.1287180	0.0070286	7.90E-83
8	SLC18A1 *	rs9644568	20071071	A	G	0.1125720	-0.2001920	0.0096479	1.80E-106
8	SLC18A1 *	rs34351848	20071686	T	TC	0.2621410	-0.1286630	0.0070820	2.30E-81
8	SLC18A1 *	rs76722925	20073987	G	A	0.0458210	-0.1106680	0.0146754	9.10E-17
8	SLC18A1 *	rs80026582	20075352	T	C	0.0428140	-0.1114180	0.0152159	2.10E-15
8	SLC18A1 *	rs79445051	20075578	G	C	0.0425645	-0.1092850	0.0152625	6.80E-15
8	SLC18A1 *	rs80302977	20076828	C	T	0.0414556	-0.1085650	0.0154979	3.70E-14
8	SLC18A1 *	rs13281248	20077573	A	G	0.0554298	-0.2405630	0.0135305	4.60E-78
8	SLC18A1 *	rs13257289	20077715	C	T	0.0567741	-0.2347680	0.0134232	2.10E-75
8	SLC18A1 *	rs28597716	20079176	G	A	0.1206360	-0.0681668	0.0095755	8.30E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	SLC18A1 *	chr8:20081391_CAAAT_C	20081391	C	CAAAT	0.1179810	-0.0707695	0.0094804	9.20E-15
8	SLC18A1 *	rs7001307	20081435	C	T	0.1164280	-0.0743319	0.0095599	8.70E-16
8	SLC18A1 *	rs12542766	20082161	G	A	0.2150000	-0.0542485	0.0074248	1.50E-13
8	SLC18A1 *	rs111648692	20082711	CTT	C	0.2151950	-0.0538604	0.0074177	2.20E-13
8	SLC18A1 *	rs35094081	20082955	AT	A	0.2157220	-0.0536301	0.0074147	3.00E-13
8	SLC18A1 *	rs11204085	20083285	C	T	0.1202900	-0.0721036	0.0093720	1.80E-15
8	SLC18A1 *	rs11204086	20083434	G	T	0.1202900	-0.0721036	0.0093720	1.80E-15
8	SLC18A1 *	rs11204087	20083516	T	C	0.1204030	-0.0720972	0.0093668	1.80E-15
8	SLC18A1 *	rs6586892	20083634	A	C	0.2118220	-0.0553823	0.0074556	5.80E-14
8	SLC18A1 *	rs12544702	20083748	C	T	0.1202040	-0.0728867	0.0093759	1.10E-15
8	SLC18A1 *	rs6989064	20083937	T	C	0.2038390	-0.0578449	0.0075687	1.50E-14
8	SLC18A1 *	rs4543559	20084343	G	A	0.2158930	-0.0541003	0.0074039	1.70E-13
8	SLC18A1 *	rs34095314	20084640	TA	T	0.1202080	-0.0726880	0.0093754	1.30E-15
8	SLC18A1 *	rs13263508	20084670	T	G	0.2002920	-0.0579436	0.0076265	2.30E-14
8	SLC18A1 *	rs34758843	20085184	T	C	0.1201590	-0.0727782	0.0093782	1.20E-15
8	SLC18A1 *	rs35005862	20085189	C	T	0.1201590	-0.0727782	0.0093782	1.20E-15
8	SLC18A1 *	rs73210856	20085295	G	A	0.1200070	-0.0730034	0.0093860	1.00E-15
8	SLC18A1 *	rs73210858	20085296	A	T	0.1200070	-0.0730034	0.0093860	1.00E-15
8	SLC18A1 *	rs11986461	20085397	A	C	0.2098990	-0.0555757	0.0074955	4.80E-14
8	SLC18A1 *	rs28475019	20085440	A	T	0.1200510	-0.0723371	0.0093853	1.70E-15
8	SLC18A1 *	rs13265868	20085516	A	G	0.1198890	-0.0721572	0.0093929	2.00E-15
8	SLC18A1 *	rs28450859	20085556	C	G	0.1197270	-0.0723600	0.0094005	1.70E-15
8	SLC18A1 *	rs13273470	20085675	C	G	0.1184790	-0.0711294	0.0094604	8.60E-15
8	SLC18A1 *	rs13275622	20085708	A	C	0.1179750	-0.0719664	0.0094895	5.80E-15
8	SLC18A1 *	rs13276972	20085797	G	A	0.1388610	-0.0606326	0.0089398	3.40E-12
8	SLC18A1 *	rs12676079	20085853	T	C	0.1156350	-0.0700379	0.0096123	4.70E-14
8	FUT10 *	rs1445190	34398333	G	A	0.4908010	0.0345649	0.0061999	1.00E-08
8	FUT10 *	rs2404558	34408317	A	T	0.4908780	0.0347677	0.0062031	8.60E-09
8	FUT10 *	rs4486200	34436234	T	C	0.4918140	0.0354335	0.0062148	5.10E-09
8	RNF122 *	rs7826177	34549022	T	C	0.4502040	0.0337611	0.0062594	3.50E-08
8	RNF122 *	rs12677593	34549378	A	G	0.4496500	0.0337269	0.0062602	3.90E-08
8	NCOA2	chr8:70131186_A_AT	70131186	AT	A	0.3658910	0.0365100	0.0063714	1.30E-08
8	NCOA2	rs34649703	70149394	C	CCAT	0.3581840	0.0371426	0.0064360	1.10E-08
8	NCOA2	rs12675772	70301470	G	C	0.3698870	0.0354190	0.0063262	3.20E-08
8	NCOA2	rs12675593	70327337	C	T	0.3719990	0.0349908	0.0063252	4.70E-08
8	NCOA2	rs13266875	70343722	T	A	0.3705810	0.0350369	0.0063230	4.80E-08
8	NCOA2	rs7012908	70377062	A	G	0.3660490	0.0362695	0.0063903	2.00E-08
8	NCOA2 *	rs35229942	70405995	A	C	0.3704480	0.0350513	0.0063326	4.90E-08
8	NCOA2 *	rs11776606	70408062	A	C	0.3696580	0.0353099	0.0063440	4.30E-08
8	NCOA2 *	rs11776287	70414380	G	A	0.3721030	0.0356789	0.0063332	2.70E-08
8	TRPS1 *	rs179456	115682885	A	G	0.3533060	-0.0351653	0.0064442	3.50E-08
8	TRPS1 *	rs17729317	115683666	A	G	0.3532110	-0.0350359	0.0064445	3.90E-08
8	TRPS1 *	rs4876612	115686812	T	C	0.3529590	-0.0350468	0.0064477	4.10E-08
8	TRPS1 *	rs751078958	115690717	A	C	0.3534920	-0.0355510	0.0064449	2.30E-08
8	TRPS1 *	rs800566	115697608	A	G	0.3532500	-0.0352008	0.0064446	3.40E-08
8	TRPS1 *	rs800575	115703162	C	T	0.3540320	-0.0349861	0.0064398	4.00E-08
8	TRPS1 *	rs800574	115705224	A	C	0.3431870	-0.0365472	0.0064752	1.10E-08
8	TRPS1 *	rs800572	115706211	A	G	0.3450940	-0.0356926	0.0064633	2.30E-08
8	TRPS1 *	rs2960151	115706393	C	A	0.3431730	-0.0364970	0.0064751	1.20E-08
8	TRPS1 *	rs800538	115710763	A	G	0.3265440	-0.0372289	0.0065485	1.00E-08
8	TRPS1 *	rs800539	115712972	G	A	0.3257730	-0.0375217	0.0065589	8.30E-09
8	TRPS1 *	rs800541	115717911	G	T	0.3285940	-0.0361710	0.0065398	2.40E-08
8	TRPS1 *	rs800542	115719218	C	T	0.3268220	-0.0370717	0.0065464	1.20E-08
8	TRPS1 *	rs800571	115720681	T	C	0.3265610	-0.0370919	0.0065471	1.20E-08
8	TRPS1 *	chr8:115722505_TAC_T	115722505	TAC	T	0.3325870	-0.0390577	0.0065482	2.60E-09
8	TRPS1 *	rs7834801	115731575	T	C	0.3322190	-0.0349809	0.0064602	3.80E-08
8	TRPS1 *	rs139674239	115731796	TG	T	0.3273930	-0.0363214	0.0064935	1.30E-08
8	TRPS1 *	rs800521	115732282	A	C	0.3300160	-0.0356820	0.0064737	2.20E-08
8	TRPS1 *	rs800520	115732360	G	T	0.3300200	-0.0356897	0.0064737	2.20E-08
8	TRPS1 *	rs71287295	115733764	C	CT	0.3319220	-0.0350220	0.0064613	3.70E-08
8	TRPS1 *	rs1880816	115733959	T	G	0.3319220	-0.0350220	0.0064613	3.70E-08
8	TRPS1 *	rs1880815	115734059	G	A	0.3319900	-0.0351681	0.0064606	3.30E-08
8	TRPS1 *	rs1880814	115734251	C	T	0.3322050	-0.0349135	0.0064602	4.00E-08
8	TRPS1 *	rs2205265	115734520	G	T	0.3319240	-0.0350307	0.0064613	3.70E-08
8	TRPS1 *	rs2205266	115734673	G	A	0.3319220	-0.0350220	0.0064613	3.70E-08
8	TRPS1 *	rs149197697	115735087	T	TTCTC	0.3343110	-0.0355597	0.0064812	2.50E-08
8	TRPS1 *	rs2736233	115735138	G	T	0.3325930	-0.0347879	0.0064691	4.40E-08
8	TRPS1 *	rs1405297	115735275	G	T	0.3319220	-0.0350220	0.0064613	3.70E-08
8	TRPS1 *	rs1830141	115735511	A	G	0.3324090	-0.0348663	0.0064668	4.50E-08
8	TRPS1 *	rs1405296	115735525	C	A	0.3321580	-0.0354801	0.0064637	2.50E-08
8	TRPS1 *	rs2960148	115735563	C	T	0.3319220	-0.0350220	0.0064613	3.70E-08
8	TRPS1 *	rs2736234	115735598	G	T	0.3319220	-0.0350220	0.0064613	3.70E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	TRPS1 *	rs2694048	115735937	C	T	0.3319040	-0.0350284	0.0064617	3.70E-08
8	TRPS1 *	rs2254555	115741374	T	G	0.3314850	-0.0348400	0.0064640	4.60E-08
8	TRPS1 *	rs5894291	115741527	A	AT	0.3320270	-0.0351153	0.0064712	3.90E-08
8	TRPS1 *	rs985161	115741917	C	T	0.3316050	-0.0348280	0.0064645	4.60E-08
8	TRPS1 *	rs1040331	115742981	T	C	0.3292140	-0.0353073	0.0064786	3.20E-08
8	TRPS1 *	rs2975510	115742985	T	C	0.3321790	-0.0348112	0.0064661	4.50E-08
8	TRPS1 *	rs2960146	115743211	A	G	0.3315160	-0.0348538	0.0064643	4.50E-08
8	TRIB1 *	rs6999569	125463528	G	A	0.1446020	-0.0732428	0.0087526	2.10E-18
8	TRIB1 *	rs2980856	125464137	G	C	0.1443270	-0.0733928	0.0087511	1.90E-18
8	TRIB1 *	rs2954017	125464631	T	C	0.4348670	0.0916244	0.0061498	3.90E-53
8	TRIB1 *	rs2954018	125464911	C	T	0.2970900	0.0874536	0.0066744	2.70E-41
8	TRIB1 *	rs2980855	125465234	C	T	0.1443320	-0.0734375	0.0087506	1.90E-18
8	TRIB1 *	rs2980854	125465255	T	C	0.1443380	-0.0734505	0.0087502	1.80E-18
8	TRIB1 *	rs2954019	125465517	A	G	0.1441920	-0.0735139	0.0087553	1.90E-18
8	TRIB1 *	rs2001945	125465736	G	C	0.4349290	0.0915557	0.0061493	4.70E-53
8	TRIB1 *	rs2980853	125466108	A	C	0.4415460	0.0900214	0.0061413	2.30E-51
8	TRIB1 *	rs2001846	125466208	T	C	0.4349560	0.0916333	0.0061502	3.60E-53
8	TRIB1 *	rs2001845	125466402	A	G	0.2971260	0.0875359	0.0066754	2.20E-41
8	TRIB1 *	rs2001844	125466503	A	G	0.4416150	0.0901718	0.0061425	1.60E-51
8	TRIB1 *	rs6982636	125467073	G	A	0.4417310	0.0901208	0.0061412	1.80E-51
8	TRIB1 *	rs6982502	125467120	C	T	0.4349650	0.0915664	0.0061488	3.90E-53
8	TRIB1 *	rs2980886	125467846	G	A	0.4417890	0.0900114	0.0061404	2.10E-51
8	TRIB1 *	rs4871603	125468125	C	T	0.3040490	0.0845445	0.0066281	3.60E-39
8	TRIB1 *	rs2980882	125468458	A	G	0.4418190	0.0899862	0.0061413	2.30E-51
8	TRIB1 *	rs2980880	125468730	G	A	0.2973280	0.0871923	0.0066699	3.70E-41
8	TRIB1 *	rs2980879	125469233	A	T	0.2971340	0.0865838	0.0066662	1.20E-40
8	TRIB1 *	rs2980876	125469452	C	T	0.2974070	0.0871168	0.0066694	4.40E-41
8	TRIB1 *	rs2980875	125469505	A	G	0.4487260	0.0890823	0.0061390	1.40E-50
8	TRIB1 *	rs2954020	125469710	A	G	0.2974850	0.0872778	0.0066688	3.50E-41
8	TRIB1 *	rs2954021	125469835	A	G	0.4407820	0.0911076	0.0061426	7.10E-53
8	TRIB1 *	rs2954022	125470379	C	A	0.4474370	0.0895540	0.0061344	3.40E-51
8	TRIB1 *	rs79658059	125470680	T	TA	0.2975290	0.0872274	0.0066708	3.70E-41
8	TRIB1 *	rs28495284	125470681	G	A	0.3102080	0.0832329	0.0067176	2.10E-37
8	TRIB1 *	rs2954024	125470688	A	G	0.2975290	0.0872274	0.0066708	3.70E-41
8	TRIB1 *	rs2980870	125471598	A	G	0.3116400	0.0847317	0.0066697	6.30E-39
8	TRIB1 *	chr8:125471601_TAA_T	125471601	TAA	T	0.3028340	0.0851702	0.0066489	1.30E-39
8	TRIB1 *	rs4336630	125472034	T	G	0.3046860	0.0840330	0.0066222	7.00E-39
8	TRIB1 *	rs2954025	125472221	C	T	0.3046930	0.0840362	0.0066220	6.90E-39
8	TRIB1 *	rs2954026	125472284	T	G	0.2978860	0.0867123	0.0066656	7.60E-41
8	TRIB1 *	rs2980862	125472396	G	C	0.2978700	0.0868260	0.0066658	6.10E-41
8	TRIB1 *	rs35575186	125472985	A	AT	0.3046960	0.0840280	0.0066220	7.00E-39
8	TRIB1 *	rs2954027	125473052	T	A	0.4479070	0.0894231	0.0061347	3.80E-51
8	TRIB1 *	rs2954028	125473054	T	C	0.2978730	0.0868179	0.0066658	6.20E-41
8	TRIB1 *	rs2980860	125473095	A	G	0.4480080	0.0894308	0.0061357	3.80E-51
8	TRIB1 *	rs7828113	125473225	A	G	0.3047660	0.0842316	0.0066232	4.40E-39
8	TRIB1 *	rs7846466	125473289	T	C	0.2979920	0.0871227	0.0066680	3.80E-41
8	TRIB1 *	chr8:125473988_G_GT	125473988	G	GT	0.3032030	0.0850468	0.0066796	4.90E-39
8	TRIB1 *	rs17321515	125474167	A	G	0.4480850	0.0896922	0.0061335	1.90E-51
8	TRIB1 *	rs2980867	125475449	T	G	0.2979430	0.0871139	0.0066682	3.00E-41
8	TRIB1 *	rs2980868	125475993	C	T	0.4482090	0.0901629	0.0061363	7.00E-52
8	TRIB1 *	rs2980869	125476008	C	T	0.4483950	0.0901274	0.0061375	8.60E-52
8	TRIB1 *	rs59871348	125476465	ATTG	A	0.3053840	0.0844817	0.0066262	2.30E-39
8	TRIB1 *	rs2980871	125476688	G	A	0.1261550	-0.0751013	0.0092277	3.30E-17
8	TRIB1 *	rs2954029	125478730	A	T	0.4479440	0.0902348	0.0061317	6.00E-52
8	TRIB1 *	rs5894757	125478769	T	TG	0.3049920	0.0842857	0.0066241	3.90E-39
8	TRIB1 *	rs2954030	125479062	T	C	0.3182630	0.0781600	0.0065533	2.90E-34
8	TRIB1 *	rs2954031	125479491	G	T	0.4617610	0.0862891	0.0061198	1.50E-47
8	TRIB1 *	rs12164213	125480206	T	C	0.4373870	0.0379329	0.0061609	5.00E-10
8	TRIB1 *	rs56116731	125480684	C	CT	0.3019460	0.0872232	0.0066887	5.20E-41
8	TRIB1 *	rs10956250	125480889	A	G	0.4373580	0.0379543	0.0061605	5.00E-10
8	TRIB1 *	rs2954032	125481150	A	G	0.2976190	0.0877567	0.0066753	7.90E-42
8	TRIB1 *	rs2954033	125481504	A	G	0.2983410	0.0876743	0.0066643	9.10E-42
8	TRIB1 *	rs4457349	125482075	G	A	0.4192100	-0.0560813	0.0061825	2.00E-20
8	TRIB1 *	chr8:125482151_G_GT	125482151	G	GT	0.4439010	0.0394153	0.0062082	1.70E-10
8	TRIB1 *	rs4350001	125482320	C	T	0.4375210	0.0380184	0.0061576	4.60E-10
8	TRIB1 *	rs4552916	125482522	A	G	0.4376490	0.0384231	0.0061589	3.10E-10
8	TRIB1 *	rs35192929	125482927	T	C	0.4367930	0.0384918	0.0061606	2.90E-10
8	TRIB1 *	rs12680798	125483251	G	C	0.0977217	-0.0843783	0.0103798	8.80E-17
8	TRIB1 *	rs7005535	125483343	T	C	0.4370580	0.0388314	0.0061645	2.20E-10
8	TRIB1 *	rs10808546	125483576	T	C	0.1257020	-0.0747512	0.0092035	3.10E-17
8	TRIB1 *	rs6470358	125483683	G	A	0.4368080	0.0389435	0.0061615	1.80E-10
8	TRIB1 *	rs16900644	125484533	C	T	0.4364580	0.0388897	0.0061683	2.00E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	TRIB1 *	rs12681878	125484683	C	T	0.4364410	0.0389174	0.0061685	1.90E-10
8	TRIB1 *	rs4870942	125486661	C	T	0.4400950	0.0390336	0.0061849	1.60E-10
8	TRIB1 *	rs72442317	125486996	CCAGT	C	0.4366330	0.0392885	0.0061677	1.20E-10
8	TRIB1 *	rs1055748815	125486998	AGTCG	A	0.4366330	0.0392885	0.0061677	1.20E-10
8	TRIB1 *	rs2980859	125487187	C	G	0.2833420	0.0946570	0.0067840	1.90E-46
8	TRIB1 *	rs4351435	125487636	G	A	0.2833420	0.0946393	0.0067841	2.00E-46
8	TRIB1 *	rs28601761	125487789	G	C	0.1508040	-0.0752989	0.0085483	3.90E-20
8	TRIB1 *	rs2980858	125488935	T	C	0.2838190	0.0946328	0.0067805	1.90E-46
8	TRIB1 *	rs11320307	125489095	CA	C	0.4360380	0.0390759	0.0061749	1.80E-10
8	TRIB1 *	rs7846135	125489286	G	A	0.4343250	0.0371428	0.0061791	1.50E-09
8	TRIB1 *	rs6987702	125492484	T	C	0.4342060	0.0394091	0.0061663	9.60E-11
8	TRIB1 *	rs75998532	125493463	C	T	0.4038890	-0.0593238	0.0062306	2.40E-22
8	TRIB1 *	rs112875651	125494452	A	G	0.1303080	-0.0731204	0.0090843	1.20E-16
8	TRIB1 *	rs2980888	125495066	T	C	0.2812670	0.0959573	0.0067890	5.40E-48
8	TRIB1 *	rs2954038	125495147	C	A	0.2814290	0.0962365	0.0067863	3.20E-48
8	TRIB1 *	rs6987904	125495783	T	C	0.4029290	-0.0589289	0.0062714	7.50E-22
8	TRIB1 *	rs6989280	125496504	G	A	0.4390280	0.0392762	0.0062511	1.40E-10
9	DMRT2 *	rs10958983	1035081	C	T	0.3721070	0.0382793	0.0063501	1.20E-08
9	DMRT2 *	rs150549203	1035756	AAAAA	A	0.3691010	0.0372728	0.0063762	3.40E-08
9	DMRT2 *	rs4741016	1036132	C	T	0.3718820	0.0379462	0.0063487	1.80E-08
9	DMRT2 *	rs12001314	1038063	C	A	0.3742520	0.0382771	0.0063360	1.20E-08
9	DMRT2 *	rs10959032	1038666	T	C	0.3724990	0.0380064	0.0063485	1.60E-08
9	PTPN3	rs75992442	109434977	G	A	0.2015930	-0.0401322	0.0076699	4.70E-08
9	PTPN3	rs57707037	109473833	C	T	0.2446480	-0.0413049	0.0072171	7.60E-10
9	PTPN3	rs60227798	109473873	T	C	0.2446990	-0.0412393	0.0072148	7.60E-10
9	PTPN3	rs76298084	109474452	T	G	0.2438430	-0.0414896	0.0072304	6.40E-10
9	PTPN3	rs58272963	109474628	A	G	0.2446410	-0.0417802	0.0072159	4.60E-10
9	PTPN3	rs59668107	109474718	A	G	0.2446370	-0.0417689	0.0072159	4.70E-10
9	PTPN3	rs78579422	109475873	T	C	0.2437940	-0.0424100	0.0072331	3.40E-10
9	PTPN3	rs75862441	109477363	T	C	0.2291880	-0.0426369	0.0074008	5.00E-10
9	PTPN3	rs41529151	109478114	G	C	0.2291470	-0.0446433	0.0073958	8.60E-11
9	PTPN3	rs56279802	109478850	T	C	0.2549080	-0.0394813	0.0071287	2.20E-09
9	PTPN3	rs77824033	109478856	C	T	0.2295460	-0.0445817	0.0073861	7.90E-11
9	PTPN3	rs796238584	109479010	TGTC	T	0.2556310	-0.0394652	0.0071355	2.30E-09
9	PTPN3	rs55727942	109479011	G	T	0.2546500	-0.0393216	0.0071567	3.30E-09
9	PTPN3	rs55824262	109479013	C	T	0.2547630	-0.0390754	0.0071544	4.10E-09
9	PTPN3	rs12376215	109479090	A	T	0.2546300	-0.0394931	0.0071324	2.20E-09
9	PTPN3	rs117969049	109480282	T	C	0.2297240	-0.0443232	0.0073783	1.00E-10
9	PTPN3	rs17793873	109482041	T	C	0.2301520	-0.0432900	0.0073695	2.60E-10
9	PTPN3	rs74928072	109482095	A	G	0.2301650	-0.0433663	0.0073685	2.50E-10
9	PTPN3	rs75024825	109482136	T	C	0.2299340	-0.0434934	0.0073660	2.30E-10
9	PTPN3	rs75113691	109483493	C	G	0.2309590	-0.0429636	0.0073473	3.30E-10
9	PTPN3	rs78919659	109483714	T	C	0.2306980	-0.0428838	0.0073490	3.80E-10
9	PTPN3	rs57906233	109485510	GA	G	0.2317590	-0.0401830	0.0073414	3.50E-09
9	PTPN3	rs78424787	109485849	A	C	0.2321710	-0.0404019	0.0073249	2.50E-09
9	PTPN3	rs59380239	109488319	T	C	0.2497390	-0.0397334	0.0070615	1.90E-09
9	PTPN3	rs139465238	109494073	A	AAGG	0.2498030	-0.0404962	0.0070566	9.50E-10
9	PTPN3	rs75577555	109495675	T	C	0.2500090	-0.0407017	0.0070537	8.00E-10
9	PTPN3	rs184172568	109497966	T	C	0.2497240	-0.0397545	0.0070714	1.70E-09
9	PTPN3 *	rs117533884	109499788	G	C	0.2500130	-0.0405254	0.0070510	8.50E-10
9	PTPN3 *	rs78042633	109502844	T	C	0.2499670	-0.0404976	0.0070517	8.10E-10
9	PTPN3 *	rs17793891	109502949	G	A	0.2503600	-0.0403430	0.0070455	1.00E-09
9	MIR3927 *	rs140269699	109506584	C	CTCTT	0.2444920	-0.0424222	0.0071383	2.30E-10
9	MIR3927 *	rs10123707	109508041	C	G	0.2752600	-0.0375302	0.0068405	4.40E-09
9	MIR3927 *	rs61358126	109511453	G	A	0.2498860	-0.0404494	0.0070552	9.60E-10
9	MIR3927 *	rs2150260	109511914	G	A	0.2817480	-0.0365022	0.0067848	1.20E-08
9	MIR3927 *	rs79437785	109512085	C	T	0.2498460	-0.0403795	0.0070563	9.90E-10
9	MIR3927 *	rs6477708	109513462	G	A	0.2815900	-0.0366555	0.0067902	1.10E-08
9	MIR3927 *	rs7341726	109513495	G	C	0.2815790	-0.0366699	0.0067903	1.10E-08
9	MIR3927 *	rs1411682	109514077	T	C	0.2815800	-0.0366911	0.0067905	1.10E-08
9	MIR3927 *	rs10124300	109515460	C	A	0.2815230	-0.0361740	0.0067882	1.60E-08
9	MIR3927 *	rs77218860	109517046	A	G	0.2468160	-0.0385133	0.0070950	7.00E-09
9	MIR3927 *	rs76636909	109518424	T	C	0.2491570	-0.0389946	0.0070593	4.10E-09
9	MIR3927 *	rs139346903	109520059	A	T	0.2491620	-0.0389469	0.0070592	4.30E-09
9	MIR3927 *	rs80070092	109521917	T	C	0.2491620	-0.0389469	0.0070592	4.30E-09
9	MIR3927 *	rs117827315	109532784	G	T	0.2502050	-0.0395046	0.0070625	2.50E-09
9	MIR3927 *	rs117527665	109533559	A	C	0.2489730	-0.0391821	0.0070674	3.50E-09
9	MIR3927 *	chr9:109535507_C_CT	109535507	CT	C	0.2458270	-0.0406309	0.0071679	1.80E-09
9	MIR3927 *	rs77274786	109536366	G	A	0.2491330	-0.0409477	0.0070933	7.70E-10
9	MIR3927 *	rs17201835	109541578	G	A	0.2522210	-0.0401365	0.0070747	8.10E-10
9	MIR3927 *	chr9:109544207_GT_G	109544207	G	GT	0.2764530	-0.0352650	0.0069155	4.50E-08
9	MIR3927 *	rs1571642	109548492	A	G	0.2557270	-0.0382056	0.0070437	6.20E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	MIR3927 *	rs75803161	109558741	A	T	0.2473540	-0.0402309	0.0071339	1.10E-09
9	MIR3927 *	rs139221760	109560788	CT	C	0.2494450	-0.0398932	0.0071243	2.30E-09
9	MIR3927 *	rs7858161	109562771	A	G	0.2545440	-0.0387588	0.0070660	4.50E-09
9	MIR3927 *	rs75001090	109565034	C	A	0.2499370	-0.0394251	0.0071241	3.20E-09
9	MIR3927 *	rs7849221	109567429	A	G	0.2481040	-0.0402817	0.0071428	1.40E-09
9	MIR3927 *	rs150040590	109573935	T	C	0.1911880	-0.0424393	0.0078347	1.40E-08
9	MIR3927 *	rs117103218	109574154	A	G	0.1887600	-0.0423158	0.0078665	1.70E-08
9	PALM2 *	rs200290358	109577536	A	AT	0.1912850	-0.0425431	0.0078191	1.40E-08
9	PALM2 *	rs200745414	109577539	C	A	0.1922990	-0.0428459	0.0077973	8.90E-09
9	PALM2 *	rs76508340	109580420	T	C	0.1784080	-0.0429798	0.0080614	1.20E-08
9	PALM2 *	rs78815286	109582984	T	G	0.1927550	-0.0422448	0.0077776	1.30E-08
9	PALM2 *	rs78864591	109583284	T	C	0.1927560	-0.0422089	0.0077776	1.40E-08
9	PALM2 *	rs17202062	109591436	C	G	0.1908710	-0.0428964	0.0078082	7.50E-09
9	PALM2 *	rs17794184	109592937	C	A	0.1906860	-0.0429665	0.0078062	7.20E-09
9	PALM2 *	rs58105812	109593130	A	T	0.1906840	-0.0429779	0.0078063	7.20E-09
9	PALM2 *	rs78927344	109593586	G	A	0.1906980	-0.0429877	0.0078065	7.20E-09
9	PALM2 *	rs10979958	109595732	A	G	0.1944360	-0.0432123	0.0077711	9.60E-09
9	PALM2 *	rs75235286	109596281	T	C	0.1956190	-0.0431542	0.0077408	7.90E-09
9	PALM2 *	rs137989413	109598306	A	C	0.1953900	-0.0428918	0.0077454	8.90E-09
10	NRBF2 *	rs10995445	63114994	T	A	0.3175510	-0.0387031	0.0066171	1.20E-09
10	NRBF2 *	rs7903602	63115551	A	G	0.3846410	0.0534786	0.0063574	1.50E-18
10	NRBF2 *	rs4414112	63115786	A	G	0.3842330	0.0539915	0.0063370	5.00E-19
10	NRBF2 *	rs4545434	63115985	C	T	0.3752270	0.0527430	0.0063608	3.20E-18
10	NRBF2 *	rs7084569	63116794	A	G	0.3165410	-0.0385735	0.0066150	1.40E-09
10	NRBF2 *	rs7084396	63116965	A	G	0.3840580	0.0534040	0.0063228	1.00E-18
10	NRBF2 *	rs35248047	63117160	A	AC	0.3873370	0.0531078	0.0063321	2.30E-18
10	NRBF2 *	rs10822138	63117400	G	A	0.3897300	0.0528530	0.0063602	5.10E-18
10	NRBF2 *	rs6479877	63118358	G	C	0.3172350	-0.0375905	0.0065651	4.10E-09
10	NRBF2 *	rs1396964	63118538	G	A	0.3872720	0.0536965	0.0062865	6.20E-19
10	NRBF2 *	rs6479878	63118657	A	G	0.3878320	0.0530298	0.0062902	1.30E-18
10	NRBF2 *	rs6479879	63118669	G	T	0.3878300	0.0530558	0.0062902	1.30E-18
10	NRBF2 *	rs6479880	63118671	A	T	0.3878300	0.0530558	0.0062902	1.30E-18
10	NRBF2 *	rs6479881	63118802	T	C	0.3871990	0.0535735	0.0062878	7.20E-19
10	NRBF2 *	rs10995447	63119761	A	G	0.3782520	0.0522555	0.0063238	4.30E-18
10	NRBF2 *	rs10761716	63122540	G	C	0.3185260	-0.0384596	0.0065691	1.60E-09
10	NRBF2 *	rs4746951	63123839	G	A	0.3782900	0.0524920	0.0063231	2.90E-18
10	NRBF2 *	rs61853335	63124977	T	C	0.3782670	0.0524972	0.0063230	2.90E-18
10	NRBF2 *	rs72824948	63126343	G	A	0.3783210	0.0524068	0.0063228	3.40E-18
10	NRBF2 *	rs10822143	63128096	T	C	0.3182330	-0.0381861	0.0065922	2.30E-09
10	NRBF2 *	rs4746974	63132292	T	G	0.3784600	0.0518139	0.0063131	6.40E-18
10	NRBF2	rs868798	63135250	G	A	0.3788250	0.0515763	0.0063069	8.00E-18
10	NRBF2	rs12416113	63136717	A	T	0.3786530	0.0515014	0.0063086	9.10E-18
10	NRBF2	rs61853336	63140115	A	G	0.3788110	0.0518443	0.0063066	5.60E-18
10	NRBF2	rs80082080	63142032	AT	A	0.2490790	-0.0407770	0.0070925	1.20E-08
10	NRBF2	rs7070052	63144054	A	G	0.3788400	0.0517760	0.0063054	6.10E-18
10	NRBF2	rs7073746	63144311	G	A	0.3160900	-0.0379490	0.0065783	2.20E-09
10	NRBF2	rs7916224	63144843	T	C	0.3878340	0.0528072	0.0062786	1.40E-18
10	NRBF2	rs4746994	63145564	A	T	0.3789180	0.0515155	0.0063008	8.10E-18
10	NRBF2	rs10733787	63147078	T	A	0.3879280	0.0526371	0.0062758	1.60E-18
10	NRBF2	chr10:63147321_AT_A	63147321	A	AT	0.3799990	0.0515768	0.0063406	1.30E-17
10	NRBF2	rs12240740	63147478	C	A	0.3879270	0.0526355	0.0062757	1.60E-18
10	NRBF2	rs11278263	63147821	T	CTGTAA	0.3144960	-0.0367974	0.0065891	6.90E-09
10	NRBF2	rs12415984	63150528	A	G	0.3789290	0.0515267	0.0062998	7.60E-18
10	NRBF2	rs35751397	63154256	TA	T	0.3159500	-0.0368894	0.0065690	5.20E-09
10	NRBF2	rs13095	63154612	C	G	0.3159520	-0.0368947	0.0065690	5.20E-09
10	NRBF2	rs1160843	63154758	C	CATA	0.3158670	-0.0367086	0.0065721	6.00E-09
10	NRBF2 *	rs7897470	63156304	G	T	0.3656090	0.0492759	0.0063965	4.60E-16
10	NRBF2 *	rs1009984	63156709	T	G	0.3876110	0.0522214	0.0062771	2.80E-18
10	NRBF2 *	rs11814792	63157799	T	C	0.3776090	0.0518103	0.0063044	6.50E-18
10	NRBF2 *	rs10733788	63158105	T	C	0.3875550	0.0523342	0.0062770	2.50E-18
10	NRBF2 *	rs61853339	63158919	C	T	0.3780130	0.0517819	0.0063000	7.00E-18
10	NRBF2 *	rs12413415	63159751	C	T	0.3750470	0.0507581	0.0063140	2.90E-17
10	NRBF2 *	rs34132715	63160401	C	CTAAA	0.3772040	0.0517231	0.0063076	8.70E-18
10	JMJD1C *	rs11817689	63164457	C	T	0.3794470	0.0517302	0.0062976	6.00E-18
10	JMJD1C *	rs3072249	63165570	CCAT	C	0.3880840	0.0527909	0.0062740	1.20E-18
10	JMJD1C *	rs4747045	63166722	T	C	0.3783350	0.0517146	0.0062986	6.00E-18
10	JMJD1C	rs1935	63168063	G	C	0.3126450	-0.0379523	0.0065898	1.30E-09
10	JMJD1C	rs1904296	63173019	C	G	0.3876490	0.0512552	0.0062858	1.10E-17
10	JMJD1C	rs4466712	63173508	C	G	0.3768670	0.0520208	0.0063033	4.30E-18
10	JMJD1C	chr10:63173739_G_GA	63173739	GA	G	0.3710800	0.0522103	0.0063613	6.20E-18
10	JMJD1C	rs35447916	63173832	CA	C	0.3148170	-0.0374238	0.0065778	2.10E-09
10	JMJD1C	rs10995453	63174571	T	C	0.3860900	0.0523371	0.0062819	2.60E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs10822145	63174788	T	C	0.3146130	-0.0374365	0.0065782	2.10E-09
10	JMJD1C	rs10995455	63176601	A	G	0.2446280	-0.0411607	0.0071245	6.80E-09
10	JMJD1C	rs907	63176919	A	G	0.3865710	0.0529355	0.0062898	1.10E-18
10	JMJD1C	rs10761721	63178644	T	G	0.3860910	0.0523395	0.0062809	2.50E-18
10	JMJD1C	rs72829170	63180529	G	A	0.3765500	0.0517058	0.0063038	8.00E-18
10	JMJD1C	rs10995459	63183050	A	G	0.3859490	0.0518683	0.0062821	5.10E-18
10	JMJD1C	rs56369591	63184054	A	AG	0.3852720	0.0524180	0.0062859	3.00E-18
10	JMJD1C	rs61853340	63184415	C	G	0.3718400	0.0502303	0.0063506	1.10E-16
10	JMJD1C	rs10740107	63184557	T	A	0.3763620	0.0512357	0.0063082	1.90E-17
10	JMJD1C	rs3211105	63185604	G	A	0.3862290	0.0523936	0.0062789	2.50E-18
10	JMJD1C	rs10733789	63188924	C	T	0.2449600	-0.0418804	0.0071234	5.20E-09
10	JMJD1C	rs10761722	63195287	C	G	0.3860660	0.0523424	0.0062829	2.70E-18
10	JMJD1C	rs10761723	63195821	T	C	0.3144970	-0.0375977	0.0065804	2.00E-09
10	JMJD1C	rs61855465	63196847	T	A	0.3771460	0.0518138	0.0062964	6.60E-18
10	JMJD1C	rs7099425	63200957	C	T	0.3775750	0.0519180	0.0062996	6.20E-18
10	JMJD1C	rs7895472	63201652	A	G	0.3128080	-0.0379816	0.0065920	1.40E-09
10	JMJD1C	rs7895610	63201899	T	C	0.3104490	-0.0375654	0.0066216	2.10E-09
10	JMJD1C	rs4379723	63203689	C	T	0.3141010	-0.0376667	0.0065852	1.90E-09
10	JMJD1C	rs12413730	63204388	T	C	0.3771290	0.0519350	0.0062952	5.50E-18
10	JMJD1C	rs1579045	63210688	G	A	0.3868630	0.0526473	0.0062707	1.70E-18
10	JMJD1C	chr10:63211997_TAAG_T	63211997	T	TAAG	0.3144070	-0.0378518	0.0065807	1.60E-09
10	JMJD1C	rs7920159	63212416	C	G	0.3868630	0.0526473	0.0062707	1.70E-18
10	JMJD1C	rs11819167	63216409	A	G	0.3771900	0.0519194	0.0062942	5.80E-18
10	JMJD1C	rs10822147	63216537	C	T	0.3868180	0.0527202	0.0062701	1.60E-18
10	JMJD1C	rs10822148	63219487	A	G	0.3869720	0.0524112	0.0062734	2.40E-18
10	JMJD1C	rs10761726	63220958	A	C	0.3867550	0.0525646	0.0062707	1.90E-18
10	JMJD1C	rs1904295	63223116	G	A	0.3873120	0.0489175	0.0063704	8.50E-16
10	JMJD1C	rs6415875	63226657	A	G	0.3782340	0.0517076	0.0062924	9.20E-18
10	JMJD1C	rs10822149	63227652	A	G	0.3145150	-0.0376392	0.0065805	1.80E-09
10	JMJD1C	rs4281380	63227938	C	A	0.3772500	0.0520447	0.0062936	5.10E-18
10	JMJD1C	rs7916868	63229171	A	T	0.3378110	0.0548978	0.0065813	7.50E-18
10	JMJD1C	rs10761727	63235733	T	C	0.3144630	-0.0378405	0.0065808	1.50E-09
10	JMJD1C	rs10761728	63235808	C	T	0.3868040	0.0526833	0.0062704	1.60E-18
10	JMJD1C	rs10761729	63235844	C	G	0.3144630	-0.0378405	0.0065808	1.50E-09
10	JMJD1C	chr10:63237348_T_TAAA	63237348	T	TAAA	0.3775620	0.0516801	0.0062959	8.40E-18
10	JMJD1C	rs4439410	63239012	C	G	0.3771720	0.0519124	0.0062944	5.60E-18
10	JMJD1C	rs7082066	63239211	A	G	0.3867380	0.0525577	0.0062710	1.80E-18
10	JMJD1C	rs7082090	63239252	A	G	0.3771720	0.0519124	0.0062944	5.60E-18
10	JMJD1C	rs4399232	63239730	T	C	0.3144960	-0.0376908	0.0065803	1.70E-09
10	JMJD1C	rs9414780	63241673	A	C	0.3771720	0.0519124	0.0062944	5.60E-18
10	JMJD1C	rs7902343	63245639	T	C	0.2856180	-0.0399486	0.0067817	1.70E-09
10	JMJD1C	rs6479891	63246696	T	C	0.3769980	0.0518862	0.0062939	5.50E-18
10	JMJD1C	chr10:63247839_TAAACAAAAAC_T	63247839	AACAA	T	0.3918070	0.0507664	0.0062916	3.10E-17
10	JMJD1C	rs10995477	63250912	C	T	0.2861370	-0.0392728	0.0067642	2.60E-09
10	JMJD1C	rs7081614	63252088	C	T	0.3865080	0.0526933	0.0062751	1.50E-18
10	JMJD1C	rs4400684	63252927	G	A	0.2856830	-0.0391232	0.0067726	2.90E-09
10	JMJD1C	rs4454603	63252990	T	C	0.2861540	-0.0395122	0.0067646	2.20E-09
10	JMJD1C	rs4403688	63253156	G	A	0.3865000	0.0526691	0.0062752	1.60E-18
10	JMJD1C	rs4595427	63253184	C	A	0.2861460	-0.0394865	0.0067645	2.20E-09
10	JMJD1C	rs4405189	63254175	G	A	0.2859800	-0.0393869	0.0067655	2.40E-09
10	JMJD1C	rs1904297	63255428	G	A	0.3864320	0.0527797	0.0062764	1.40E-18
10	JMJD1C	rs7070693	63256402	A	G	0.3864400	0.0526705	0.0062764	1.70E-18
10	JMJD1C	rs7088799	63256414	G	T	0.2860020	-0.0394346	0.0067594	2.30E-09
10	JMJD1C	rs7896910	63256961	A	G	0.2463210	-0.0416478	0.0070975	3.80E-09
10	JMJD1C	rs10761730	63257293	C	T	0.3773560	0.0519795	0.0063076	5.90E-18
10	JMJD1C	rs10822150	63257736	G	A	0.3864080	0.0524856	0.0062757	2.10E-18
10	JMJD1C	rs11370668	63260747	G	GC	0.3822080	0.0501697	0.0063262	6.00E-17
10	JMJD1C	rs35843321	63260755	A	AT	0.3916990	0.0504411	0.0063049	3.30E-17
10	JMJD1C	rs9415680	63261130	A	G	0.3762020	0.0516429	0.0063029	6.10E-18
10	JMJD1C	chr10:63262822_AC_A	63262822	AC	A	0.3773540	0.0521047	0.0063006	3.60E-18
10	JMJD1C	rs7098181	63267383	T	G	0.2863200	-0.0386308	0.0067553	3.60E-09
10	JMJD1C	rs10761731	63267850	T	A	0.2862950	-0.0386416	0.0067553	3.70E-09
10	JMJD1C	rs10761732	63268497	C	T	0.3858620	0.0524154	0.0062783	1.80E-18
10	JMJD1C	rs7916282	63272051	A	T	0.3891350	0.0507683	0.0064089	1.00E-16
10	JMJD1C	rs7909555	63273348	T	C	0.3879560	0.0501212	0.0062724	6.00E-17
10	JMJD1C	rs9415682	63274057	G	T	0.3767430	0.0518772	0.0063006	5.90E-18
10	JMJD1C	rs10761733	63275024	T	C	0.4040790	0.0496524	0.0062872	1.20E-16
10	JMJD1C	rs10822151	63276907	G	C	0.3756160	0.0513014	0.0063041	1.20E-17
10	JMJD1C	rs9787438	63278270	C	G	0.2868060	-0.0382079	0.0067522	6.10E-09
10	JMJD1C	rs10761734	63281453	C	T	0.3852580	0.0522679	0.0062783	2.80E-18
10	JMJD1C	rs10740110	63283461	A	G	0.3756450	0.0514062	0.0063036	1.10E-17
10	JMJD1C	rs10761735	63284158	A	G	0.3791370	0.0514782	0.0063108	1.00E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs9414786	63284562	T	A	0.3756450	0.0514062	0.0063036	1.10E-17
10	JMJD1C	rs4417159	63285938	T	A	0.3852550	0.0522517	0.0062783	2.90E-18
10	JMJD1C	rs67907125	63286034	GA	G	0.3756450	0.0514062	0.0063036	1.10E-17
10	JMJD1C	rs10995493	63287266	C	T	0.3852570	0.0522569	0.0062782	2.90E-18
10	JMJD1C	rs10761736	63288009	A	T	0.3852970	0.0523490	0.0062788	2.50E-18
10	JMJD1C	rs7080386	63288546	A	C	0.2868060	-0.0382079	0.0067522	6.10E-09
10	JMJD1C	rs67135607	63289318	CAT	C	0.3853430	0.0521585	0.0062792	3.30E-18
10	JMJD1C	rs7074351	63290343	A	T	0.3756890	0.0515087	0.0063039	9.00E-18
10	JMJD1C	rs7075195	63290899	G	A	0.2872780	-0.0387276	0.0067475	4.00E-09
10	JMJD1C	rs4486510	63291134	C	G	0.3751270	0.0513953	0.0063057	1.10E-17
10	JMJD1C	rs10761737	63292445	C	T	0.2871320	-0.0389931	0.0067499	3.20E-09
10	JMJD1C	rs6479892	63292472	A	G	0.3756510	0.0514003	0.0063037	1.10E-17
10	JMJD1C	rs7084707	63292782	T	C	0.2873040	-0.0388029	0.0067477	3.70E-09
10	JMJD1C	rs11408050	63293789	A	AT	0.3862590	0.0515323	0.0062861	8.90E-18
10	JMJD1C	rs7913332	63293890	A	T	0.3852620	0.0522300	0.0062783	3.00E-18
10	JMJD1C	rs7093899	63294576	A	G	0.3852590	0.0522149	0.0062784	3.10E-18
10	JMJD1C	rs5785566	63295026	TA	T	0.2871960	-0.0390863	0.0067493	2.60E-09
10	JMJD1C	rs7907462	63295773	T	C	0.3857700	0.0521283	0.0062813	3.30E-18
10	JMJD1C	rs9414788	63296952	A	G	0.3756310	0.0514168	0.0063042	1.10E-17
10	JMJD1C	rs10822153	63297053	A	C	0.2874340	-0.0387670	0.0067463	3.70E-09
10	JMJD1C	rs12773283	63298464	C	T	0.3756360	0.0514015	0.0063041	1.10E-17
10	JMJD1C	rs10822154	63299284	C	T	0.3852600	0.0522169	0.0062785	3.10E-18
10	JMJD1C	rs7920768	63300754	C	T	0.3756500	0.0513756	0.0063040	1.10E-17
10	JMJD1C	chr10:63300891_C_CA	63300891	C	CA	0.3902140	0.0539490	0.0063119	4.00E-19
10	JMJD1C	rs10761739	63302248	C	G	0.2871970	-0.0386462	0.0067470	4.20E-09
10	JMJD1C	rs7073753	63303060	T	C	0.2872090	-0.0384741	0.0067474	4.80E-09
10	JMJD1C	rs10761740	63303503	G	A	0.3852810	0.0522501	0.0062787	3.00E-18
10	JMJD1C	rs74506613	63304076	A	CTTTGC	0.2869930	-0.0385785	0.0067546	4.80E-09
10	JMJD1C	rs61855497	63304084	A	T	0.2861190	-0.0384982	0.0067602	4.80E-09
10	JMJD1C	rs7100372	63304484	T	C	0.3756610	0.0514161	0.0063043	1.10E-17
10	JMJD1C	rs7896676	63305542	T	C	0.3579600	0.0525171	0.0064575	1.60E-17
10	JMJD1C	rs7896677	63305545	T	G	0.3587130	0.0523960	0.0064624	2.20E-17
10	JMJD1C	rs7897326	63306059	T	C	0.3852520	0.0522205	0.0062785	3.10E-18
10	JMJD1C	rs10761741	63306426	T	G	0.2871180	-0.0385077	0.0067475	4.50E-09
10	JMJD1C	rs7092139	63306540	A	C	0.3852880	0.0522167	0.0062789	3.20E-18
10	JMJD1C	rs7092539	63306749	C	T	0.3856150	0.0518681	0.0062833	6.80E-18
10	JMJD1C	rs7922587	63309854	C	T	0.2869590	-0.0383505	0.0067520	5.00E-09
10	JMJD1C	rs7085869	63310403	C	T	0.3756400	0.0513875	0.0063043	1.10E-17
10	JMJD1C	rs7070296	63310678	A	T	0.2873760	-0.0385113	0.0067465	4.50E-09
10	JMJD1C	rs10822155	63311455	A	C	0.2871900	-0.0384261	0.0067480	5.10E-09
10	JMJD1C	rs67173357	63312116	TG	T	0.4193190	0.0465440	0.0062228	7.40E-15
10	JMJD1C	rs9299455	63313841	A	G	0.3747010	0.0513614	0.0063096	1.10E-17
10	JMJD1C	chr10:63314548_A_AAC	63314548	AAC	A	0.2872970	-0.0384825	0.0067473	4.70E-09
10	JMJD1C	rs9733126	63314727	C	A	0.3850030	0.0520729	0.0062833	4.40E-18
10	JMJD1C	rs9414793	63315349	G	A	0.3756410	0.0514233	0.0063046	1.10E-17
10	JMJD1C	rs7090111	63318234	G	C	0.2872200	-0.0384801	0.0067475	4.80E-09
10	JMJD1C	rs7899715	63318695	T	C	0.3757160	0.0512836	0.0063048	1.30E-17
10	JMJD1C	rs4518976	63319017	C	T	0.3802730	0.0523620	0.0063200	4.20E-18
10	JMJD1C	rs10822156	63320967	C	T	0.2873710	-0.0385656	0.0067466	4.30E-09
10	JMJD1C	rs10740112	63322315	G	A	0.3852720	0.0521444	0.0062793	3.40E-18
10	JMJD1C	rs10740113	63322516	T	C	0.3852720	0.0521444	0.0062793	3.40E-18
10	JMJD1C	rs10740114	63322659	A	G	0.3852720	0.0521444	0.0062793	3.40E-18
10	JMJD1C	rs34979184	63323439	GA	G	0.3852740	0.0521495	0.0062792	3.30E-18
10	JMJD1C	rs10761742	63325288	G	A	0.2874720	-0.0386457	0.0067460	4.10E-09
10	JMJD1C	rs4525102	63326513	C	T	0.3756380	0.0514805	0.0063047	9.80E-18
10	JMJD1C	rs7899503	63327708	C	G	0.3756330	0.0514706	0.0063047	9.80E-18
10	JMJD1C	rs12767177	63327882	C	G	0.3861070	0.0513271	0.0062844	1.20E-17
10	JMJD1C	chr10:63329478_GA_G	63329478	GA	G	0.3775810	0.0498160	0.0063629	3.30E-16
10	JMJD1C	rs7092504	63329679	A	G	0.3756360	0.0514492	0.0063048	1.00E-17
10	JMJD1C	rs10822157	63329720	A	G	0.3852640	0.0521690	0.0062795	3.20E-18
10	JMJD1C	rs4133250	63332645	G	A	0.3756320	0.0514319	0.0063048	1.00E-17
10	JMJD1C	rs7918743	63333302	T	C	0.3852410	0.0522378	0.0062794	3.00E-18
10	JMJD1C	rs7902187	63333375	C	T	0.3852410	0.0522378	0.0062794	3.00E-18
10	JMJD1C	rs10822158	63334623	G	A	0.2872800	-0.0384486	0.0067486	4.90E-09
10	JMJD1C	rs10995506	63334706	A	G	0.3756350	0.0514416	0.0063049	1.00E-17
10	JMJD1C	rs10740115	63335230	A	G	0.2868960	-0.0386714	0.0067544	4.30E-09
10	JMJD1C	rs10740116	63335232	C	T	0.2868960	-0.0386714	0.0067544	4.30E-09
10	JMJD1C	rs12219332	63335932	G	C	0.3756720	0.0513821	0.0063054	1.10E-17
10	JMJD1C	rs10761743	63336258	C	T	0.3853530	0.0520117	0.0062804	4.10E-18
10	JMJD1C	rs10822159	63336490	T	C	0.2871590	-0.0383760	0.0067491	5.40E-09
10	JMJD1C	rs10740117	63338517	G	A	0.3756210	0.0514365	0.0063050	1.10E-17
10	JMJD1C	rs6479894	63338981	T	C	0.3756220	0.0514395	0.0063050	1.10E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs56674933	63339623	T	TAA	0.3844430	0.0518850	0.0062850	5.00E-18
10	JMJD1C	rs71025161	63340059	C	CAATA	0.3823040	0.0520816	0.0063182	7.00E-18
10	JMJD1C	rs10733790	63340574	G	C	0.3720200	0.0517615	0.0063305	1.00E-17
10	JMJD1C	rs10761744	63341266	C	G	0.3756210	0.0514458	0.0063049	1.10E-17
10	JMJD1C	rs10761745	63341311	G	C	0.3758350	0.0511479	0.0063122	1.90E-17
10	JMJD1C	rs10740118	63341447	C	G	0.2873620	-0.0383411	0.0067476	5.40E-09
10	JMJD1C	rs7091664	63342040	G	A	0.3756210	0.0514458	0.0063049	1.10E-17
10	JMJD1C	rs7896518	63344740	G	A	0.2871830	-0.0384780	0.0067488	4.90E-09
10	JMJD1C	rs10761746	63345134	A	G	0.3852300	0.0522447	0.0062793	3.00E-18
10	JMJD1C	rs7081275	63346791	G	T	0.3756940	0.0512211	0.0063054	1.40E-17
10	JMJD1C	chr10:63348205_CAA_C	63348205	CAA	C	0.3721030	0.0523200	0.0063289	5.00E-18
10	JMJD1C	rs7895348	63349781	C	A	0.3756350	0.0514764	0.0063048	9.90E-18
10	JMJD1C	rs7073932	63350160	C	T	0.3852390	0.0522945	0.0062793	2.80E-18
10	JMJD1C	rs10761748	63350216	T	G	0.3852390	0.0522945	0.0062793	2.80E-18
10	JMJD1C	rs10822160	63353036	G	T	0.2825820	-0.0382072	0.0068075	9.20E-09
10	JMJD1C	rs7913278	63353774	G	A	0.3860910	0.0522859	0.0062790	2.70E-18
10	JMJD1C	rs10761749	63354049	C	T	0.4185450	0.0488713	0.0062451	3.70E-16
10	JMJD1C	rs200427687	63354672	G	GCTT	0.3751720	0.0515293	0.0063171	1.10E-17
10	JMJD1C	rs149520237	63354674	T	TTTGT	0.3847980	0.0523054	0.0062913	3.30E-18
10	JMJD1C	rs9415692	63355392	A	G	0.3745330	0.0515018	0.0063116	9.90E-18
10	JMJD1C	rs7082926	63355771	T	G	0.3845390	0.0523026	0.0062858	3.30E-18
10	JMJD1C	rs7083356	63356028	T	A	0.3843100	0.0525643	0.0062837	2.10E-18
10	JMJD1C	rs35971912	63357004	C	CA	0.3843620	0.0517397	0.0062890	7.20E-18
10	JMJD1C	rs10822161	63358443	A	G	0.2872870	-0.0385904	0.0067487	4.30E-09
10	JMJD1C	rs9415693	63360127	C	T	0.3758620	0.0514689	0.0063064	1.10E-17
10	JMJD1C	rs12355784	63361805	A	C	0.2750520	-0.0381784	0.0068661	2.70E-08
10	JMJD1C	rs144958118	63362473	TATAT.	T	0.3859950	0.0521270	0.0062864	4.10E-18
10	JMJD1C	rs9629895	63363027	A	C	0.3852960	0.0520392	0.0062790	4.10E-18
10	JMJD1C	rs10822162	63364320	A	G	0.3852960	0.0520194	0.0062791	4.20E-18
10	JMJD1C	rs10822163	63364338	G	C	0.2876400	-0.0380554	0.0067475	7.40E-09
10	JMJD1C	rs10740119	63365477	T	G	0.3844260	0.0522733	0.0062828	3.20E-18
10	JMJD1C	rs6479896	63367072	C	T	0.2873040	-0.0386333	0.0067492	4.30E-09
10	JMJD1C	rs10822164	63367498	A	G	0.2873040	-0.0386333	0.0067492	4.30E-09
10	JMJD1C	rs7909692	63368517	T	A	0.3846330	0.0522684	0.0062845	3.30E-18
10	JMJD1C	rs10761750	63368859	A	G	0.2873070	-0.0386120	0.0067491	4.40E-09
10	JMJD1C	rs9414799	63369842	C	T	0.3737510	0.0521634	0.0063197	4.30E-18
10	JMJD1C	rs4746119	63370157	C	T	0.3756740	0.0512564	0.0063045	1.40E-17
10	JMJD1C	rs9414800	63371522	A	T	0.3748270	0.0514620	0.0063082	1.10E-17
10	JMJD1C	rs10546984	63371680	C	CATA	0.2873190	-0.0386480	0.0067488	4.20E-09
10	JMJD1C	rs2393967	63373396	C	A	0.2483100	-0.0405989	0.0070658	7.90E-09
10	JMJD1C	rs7923609	63374062	G	A	0.2877810	-0.0384675	0.0067450	4.90E-09
10	JMJD1C	rs9415696	63374588	T	A	0.3748110	0.0516097	0.0063077	8.90E-18
10	JMJD1C	rs2893919	63375018	A	G	0.2874270	-0.0385638	0.0067469	4.50E-09
10	JMJD1C	rs2393966	63375054	G	T	0.2874270	-0.0385638	0.0067469	4.50E-09
10	JMJD1C	rs9415697	63375377	C	T	0.3748240	0.0516403	0.0063076	8.60E-18
10	JMJD1C	rs7076310	63375912	A	C	0.2874270	-0.0385638	0.0067469	4.50E-09
10	JMJD1C	rs6479897	63376868	C	T	0.3844420	0.0524057	0.0062817	2.50E-18
10	JMJD1C	rs4310508	63378813	G	A	0.2874270	-0.0385638	0.0067469	4.50E-09
10	JMJD1C	rs7910927	63379150	G	T	0.2879800	-0.0390048	0.0067486	2.80E-09
10	JMJD1C	rs6479899	63379287	T	A	0.3757780	0.0518095	0.0063176	9.40E-18
10	JMJD1C	rs724553	63380624	C	G	0.3748240	0.0516403	0.0063076	8.60E-18
10	JMJD1C	rs2393969	63380680	C	A	0.2875060	-0.0384888	0.0067475	4.70E-09
10	JMJD1C	rs9415699	63383798	C	T	0.3756660	0.0514247	0.0063039	1.10E-17
10	JMJD1C	rs9415700	63385805	T	C	0.3035250	0.0457585	0.0066505	1.10E-13
10	JMJD1C	rs10822165	63387199	T	C	0.3852810	0.0521940	0.0062783	3.20E-18
10	JMJD1C	rs71025168	63387563	GA	G	0.3861790	0.0518271	0.0062806	5.40E-18
10	JMJD1C	rs10995527	63387659	A	G	0.2950240	-0.0376060	0.0067279	9.50E-09
10	JMJD1C	chr10:63390573_TACA_T	63390573	TACA	T	0.3865200	0.0527010	0.0062979	2.20E-18
10	JMJD1C	rs9414802	63391622	C	T	0.3123000	0.0466512	0.0066036	3.10E-14
10	JMJD1C	rs9415701	63391749	C	T	0.3026780	0.0460166	0.0066566	8.60E-14
10	JMJD1C	rs4746125	63393125	A	G	0.3060560	0.0461408	0.0066491	8.10E-14
10	JMJD1C	rs10740122	63395451	C	A	0.3839900	0.0524230	0.0062867	2.70E-18
10	JMJD1C	rs10822167	63398991	C	T	0.3858080	0.0527092	0.0062823	1.60E-18
10	JMJD1C	rs67434572	63399012	A	AAAG	0.2874310	-0.0386356	0.0067486	4.30E-09
10	JMJD1C	rs4745706	63399820	C	T	0.3709810	0.0514493	0.0063580	2.10E-17
10	JMJD1C	rs12415038	63401098	G	A	0.3762770	0.0520354	0.0063057	5.00E-18
10	JMJD1C	rs9415705	63401790	G	T	0.3752020	0.0517342	0.0063023	8.00E-18
10	JMJD1C	rs10740123	63404755	A	G	0.3134170	0.0468682	0.0065914	2.10E-14
10	JMJD1C	rs10822168	63405424	A	G	0.2867080	-0.0389707	0.0067556	3.00E-09
10	JMJD1C	chr10:63407820_CA_C	63407820	C	CA	0.3058290	0.0451920	0.0066628	2.00E-13
10	JMJD1C	rs10822170	63411395	G	T	0.3866400	0.0519557	0.0062909	6.70E-18
10	JMJD1C	rs10761755	63412212	G	A	0.3861180	0.0525569	0.0062767	2.10E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs10761756	63412568	T	C	0.2872660	-0.0384191	0.0067483	5.20E-09
10	JMJD1C	rs10761757	63412790	C	G	0.3861170	0.0525601	0.0062767	2.10E-18
10	JMJD1C	rs10761758	63412987	T	A	0.2865560	-0.0389165	0.0067591	3.40E-09
10	JMJD1C	rs71837985	63413039	A	AAAC	0.2875210	-0.0388020	0.0067486	4.00E-09
10	JMJD1C	rs10761759	63414032	G	T	0.3139540	0.0478272	0.0066050	7.30E-15
10	JMJD1C	rs61853587	63414817	C	G	0.3034960	0.0467537	0.0066490	3.70E-14
10	JMJD1C	rs7909269	63418006	A	G	0.2872650	-0.0387111	0.0067482	4.20E-09
10	JMJD1C	rs35999426	63418722	T	TG	0.3755440	0.0519857	0.0063058	6.30E-18
10	JMJD1C	rs10761760	63419392	C	A	0.2844350	-0.0381899	0.0067952	6.50E-09
10	JMJD1C	rs10761761	63419398	T	A	0.3895400	0.0518102	0.0062913	6.70E-18
10	JMJD1C	rs10995530	63419654	G	A	0.3131710	0.0471399	0.0065980	1.60E-14
10	JMJD1C	rs11818194	63420692	A	G	0.3646960	0.0504252	0.0065013	1.70E-16
10	JMJD1C	rs6479901	63421016	C	A	0.3853370	0.0526154	0.0062798	2.00E-18
10	JMJD1C	rs7077580	63421125	A	G	0.2872630	-0.0387024	0.0067481	4.20E-09
10	JMJD1C	rs35654741	63425460	CAT	C	0.3034060	0.0464707	0.0066511	5.10E-14
10	JMJD1C	rs10740124	63426034	C	T	0.3130800	0.0472737	0.0065977	1.40E-14
10	JMJD1C	rs9415706	63426587	T	C	0.3035070	0.0467912	0.0066491	3.50E-14
10	JMJD1C	rs72837019	63427258	C	T	0.3130800	0.0472737	0.0065977	1.40E-14
10	JMJD1C	rs61853589	63427351	A	T	0.3040560	0.0469561	0.0066515	2.40E-14
10	JMJD1C	rs9414803	63428309	A	G	0.3035050	0.0467852	0.0066491	3.50E-14
10	JMJD1C	rs9415707	63428530	C	T	0.3043300	0.0467236	0.0066435	3.60E-14
10	JMJD1C	rs10761764	63429143	C	G	0.3132260	0.0471894	0.0065987	1.60E-14
10	JMJD1C	rs10761765	63429213	A	G	0.3130790	0.0472597	0.0065976	1.50E-14
10	JMJD1C	rs12413029	63429366	C	T	0.3035070	0.0467769	0.0066491	3.60E-14
10	JMJD1C	rs9415708	63430282	C	G	0.3035070	0.0467769	0.0066491	3.60E-14
10	JMJD1C	rs7924036	63431885	G	T	0.3325160	0.0506814	0.0064958	4.50E-17
10	JMJD1C	rs10761767	63432671	T	C	0.3126170	0.0472250	0.0065965	1.50E-14
10	JMJD1C	rs7917169	63433181	T	C	0.3135990	0.0470416	0.0065933	1.70E-14
10	JMJD1C	rs10761768	63434369	C	A	0.3136850	0.0472327	0.0065896	1.30E-14
10	JMJD1C	rs72837025	63434731	C	A	0.3043830	0.0468109	0.0066435	3.20E-14
10	JMJD1C	rs12784772	63435695	A	T	0.3043380	0.0469021	0.0066430	2.80E-14
10	JMJD1C	rs77494594	63437549	C	A	0.3035370	0.0470707	0.0066482	2.40E-14
10	JMJD1C	rs10437345	63443186	C	T	0.3035310	0.0470223	0.0066485	2.50E-14
10	JMJD1C	rs2616631	63448154	A	T	0.3030740	0.0467984	0.0066480	3.30E-14
10	JMJD1C	rs2466128	63448561	C	T	0.3030740	0.0467984	0.0066480	3.30E-14
10	JMJD1C	rs2719815	63450534	C	G	0.3030740	0.0467984	0.0066480	3.30E-14
10	JMJD1C	rs2616630	63453579	C	A	0.3030740	0.0467984	0.0066480	3.30E-14
10	JMJD1C	rs2616629	63454056	C	T	0.3030740	0.0467984	0.0066480	3.30E-14
10	JMJD1C	rs10822172	63455478	T	C	0.3129470	0.0472312	0.0065980	1.50E-14
10	JMJD1C	rs12573212	63458665	A	C	0.3125530	0.0473158	0.0065975	1.30E-14
10	JMJD1C	rs7074735	63459519	T	A	0.3127920	0.0473602	0.0065961	1.30E-14
10	JMJD1C	rs7075205	63459834	T	C	0.3126230	0.0473350	0.0065966	1.30E-14
10	JMJD1C	rs10995540	63460170	C	G	0.3126230	0.0473350	0.0065966	1.30E-14
10	JMJD1C	rs2616628	63460197	C	G	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C	rs10159609	63461168	C	T	0.3126230	0.0473350	0.0065966	1.30E-14
10	JMJD1C	chr10:63464698_CA_C	63464698	CA	C	0.3305780	0.0512128	0.0065197	3.00E-17
10	JMJD1C	rs2393980	63464750	G	C	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C, JN	rs1061259	63465484	G	C	0.3129520	0.0474059	0.0065994	1.20E-14
10	JMJD1C *	rs58806797	63466790	A	AT	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C *	rs10995541	63473575	G	T	0.3123660	0.0471361	0.0065992	1.60E-14
10	JMJD1C *	rs59215788	63474074	G	A	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C *	chr10:63474104_TAATA_T	63474104	T	TAATA	0.3319420	0.0391076	0.0065037	4.00E-11
10	JMJD1C *	rs59246603	63474182	C	T	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C *	chr10:63474856_T_TA	63474856	TA	T	0.3128060	0.0473053	0.0065996	1.30E-14
10	JMJD1C *	rs12414159	63479017	T	A	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C *	rs10995543	63479787	C	T	0.3030670	0.0468449	0.0066482	3.10E-14
10	JMJD1C *	rs10761773	63480322	G	C	0.3224320	0.0477728	0.0066400	7.90E-15
10	JMJD1C *	rs4746138	63481981	G	A	0.3029190	0.0469303	0.0066501	2.60E-14
10	JMJD1C *	rs2393978	63482050	C	A	0.3134920	0.0471706	0.0065942	1.80E-14
10	JMJD1C *	rs10822173	63483842	A	T	0.3126130	0.0473525	0.0065966	1.30E-14
10	JMJD1C *	rs7915680	63484544	C	T	0.3126130	0.0473525	0.0065966	1.30E-14
10	JMJD1C *	rs7085862	63486687	T	G	0.3126130	0.0473525	0.0065966	1.30E-14
10	JMJD1C *	rs2893922	63487259	G	T	0.3030970	0.0468799	0.0066488	3.00E-14
10	JMJD1C *	chr10:63488541_TA_T	63488541	TA	T	0.3130380	0.0470908	0.0065983	1.80E-14
10	JMJD1C *	rs9919452	63488812	T	C	0.3126080	0.0473625	0.0065966	1.30E-14
10	JMJD1C *	rs10740128	63490783	A	G	0.3108910	0.0472746	0.0066169	1.40E-14
10	JMJD1C *	rs10761776	63491217	C	T	0.3125090	0.0474046	0.0065979	1.30E-14
10	JMJD1C *	rs2393976	63493679	C	G	0.3041440	0.0461862	0.0066447	6.30E-14
10	REEP3 *	rs7910662	63493940	C	T	0.3123330	0.0471308	0.0066003	1.70E-14
10	REEP3 *	chr10:63495406_TA_T	63495406	T	TA	0.3029890	0.0469414	0.0066490	2.80E-14
10	REEP3 *	rs10822175	63495414	A	T	0.3077120	0.0475571	0.0066543	1.80E-14
10	REEP3 *	rs4746149	63497633	C	T	0.3030760	0.0468869	0.0066480	3.00E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	REEP3 *	rs72837056	63500718	G	T	0.3026300	0.0469616	0.0066536	3.00E-14
10	REEP3 *	rs2893924	63501594	A	G	0.3126270	0.0473705	0.0065963	1.20E-14
10	REEP3 *	rs2393981	63501605	A	G	0.3126270	0.0473705	0.0065963	1.20E-14
10	REEP3 *	rs9971294	63503108	A	G	0.3126270	0.0473705	0.0065963	1.20E-14
10	REEP3 *	rs76677248	63503505	C	CAT	0.3030830	0.0468574	0.0066479	3.10E-14
10	REEP3 *	rs80026135	63505240	G	C	0.3026020	0.0469386	0.0066595	3.30E-14
10	REEP3 *	rs11815969	63506095	T	C	0.3030840	0.0468491	0.0066479	3.10E-14
10	REEP3 *	rs7078456	63509719	C	T	0.3032490	0.0466916	0.0066472	3.90E-14
10	REEP3 *	rs7083823	63510912	G	C	0.3132810	0.0468384	0.0065998	2.30E-14
10	REEP3 *	chr10:63512289_C_CT	63512289	CT	C	0.2952130	0.0467299	0.0067513	1.20E-13
10	REEP3 *	rs7097698	63513635	G	A	0.3126800	0.0474392	0.0065991	1.30E-14
10	REEP3 *	rs7068144	63514500	C	G	0.3126770	0.0474518	0.0065991	1.20E-14
10	REEP3 *	rs72837070	63514919	C	T	0.3031380	0.0469142	0.0066505	3.10E-14
10	REEP3 *	chr10:63514949_A_AT	63514949	AT	A	0.3005860	0.0470047	0.0066852	3.00E-14
10	REEP3 *	rs35605123	63516140	GA	G	0.3130980	0.0468628	0.0066002	2.50E-14
10	REEP3 *	rs61853635	63516750	G	T	0.3031460	0.0468994	0.0066505	3.20E-14
10	REEP3 *	rs7082076	63517185	C	G	0.3141500	0.0477740	0.0066068	9.40E-15
10	REEP3 *	rs4745729	63517323	G	A	0.3031220	0.0468778	0.0066511	3.20E-14
10	REEP3 *	rs10740133	63517676	C	T	0.3126630	0.0474351	0.0065995	1.30E-14
10	REEP3 *	rs12416349	63517783	T	C	0.3002910	0.0477780	0.0067091	2.20E-14
10	REEP3 *	rs7358191	63519028	A	C	0.3126630	0.0474351	0.0065995	1.30E-14
10	REEP3 *	rs7358152	63519138	T	C	0.3126630	0.0474351	0.0065995	1.30E-14
10	REEP3 *	rs10822179	63520404	T	C	0.3126630	0.0474351	0.0065995	1.30E-14
10	REEP3	rs10761780	63524272	C	T	0.3032090	0.0469013	0.0066509	3.00E-14
10	REEP3	rs10761781	63524843	T	C	0.3031260	0.0468039	0.0066516	3.50E-14
10	REEP3	rs12412946	63529792	G	T	0.2954150	0.0464895	0.0067524	7.50E-14
10	REEP3	rs12414188	63529854	G	A	0.3024460	0.0469334	0.0066604	3.30E-14
10	REEP3	rs11375382	63530178	A	AC	0.3030840	0.0467440	0.0066514	3.80E-14
10	REEP3	rs5785580	63530494	AT	A	0.3310940	0.0504954	0.0065020	6.40E-17
10	REEP3	rs7087279	63532176	T	A	0.3031330	0.0469694	0.0066506	2.80E-14
10	REEP3	rs59035163	63532283	G	C	0.3031330	0.0469694	0.0066506	2.80E-14
10	REEP3	rs12413081	63533959	T	C	0.3031330	0.0469694	0.0066506	2.80E-14
10	REEP3	rs16918567	63534910	C	A	0.3029870	0.0466487	0.0066526	3.70E-14
10	REEP3	rs16918573	63541045	A	T	0.3006570	0.0468725	0.0066644	3.10E-14
10	REEP3	rs16918575	63541565	G	A	0.3006580	0.0468574	0.0066643	3.20E-14
10	REEP3	rs147232123	63541637	G	GT	0.3006580	0.0468574	0.0066643	3.20E-14
10	REEP3	rs12414796	63543327	A	G	0.3006230	0.0467879	0.0066648	3.50E-14
10	REEP3	rs61853639	63545353	T	G	0.3012050	0.0465319	0.0066608	4.50E-14
10	REEP3	rs4746195	63547893	G	A	0.3012450	0.0465459	0.0066592	4.30E-14
10	REEP3	rs4469774	63550017	T	G	0.3022850	0.0461365	0.0066609	9.70E-14
10	REEP3	rs61853642	63554019	A	G	0.2851540	0.0458909	0.0067641	3.90E-13
10	REEP3	rs9919429	63554059	G	A	0.3130870	0.0494658	0.0065930	1.10E-15
10	REEP3	rs2163188	63554951	C	G	0.3132370	0.0492117	0.0065935	1.30E-15
10	REEP3	rs2393984	63555211	G	A	0.3130890	0.0494585	0.0065929	1.10E-15
10	REEP3	rs6479905	63555471	G	A	0.3111060	0.0511594	0.0066104	2.40E-16
10	REEP3	rs12411988	63555637	C	G	0.2853440	0.0456901	0.0067631	4.80E-13
10	REEP3	rs12412012	63556003	T	C	0.2852690	0.0457247	0.0067631	4.60E-13
10	REEP3	rs7919685	63556040	T	G	0.3132080	0.0492931	0.0065921	1.30E-15
10	REEP3	rs61117531	63556475	T	TACTC	0.3128050	0.0495775	0.0066086	9.10E-16
10	REEP3	rs12247907	63557285	C	G	0.3132040	0.0493339	0.0065923	1.20E-15
10	REEP3	rs7070761	63557296	T	A	0.3132040	0.0493339	0.0065923	1.20E-15
10	REEP3	rs10761785	63559006	G	T	0.3147330	0.0494803	0.0065876	1.10E-15
10	REEP3	rs61579729	63559553	G	A	0.2852670	0.0457809	0.0067633	4.30E-13
10	REEP3	rs7898861	63559918	C	T	0.3121000	0.0492474	0.0066082	1.60E-15
10	REEP3	rs16918599	63560319	C	T	0.2852430	0.0457960	0.0067636	4.30E-13
10	REEP3	rs16918600	63560690	A	C	0.2852430	0.0457960	0.0067636	4.30E-13
10	REEP3	rs11812934	63560970	A	G	0.2852460	0.0457778	0.0067637	4.30E-13
10	REEP3	rs16918601	63561291	A	C	0.2852630	0.0459802	0.0067658	3.50E-13
10	REEP3	rs12245149	63561387	A	C	0.3131840	0.0495291	0.0065951	1.00E-15
10	REEP3	rs12245367	63561704	T	C	0.3127350	0.0495372	0.0066136	1.30E-15
10	REEP3	rs16918603	63561712	G	A	0.2847960	0.0462078	0.0067854	3.60E-13
10	REEP3	rs4746201	63562621	T	G	0.2848440	0.0462630	0.0067885	3.30E-13
10	REEP3	rs10666196	63562704	ATCAG	A	0.3128100	0.0496577	0.0066169	1.10E-15
10	REEP3	rs7899657	63563505	A	G	0.3128260	0.0496322	0.0066177	1.10E-15
10	REEP3	rs4746203	63564237	T	G	0.3123110	0.0498333	0.0066248	9.90E-16
10	REEP3	rs10822181	63565366	A	G	0.3131180	0.0494145	0.0066227	1.40E-15
10	REEP3	rs4746204	63568758	T	C	0.3129950	0.0497775	0.0066253	1.00E-15
10	REEP3	rs7907451	63568980	A	T	0.3130040	0.0497575	0.0066254	1.10E-15
10	REEP3	rs4746205	63569758	G	A	0.3130130	0.0497856	0.0066266	1.10E-15
10	REEP3	rs7100409	63570435	A	T	0.3130050	0.0497848	0.0066270	1.10E-15
10	REEP3	rs7100413	63570448	C	T	0.3130080	0.0497703	0.0066271	1.10E-15
10	REEP3	rs61853655	63570645	G	A	0.2846860	0.0459176	0.0068038	5.90E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	REEP3	rs3847325	63571751	C	G	0.3134390	0.0493902	0.0066254	1.80E-15
10	REEP3	rs3847326	63572099	G	A	0.3154340	0.0481010	0.0066189	7.50E-15
10	REEP3	chr10:63572305_C_CT	63572305	CT	C	0.2991490	0.0474853	0.0067412	2.50E-14
10	REEP3	rs6479908	63573888	G	C	0.3056540	0.0477275	0.0066693	1.60E-14
10	REEP3	rs7090758	63575555	C	T	0.3056670	0.0475940	0.0066696	1.90E-14
10	REEP3	rs7077256	63576425	G	A	0.3056990	0.0477199	0.0066700	1.60E-14
10	REEP3	rs7902616	63576613	A	G	0.3056990	0.0477199	0.0066700	1.60E-14
10	REEP3	rs10822183	63577381	C	T	0.3055420	0.0478448	0.0066719	1.40E-14
10	REEP3	rs7910951	63578544	G	A	0.3056980	0.0477168	0.0066700	1.60E-14
10	REEP3	rs7911761	63578993	G	C	0.3057150	0.0476667	0.0066703	1.80E-14
10	REEP3	rs11817901	63580123	A	G	0.2868010	0.0446482	0.0067966	2.00E-12
10	REEP3	rs12768534	63581137	A	G	0.3056940	0.0476998	0.0066700	1.70E-14
10	REEP3	rs16918638	63583371	C	T	0.2879580	0.0446840	0.0067905	2.20E-12
10	REEP3	rs61853658	63590037	T	C	0.2819710	0.0431264	0.0068468	1.80E-11
10	REEP3	chr10:63590519_AT_A	63590519	AT	A	0.3098970	0.0464419	0.0066764	1.10E-13
10	REEP3	rs11817169	63596549	G	A	0.2833550	0.0429467	0.0068523	2.60E-11
10	REEP3	rs4746244	63599941	T	C	0.2814860	0.0429335	0.0068731	3.00E-11
10	REEP3	rs11818738	63604971	C	A	0.2852460	0.0419282	0.0068872	7.20E-11
10	REEP3 *	rs2565187	63632093	C	T	0.2327730	0.0387479	0.0072671	1.80E-08
10	REEP3 *	rs2565186	63632270	A	G	0.2327470	0.0387078	0.0072672	1.90E-08
10	REEP3 *	rs1268639	63632720	A	G	0.2329050	0.0388513	0.0072629	1.80E-08
10	REEP3 *	rs1255495	63634690	G	A	0.2331590	0.0386257	0.0072493	2.00E-08
10	OIT3	rs11000447	72920381	T	G	0.2415890	0.0438623	0.0071925	8.40E-10
10	OIT3	rs41280378	72932888	G	T	0.2527460	0.0414069	0.0071313	3.00E-09
10	CYP26A1 *	rs11812460	93072371	G	A	0.1738050	0.0461800	0.0082681	2.00E-08
10	CYP26A1 *	rs61863116	93078631	G	A	0.1264410	0.0547489	0.0093216	5.40E-09
10	CYP26A1 *	rs2068888	93079885	G	A	0.1900280	0.0597742	0.0078015	1.40E-15
10	CYP26A1 *	rs4418728	93079967	G	T	0.1899420	0.0595268	0.0078063	2.10E-15
10	CYP26A1 *	rs10882140	93082456	G	T	0.1610870	0.0534149	0.0083568	1.70E-11
10	CYP26A1 *	rs10786068	93082720	C	G	0.1606610	0.0539183	0.0083615	1.30E-11
10	CYP26A1 *	rs12359135	93083778	T	C	0.1660950	0.0507172	0.0082671	1.60E-10
10	CYP26A1 *	rs10748591	93084109	C	G	0.1534490	0.0538689	0.0085224	3.30E-11
10	CYP26A1 *	rs10882141	93084327	G	A	0.1564250	0.0535960	0.0084483	3.00E-11
10	CYP26A1 *	rs913423	93085279	G	A	0.1613260	0.0532201	0.0083200	1.40E-11
10	CYP26A1 *	rs10786069	93085789	C	T	0.1623790	0.0518673	0.0083112	2.60E-11
10	CYP26A1 *	rs10610109	93086224	TCA	T	0.1571470	0.0502565	0.0084685	1.70E-10
10	CYP26A1 *	rs7080494	93086336	G	A	0.1508880	0.0518872	0.0087289	1.40E-10
10	GPAM	rs2487294	112178183	G	T	0.2857440	-0.0375942	0.0067800	3.90E-08
10	GPAM	chr10:112178572_AAAAC_A	112178572	AAAAC	A	0.2852900	-0.0376961	0.0067872	4.20E-08
10	GPAM *	rs55645497	112225671	A	T	0.3605530	0.0367450	0.0065269	4.50E-09
10	GPAM *	rs12413488	112227082	A	G	0.3611870	0.0378540	0.0065053	1.10E-09
10	GPAM *	rs4573621	112227790	G	A	0.3636080	0.0380919	0.0064842	7.90E-10
10	GPAM *	rs12571496	112228257	A	C	0.3624390	0.0374658	0.0064960	1.50E-09
10	GPAM *	rs60191209	112229237	C	T	0.3654220	0.0373773	0.0064715	1.60E-09
10	GPAM *	rs57128949	112231292	T	C	0.3572470	0.0384427	0.0064290	1.10E-09
10	GPAM *	rs7082582	112231639	C	T	0.4019300	-0.0378575	0.0062686	3.10E-09
10	GPAM *	rs10885316	112232239	T	C	0.3839740	-0.0382532	0.0062896	3.20E-09
10	GPAM *	rs7922421	112232800	C	T	0.3843320	-0.0378198	0.0062779	4.20E-09
10	GPAM *	rs12572599	112233103	G	T	0.3516450	0.0362503	0.0064012	6.40E-09
10	GPAM *	rs12572629	112233303	C	T	0.3530560	0.0360008	0.0063946	7.00E-09
10	GPAM *	rs4491148	112233558	G	A	0.3920670	-0.0364071	0.0062534	1.40E-08
10	TECTB *	rs4360631	112233724	G	A	0.3925390	-0.0365161	0.0062593	1.30E-08
10	TECTB *	rs2001737	112236289	T	C	0.3937660	0.0334052	0.0062545	4.20E-08
10	TECTB *	rs4918725	112237665	T	A	0.3880240	-0.0359121	0.0062737	2.30E-08
10	TECTB *	rs61383545	112238312	C	G	0.3547360	0.0348231	0.0063904	2.50E-08
10	TECTB *	rs7902884	112238713	T	C	0.3807420	-0.0369085	0.0062909	9.50E-09
10	TECTB *	rs12416473	112240658	T	C	0.3552950	0.0347047	0.0063961	2.90E-08
10	TECTB *	rs2419611	112241185	C	T	0.3893030	-0.0367424	0.0062837	9.70E-09
10	TECTB *	rs1986539	112241256	C	T	0.3845420	-0.0364326	0.0062925	1.40E-08
10	TECTB *	rs1986540	112241510	C	T	0.3885070	-0.0366812	0.0062752	1.10E-08
10	TECTB *	rs4285809	112242269	T	C	0.3552420	0.0346104	0.0063974	3.20E-08
10	TECTB *	rs4285810	112242632	T	C	0.3555540	0.0345518	0.0063950	3.30E-08
10	TECTB *	rs7913225	112243566	T	G	0.3538370	0.0347711	0.0063996	2.70E-08
10	TECTB *	rs67991485	112244107	C	A	0.3556410	0.0346030	0.0063950	3.30E-08
10	TECTB *	rs4918727	112244521	T	C	0.3541560	0.0348389	0.0064009	2.50E-08
10	TECTB *	rs11195850	112246212	C	T	0.4022950	0.0336380	0.0062428	3.50E-08
10	TECTB *	rs1887137	112246848	A	G	0.3536840	0.0348848	0.0064056	2.60E-08
10	TECTB *	chr10:112246861_CA_C	112246861	CA	C	0.3831040	-0.0369648	0.0063207	1.00E-08
10	TECTB *	rs11195851	112247704	A	G	0.3818640	-0.0375320	0.0062881	5.80E-09
10	TECTB *	rs7903487	112248173	C	G	0.4044710	0.0336969	0.0062373	4.00E-08
10	TECTB *	rs1926563	112248810	T	C	0.3856960	-0.0363707	0.0062794	1.60E-08
10	TECTB *	rs10787433	112249254	C	T	0.4044590	0.0336731	0.0062372	4.10E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	TECTB *	rs34549369	112251411	CGT	C	0.3880510	-0.0358470	0.0062806	2.50E-08
10	TECTB *	rs55875049	112252320	G	A	0.3542420	0.0349923	0.0063911	2.60E-08
10	TECTB *	rs4918730	112253508	C	G	0.3529120	0.0348525	0.0064108	3.80E-08
10	TECTB *	rs7897127	112258898	A	G	0.4018460	0.0335109	0.0062360	4.50E-08
10	TECTB *	rs7897067	112259026	T	C	0.4018910	0.0335650	0.0062356	4.40E-08
10	TECTB *	rs12357806	112259592	T	C	0.4017580	0.0335651	0.0062372	4.40E-08
10	TECTB *	rs4917629	112259662	T	C	0.4018910	0.0335650	0.0062356	4.40E-08
10	TECTB *	rs4917630	112260072	A	G	0.4019310	0.0335176	0.0062347	4.50E-08
10	TECTB *	rs10787434	112260540	A	G	0.3821110	-0.0379373	0.0062822	3.90E-09
10	TECTB *	rs72403542	112260761	G	GT	0.3541790	0.0349493	0.0063954	2.80E-08
10	TECTB *	rs11195857	112262808	A	G	0.3537360	0.0345004	0.0063922	3.90E-08
10	TECTB *	rs57594838	112265424	G	T	0.3612820	0.0351185	0.0063641	2.20E-08
10	TECTB *	rs10787435	112265744	C	G	0.3804390	-0.0377062	0.0062890	5.10E-09
10	TECTB *	rs66870305	112266021	T	A	0.3538810	0.0347418	0.0063916	3.30E-08
10	TECTB *	rs7084806	112267063	A	G	0.3797330	-0.0374723	0.0062934	5.90E-09
10	TECTB *	rs17672352	112268722	T	C	0.3537610	0.0344777	0.0063920	3.90E-08
10	TECTB *	rs2419613	112268780	A	G	0.3799200	-0.0377583	0.0062902	4.40E-09
10	TECTB *	rs6585147	112270962	C	T	0.3827190	-0.0375318	0.0062832	5.80E-09
10	TECTB *	rs4918733	112276040	C	G	0.3885020	-0.0372802	0.0062909	6.60E-09
10	TECTB *	rs10885323	112277720	G	A	0.3816760	-0.0376422	0.0062908	4.90E-09
10	TECTB *	rs7912328	112280463	A	G	0.3766010	-0.0367360	0.0063255	1.30E-08
10	TECTB *	rs4918734	112281088	C	A	0.3873700	-0.0355742	0.0062860	3.80E-08
10	TECTB	rs7904701	112287050	T	A	0.3880870	-0.0361994	0.0062828	1.70E-08
10	TECTB	rs943265	112287637	C	T	0.3643340	0.0357730	0.0063594	1.20E-08
10	TECTB	rs2419616	112288272	C	T	0.3849390	-0.0356086	0.0063222	3.90E-08
10	TECTB	rs4918735	112289877	C	T	0.3820880	-0.0369948	0.0063527	1.20E-08
10	TECTB	rs11195876	112289955	T	C	0.3780790	-0.0374247	0.0063623	8.60E-09
10	WDR11 *	rs2246730	121131141	C	T	0.3758050	-0.0371973	0.0063560	4.70E-08
10	WDR11 *	rs1873446	121131995	C	T	0.3754910	-0.0370628	0.0063478	4.60E-08
10	WDR11 *	rs1907239	121135315	A	C	0.3674860	0.0385825	0.0063357	1.20E-09
10	WDR11 *	rs2250266	121138399	A	G	0.3660840	0.0390108	0.0063468	7.30E-10
10	WDR11 *	rs1907240	121138445	G	A	0.4139620	-0.0418626	0.0062024	1.00E-10
10	WDR11 *	rs1907241	121138470	G	T	0.4134500	-0.0424073	0.0062023	5.60E-11
10	WDR11 *	rs2257129	121139183	T	C	0.4110220	-0.0428991	0.0062089	2.50E-11
10	WDR11 *	rs2263985	121143992	C	T	0.4110290	-0.0434753	0.0062120	1.40E-11
10	WDR11 *	rs2451876	121144368	T	C	0.4109380	-0.0433688	0.0062109	1.60E-11
10	WDR11 *	rs2263983	121145186	T	C	0.4109330	-0.0433332	0.0062108	1.60E-11
10	WDR11 *	rs2220607	121146746	C	A	0.4124810	-0.0435944	0.0062072	1.20E-11
10	WDR11 *	rs2172073	121150111	C	A	0.4126560	-0.0438173	0.0062070	8.40E-12
10	WDR11 *	rs1907256	121150416	A	G	0.3709890	0.0390286	0.0063261	3.50E-10
10	WDR11 *	rs2263997	121151174	A	C	0.3675420	0.0396505	0.0063671	2.10E-10
10	WDR11 *	rs7098433	121153961	C	T	0.4127630	-0.0434002	0.0062042	1.30E-11
10	WDR11 *	rs17101518	121155455	G	A	0.3658960	-0.0431409	0.0063433	6.70E-11
10	WDR11 *	rs58846742	121155542	C	G	0.3167750	-0.0402890	0.0065621	1.90E-09
10	WDR11 *	rs72631105	121155831	A	G	0.3524420	0.0406459	0.0063951	1.10E-10
10	WDR11 *	rs56351107	121155983	G	C	0.3657410	-0.0431676	0.0063412	6.00E-11
10	WDR11 *	rs17101521	121156039	C	T	0.3647910	-0.0432794	0.0063515	5.80E-11
10	WDR11 *	rs56132357	121156071	A	T	0.3154900	-0.0402830	0.0065796	2.00E-09
10	WDR11 *	rs59313277	121156141	T	G	0.3655830	-0.0429742	0.0063432	7.40E-11
10	WDR11 *	chr10:121156208_T_TA	121156208	TA	T	0.3578730	-0.0437478	0.0064432	4.10E-11
10	WDR11 *	rs73366917	121156240	A	G	0.3652070	-0.0429106	0.0063448	8.00E-11
10	WDR11 *	rs17101524	121156265	A	C	0.3657410	-0.0431676	0.0063412	6.00E-11
10	WDR11 *	rs59082214	121156440	A	ACACA	0.3595500	-0.0394363	0.0064181	2.80E-09
10	WDR11 *	rs4752500	121156448	T	A	0.3680700	-0.0429978	0.0063520	7.00E-11
10	WDR11 *	rs1907266	121156628	T	C	0.4125470	-0.0432409	0.0062036	1.60E-11
10	WDR11 *	rs7920116	121156957	C	T	0.3657410	-0.0431676	0.0063412	6.00E-11
10	WDR11 *	rs7903585	121157114	G	A	0.3641940	-0.0435487	0.0063526	4.60E-11
10	WDR11 *	rs7903948	121157125	A	G	0.3656160	-0.0433951	0.0063422	4.50E-11
10	WDR11 *	rs7903733	121157208	G	A	0.3167860	-0.0403005	0.0065619	1.80E-09
10	WDR11 *	rs10710843	121157294	C	CA	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs7904102	121157377	G	C	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs58960052	121157487	A	G	0.3167860	-0.0403005	0.0065619	1.80E-09
10	WDR11 *	rs59754371	121157811	C	T	0.3650530	-0.0427813	0.0063489	9.20E-11
10	WDR11 *	rs57615383	121157842	A	G	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs112209982	121158067	A	G	0.3616810	-0.0427652	0.0063797	1.10E-10
10	WDR11 *	rs58324269	121158215	G	A	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs60089052	121158221	C	T	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs58217496	121158313	C	T	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs60711290	121158469	T	G	0.3657370	-0.0432219	0.0063407	5.50E-11
10	WDR11 *	rs57142282	121158561	T	C	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs17101530	121158601	C	T	0.3657840	-0.0433595	0.0063408	5.10E-11
10	WDR11 *	rs71945618	121158703	AG	A	0.3657400	-0.0432463	0.0063405	5.40E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	WDR11 *	rs73366943	121158995	G	A	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs17101534	121159361	C	T	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs11199803	121159565	G	A	0.3657400	-0.0432463	0.0063405	5.40E-11
10	WDR11 *	rs11199804	121159660	G	C	0.3657390	-0.0432452	0.0063405	5.40E-11
10	WDR11 *	rs11199805	121159692	T	C	0.3657390	-0.0432452	0.0063405	5.40E-11
10	WDR11 *	rs11199806	121159795	A	G	0.3657430	-0.0432401	0.0063405	5.40E-11
10	WDR11 *	rs7917346	121160328	G	A	0.3658630	-0.0429596	0.0063413	7.30E-11
10	WDR11 *	rs7902796	121160495	C	T	0.3167900	-0.0402910	0.0065619	1.90E-09
10	WDR11 *	rs7902919	121160588	C	T	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs7917833	121160641	A	C	0.3657470	-0.0432764	0.0063407	5.20E-11
10	WDR11 *	rs7917847	121160676	A	C	0.3168370	-0.0405209	0.0065626	1.50E-09
10	WDR11 *	rs2130786	121161069	C	T	0.4125810	-0.0432488	0.0062030	1.60E-11
10	WDR11 *	rs1907267	121161442	T	C	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs1907268	121161733	C	T	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs1907269	121161835	C	A	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs6585696	121162049	G	A	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs6585697	121162083	T	C	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs6585698	121162088	G	T	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs6585699	121162146	C	T	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs6585700	121162243	C	G	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs6585701	121162277	C	T	0.3657420	-0.0432314	0.0063405	5.50E-11
10	WDR11 *	rs7920041	121162857	C	T	0.3657470	-0.0432197	0.0063406	5.60E-11
10	WDR11 *	rs7920045	121162867	C	T	0.3167920	-0.0403084	0.0065619	1.80E-09
10	WDR11 *	rs7906567	121162944	C	A	0.3657470	-0.0432197	0.0063406	5.60E-11
10	WDR11 *	rs59296617	121163320	A	T	0.3657470	-0.0432197	0.0063406	5.60E-11
10	WDR11 *	rs11199810	121164064	C	T	0.3657470	-0.0432197	0.0063406	5.60E-11
10	WDR11 *	rs60590589	121164227	AAAAC	A	0.3657940	-0.0431412	0.0063412	6.00E-11
10	WDR11 *	rs7087606	121164303	T	C	0.3657040	-0.0432026	0.0063405	5.80E-11
10	WDR11 *	rs6585702	121164396	T	G	0.3657040	-0.0432026	0.0063405	5.80E-11
10	WDR11 *	rs6585703	121164626	A	G	0.3657490	-0.0432328	0.0063406	5.50E-11
10	WDR11 *	rs7915733	121165125	A	C	0.3657610	-0.0432753	0.0063407	5.30E-11
10	WDR11 *	rs10788141	121165340	G	T	0.4126350	-0.0431026	0.0062028	1.90E-11
10	WDR11 *	rs1907272	121165648	A	G	0.3164830	-0.0405761	0.0065666	1.40E-09
10	WDR11 *	rs1907273	121165771	C	T	0.3167910	-0.0403915	0.0065626	1.70E-09
10	WDR11 *	rs1907274	121165824	T	G	0.3657580	-0.0432953	0.0063410	5.20E-11
10	WDR11 *	rs7096589	121165945	G	A	0.3167910	-0.0403915	0.0065626	1.70E-09
10	WDR11 *	rs7080940	121166105	A	T	0.3167910	-0.0403915	0.0065626	1.70E-09
10	WDR11 *	rs6585704	121166509	G	A	0.3168590	-0.0403583	0.0065628	1.70E-09
10	WDR11 *	rs7920839	121166658	T	C	0.3168590	-0.0403583	0.0065628	1.70E-09
10	WDR11 *	rs7921081	121166703	T	G	0.3168160	-0.0402397	0.0065635	1.90E-09
10	WDR11 *	rs17559591	121166830	G	A	0.3168160	-0.0402397	0.0065635	1.90E-09
10	WDR11 *	rs7921353	121166901	A	G	0.3184670	-0.0402498	0.0065676	1.80E-09
10	WDR11 *	rs7893136	121166946	T	C	0.3168160	-0.0402397	0.0065635	1.90E-09
10	WDR11 *	rs6585705	121167044	C	T	0.3163830	-0.0405321	0.0065669	1.40E-09
10	WDR11 *	rs6585706	121167075	G	A	0.3159010	-0.0404132	0.0065739	1.70E-09
10	WDR11 *	rs6585707	121167285	G	C	0.3168160	-0.0402397	0.0065635	1.90E-09
10	WDR11 *	rs6585708	121167429	T	C	0.3657410	-0.0432546	0.0063419	5.30E-11
10	WDR11 *	rs7897890	121168240	T	C	0.3162600	-0.0398220	0.0065667	2.90E-09
10	WDR11 *	rs11199811	121169559	A	C	0.3164910	-0.0399302	0.0065671	2.60E-09
10	WDR11 *	rs10886862	121169894	C	T	0.4123390	-0.0430248	0.0062070	1.90E-11
10	WDR11 *	rs35326857	121169898	G	T	0.3704220	0.0395881	0.0063279	1.40E-10
10	WDR11 *	rs10886863	121169979	T	C	0.4123390	-0.0430248	0.0062070	1.90E-11
10	WDR11 *	rs10886864	121170023	C	T	0.4123390	-0.0430248	0.0062070	1.90E-11
10	WDR11 *	rs7071036	121171054	C	T	0.3655310	-0.0430941	0.0063447	6.30E-11
10	WDR11 *	rs7071062	121171098	C	T	0.3655310	-0.0430941	0.0063447	6.30E-11
10	WDR11 *	rs11199812	121171431	A	G	0.3161680	-0.0407444	0.0065713	1.20E-09
10	WDR11 *	rs1873449	121172138	T	G	0.3621620	-0.0436626	0.0063689	4.00E-11
10	WDR11 *	rs754227	121172490	C	T	0.3685040	-0.0433835	0.0063501	3.70E-11
10	WDR11 *	rs3962120	121177844	A	C	0.3626230	-0.0452084	0.0064449	6.30E-12
10	WDR11 *	rs191959515	121178085	T	C	0.3244160	-0.0457963	0.0066215	8.70E-12
10	WDR11 *	rs200553592	121178117	A	TAGAT	0.3239490	-0.0450525	0.0066210	1.90E-11
10	WDR11 *	rs75208023	121179679	T	C	0.2297110	-0.0399776	0.0072837	4.50E-08
10	WDR11 *	rs7085142	121179860	C	T	0.4213490	0.0354257	0.0062217	2.60E-09
10	WDR11 *	rs35805626	121180026	A	ATG	0.2297040	-0.0401214	0.0072829	4.00E-08
10	WDR11 *	rs10788142	121181315	C	T	0.3782750	0.0387893	0.0063165	2.90E-10
10	WDR11 *	rs1907279	121181633	C	G	0.4241000	0.0340478	0.0062107	8.80E-09
10	WDR11 *	rs1907282	121182017	A	G	0.3862900	0.0380867	0.0062804	3.60E-10
10	WDR11 *	rs1907284	121182265	G	T	0.3868240	0.0379959	0.0062829	4.50E-10
10	WDR11 *	rs6585711	121182277	A	G	0.4305940	0.0343098	0.0061829	5.30E-09
10	WDR11 *	rs12219793	121183786	G	T	0.2323130	-0.0403036	0.0072398	2.70E-08
10	WDR11 *	rs1907285	121183933	G	A	0.2321850	-0.0400559	0.0072441	3.50E-08
10	WDR11 *	rs11199816	121184848	C	T	0.2323830	-0.0405307	0.0072408	2.40E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	WDR11 *	rs11199817	121184912	A	G	0.2323380	-0.0405000	0.0072399	2.40E-08
10	WDR11 *	rs3943077	121185572	G	A	0.3881070	0.0382851	0.0063108	4.10E-10
10	WDR11 *	rs7088428	121185738	G	T	0.3866960	0.0377047	0.0062874	5.70E-10
10	WDR11 *	rs17101591	121187689	T	C	0.2266280	-0.0414345	0.0073048	2.60E-08
10	WDR11 *	rs12221113	121187774	G	T	0.2266870	-0.0418259	0.0073022	1.80E-08
10	WDR11 *	rs35234305	121188328	C	CT	0.4035300	0.0320146	0.0062421	2.50E-08
10	WDR11 *	rs10788144	121188708	T	C	0.4026150	0.0328085	0.0062631	1.40E-08
10	WDR11 *	rs7089185	121189319	A	G	0.4022760	0.0327453	0.0062408	1.30E-08
10	WDR11 *	rs1907287	121189936	A	G	0.4014690	0.0329279	0.0062430	1.30E-08
10	WDR11 *	rs2901288	121192680	A	G	0.4019960	0.0329848	0.0062405	1.20E-08
10	FGFR2 *	rs7077138	121195851	A	T	0.4025390	0.0330170	0.0062422	1.10E-08
10	FGFR2 *	rs7067847	121197234	T	C	0.4020320	0.0327231	0.0062427	1.50E-08
10	FGFR2 *	chr10:121197901_A_AT	121197901	AT	A	0.4019610	0.0330547	0.0062582	1.30E-08
10	FGFR2 *	rs7082125	121199983	T	G	0.4020590	0.0334911	0.0062467	7.70E-09
10	FGFR2 *	rs12358575	121203420	T	C	0.3331130	0.0351831	0.0064874	2.60E-09
10	FGFR2 *	rs11199828	121205116	A	G	0.3271640	0.0378437	0.0066638	5.10E-10
10	FGFR2 *	rs10788149	121207656	G	A	0.3200910	0.0417647	0.0065481	9.90E-12
10	FGFR2 *	rs10749408	121208012	C	T	0.3195500	0.0422622	0.0065571	5.50E-12
10	FGFR2 *	rs2172071	121208516	C	T	0.3184490	0.0421100	0.0065678	7.40E-12
10	FGFR2 *	rs11199830	121208601	T	C	0.3369970	-0.0345887	0.0064706	3.60E-08
10	FGFR2 *	rs11592107	121209450	A	G	0.3184730	0.0420125	0.0065683	8.50E-12
10	FGFR2 *	rs1907218	121210702	T	C	0.3184200	0.0422299	0.0065678	6.80E-12
10	FGFR2 *	rs1907219	121210790	A	G	0.3374820	-0.0350076	0.0064614	2.40E-08
10	FGFR2 *	rs1907220	121211409	A	G	0.3182970	0.0423665	0.0065700	5.80E-12
10	FGFR2 *	rs1994655	121211732	T	G	0.3183060	0.0423561	0.0065699	5.90E-12
10	FGFR2 *	rs1907221	121212913	C	T	0.3192760	0.0418643	0.0065533	9.70E-12
10	FGFR2 *	rs1907225	121216119	C	T	0.3187240	0.0422244	0.0065673	8.20E-12
10	FGFR2 *	rs10749409	121217052	C	G	0.3187660	0.0420108	0.0065677	1.20E-11
10	FGFR2 *	rs11199835	121217643	G	A	0.3188200	0.0421041	0.0065680	1.10E-11
10	FGFR2 *	rs1907228	121219430	G	A	0.4972710	-0.0397415	0.0061282	3.50E-11
10	FGFR2 *	rs7093348	121221734	C	T	0.4951520	-0.0397210	0.0061379	2.80E-11
10	FGFR2 *	rs1907231	121221742	T	A	0.4951520	-0.0397210	0.0061379	2.80E-11
10	FGFR2 *	rs10886871	121222283	A	C	0.3354970	-0.0354917	0.0064803	2.20E-08
10	FGFR2 *	rs2420922	121223863	G	A	0.4971780	-0.0393147	0.0061148	5.00E-11
10	FGFR2 *	rs7920546	121224230	G	A	0.4971750	-0.0393103	0.0061149	5.00E-11
10	FGFR2 *	rs7921069	121224591	A	C	0.3355980	-0.0353590	0.0064696	2.30E-08
10	FGFR2 *	rs7098079	121224699	G	C	0.4935930	-0.0383723	0.0061206	1.40E-10
10	FGFR2 *	rs11595340	121225312	T	C	0.3355980	-0.0353590	0.0064696	2.30E-08
10	FGFR2 *	rs10886873	121225604	T	C	0.3356250	-0.0353435	0.0064693	2.40E-08
10	FGFR2 *	rs56124706	121226884	A	T	0.3355450	-0.0353019	0.0064706	2.50E-08
10	FGFR2 *	rs11199837	121227134	A	T	0.4972070	-0.0394944	0.0061155	4.20E-11
10	FGFR2 *	rs1907232	121227612	A	G	0.4958570	-0.0385585	0.0061141	1.20E-10
10	FGFR2 *	rs1907233	121227775	T	C	0.3362230	-0.0359237	0.0064724	1.40E-08
10	FGFR2 *	rs11199838	121228771	A	G	0.3355210	-0.0354317	0.0064716	2.20E-08
10	FGFR2 *	rs4752518	121229421	T	C	0.3000410	0.0390161	0.0066909	5.00E-10
10	FGFR2 *	rs11597855	121229534	T	C	0.4972020	-0.0394374	0.0061157	4.80E-11
10	FGFR2 *	rs4500422	121230633	A	G	0.4867890	-0.0393023	0.0061387	5.70E-11
10	FGFR2 *	rs11199840	121230824	G	A	0.4868740	-0.0393725	0.0061398	5.10E-11
10	FGFR2 *	rs11199842	121230972	C	T	0.4864730	-0.0392686	0.0061509	5.90E-11
10	FGFR2 *	rs11199843	121230977	C	T	0.4870110	-0.0391851	0.0061560	6.50E-11
10	FGFR2 *	rs10886874	121232008	A	G	0.4942740	-0.0395947	0.0061661	2.80E-11
10	FGFR2 *	rs4294510	121232748	A	G	0.4856940	-0.0388266	0.0061403	9.90E-11
10	FGFR2 *	rs11199844	121232928	T	C	0.3252650	-0.0359531	0.0065460	1.80E-08
10	FGFR2 *	rs11199845	121232961	T	C	0.3252730	-0.0359473	0.0065459	1.80E-08
10	FGFR2 *	rs10886876	121233331	G	C	0.4867610	-0.0399049	0.0061376	2.60E-11
10	FGFR2 *	rs60834189	121233878	A	AT	0.4832690	-0.0407438	0.0061591	1.20E-11
10	FGFR2 *	rs11199848	121235094	G	A	0.4868000	-0.0393873	0.0061443	5.30E-11
10	FGFR2 *	rs12217412	121235456	C	T	0.4894230	-0.0393720	0.0061520	5.10E-11
10	FGFR2 *	rs12220647	121235627	A	C	0.3243990	-0.0360421	0.0065578	1.50E-08
10	FGFR2 *	rs11199850	121236106	T	C	0.4849890	-0.0391955	0.0061491	6.00E-11
10	FGFR2 *	rs11199851	121237414	C	A	0.3055260	0.0397006	0.0066820	2.90E-10
10	FGFR2 *	rs878409	121240036	A	G	0.4965100	-0.0400808	0.0061289	1.80E-11
10	FGFR2 *	rs12358504	121240352	G	A	0.2827550	0.0398948	0.0068437	7.30E-10
10	FGFR2 *	rs12245393	121240386	T	C	0.4965140	-0.0401209	0.0061295	1.70E-11
10	FGFR2 *	rs4751828	121241030	A	G	0.2802580	0.0399474	0.0068779	9.00E-10
10	FGFR2 *	rs145325908	121241120	TG	T	0.4946300	-0.0388480	0.0062292	8.70E-11
10	FGFR2 *	rs5016035	121241124	G	T	0.4939900	-0.0382652	0.0062231	1.70E-10
11	DAGLA *	rs7925523	61675020	A	G	0.2534830	-0.0629896	0.0070109	1.00E-18
11	DAGLA *	rs60399071	61675683	A	G	0.2536090	-0.0629915	0.0070118	1.00E-18
11	DAGLA *	rs151242175	61679851	T	C	0.2530620	-0.0627098	0.0070276	1.90E-18
11	DAGLA *	rs115702847	61679884	A	T	0.2530660	-0.0627109	0.0070276	1.90E-18
11	DAGLA *	rs11230779	61682061	A	G	0.4919180	-0.0327372	0.0061810	3.20E-08

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11	DAGLA	rs34700917	61682076	TG	T	0.4914870	-0.0329164	0.0061844	3.00E-08
11	DAGLA	rs59200224	61682665	G	A	0.2535710	-0.0627547	0.0070199	1.50E-18
11	DAGLA	rs59371352	61682823	A	G	0.2537590	-0.0628197	0.0070310	1.60E-18
11	DAGLA	rs72918042	61684076	G	C	0.2535800	-0.0627795	0.0070198	1.50E-18
11	DAGLA	rs61898525	61686132	G	A	0.4919230	-0.0323884	0.0061763	4.30E-08
11	DAGLA	rs35404524	61687658	C	CTT	0.2535890	-0.0625653	0.0070206	2.00E-18
11	DAGLA	rs4963308	61688954	A	G	0.2535830	-0.0626738	0.0070217	1.70E-18
11	DAGLA	rs883724	61690385	T	C	0.2532160	-0.0622121	0.0070264	3.10E-18
11	DAGLA	rs11827215	61691123	A	G	0.2539550	-0.0619758	0.0070167	3.80E-18
11	DAGLA	rs72315101	61695289	C	CTCTG	0.2535880	-0.0626605	0.0070236	1.70E-18
11	DAGLA	rs60507107	61696297	T	C	0.2535470	-0.0624247	0.0070242	2.30E-18
11	DAGLA	rs17827816	61697053	T	C	0.4399030	-0.0351643	0.0062349	5.70E-09
11	DAGLA	rs198453	61697078	C	T	0.4924560	-0.0326394	0.0061668	3.60E-08
11	DAGLA	rs2097853	61698795	T	G	0.2537120	-0.0623449	0.0070243	2.60E-18
11	DAGLA	rs81659	61699580	G	A	0.4660940	-0.0381259	0.0062070	1.90E-10
11	DAGLA	rs58217294	61702031	A	T	0.2537370	-0.0623314	0.0070256	2.80E-18
11	DAGLA	rs12274157	61710175	C	A	0.2538820	-0.0623968	0.0070292	3.30E-18
11	DAGLA	rs731842	61712719	C	T	0.2539950	-0.0624356	0.0070281	2.90E-18
11	DAGLA	rs2107617	61714167	G	C	0.3044660	-0.0549757	0.0066855	6.10E-16
11	DAGLA	rs17156244	61714923	G	T	0.2540830	-0.0625785	0.0070266	2.40E-18
11	DAGLA	rs198435	61715852	C	G	0.2510930	-0.0620538	0.0070629	5.60E-18
11	DAGLA	rs2903825	61721496	T	C	0.2612890	-0.0627658	0.0069686	1.10E-18
11	DAGLA	rs9735635	61723408	A	C	0.2606860	-0.0629399	0.0069740	9.70E-19
11	DAGLA	rs4963243	61726855	A	G	0.2616820	-0.0632641	0.0069614	4.50E-19
11	DAGLA	rs2240287	61738111	A	G	0.2640960	-0.0620374	0.0069520	1.90E-18
11	DAGLA	rs2240286	61738982	C	T	0.2641080	-0.0619090	0.0069533	2.30E-18
11	DAGLA	rs4963255	61740134	A	G	0.2641310	-0.0620805	0.0069546	2.00E-18
11	DAGLA	rs3741252	61744026	T	C	0.2614780	-0.0622214	0.0069953	2.20E-18
11	MYRF	rs174528	61776027	T	C	0.4021760	-0.0705933	0.0062469	3.70E-29
11	MYRF	rs174529	61776489	T	C	0.4022870	-0.0703166	0.0062497	6.90E-29
11	MYRF	rs174530	61779120	A	G	0.4117120	-0.0728220	0.0062179	4.00E-31
11	MYRF	rs108499	61779765	C	T	0.4151020	-0.0730680	0.0062102	1.60E-31
11	MYRF	rs509360	61781087	A	G	0.4022220	-0.0698844	0.0062514	1.30E-28
11	MYRF	rs174533	61781553	G	A	0.4147520	-0.0722263	0.0062164	8.80E-31
11	MYRF	rs174534	61781986	A	G	0.4115120	-0.0718944	0.0062223	2.30E-30
11	MYRF	rs174535	61783884	T	C	0.4106490	-0.0722685	0.0062181	1.30E-30
11	MYRF	rs174536	61784455	A	C	0.4132180	-0.0730267	0.0062166	2.40E-31
11	MYRF	rs174537	61785208	G	T	0.4141110	-0.0731799	0.0062104	1.70E-31
11	TMEM258	rs102275	61790331	T	C	0.4137110	-0.0734431	0.0062101	8.90E-32
11	TMEM258	rs102274	61790354	T	C	0.4138730	-0.0735384	0.0062110	8.00E-32
11	TMEM258	rs174538	61792609	G	A	0.4162490	-0.0729611	0.0062054	2.10E-31
11	FEN1	rs4246215	61796827	G	T	0.4141740	-0.0736016	0.0062094	7.40E-32
11	FADS1 *	rs174541	61798436	T	C	0.4140000	-0.0740401	0.0062131	3.50E-32
11	FADS1	rs174544	61800281	C	A	0.4231340	-0.0739127	0.0062097	4.90E-32
11	FADS1	rs174545	61801834	C	G	0.4144200	-0.0734832	0.0062088	9.00E-32
11	FADS1	rs174546	61802358	C	T	0.4144600	-0.0737875	0.0062094	5.00E-32
11	FADS1	rs174547	61803311	T	C	0.4143440	-0.0732142	0.0062110	1.60E-31
11	FADS1	rs174548	61803876	C	G	0.4221640	-0.0747045	0.0061961	7.60E-33
11	FADS1	rs174549	61803910	G	A	0.4226540	-0.0744463	0.0061988	1.50E-32
11	FADS1	rs174550	61804006	T	C	0.4143940	-0.0738048	0.0062089	4.80E-32
11	FADS1	rs174553	61807686	A	G	0.4147310	-0.0738720	0.0062090	4.50E-32
11	FADS1	rs72643557	61811955	T	C	0.4112140	-0.0743333	0.0062371	4.60E-32
11	FADS1	rs174554	61811991	A	G	0.4147510	-0.0739556	0.0062086	3.90E-32
11	FADS1	rs174555	61812288	T	C	0.4220380	-0.0747526	0.0061966	6.90E-33
11	FADS1	rs174556	61813163	C	T	0.4220870	-0.0747713	0.0061967	6.50E-33
11	FADS1	rs174559	61814184	G	A	0.4237900	-0.0748078	0.0061950	6.20E-33
11	FADS1	rs174560	61814292	T	C	0.4220740	-0.0749437	0.0061970	4.80E-33
11	FADS1, MIF	rs174561	61815236	T	C	0.4220540	-0.0748944	0.0061981	5.20E-33
11	FADS2	rs174562	61817672	A	G	0.4139960	-0.0741560	0.0062151	2.80E-32
11	FADS2	rs35473591	61818856	C	CT	0.4142080	-0.0738265	0.0062146	5.20E-32
11	FADS2	rs174564	61820833	A	G	0.4130810	-0.0730346	0.0062227	2.70E-31
11	FADS2	rs28456	61822009	A	G	0.4207950	-0.0731574	0.0062153	2.00E-31
11	FADS2	rs174565	61824164	C	G	0.4150380	-0.0724609	0.0062199	6.60E-31
11	FADS2	chr11:61824525_A_AAG	61824525	A	AAG	0.4172920	-0.0722417	0.0062370	1.20E-30
11	FADS2	rs174566	61824890	A	G	0.4130810	-0.0730000	0.0062226	2.90E-31
11	FADS2	rs174567	61825533	A	G	0.4159730	-0.0745859	0.0062144	1.80E-32
11	FADS2	rs174568	61826344	C	T	0.4149930	-0.0741253	0.0062125	3.00E-32
11	FADS2	rs3834458	61827448	CT	C	0.4141870	-0.0742221	0.0062171	2.70E-32
11	FADS2	rs5792235	61828850	CA	C	0.4131360	-0.0732189	0.0062135	2.10E-31
11	FADS2	rs99780	61829161	C	T	0.4131420	-0.0732216	0.0062136	2.00E-31
11	FADS2	rs174570	61829740	C	T	0.4151610	-0.0727442	0.0062091	4.00E-31
11	FADS2	rs1535	61830500	A	G	0.4130680	-0.0731724	0.0062126	2.10E-31

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	FADS2	rs174574	61832870	C	A	0.4131250	-0.0726625	0.0062160	6.30E-31
11	FADS2	rs2524296	61833906	T	C	0.4388760	0.0597347	0.0061697	1.50E-21
11	FADS2	rs2845574	61834400	T	C	0.4436710	0.0609137	0.0061406	2.00E-22
11	FADS2	rs2845573	61834436	G	A	0.4490920	0.0605745	0.0061393	4.10E-22
11	FADS2	rs199649489	61834989	A	C	0.4316580	-0.0690781	0.0063136	2.80E-27
11	FADS2	rs2727270	61835765	T	C	0.4459500	0.0614341	0.0061375	7.20E-23
11	FADS2	rs2727271	61835886	T	A	0.4459790	0.0610626	0.0061377	1.40E-22
11	FADS2	rs174576	61836038	C	A	0.4126860	-0.0723598	0.0062165	1.20E-30
11	FADS2	rs2524299	61837310	T	A	0.4462200	0.0612598	0.0061355	7.50E-23
11	FADS2	rs174577	61837342	C	A	0.4128190	-0.0722470	0.0062152	1.40E-30
11	FADS2	rs2072113	61837495	T	C	0.4459290	0.0616266	0.0061384	4.80E-23
11	FADS2	rs2072114	61837743	G	A	0.4458850	0.0611607	0.0061375	1.20E-22
11	FADS2	rs174578	61838027	T	A	0.4130350	-0.0720545	0.0062174	1.70E-30
11	FADS2	rs174580	61839170	A	G	0.4124200	-0.0722154	0.0062207	1.70E-30
11	FADS2	rs174581	61839211	G	A	0.4125400	-0.0722114	0.0062216	1.70E-30
11	FADS2	rs2727265	61841532	A	C	0.4464540	0.0617116	0.0061750	1.00E-22
11	FADS2	rs174583	61842278	C	T	0.4120770	-0.0720804	0.0062181	2.20E-30
11	FADS2	rs174584	61843278	G	A	0.4117630	-0.0719980	0.0062218	3.00E-30
11	FADS2	rs2526680	61843744	T	C	0.4483470	0.0605337	0.0061483	4.50E-22
11	FADS2	rs2845572	61847123	A	G	0.4447800	0.0606241	0.0061488	4.20E-22
11	FADS2	rs2851682	61848540	G	A	0.4452250	0.0599230	0.0061400	1.00E-21
11	FADS2	rs2727263	61850540	T	C	0.4462390	0.0611114	0.0061639	2.70E-22
11	FADS2	rs174592	61851136	A	G	0.4089970	-0.0720661	0.0062191	1.80E-30
11	FADS2	rs174594	61852357	A	C	0.4089040	-0.0727639	0.0062294	5.60E-31
11	FADS2	rs72643559	61852802	C	T	0.4051950	-0.0729344	0.0062626	7.80E-31
11	FADS2	chr11:61853156_AAACAAC_A	61853156_AAACAAC_A	A	A	0.4089690	-0.0706799	0.0062534	3.30E-29
11	FADS2	rs174598	61853722	G	A	0.4102720	-0.0724034	0.0062209	1.10E-30
11	FADS2	rs174599	61854084	G	C	0.4081410	-0.0727520	0.0062282	5.90E-31
11	FADS2	rs174600	61854755	T	C	0.4096670	-0.0724214	0.0062315	1.60E-30
11	FADS2	rs174601	61855668	C	T	0.4044090	-0.0722915	0.0062336	1.20E-30
11	FADS2 *	rs174626	61869585	G	A	0.3186720	0.0360513	0.0065461	3.70E-08
11	FADS3	rs174453	61878495	G	C	0.3009690	0.0475672	0.0067547	2.10E-12
11	FADS3	rs174634	61879915	G	C	0.3087450	0.0475068	0.0066904	1.60E-12
11	FADS3	rs174635	61879955	T	G	0.3087460	0.0474999	0.0066904	1.60E-12
11	FADS3	rs174454	61883275	G	A	0.3117290	0.0449140	0.0066358	1.20E-11
11	FADS3	rs1000778	61887833	A	G	0.3031790	0.0434270	0.0066139	7.20E-11
11	FADS3	rs174455	61888645	G	A	0.3904360	0.0421283	0.0062461	1.60E-11
11	FADS3	rs174456	61888710	C	A	0.3027960	0.0435494	0.0066200	6.60E-11
11	FADS3	rs36047269	61888782	T	TC	0.3027890	0.0435601	0.0066201	6.50E-11
11	FADS3	rs5792240	61889069	A	AT	0.3129570	0.0441363	0.0065953	1.90E-11
11	FADS3	rs1151144	61889113	T	C	0.3136120	0.0438851	0.0065840	2.00E-11
11	FADS3	rs1295988	61889186	A	C	0.3033950	0.0433607	0.0066236	8.30E-11
11	FADS3	rs174457	61889503	T	C	0.3127010	0.0444745	0.0065916	1.10E-11
11	FADS3	rs174458	61889523	C	T	0.3134700	0.0450717	0.0065864	6.10E-12
11	FADS3	rs174459	61889578	C	T	0.3131820	0.0445297	0.0065878	9.80E-12
11	FADS3	rs174460	61889638	C	T	0.3136850	0.0450181	0.0065865	6.50E-12
11	FADS3	rs174461	61889929	A	C	0.3138730	0.0459188	0.0066017	3.10E-12
11	FADS3	rs174462	61890194	A	G	0.3068770	0.0465322	0.0066864	3.10E-12
11	FADS3	rs174463	61890366	G	A	0.3127170	0.0447578	0.0066513	1.50E-11
11	FADS3	rs174464	61890454	A	G	0.3127380	0.0445548	0.0066565	2.10E-11
11	FADS3	rs693672	61891157	T	C	0.2956060	0.0449494	0.0067626	4.60E-11
11	FADS3	rs174465	61891328	C	T	0.3017050	0.0444212	0.0067215	7.10E-11
11	FADS3 *	rs35870730	61891648	A	AC	0.2930000	0.0486932	0.0068411	2.00E-12
11	RAB3IL1	rs174469	61899971	T	C	0.3304950	0.0448562	0.0066029	2.30E-11
11	RAB3IL1	rs174473	61904763	C	T	0.3647490	0.0461834	0.0064504	1.30E-12
11	RAB3IL1	rs174474	61904793	C	T	0.3318600	0.0453524	0.0065933	1.60E-11
11	RAB3IL1	rs174479	61911282	G	C	0.3382070	0.0430286	0.0064145	2.30E-11
11	BEST1 *	rs2521572	61944003	G	T	0.4135990	0.0344279	0.0061633	2.10E-08
11	BUD13 *	rs191081678	116505105	T	G	0.0117429	0.2404330	0.0284041	5.90E-18
11	BUD13 *	rs79859462	116509279	A	G	0.0220809	0.1499630	0.0207987	1.60E-13
11	BUD13 *	rs188115846	116511441	A	G	0.0204079	0.1734420	0.0216757	4.90E-16
11	BUD13 *	rs140673349	116525979	A	G	0.0158909	0.2648630	0.0245319	5.50E-28
11	BUD13 *	rs150997570	116546725	A	G	0.0139021	0.1757050	0.0261433	7.10E-11
11	BUD13 *	rs56970059	116577861	C	T	0.1291600	-0.0518070	0.0090931	1.30E-08
11	BUD13 *	rs61904846	116578975	A	G	0.0628049	-0.0713346	0.0125386	2.40E-08
11	BUD13 *	rs144641996	116579022	T	A	0.0356997	0.1251210	0.0165745	1.90E-13
11	BUD13 *	rs114594921	116602565	C	T	0.0508974	0.1059780	0.0140899	6.70E-14
11	BUD13 *	rs74733106	116608826	T	G	0.0558359	0.0928095	0.0132468	5.70E-12
11	BUD13 *	rs116585768	116615113	A	G	0.0583319	0.1057560	0.0130924	1.00E-15
11	BUD13 *	rs11216040	116617822	A	G	0.0843208	0.0589469	0.0109400	3.20E-08
11	BUD13 *	rs10891999	116618165	T	A	0.1461850	0.0839173	0.0086977	3.10E-22
11	BUD13 *	rs12365864	116618319	G	A	0.0847773	0.0590809	0.0109062	2.70E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs11216043	116619262	C	T	0.1450110	0.0833391	0.0087206	1.00E-21
11	BUD13 *	rs148093284	116620192	C	T	0.0301276	0.1454900	0.0180431	4.50E-17
11	BUD13 *	rs12365322	116620253	G	T	0.0857577	0.0588527	0.0108462	2.60E-08
11	BUD13 *	rs182744169	116620615	C	T	0.0128562	0.1868960	0.0271637	7.70E-12
11	BUD13 *	rs61904858	116621390	G	A	0.0867154	0.0603600	0.0107803	1.10E-08
11	BUD13 *	rs11216045	116621694	C	T	0.1461490	0.0826304	0.0086917	2.00E-21
11	BUD13 *	rs11216046	116621984	T	G	0.0843974	0.0596745	0.0109505	2.70E-08
11	BUD13 *	rs79801428	116623547	A	G	0.0832195	-0.1049320	0.0112437	3.90E-21
11	BUD13 *	rs11216048	116624342	G	A	0.0875699	-0.1000530	0.0109093	1.00E-20
11	BUD13 *	rs11216049	116624458	C	T	0.0878015	-0.0991173	0.0108930	2.30E-20
11	BUD13 *	rs11216050	116624597	T	C	0.0882809	-0.0990484	0.0108576	1.80E-20
11	BUD13 *	rs112305884	116625067	T	C	0.0897244	-0.0962555	0.0107476	1.00E-19
11	BUD13 *	rs112494128	116625184	T	C	0.0898249	-0.0959115	0.0107360	1.20E-19
11	BUD13 *	rs7114844	116625470	A	G	0.1424760	0.0982873	0.0087137	9.00E-30
11	BUD13 *	rs4340085	116625592	T	C	0.0902427	-0.0973360	0.0107064	3.00E-20
11	BUD13 *	rs7114993	116625593	T	G	0.1420770	0.0990532	0.0087245	4.50E-30
11	BUD13 *	rs2156122	116625906	A	C	0.1428990	0.1017560	0.0086939	8.30E-32
11	BUD13 *	rs77984767	116626027	G	A	0.0911173	-0.0941547	0.0106498	3.70E-19
11	BUD13 *	rs77623050	116626231	T	C	0.0890773	-0.0950243	0.0107762	4.50E-19
11	BUD13 *	rs78485217	116626244	A	T	0.0882099	-0.0957095	0.0108382	5.00E-19
11	BUD13 *	rs147788053	116626296	CAT	C	0.0776658	-0.0928439	0.0115777	4.60E-16
11	BUD13 *	rs77966841	116627973	AC	A	0.0927161	-0.0951712	0.0105220	6.30E-20
11	BUD13 *	rs10892000	116628145	G	T	0.1479360	0.0967584	0.0085970	1.60E-29
11	BUD13 *	rs11216054	116628234	C	T	0.1479510	0.0968620	0.0085968	1.50E-29
11	BUD13 *	rs61270867	116628783	G	A	0.1738830	-0.0475481	0.0081113	4.20E-09
11	BUD13 *	rs11216055	116629871	T	C	0.0936201	-0.0944336	0.0104538	6.60E-20
11	BUD13 *	rs11216056	116629912	A	C	0.0936585	-0.0942191	0.0104514	8.00E-20
11	BUD13 *	rs11216057	116630051	T	C	0.0936060	-0.0940460	0.0104472	8.70E-20
11	BUD13 *	rs77649044	116630336	C	T	0.0936336	-0.0940120	0.0104424	8.60E-20
11	BUD13 *	rs76055915	116630355	T	C	0.0936394	-0.0940022	0.0104421	8.70E-20
11	BUD13 *	rs74424292	116630372	T	A	0.0936424	-0.0939127	0.0104419	9.20E-20
11	BUD13 *	rs76267862	116630652	C	CCTT	0.0938186	-0.0949758	0.0104310	3.50E-20
11	BUD13 *	rs11216059	116631270	A	C	0.0939804	-0.0962047	0.0104209	1.10E-20
11	BUD13 *	rs11216060	116631550	A	G	0.0945918	-0.0954488	0.0103984	2.50E-20
11	BUD13 *	rs58675830	116631757	TATTG	T	0.0939509	-0.0971674	0.0104200	4.50E-21
11	BUD13 *	rs11216061	116632035	C	T	0.0939312	-0.0975099	0.0104214	3.60E-21
11	BUD13 *	rs11216062	116632051	A	C	0.0939430	-0.0975241	0.0104208	3.50E-21
11	BUD13 *	rs11216063	116632059	A	T	0.0939430	-0.0975241	0.0104208	3.50E-21
11	BUD13 *	rs11216064	116632106	C	G	0.0939459	-0.0974801	0.0104206	3.70E-21
11	BUD13 *	rs4502019	116632117	G	C	0.1438620	0.0965792	0.0087317	2.90E-28
11	BUD13 *	rs60952109	116632129	CT	C	0.0941308	-0.0973105	0.0104109	4.00E-21
11	BUD13 *	rs7946423	116632686	T	A	0.1456240	0.0950211	0.0087122	1.20E-27
11	BUD13 *	rs2096961	116632927	A	G	0.0918573	-0.0983324	0.0105444	4.40E-21
11	BUD13 *	rs11216067	116633660	G	A	0.0934428	-0.0982851	0.0104616	2.80E-21
11	BUD13 *	rs76801336	116634037	C	T	0.0927313	-0.0979255	0.0105104	5.00E-21
11	BUD13 *	rs59232710	116634267	G	A	0.0916970	-0.0984209	0.0105937	6.20E-21
11	BUD13 *	rs11216068	116634522	T	C	0.1365630	0.1045040	0.0090223	6.00E-31
11	BUD13 *	rs10892001	116634723	A	G	0.1402980	0.1080470	0.0089344	1.40E-33
11	BUD13 *	rs10892002	116634775	C	G	0.1401560	0.1082090	0.0089389	1.40E-33
11	BUD13 *	rs2077334	116635693	A	C	0.0897149	-0.1043550	0.0107699	6.40E-23
11	BUD13 *	rs530592323	116636052	G	GCATG	0.0260018	0.1155890	0.0193108	3.10E-09
11	BUD13 *	rs201535154	116636067	T	C	0.0245838	0.1309630	0.0198912	5.80E-11
11	BUD13 *	rs199523826	116636068	G	A	0.0243021	0.1269470	0.0199852	2.60E-10
11	BUD13 *	rs77983701	116636339	C	T	0.0899778	-0.1064750	0.0107727	7.60E-24
11	BUD13 *	rs74948313	116636865	G	A	0.0955782	-0.1212130	0.0105837	1.60E-31
11	BUD13 *	rs76747451	116638116	G	T	0.0834730	-0.1189110	0.0111370	1.10E-27
11	BUD13 *	rs725524	116639652	A	G	0.0837197	-0.1204930	0.0111078	1.60E-28
11	BUD13 *	rs79315770	116639825	A	T	0.0837944	-0.1201080	0.0111018	2.20E-28
11	BUD13 *	rs184616707	116639841	G	C	0.0293437	0.3093820	0.0182085	2.40E-66
11	BUD13 *	rs117437529	116641735	T	C	0.0875302	-0.1174650	0.0108126	2.50E-28
11	BUD13 *	rs116892227	116642030	A	G	0.0888783	-0.1201170	0.0107100	7.70E-30
11	BUD13 *	rs1145184	116642465	A	G	0.1375750	0.1148600	0.0089413	3.80E-39
11	BUD13 *	rs117239953	116642471	C	T	0.0924163	-0.1175250	0.0104986	1.70E-29
11	BUD13 *	rs116859831	116642711	C	T	0.0926037	-0.1180070	0.0104878	8.70E-30
11	BUD13 *	rs78642155	116643375	C	G	0.0920754	-0.1182330	0.0105212	1.10E-29
11	BUD13 *	rs116948654	116643602	C	T	0.0921552	-0.1184980	0.0105243	8.70E-30
11	BUD13 *	rs117689643	116643612	T	G	0.0921562	-0.1184950	0.0105245	8.90E-30
11	BUD13 *	rs191049803	116643878	A	G	0.0202301	-0.1507370	0.0214997	4.50E-12
11	BUD13 *	rs1145185	116643982	A	G	0.1374220	0.1178820	0.0088730	2.70E-41
11	BUD13 *	rs78221557	116644811	A	G	0.2130600	0.0744307	0.0075468	4.70E-24
11	BUD13 *	rs71480306	116644840	C	T	0.1422660	0.1206630	0.0087071	1.30E-44
11	BUD13 *	rs11216072	116645635	C	T	0.0262644	-0.1333340	0.0190491	2.30E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	chr11:116645661_CA_C	116645661	C	CA	0.0984836	-0.1090920	0.0104005	4.60E-26
11	BUD13 *	rs139668970	116645673	T	TAAAC	0.1416700	0.1201240	0.0087140	3.10E-44
11	BUD13 *	rs869271932	116645674	A	AAAC	0.1424740	0.1208740	0.0086902	9.00E-45
11	BUD13 *	rs2212428	116645870	T	C	0.0919666	-0.1224680	0.0105675	1.30E-31
11	BUD13 *	rs1002037	116646019	C	G	0.0965668	-0.1214840	0.0103803	2.40E-32
11	BUD13 *	rs71480307	116646156	A	G	0.1419790	0.1217000	0.0087017	2.90E-45
11	BUD13 *	rs35165288	116646608	C	T	0.1426080	0.1211260	0.0086849	6.00E-45
11	BUD13 *	rs1124874	116647291	A	G	0.0893623	-0.1187400	0.0107033	4.10E-29
11	BUD13 *	rs117338034	116648026	G	T	0.0893297	-0.1189360	0.0107074	3.20E-29
11	BUD13 *	rs1240771	116648172	G	A	0.2290210	0.0706853	0.0072168	7.80E-24
11	BUD13 *	rs73580632	116648184	T	C	0.0893140	-0.1188670	0.0107087	3.50E-29
11	BUD13 *	rs1261672	116648243	G	A	0.2284960	0.0712227	0.0072217	3.90E-24
11	BUD13 *	rs1240772	116648412	C	G	0.3207270	0.0798099	0.0066059	3.80E-35
11	BUD13 *	rs76234156	116648464	A	C	0.0847706	0.0605646	0.0109915	1.40E-08
11	BUD13 *	rs513533	116648641	G	A	0.1154020	0.1509980	0.0095333	2.20E-57
11	BUD13 *	rs516043	116648867	G	C	0.1154690	0.1505030	0.0095307	4.40E-57
11	BUD13 *	rs516226	116648938	T	C	0.2941220	0.0501674	0.0068006	8.70E-14
11	BUD13 *	rs499790	116649022	T	C	0.1154500	0.1505130	0.0095304	4.30E-57
11	BUD13 *	rs504268	116649487	T	C	0.1154520	0.1505690	0.0095302	3.80E-57
11	BUD13 *	rs544479	116649681	C	T	0.1154570	0.1504640	0.0095298	4.60E-57
11	BUD13 *	rs506222	116649717	C	A	0.1154590	0.1504630	0.0095298	4.60E-57
11	BUD13 *	rs1240773	116649810	T	G	0.2291670	0.0724150	0.0072062	5.30E-25
11	BUD13 *	rs549125	116650209	G	C	0.1193890	0.1574860	0.0093927	3.50E-64
11	BUD13 *	rs533668	116650418	G	T	0.1193910	0.1576450	0.0093926	2.60E-64
11	BUD13 *	rs573985	116650599	A	G	0.1192320	0.1577210	0.0093976	3.20E-64
11	BUD13 *	rs575906	116650841	G	A	0.1195840	0.1578730	0.0093868	1.80E-64
11	BUD13 *	rs143762798	116650954	A	G	0.0206352	-0.1952070	0.0213859	1.70E-19
11	BUD13 *	rs562756	116651258	C	G	0.1193170	0.1578920	0.0093962	2.30E-64
11	BUD13 *	rs491022	116651271	C	T	0.1374890	0.1240200	0.0089519	3.30E-44
11	BUD13 *	rs563796	116651394	G	A	0.1202480	0.1574880	0.0093570	2.40E-64
11	BUD13 *	rs563917	116651439	T	C	0.1202740	0.1575260	0.0093555	2.20E-64
11	BUD13 *	rs492182	116651447	A	G	0.1202990	0.1576760	0.0093543	1.60E-64
11	BUD13 *	rs5795043	116651516	T	TC	0.1112830	0.1517480	0.0097519	6.90E-56
11	BUD13 *	rs565607	116651613	T	C	0.1202260	0.1577090	0.0093560	1.30E-64
11	BUD13 *	rs567576	116651842	G	A	0.1201480	0.1580510	0.0093485	5.30E-65
11	BUD13 *	rs567599	116651848	T	G	0.1201690	0.1580390	0.0093477	5.20E-65
11	BUD13 *	rs3017237	116651908	C	G	0.1203300	0.1575520	0.0093396	1.00E-64
11	BUD13 *	rs480028	116652053	G	C	0.1203660	0.1574470	0.0093365	1.10E-64
11	BUD13 *	rs480878	116652137	A	G	0.1208530	0.1568360	0.0093259	2.30E-64
11	BUD13 *	rs499563	116652244	T	C	0.1204960	0.1577720	0.0093327	5.40E-65
11	BUD13 *	rs138535309	116652253	C	CTT	0.1202770	0.1576380	0.0093390	8.70E-65
11	BUD13 *	rs202191031	116652259	A	AAGTGC	0.1202770	0.1576380	0.0093390	8.70E-65
11	BUD13 *	rs79770434	116652448	T	C	0.0861211	-0.1214430	0.0109055	1.90E-29
11	BUD13 *	rs483747	116652450	C	T	0.1203950	0.1575530	0.0093349	9.10E-65
11	BUD13 *	rs141584077	116652587	T	A	0.1125940	0.1488190	0.0096930	1.00E-53
11	BUD13 *	rs523980	116652589	T	A	0.1074860	0.1461010	0.0099291	2.70E-49
11	BUD13 *	rs485638	116652656	C	G	0.1203920	0.1575670	0.0093350	8.90E-65
11	BUD13 *	rs117742492	116652940	A	G	0.0859741	-0.1220170	0.0109214	1.10E-29
11	BUD13 *	rs528647	116653104	T	C	0.1203850	0.1575870	0.0093344	8.70E-65
11	BUD13 *	rs528732	116653127	A	G	0.1203850	0.1575870	0.0093344	8.70E-65
11	BUD13 *	rs3017778	116653214	T	C	0.1203480	0.1574940	0.0093363	1.10E-64
11	BUD13 *	rs3017779	116653271	T	C	0.1203090	0.1575370	0.0093373	9.90E-65
11	BUD13 *	rs76860051	116654589	C	A	0.0856162	-0.1242840	0.0109537	1.20E-30
11	BUD13 *	rs79862998	116654602	A	G	0.0854554	-0.1249900	0.0109654	6.60E-31
11	BUD13 *	rs480823	116655013	C	T	0.1154110	0.1673220	0.0096088	1.40E-68
11	BUD13 *	rs481843	116655150	T	C	0.1146130	0.1655780	0.0096498	1.20E-66
11	BUD13 *	rs116857027	116655278	T	C	0.0853971	-0.1257050	0.0109734	3.80E-31
11	BUD13 *	rs34485603	116655315	C	CCT	0.1146000	0.1654510	0.0096569	1.80E-66
11	BUD13 *	rs486394	116655605	C	A	0.1178960	0.1693590	0.0095569	6.20E-71
11	BUD13 *	rs34821424	116657330	A	T	0.0964202	0.0726203	0.0104386	1.90E-12
11	BUD13 *	rs78347813	116658413	T	C	0.0847463	-0.1351990	0.0109728	1.20E-35
11	BUD13 *	rs117935983	116658471	G	T	0.1821730	0.0667733	0.0080013	2.60E-17
11	BUD13 *	rs71480309	116659239	T	C	0.0983171	0.0702031	0.0103072	5.00E-12
11	BUD13 *	rs1892947	116659344	A	G	0.0869120	-0.1374530	0.0108040	5.60E-38
11	BUD13 *	rs116905034	116659391	C	G	0.0647560	0.1119480	0.0125738	2.50E-20
11	BUD13 *	rs11216080	116660281	T	G	0.0979717	0.0695232	0.0103087	7.40E-12
11	BUD13 *	rs146893332	116660321	AGGGGC	T	0.0650380	0.1127930	0.0125426	1.40E-20
11	BUD13 *	rs117889066	116660333	C	G	0.0876652	-0.1381030	0.0107442	1.40E-38
11	BUD13 *	rs117293980	116660758	G	T	0.0876598	-0.1379690	0.0107445	1.60E-38
11	BUD13 *	rs2155216	116661022	T	C	0.1919360	0.0591526	0.0077261	6.20E-15
11	BUD13 *	rs2186670	116661233	T	C	0.1919620	0.0593965	0.0077254	4.80E-15
11	BUD13 *	rs7117145	116661252	T	A	0.0878326	-0.1367780	0.0107317	6.20E-38

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs1944153	116661504	C	T	0.1919830	0.0594423	0.0077245	4.30E-15
11	BUD13 *	rs78198334	116661566	C	G	0.0878392	-0.1366680	0.0107309	7.10E-38
11	BUD13 *	rs118175510	116661831	C	T	0.0822048	0.1968080	0.0111554	1.60E-70
11	BUD13 *	rs79291519	116662593	T	C	0.0865104	-0.1367500	0.0108016	2.80E-37
11	BUD13 *	rs75942205	116662878	C	T	0.0867754	-0.1370330	0.0107827	1.30E-37
11	BUD13 *	rs61659529	116662911	G	A	0.0867631	-0.1365450	0.0107848	2.40E-37
11	BUD13 *	rs486915	116663571	T	A	0.3682650	-0.1365950	0.0064510	7.30E-104
11	BUD13 *	rs146134775	116663577	C	CT	0.0867329	-0.1356510	0.0107948	6.90E-37
11	BUD13 *	rs76547220	116663833	G	T	0.0868005	-0.1366680	0.0107840	2.10E-37
11	BUD13 *	rs567209	116664111	T	C	0.1676570	0.0726918	0.0082120	1.30E-19
11	BUD13 *	rs12802672	116664246	G	A	0.0933411	0.0857506	0.0105149	1.70E-16
11	BUD13 *	rs2105609	116664370	A	G	0.0868001	-0.1366770	0.0107842	2.10E-37
11	BUD13 *	rs2105610	116664409	C	T	0.0863973	-0.1361380	0.0108101	5.10E-37
11	BUD13 *	rs77226464	116664718	T	C	0.0868996	-0.1364300	0.0107804	2.40E-37
11	BUD13 *	rs190069353	116664907	A	C	0.0867767	-0.1366240	0.0107869	2.40E-37
11	BUD13 *	rs117014628	116664914	T	C	0.0867953	-0.1365490	0.0107854	2.50E-37
11	BUD13 *	rs1240776	116665564	T	C	0.3746720	-0.1394920	0.0062975	3.80E-113
11	BUD13 *	rs12803249	116665701	G	A	0.1676580	0.0730384	0.0082105	9.30E-20
11	BUD13 *	rs1240777	116665759	C	T	0.2001710	0.0583639	0.0075944	4.30E-15
11	BUD13 *	rs1240778	116665773	C	A	0.3707370	0.0857315	0.0063759	4.50E-43
11	BUD13 *	rs10892010	116665939	C	A	0.2481690	0.0689973	0.0071308	7.20E-23
11	BUD13 *	rs79063991	116666103	T	C	0.0867945	-0.1365460	0.0107860	2.50E-37
11	BUD13 *	rs61906081	116666342	A	G	0.1676680	0.0730236	0.0082102	9.50E-20
11	BUD13 *	rs118103820	116666399	G	A	0.0867945	-0.1365460	0.0107860	2.50E-37
11	BUD13 *	rs6589557	116667044	T	C	0.4240990	0.0953893	0.0061577	3.40E-56
11	BUD13 *	rs140973748	116667081	C	T	0.0868006	-0.1365570	0.0107859	2.40E-37
11	BUD13 *	rs35933073	116667129	A	C	0.1676860	0.0729623	0.0082095	9.80E-20
11	BUD13 *	rs6589558	116667225	A	G	0.4241000	0.0953909	0.0061577	3.40E-56
11	BUD13 *	rs1784125	116667245	C	G	0.2001580	0.0584915	0.0075938	3.80E-15
11	BUD13 *	rs12787592	116667257	C	G	0.1676990	0.0728627	0.0082093	1.10E-19
11	BUD13 *	rs143380339	116667386	A	C	0.0868006	-0.1365570	0.0107859	2.40E-37
11	BUD13 *	rs1784126	116667498	T	G	0.3726630	-0.1387770	0.0063004	5.80E-112
11	BUD13 *	rs57258844	116667690	C	G	0.0935029	0.0870833	0.0105002	5.00E-17
11	BUD13 *	rs1784127	116667859	A	G	0.3729900	-0.1388260	0.0062990	4.70E-112
11	BUD13 *	rs1784128	116667972	A	G	0.3730010	-0.1388040	0.0062990	5.30E-112
11	BUD13 *	rs1632755	116668134	C	A	0.2002190	0.0584850	0.0075947	3.90E-15
11	BUD13 *	rs112464350	116668341	A	C	0.0935149	0.0872218	0.0104996	4.50E-17
11	BUD13 *	rs1787682	116668486	G	C	0.2001610	0.0584822	0.0075938	3.80E-15
11	BUD13 *	rs150937658	116668605	G	A	0.0996027	-0.1351260	0.0102694	2.40E-39
11	BUD13 *	rs9681206	116668801	T	C	0.2500840	0.0668762	0.0071082	9.60E-22
11	BUD13 *	rs112550319	116669092	G	C	0.0935390	0.0875765	0.0104984	3.40E-17
11	BUD13 *	rs1784131	116669151	C	T	0.1999160	0.0585732	0.0075985	3.80E-15
11	BUD13 *	rs11216085	116669432	C	T	0.2501280	0.0670975	0.0071084	7.80E-22
11	BUD13 *	rs2846015	116669722	T	C	0.2001560	0.0584991	0.0075938	3.80E-15
11	BUD13 *	rs3016354	116670075	C	T	0.2001620	0.0584563	0.0075935	3.90E-15
11	BUD13 *	rs3017337	116670090	T	C	0.2003100	0.0591338	0.0075946	1.90E-15
11	BUD13 *	rs7925553	116670267	G	A	0.1678930	0.0726926	0.0082025	1.30E-19
11	BUD13 *	rs144188664	116670317	T	A	0.0868070	-0.1365840	0.0107870	2.40E-37
11	BUD13 *	rs1784133	116670700	T	C	0.2001610	0.0584540	0.0075935	3.90E-15
11	BUD13 *	rs1787686	116670755	A	G	0.2858380	-0.1062130	0.0067534	1.20E-58
11	BUD13 *	rs2846016	116670822	T	C	0.1998940	0.0591141	0.0075983	2.10E-15
11	BUD13 *	rs36195057	116671530	A	G	0.2502470	0.0670517	0.0071062	8.10E-22
11	BUD13 *	rs1787692	116671779	G	T	0.4591740	0.0361475	0.0061831	1.20E-09
11	BUD13 *	rs148462279	116672020	G	A	0.0868124	-0.1364980	0.0107874	2.70E-37
11	BUD13 *	rs75930640	116672095	T	G	0.2001580	0.0584144	0.0075935	4.10E-15
11	BUD13 *	rs144256947	116672308	C	T	0.0867327	-0.1367960	0.0107936	2.20E-37
11	BUD13 *	rs111446876	116672353	T	TA	0.2501860	0.0672308	0.0071073	6.20E-22
11	BUD13 *	rs113264811	116672394	T	C	0.2019680	0.0578309	0.0075734	6.80E-15
11	BUD13 *	rs12294322	116672835	G	A	0.2001510	0.0584094	0.0075934	4.10E-15
11	BUD13 *	chr11:116672851_TA_T	116672851	TA	T	0.2858390	-0.1062170	0.0067534	1.20E-58
11	BUD13 *	chr11:116673046_T_TA	116673046	TA	T	0.0920279	0.0917532	0.0105865	1.40E-18
11	BUD13 *	rs74724948	116673298	T	A	0.1975650	0.0545561	0.0076428	2.50E-13
11	BUD13 *	chr11:116674066_A_ATATT	116674066	ATATT	A	0.0863955	-0.1373200	0.0108189	1.20E-37
11	BUD13 *	rs180815846	116674155	G	T	0.2441140	0.0668467	0.0071878	4.60E-21
11	BUD13 *	rs559604795	116674196	T	A	0.0936282	0.0876664	0.0104930	3.00E-17
11	BUD13 *	rs71466774	116674354	A	T	0.0912345	0.0849729	0.0106359	8.20E-16
11	BUD13 *	rs117179746	116674534	A	G	0.0865483	-0.1370580	0.0108095	1.80E-37
11	BUD13 *	rs3016355	116674778	T	A	0.2001580	0.0583385	0.0075929	4.30E-15
11	BUD13 *	rs11530558	116674881	C	A	0.0254342	0.1811940	0.0193899	5.80E-21
11	BUD13 *	rs1787688	116675006	C	T	0.2853950	-0.1059760	0.0067597	2.60E-58
11	BUD13 *	rs78106248	116675263	CA	C	0.1720550	0.0723076	0.0081456	9.00E-20
11	BUD13 *	rs61906102	116675786	C	T	0.1723070	0.0715915	0.0081392	1.90E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs116944258	116675916	A	C	0.0869479	-0.1369350	0.0107905	1.80E-37
11	BUD13 *	rs58672319	116676219	T	TG	0.2849130	-0.1058310	0.0067625	3.40E-58
11	BUD13 *	rs1960036	116676692	A	C	0.1722990	0.0716393	0.0081385	1.80E-19
11	BUD13 *	rs1614444	116676831	G	A	0.2004170	0.0581161	0.0075970	5.50E-15
11	BUD13 *	rs59371082	116677028	G	A	0.0939559	0.0885741	0.0104795	1.30E-17
11	BUD13 *	rs372407480	116677221	A	C	0.0141155	0.2249800	0.0258895	1.30E-18
11	BUD13 *	rs868329903	116677410	C	A	0.0674358	-0.1409350	0.0123114	2.90E-31
11	BUD13 *	rs12801136	116677632	A	G	0.1723290	0.0716240	0.0081377	1.80E-19
11	BUD13 *	rs79678269	116678255	C	G	0.0870474	-0.1371050	0.0107891	1.50E-37
11	BUD13 *	rs1005705	116678399	C	A	0.0869308	-0.1371490	0.0107932	1.50E-37
11	BUD13 *	rs74792494	116678691	C	A	0.1975740	0.0553582	0.0076336	9.80E-14
11	BUD13 *	chr11:116678728_T_TGA	116678728	TGA	T	0.0869357	-0.1371190	0.0107931	1.50E-37
11	BUD13 *	chr11:116678738_A_AGAAT	116678738	AGAAT	A	0.1980960	0.0590183	0.0076439	3.00E-15
11	BUD13 *	rs58060512	116678740	A	AAT	0.1709930	0.0703333	0.0082128	2.20E-18
11	BUD13 *	rs1787687	116679179	G	A	0.2001940	0.0583027	0.0075903	4.30E-15
11	BUD13 *	rs35963862	116679180	C	T	0.1683070	0.0722146	0.0081912	2.10E-19
11	BUD13 *	rs117830617	116679254	A	G	0.0869392	-0.1371210	0.0107935	1.50E-37
11	BUD13 *	rs61906104	116679398	G	A	0.1723990	0.0714366	0.0081350	2.20E-19
11	BUD13 *	rs11216091	116679966	G	A	0.0216015	-0.1471180	0.0209553	3.50E-12
11	BUD13 *	rs12417015	116680059	G	A	0.1973460	0.0549267	0.0076373	1.50E-13
11	BUD13 *	chr11:116681564_G_GA	116681564	GA	G	0.1724440	0.0714886	0.0081335	2.10E-19
11	BUD13 *	rs1787717	116682049	T	C	0.3703180	-0.1391560	0.0063202	1.10E-111
11	BUD13 *	rs12806224	116682098	C	T	0.1722050	0.0717850	0.0081415	1.60E-19
11	BUD13 *	rs113194822	116682143	A	G	0.0928147	0.0922691	0.0105499	2.20E-18
11	BUD13 *	rs12805061	116682308	G	A	0.1724940	0.0715926	0.0081325	1.80E-19
11	BUD13 *	rs5795046	116682757	T	TG	0.3703020	-0.1388510	0.0063209	4.00E-111
11	BUD13 *	rs11826999	116683062	A	G	0.1725970	0.0712609	0.0081327	2.80E-19
11	BUD13 *	rs71480312	116683372	T	C	0.0989834	0.0853768	0.0102388	6.50E-17
11	BUD13 *	rs66560466	116683783	T	TG	0.2839840	-0.1055380	0.0067570	7.90E-58
11	BUD13 *	rs35310854	116684317	TA	T	0.1726160	0.0715858	0.0081329	2.00E-19
11	BUD13 *	rs117341026	116684410	A	G	0.0858295	-0.1411710	0.0108796	5.00E-39
11	BUD13 *	rs7932330	116684491	G	A	0.2470610	0.0669783	0.0071553	1.90E-21
11	BUD13 *	rs182999532	116684639	A	G	0.0106460	-0.1627560	0.0296687	2.60E-08
11	BUD13 *	rs35681250	116684670	T	A	0.1728280	0.0712839	0.0081365	2.90E-19
11	BUD13 *	rs3016357	116684699	T	C	0.2916960	-0.1088040	0.0067908	6.20E-61
11	BUD13 *	rs1145213	116684706	G	A	0.2950140	-0.1021730	0.0067870	7.50E-54
11	BUD13 *	rs77835865	116684713	G	A	0.1726110	0.0714578	0.0081331	2.40E-19
11	BUD13 *	rs956832572	116684717	T	A	0.0144258	0.2259090	0.0256138	5.10E-19
11	BUD13 *	rs71037408	116684780	C	CTG	0.0920037	0.0924866	0.0105968	1.70E-18
11	BUD13 *	rs61906112	116685049	A	T	0.1725490	0.0715136	0.0081348	2.20E-19
11	BUD13 *	rs17092638	116685520	G	C	0.1725580	0.0719290	0.0081372	1.40E-19
11	BUD13 *	rs1145212	116686149	A	G	0.4523740	0.0920260	0.0062034	1.70E-51
11	BUD13 *	rs2156120	116686439	G	A	0.2500350	0.0687792	0.0071232	6.50E-23
11	BUD13 *	rs1145211	116686500	A	C	0.2835670	-0.1071770	0.0067924	4.00E-59
11	BUD13 *	rs17092642	116686532	C	T	0.1724990	0.0725948	0.0081453	7.40E-20
11	BUD13 *	rs947990	116686598	T	G	0.0619193	-0.1516310	0.0126722	8.80E-33
11	BUD13 *	rs11216093	116687166	C	A	0.2507130	0.0692407	0.0071259	3.60E-23
11	BUD13 *	rs61906115	116687529	A	T	0.1681900	0.0738863	0.0082108	3.80E-20
11	BUD13 *	rs12799766	116687711	A	G	0.1682100	0.0737923	0.0082107	4.00E-20
11	BUD13 *	rs12799441	116687799	T	A	0.1683250	0.0738774	0.0082089	3.80E-20
11	BUD13 *	rs12799449	116687809	G	A	0.1683570	0.0740140	0.0082103	3.40E-20
11	BUD13 *	rs80134543	116688524	C	CTT	0.0802926	0.1133440	0.0113389	9.30E-24
11	BUD13 *	rs77277788	116688720	T	C	0.0925714	0.0912449	0.0105393	3.40E-18
11	BUD13 *	rs11824135	116688837	T	G	0.2014630	0.0477555	0.0077170	1.20E-10
11	BUD13 *	rs11828763	116688947	G	A	0.2122340	0.0534947	0.0075162	3.00E-13
11	BUD13 *	rs3016360	116689027	C	T	0.2127280	0.0536892	0.0075065	4.10E-13
11	BUD13 *	rs1787716	116689458	A	G	0.1986100	0.0632460	0.0076366	4.30E-17
11	BUD13 *	rs1787715	116689609	T	C	0.1986050	0.0631793	0.0076365	4.60E-17
11	BUD13 *	rs1623797	116689731	T	C	0.4324560	-0.1172870	0.0062038	5.00E-83
11	BUD13 *	rs34937367	116689808	C	T	0.1987320	0.0633416	0.0076366	3.70E-17
11	BUD13 *	rs74330350	116689812	G	A	0.1987320	0.0633416	0.0076366	3.70E-17
11	BUD13 *	rs79280888	116689813	G	A	0.1987320	0.0633416	0.0076366	3.70E-17
11	BUD13 *	rs1787714	116689894	A	G	0.2464520	-0.1382440	0.0071752	2.80E-86
11	BUD13 *	rs1787713	116689895	G	C	0.2464520	-0.1382440	0.0071752	2.80E-86
11	BUD13 *	rs12291024	116689951	G	T	0.3659220	0.0807859	0.0063588	9.00E-39
11	BUD13 *	rs1787711	116690062	G	A	0.1986450	0.0629021	0.0076348	5.70E-17
11	BUD13 *	rs3017232	116690167	T	C	0.1989620	0.0632469	0.0076298	3.70E-17
11	BUD13 *	rs3017231	116690232	A	G	0.1986520	0.0629220	0.0076345	5.70E-17
11	BUD13 *	rs3017230	116690245	C	G	0.1986530	0.0629105	0.0076344	5.80E-17
11	BUD13 *	rs3017229	116690251	A	G	0.2481520	-0.1398800	0.0071494	1.10E-88
11	BUD13 *	rs3017228	116690276	G	A	0.1986530	0.0629105	0.0076344	5.80E-17
11	BUD13 *	rs1787710	116690486	A	G	0.1986620	0.0627526	0.0076342	6.90E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs76483212	116690550	A	G	0.0924544	0.0950505	0.0105221	1.20E-19
11	BUD13 *	rs1787709	116690612	G	C	0.1986480	0.0626590	0.0076338	7.60E-17
11	BUD13 *	rs1784123	116690665	C	T	0.1986450	0.0627326	0.0076337	7.00E-17
11	BUD13 *	rs1787708	116690677	A	G	0.1986710	0.0626996	0.0076330	7.40E-17
11	BUD13 *	rs116505113	116690754	A	C	0.1981350	0.0598766	0.0076460	1.60E-15
11	BUD13 *	rs116166656	116690755	A	T	0.1981350	0.0598766	0.0076460	1.60E-15
11	BUD13 *	rs116365797	116690756	A	C	0.1981340	0.0598929	0.0076460	1.50E-15
11	BUD13 *	rs118013839	116690798	A	G	0.0837362	-0.1481810	0.0110390	9.50E-42
11	BUD13 *	rs1784122	116690985	A	T	0.1986980	0.0627051	0.0076318	7.50E-17
11	BUD13 *	rs1784121	116691074	T	G	0.4317020	-0.1168870	0.0062094	1.90E-82
11	BUD13 *	rs1784120	116691143	G	C	0.1987000	0.0627475	0.0076318	7.10E-17
11	BUD13 *	rs1787706	116691212	A	G	0.1986940	0.0627859	0.0076320	6.70E-17
11	BUD13 *	rs1787705	116691222	A	G	0.1986960	0.0627691	0.0076319	6.80E-17
11	BUD13 *	rs1787704	116691280	T	C	0.4330810	-0.1183790	0.0062026	1.30E-84
11	BUD13 *	rs1787703	116691550	T	C	0.1986910	0.0627344	0.0076320	7.10E-17
11	BUD13 *	rs1787702	116691572	A	G	0.1986910	0.0627344	0.0076320	7.10E-17
11	BUD13 *	rs11216096	116691864	A	C	0.3661670	0.0813567	0.0063514	2.70E-39
11	BUD13 *	rs117393825	116691971	T	C	0.1001480	-0.1374250	0.0102339	3.10E-41
11	BUD13 *	rs35256265	116691985	ACC	A	0.1987030	0.0629101	0.0076323	6.00E-17
11	BUD13 *	rs1784119	116692089	T	C	0.2481130	-0.1403730	0.0071480	2.70E-89
11	BUD13 *	rs12785772	116692892	A	G	0.3661970	0.0809723	0.0063537	6.20E-39
11	BUD13 *	rs12785990	116692990	A	G	0.3642190	0.0821620	0.0063616	7.40E-40
11	BUD13 *	rs79962987	116693078	T	G	0.0392205	-0.1817050	0.0156594	2.00E-32
11	BUD13 *	rs12420888	116693106	G	C	0.3644800	0.0822458	0.0063581	5.60E-40
11	BUD13 *	rs1787701	116693276	C	G	0.3361110	-0.1701820	0.0065335	3.00E-154
11	BUD13 *	chr11:116693645_G_GCA	116693645	GCA	G	0.1863310	0.0588488	0.0078969	2.60E-14
11	BUD13 *	rs117889337	116693777	T	C	0.0830397	-0.1488830	0.0110815	1.10E-41
11	BUD13 *	rs1787699	116693837	G	A	0.2474050	-0.1409600	0.0071612	8.00E-90
11	BUD13 *	rs1787698	116693846	T	C	0.2474020	-0.1409260	0.0071612	8.70E-90
11	BUD13 *	rs1784118	116694339	T	C	0.2501430	-0.1415570	0.0071285	3.40E-91
11	BUD13 *	rs12293222	116694593	A	G	0.2862700	0.0942524	0.0067945	6.60E-44
11	BUD13 *	rs111226221	116694718	T	C	0.0921724	0.0933717	0.0105432	5.70E-19
11	BUD13 *	rs117607796	116694887	A	C	0.0834866	-0.1487610	0.0110538	7.20E-42
11	BUD13 *	rs116978945	116694974	T	C	0.0909422	0.0850174	0.0106099	1.10E-15
11	BUD13 *	rs111218525	116695822	T	C	0.2060950	0.0741920	0.0075922	2.90E-23
11	BUD13 *	rs59854309	116696047	T	C	0.2555700	-0.1455380	0.0071517	3.00E-95
11	BUD13 *	rs60954647	116696217	T	C	0.4091640	-0.0856577	0.0063220	9.20E-43
11	BUD13 *	rs1784106	116696733	A	C	0.2522870	-0.1423570	0.0071151	4.80E-92
11	BUD13 *	rs78888567	116696897	A	G	0.0961432	0.0928868	0.0103555	2.90E-19
11	BUD13 *	rs4938300	116696903	T	C	0.2030020	0.0825334	0.0076033	2.30E-28
11	BUD13 *	rs10892017	116697165	C	G	0.3599610	0.0890183	0.0063396	7.20E-47
11	BUD13 *	rs66473272	116697382	G	GT	0.3527390	0.0916216	0.0064180	5.60E-48
11	BUD13 *	rs11605568	116697452	A	G	0.3599010	0.0890250	0.0063392	6.90E-47
11	BUD13 *	rs11606013	116697509	T	G	0.3599670	0.0889486	0.0063385	8.50E-47
11	BUD13 *	rs140078194	116697574	A	C	0.0866758	-0.1470470	0.0108651	8.60E-42
11	BUD13 *	rs11608173	116697648	A	T	0.3599680	0.0889310	0.0063383	8.90E-47
11	BUD13 *	rs1787689	116697666	G	A	0.4430220	-0.1204390	0.0061591	1.30E-87
11	BUD13 *	rs1787690	116697800	T	G	0.2520080	-0.1421990	0.0071022	5.30E-92
11	BUD13 *	rs1787691	116697997	A	G	0.4423880	-0.1202750	0.0061572	1.40E-87
11	BUD13 *	rs947986	116698488	A	G	0.2507280	-0.1420870	0.0071167	1.10E-91
11	BUD13 *	rs3017338	116698629	A	G	0.4423270	-0.1167480	0.0061660	2.50E-82
11	BUD13 *	rs71037412	116699941	CA	C	0.4448820	-0.1174420	0.0061446	9.60E-84
11	BUD13 *	rs1145191	116700002	G	C	0.4448820	-0.1174420	0.0061446	9.60E-84
11	BUD13 *	rs200445365	116700100	A	AAAAA	0.0865011	-0.1481110	0.0108788	2.40E-42
11	BUD13 *	rs150808564	116700125	T	C	0.0417602	-0.1546480	0.0152516	2.40E-24
11	BUD13 *	rs1145193	116700226	G	A	0.4460960	-0.1181450	0.0061423	7.10E-85
11	BUD13 *	rs1145194	116700252	A	C	0.2495560	-0.1430520	0.0071375	5.50E-92
11	BUD13 *	rs11601168	116700422	A	T	0.0782348	-0.1637480	0.0113206	4.90E-48
11	BUD13 *	rs1145195	116700534	A	G	0.4450380	-0.1171930	0.0061442	2.20E-83
11	BUD13 *	rs11601584	116700568	C	T	0.3487160	0.0915744	0.0063557	2.00E-49
11	BUD13 *	rs61905066	116700892	G	A	0.2067880	0.0439688	0.0075530	8.00E-09
11	BUD13 *	rs1892948	116701373	T	C	0.2060430	0.0439245	0.0075635	8.90E-09
11	BUD13 *	rs1145196	116701489	T	C	0.4452830	-0.1176920	0.0061451	4.30E-84
11	BUD13 *	rs1240783	116701809	C	T	0.4452430	-0.1176880	0.0061456	4.40E-84
11	BUD13 *	rs11216100	116701814	G	C	0.3444500	0.0949772	0.0063839	3.80E-52
11	BUD13 *	rs879858	116702404	A	G	0.2059020	0.0438815	0.0075736	9.00E-09
11	BUD13 *	rs947989	116702805	A	C	0.4518470	-0.1178380	0.0062444	4.90E-82
11	BUD13 *	rs882398	116703122	C	T	0.2066810	0.0434134	0.0075704	1.30E-08
11	BUD13 *	rs77206548	116703747	A	G	0.0867674	-0.1473250	0.0108658	6.70E-42
11	BUD13 *	rs11216103	116703772	A	G	0.2031740	0.0421046	0.0076254	4.00E-08
11	BUD13 *	rs1240782	116703868	A	G	0.3522990	-0.0741242	0.0064519	7.20E-32
11	BUD13 *	rs10617144	116703898	CTG	C	0.3521310	-0.0736560	0.0064534	1.90E-31

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs1240781	116704101	T	C	0.2446130	-0.1402190	0.0071981	3.50E-87
11	BUD13 *	rs1268832	116704513	T	G	0.3051690	-0.0484165	0.0066987	1.40E-13
11	BUD13 *	rs4938301	116704757	A	G	0.2058840	0.0760066	0.0075699	2.80E-24
11	BUD13 *	rs1263058	116704839	A	G	0.3070130	-0.0443476	0.0066779	1.10E-11
11	BUD13 *	rs76124005	116704898	G	T	0.0872834	-0.1472950	0.0108370	3.70E-42
11	BUD13 *	rs12574790	116704971	T	C	0.0160592	-0.1365800	0.0244646	1.70E-09
11	BUD13 *	rs74939223	116705164	G	A	0.0872937	-0.1476580	0.0108392	2.50E-42
11	BUD13 *	rs59873384	116705494	T	C	0.0872096	-0.1473780	0.0108433	3.50E-42
11	BUD13 *	rs12802944	116705684	C	T	0.2043020	0.0802212	0.0075942	7.30E-27
11	BUD13 *	rs1263056	116705699	A	G	0.3432500	-0.1721310	0.0065122	8.60E-157
11	BUD13 *	rs1263055	116706327	A	G	0.2521750	-0.1431450	0.0071281	5.00E-92
11	BUD13 *	rs11216105	116706725	A	G	0.2523250	-0.1432990	0.0071304	2.40E-92
11	BUD13 *	rs117684324	116707255	T	A	0.0872802	-0.1471190	0.0108388	4.20E-42
11	BUD13 *	rs12221682	116707501	G	C	0.3083240	-0.0819153	0.0066911	3.30E-35
11	BUD13 *	rs11216107	116708947	C	T	0.4961890	0.0822149	0.0061224	4.30E-41
11	BUD13 *	rs148075162	116709936	C	G	0.0157826	0.2576010	0.0244516	3.80E-27
11	BUD13 *	rs61346349	116710082	G	A	0.1783320	-0.1857270	0.0079734	2.50E-124
11	BUD13 *	rs11216109	116710099	G	C	0.3099610	0.2244300	0.0065739	3.50E-261
11	BUD13 *	rs75476300	116710153	C	G	0.0545363	0.3264700	0.0134229	1.80E-133
11	BUD13 *	rs59620302	116710443	G	C	0.0862703	-0.1481370	0.0108715	2.30E-42
11	BUD13 *	rs2367970	116710925	A	G	0.3101250	0.2247520	0.0065748	8.30E-262
11	BUD13 *	rs77574778	116711084	T	C	0.0863513	-0.1477350	0.0108645	3.60E-42
11	BUD13 *	rs77646493	116711464	A	C	0.0863329	-0.1477860	0.0108651	3.80E-42
11	BUD13 *	rs74360954	116711826	T	C	0.0863683	-0.1477290	0.0108621	4.20E-42
11	BUD13 *	rs7480302	116712301	G	A	0.4943220	0.0814308	0.0060797	9.80E-41
11	BUD13 *	rs6589562	116712723	A	G	0.3107000	0.2239240	0.0065725	1.00E-259
11	BUD13 *	rs886022	116712797	A	C	0.2349950	-0.1691870	0.0072470	6.50E-124
11	BUD13 *	rs117450838	116712972	A	G	0.0683655	-0.1732420	0.0120719	1.90E-48
11	BUD13 *	rs151007118	116713148	T	G	0.0998087	0.2424860	0.0102359	4.50E-125
11	BUD13 *	rs1144035	116713601	C	T	0.2359410	-0.1691450	0.0072367	3.20E-124
11	BUD13 *	rs117837319	116713731	C	A	0.0848100	-0.1459790	0.0109626	1.70E-40
11	BUD13 *	rs4938302	116713788	C	T	0.4943930	0.0812200	0.0060745	1.20E-40
11	BUD13 *	rs4938303	116714271	C	T	0.4943350	0.0814708	0.0060703	6.20E-41
11	BUD13 *	rs79886324	116714728	A	G	0.0866601	-0.1492480	0.0108466	4.80E-43
11	BUD13 *	rs2000571	116714817	A	G	0.3095860	0.2255180	0.0065851	8.60E-263
11	BUD13 *	rs17119918	116714897	A	G	0.1079920	-0.1656660	0.0098563	1.40E-65
11	BUD13 *	rs34100096	116714909	A	G	0.1028670	0.0603894	0.0100082	1.80E-10
11	BUD13 *	rs117785509	116715515	A	G	0.0867137	-0.1488410	0.0108477	9.50E-43
11	BUD13 *	rs7350481	116715567	T	C	0.2351070	0.3483300	0.0071604	4.7E-527
11	BUD13 *	rs7926828	116715707	C	T	0.3129840	0.2386340	0.0065629	4.30E-296
11	BUD13 *	rs5795050	116716065	T	TC	0.1011540	0.0578243	0.0100773	1.30E-09
11	BUD13 *	rs151061355	116716138	A	G	0.0874632	-0.1509720	0.0108046	2.10E-44
11	BUD13 *	rs555105607	116716397	CT	C	0.0876972	-0.1508670	0.0107767	1.70E-44
11	BUD13 *	rs373804009	116716399	T	TG	0.0872540	-0.1505680	0.0108072	5.50E-44
11	BUD13 *	rs142290703	116716430	A	G	0.0876972	-0.1508670	0.0107767	1.70E-44
11	BUD13 *	rs17119920	116717173	G	C	0.1007840	0.0559004	0.0100857	4.60E-09
11	BUD13 *	rs76542665	116717237	A	C	0.1007950	0.0558413	0.0100852	5.00E-09
11	BUD13 *	rs4938304	116717709	T	C	0.0790677	-0.1715050	0.0112334	6.60E-53
11	BUD13 *	rs79408961	116717877	T	C	0.0542620	0.3380690	0.0134288	1.80E-143
11	BUD13 *	rs4938305	116717913	T	C	0.3114730	0.2447690	0.0065944	8.0E-309
11	BUD13 *	rs1262892	116718188	A	G	0.1011070	0.0556638	0.0100625	4.60E-09
11	BUD13 *	rs180378	116718193	A	G	0.3124650	0.2441990	0.0065866	6.60E-308
11	BUD13 *	rs10711344	116718401	TA	T	0.3117200	0.2448100	0.0065929	4.8E-309
11	BUD13 *	rs180377	116718411	T	C	0.3124100	0.2442700	0.0065872	5.70E-308
11	BUD13 *	rs56881207	116718802	T	C	0.1014780	0.0548911	0.0100379	6.10E-09
11	BUD13 *	rs10892020	116718936	G	C	0.3112810	0.2443100	0.0065977	2.40E-307
11	BUD13 *	rs12419326	116719152	A	G	0.1015630	0.0546091	0.0100320	7.10E-09
11	BUD13 *	rs180376	116719323	C	G	0.3287420	-0.0834737	0.0065264	2.00E-38
11	BUD13 *	rs118046012	116719812	A	G	0.0860766	-0.1533990	0.0108661	2.30E-45
11	BUD13 *	rs6589563	116720071	A	G	0.1026910	0.0554209	0.0099769	4.50E-09
11	BUD13 *	rs180375	116720324	T	C	0.3288540	-0.0837260	0.0065241	1.20E-38
11	BUD13 *	rs116962103	116720402	A	G	0.0216920	-0.1713530	0.0209515	1.20E-15
11	BUD13 *	rs12421490	116720725	G	T	0.1019210	0.0542051	0.0100093	8.60E-09
11	BUD13 *	rs180373	116720837	A	C	0.1663120	-0.1943450	0.0082036	6.50E-131
11	BUD13 *	rs147232672	116721147	A	C	0.0116128	0.2949110	0.0284047	8.00E-26
11	BUD13 *	rs180372	116721218	A	G	0.3279710	-0.0835407	0.0065273	2.50E-38
11	BUD13 *	rs180371	116721487	A	G	0.4173440	-0.1254400	0.0061843	8.30E-93
11	BUD13 *	rs143315658	116721532	C	T	0.0865197	-0.1524010	0.0108367	4.30E-45
11	BUD13 *	rs180370	116721649	T	C	0.3279710	-0.0835407	0.0065273	2.50E-38
11	BUD13 *	rs74680844	116721744	C	G	0.1647650	-0.1964250	0.0082304	2.30E-132
11	BUD13 *	rs79100692	116722391	A	G	0.1644510	-0.1966480	0.0082382	1.70E-132
11	BUD13 *	rs79826170	116723038	C	T	0.1018600	0.0543713	0.0100145	8.30E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs12420920	116723315	A	G	0.1644550	-0.1966300	0.0082381	1.80E-132
11	BUD13 *	rs12421191	116723578	T	C	0.1644550	-0.1966300	0.0082381	1.80E-132
11	BUD13 *	rs75779227	116724640	T	C	0.1018570	0.0541080	0.0100147	9.70E-09
11	BUD13 *	rs180365	116725458	T	C	0.2942770	-0.1879440	0.0067682	1.70E-174
11	BUD13 *	rs61905078	116725593	C	A	0.1636180	-0.1926290	0.0082633	1.10E-126
11	BUD13 *	rs11216118	116725679	T	C	0.0767683	0.3859290	0.0114690	3.50E-254
11	BUD13 *	rs180364	116726036	G	A	0.2558610	-0.2033960	0.0070388	1.10E-190
11	BUD13 *	rs78347254	116726040	A	G	0.1008490	0.0568658	0.0100752	2.30E-09
11	BUD13 *	rs146714678	116726114	G	T	0.0923900	-0.1849520	0.0105653	3.60E-72
11	BUD13 *	rs75662937	116726178	T	C	0.0347830	0.6016120	0.0165937	5.90E-296
11	BUD13 *	rs144027752	116726289	A	G	0.0100566	0.2821510	0.0303919	1.20E-20
11	BUD13 *	rs180363	116727173	C	T	0.2542430	-0.2075680	0.0070384	1.70E-198
11	BUD13 *	rs78484485	116727349	A	G	0.2525900	-0.2088870	0.0070516	7.80E-200
11	BUD13 *	rs10892023	116727532	T	C	0.3087960	0.2484420	0.0066116	9.5E-317
11	BUD13 *	rs180361	116727933	T	C	0.3285170	-0.0828891	0.0065277	9.10E-38
11	BUD13 *	rs139628269	116727934	A	G	0.0141739	-0.1391190	0.0257641	3.10E-08
11	BUD13 *	rs139283556	116728079	T	C	0.0129402	0.2718330	0.0268417	1.50E-24
11	BUD13 *	rs180360	116728272	G	A	0.2535780	-0.2088620	0.0070441	2.40E-200
11	BUD13 *	rs180357	116728788	C	T	0.1029580	0.0547314	0.0099765	7.60E-09
11	BUD13 *	rs76240380	116728819	A	G	0.0349549	0.6015250	0.0165533	2.70E-297
11	BUD13 *	rs76986530	116728870	A	G	0.1018380	0.0537101	0.0100169	1.20E-08
11	BUD13 *	rs7123583	116729305	C	T	0.4342270	-0.0538983	0.0061909	4.30E-18
11	BUD13 *	rs189131104	116730452	A	C	0.0170796	-0.1607020	0.0234762	1.80E-12
11	BUD13 *	rs141882698	116730622	C	A	0.0918176	-0.1856620	0.0105965	2.80E-72
11	BUD13 *	rs4938306	116730762	T	G	0.1001300	0.0534159	0.0101015	1.90E-08
11	BUD13 *	rs108533	116730995	T	A	0.3307850	-0.0829544	0.0065158	4.20E-38
11	BUD13 *	rs3212282	116731229	A	G	0.3098840	0.2476910	0.0065974	4.3E-316
11	BUD13 *	rs75387300	116731683	A	G	0.1640140	-0.1979470	0.0082450	6.20E-134
11	BUD13 *	rs2008915	116732418	C	G	0.3086590	0.2486980	0.0066037	2.0E-318
11	BUD13 *	rs60273659	116732424	T	C	0.0991780	0.0554429	0.0101463	6.60E-09
11	BUD13 *	rs74503308	116732841	A	G	0.0992099	0.0547610	0.0101456	1.10E-08
11	BUD13 *	rs1893460	116732961	A	G	0.3338530	-0.2358240	0.0064917	5.30E-297
11	BUD13 *	rs78192008	116733154	G	A	0.0991430	0.0549417	0.0101502	9.10E-09
11	BUD13 *	rs4938307	116733798	A	G	0.2434150	-0.2151100	0.0071008	5.70E-209
11	BUD13 *	rs117170971	116734549	A	G	0.0880828	-0.1502450	0.0107458	2.00E-44
11	BUD13 *	rs79210888	116734607	T	C	0.0980586	0.0537956	0.0102099	2.30E-08
11	BUD13 *	rs1013526	116735178	G	A	0.0998760	0.0536634	0.0101184	1.90E-08
11	BUD13 *	chr11:116735204_C_CT	116735204	CT	C	0.0138441	0.2226000	0.0261418	1.40E-17
11	BUD13 *	rs138202725	116735858	ATAGT	A	0.0999028	0.0534351	0.0101160	2.20E-08
11	BUD13 *	rs1974718	116736050	G	A	0.2042370	0.3076280	0.0075214	2.2E-372
11	BUD13 *	rs68149171	116736335	T	TTCTG	0.2416520	-0.2143160	0.0071224	3.50E-206
11	BUD13 *	rs1558860	116736652	A	C	0.2039940	0.3088690	0.0075220	2.8E-375
11	BUD13 *	rs1558861	116736721	C	T	0.2040230	0.3085850	0.0075206	9.6E-375
11	BUD13 *	chr11:116736812_G_GA	116736812	GA	G	0.0980254	0.0525525	0.0102203	4.90E-08
11	BUD13 *	rs114554198	116736935	T	C	0.0105533	0.2322570	0.0298465	1.30E-15
11	BUD13 *	rs77032561	116738180	C	T	0.1006480	0.0544734	0.0100863	1.30E-08
11	BUD13 *	rs180350	116739332	T	C	0.2792180	-0.1982950	0.0068267	5.50E-191
11	BUD13 *	rs10466588	116739533	G	A	0.1007090	0.0543618	0.0100834	1.30E-08
11	BUD13 *	rs61905084	116739578	C	T	0.3406250	-0.2393990	0.0064496	5.1E-310
11	BUD13 *	rs9326246	116741017	C	G	0.2039180	0.3090570	0.0075303	4.1E-375
11	BUD13 *	rs180349	116741111	A	T	0.2044290	0.3084730	0.0075235	3.3E-374
11	BUD13 *	rs17092646	116741248	C	G	0.1004600	0.0537400	0.0100983	2.30E-08
11	BUD13 *	rs180348	116741279	A	G	0.0676465	-0.1628250	0.0121343	5.10E-41
11	BUD13 *	rs10466533	116741412	G	A	0.1011780	0.0530474	0.0100708	2.90E-08
11	BUD13 *	rs11216125	116741558	A	G	0.2590320	-0.2112510	0.0069289	7.30E-212
11	BUD13 *	chr11:116741689_AACACACACACACAC_A	116741689	A	.CACAC	0.0711018	0.5399600	0.0119088	1.6E-463
11	BUD13 *	rs180346	116741943	C	A	0.2786430	-0.1972740	0.0068160	1.40E-189
11	BUD13 *	rs117788500	116742318	C	G	0.0840144	-0.1521590	0.0109826	2.30E-43
11	BUD13 *	rs17518841	116744528	A	G	0.0843615	-0.1528750	0.0109574	6.90E-44
11	BUD13 *	rs4938308	116745386	T	C	0.0981043	0.0532040	0.0102091	3.70E-08
11	BUD13 *	rs11216126	116746524	C	A	0.2561410	-0.2178980	0.0069426	1.50E-224
11	BUD13 *	rs180339	116747066	T	C	0.4407740	-0.1995350	0.0061475	5.20E-236
11	BUD13 *	rs45539536	116747179	T	C	0.0844485	-0.1523510	0.0109539	1.30E-43
11	BUD13	rs34637368	116748889	A	G	0.2497970	-0.2143940	0.0070653	2.90E-210
11	BUD13	rs141923916	116749021	GA	G	0.0845439	-0.1529870	0.0109457	5.70E-44
11	BUD13	rs11216129	116749540	A	C	0.2514760	-0.2183320	0.0070123	1.80E-221
11	BUD13	rs57950207	116749954	C	T	0.0846225	-0.1529230	0.0109466	6.60E-44
11	BUD13	rs17440396	116751054	A	G	0.0833443	-0.1520010	0.0110286	1.00E-42
11	BUD13	rs74368849	116751583	A	G	0.0667423	0.5454510	0.0122799	2.8E-446
11	BUD13	chr11:116752497_TA_T	116752497	TA	T	0.3038560	0.2650700	0.0066195	2.8E-360
11	BUD13	rs180327	116752943	C	T	0.3051250	0.2643450	0.0066085	2.7E-359
11	BUD13	rs6589564	116753437	C	G	0.2018900	0.3188020	0.0075550	1.2E-396

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13	rs180326	116753987	G	T	0.2037410	0.3166430	0.0075257	9.9E-394
11	BUD13	rs7930786	116754011	C	G	0.2021090	0.3188810	0.0075562	7.6E-397
11	BUD13	rs117728849	116754200	T	C	0.1003360	0.0550924	0.0101040	9.30E-09
11	BUD13	rs12421652	116755159	T	G	0.2528300	-0.2185920	0.0069974	1.00E-222
11	BUD13	rs77112220	116755510	T	C	0.0843734	-0.1530050	0.0109559	6.20E-44
11	BUD13	rs182500870	116755846	A	T	0.0113219	0.5855780	0.0287940	1.90E-95
11	BUD13	rs180322	116756019	C	T	0.3578900	-0.1606070	0.0063288	1.70E-146
11	BUD13	rs4938309	116756339	T	C	0.2530550	-0.2189430	0.0069958	1.80E-223
11	BUD13	rs117685786	116756907	C	T	0.0437545	-0.1577750	0.0148887	3.20E-26
11	BUD13	rs2075295	116757685	C	T	0.4408720	-0.1996790	0.0061470	2.60E-236
11	BUD13	rs17519093	116759189	A	G	0.0845766	-0.1526810	0.0109427	6.80E-44
11	BUD13	rs75955612	116759802	T	A	0.0423962	0.2804010	0.0151355	1.20E-78
11	BUD13	rs3741301	116760675	C	T	0.2812880	-0.1969700	0.0067946	2.80E-190
11	BUD13	rs3825041	116760991	T	C	0.2003960	0.3184400	0.0075760	1.0E-393
11	BUD13	rs139872819	116761196	C	T	0.0844152	-0.1520520	0.0109477	2.20E-43
11	BUD13	rs11602240	116762082	C	T	0.2569920	-0.2195370	0.0069603	5.50E-227
11	BUD13	rs918144	116763109	T	C	0.4413410	-0.1995990	0.0061486	2.80E-236
11	BUD13	rs10488698	116763231	A	G	0.0837812	-0.1525160	0.0109851	1.70E-43
11	BUD13	rs17440824	116763457	T	C	0.0864724	-0.1448380	0.0108339	1.00E-40
11	BUD13	rs116877083	116763581	C	A	0.0863992	-0.1455830	0.0108368	4.30E-41
11	BUD13	rs17119975	116763841	C	T	0.2543930	-0.2191840	0.0069971	4.90E-224
11	BUD13	rs2187126	116765068	G	A	0.0407536	-0.1332540	0.0153850	1.10E-17
11	BUD13	rs75542782	116766286	A	G	0.0407351	-0.1336650	0.0153887	8.80E-18
11	BUD13	rs141740187	116766961	T	G	0.1068030	0.0551179	0.0098350	2.90E-09
11	BUD13	rs532088210	116767607	G	A	0.0144182	-0.1917440	0.0257504	3.00E-14
11	BUD13	rs57643109	116768035	A	G	0.0407874	-0.1339790	0.0153797	7.20E-18
11	BUD13	rs78908794	116768138	C	T	0.1086570	0.0548070	0.0097523	2.70E-09
11	BUD13	rs10790162	116768388	A	G	0.2006540	0.3208890	0.0075817	1.9E-399
11	BUD13	rs1268353	116768976	T	C	0.3005040	-0.2298280	0.0066528	1.20E-270
11	BUD13	rs1263149	116769225	G	A	0.4544210	-0.1969580	0.0061104	3.10E-232
11	BUD13	rs622604	116769346	C	T	0.3035430	-0.2298220	0.0066214	8.90E-274
11	BUD13	rs610675	116769378	A	T	0.3035470	-0.2298330	0.0066214	8.30E-274
11	BUD13	rs6589565	116769521	A	G	0.2014770	0.3216940	0.0075668	8.7E-403
11	BUD13	rs623908	116769652	G	A	0.3036720	-0.2302220	0.0066203	1.00E-274
11	BUD13	rs4938311	116769888	T	C	0.1075180	0.0541111	0.0097990	3.70E-09
11	BUD13	rs1263151	116770312	T	C	0.3845910	-0.0350662	0.0062576	2.00E-08
11	BUD13	rs181315084	116770469	C	T	0.0128548	0.2814560	0.0269435	7.00E-26
11	BUD13	rs117579298	116771384	G	A	0.0408057	-0.1331420	0.0153761	1.00E-17
11	BUD13	rs79110162	116772295	G	A	0.0408029	-0.1331070	0.0153767	1.00E-17
11	BUD13 *	rs12422076	116773572	G	A	0.0699820	-0.1748040	0.0119573	3.80E-50
11	BUD13 *	rs141740837	116774378	T	TCA	0.0408081	-0.1331480	0.0153755	9.90E-18
11	BUD13 *	rs2041967	116774433	G	A	0.4104830	-0.1810050	0.0061876	1.60E-192
11	BUD13 *	rs7118999	116774559	T	C	0.3853260	-0.0355685	0.0062499	1.20E-08
11	BUD13 *	rs45443305	116774966	A	C	0.1061210	0.0517413	0.0098432	1.80E-08
11	BUD13 *	rs11216135	116775346	G	C	0.3012710	-0.2310110	0.0066354	1.60E-274
11	ZPR1 *	rs11602073	116776142	T	C	0.3008450	-0.2286350	0.0066363	3.30E-269
11	ZPR1 *	rs11216136	116776404	G	T	0.3033420	-0.2294310	0.0066206	1.10E-272
11	ZPR1 *	rs2160669	116776891	C	T	0.2028050	0.3217370	0.0075431	1.6E-405
11	ZPR1 *	rs78296522	116778060	A	C	0.0408039	-0.1331450	0.0153761	1.00E-17
11	ZPR1 *	rs964184	116778201	G	C	0.2032670	0.3216060	0.0075361	5.3E-406
11	ZPR1	rs75198898	116779090	A	G	0.0662731	0.5989900	0.0122357	2.6E-538
11	ZPR1	rs113932726	116779922	T	C	0.0655430	0.6015680	0.0123031	1.4E-536
11	ZPR1	rs34248274	116779950	C	CTAGT	0.3010840	-0.2291600	0.0066299	1.40E-270
11	ZPR1	rs11604424	116780399	C	T	0.3534080	0.2269770	0.0063525	1.30E-289
11	ZPR1	rs200405951	116780493	G	C	0.0111311	0.5341570	0.0289961	6.10E-79
11	ZPR1	rs1942478	116780747	G	T	0.3028740	-0.2311300	0.0066215	5.00E-276
11	ZPR1	rs9633942	116781154	C	T	0.0250266	-0.1441290	0.0195699	3.10E-13
11	ZPR1	rs139753514	116781213	G	GA	0.1058100	0.0537048	0.0098705	8.10E-09
11	ZPR1	rs4417316	116781585	T	C	0.3008100	-0.2297130	0.0066250	2.60E-272
11	ZPR1	rs6589566	116781707	G	A	0.2031840	0.3214220	0.0075382	2.5E-405
11	ZPR1	rs190443984	116781741	A	G	0.0149581	-0.1370530	0.0251744	3.40E-08
11	ZPR1	rs7483863	116781775	A	G	0.2031840	0.3214220	0.0075382	2.5E-405
11	ZPR1	rs2075290	116782580	C	T	0.2213260	0.2862010	0.0073077	2.3E-341
11	ZPR1	rs76836072	116783046	T	C	0.0408602	-0.1337870	0.0153651	8.20E-18
11	ZPR1	rs603446	116783719	T	C	0.2790180	-0.2012380	0.0067733	3.50E-200
11	ZPR1	rs74662600	116784243	A	G	0.1049540	0.0526265	0.0098964	1.50E-08
11	ZPR1	rs139678706	116784368	A	G	0.0186544	-0.2169100	0.0225734	1.80E-21
11	ZPR1	rs10750096	116786072	C	A	0.2032270	0.3218540	0.0075384	2.7E-406
11	ZPR1	rs3741298	116786845	C	T	0.3627070	0.2216700	0.0063093	3.60E-280
11	ZPR1	rs3741297	116786951	T	C	0.0651757	0.6149740	0.0123280	2.9E-559
11	APOA5	rs2266788	116789970	G	A	0.2031630	0.3221530	0.0075419	1.3E-406
11	APOA5	rs2075291	116790676	A	C	0.0652237	0.6173950	0.0123160	1.4E-564

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	APOA5	rs3135507	116790772	T	C	0.1039890	0.0589322	0.0099647	5.80E-10
11	APOA5	rs2072560	116791110	T	C	0.2021840	0.3233810	0.0075686	5.6E-407
11	APOA5	rs651821	116791863	C	T	0.2709740	0.4536030	0.0068455	2.3E-979
11	APOA5 *	rs34003087	116792880	T	C	0.0403630	-0.1299070	0.0155104	8.80E-17
11	APOA5 *	rs662799	116792991	G	A	0.2712310	0.4524820	0.0068391	4.1E-976
11	APOA5 *	rs17120035	116793135	T	C	0.0819062	-0.1691090	0.0111357	8.60E-53
11	APOA5 *	rs7103224	116793250	A	G	0.0818766	-0.1690010	0.0111378	1.10E-52
11	APOA5 *	rs10750097	116793324	G	A	0.4346660	0.0640109	0.0062185	2.10E-24
11	APOA5 *	rs1787680	116794060	A	T	0.2656610	-0.2074200	0.0070115	2.80E-198
11	APOA5 *	rs9804646	116794363	T	C	0.2194970	-0.2088570	0.0074863	2.20E-177
11	APOA5 *	rs35904674	116795383	T	C	0.0542608	-0.1570910	0.0134881	1.40E-32
11	APOA5 *	chr11:116795401_C_CA	116795401	CA	C	0.0533214	-0.1589900	0.0136242	1.30E-32
11	APOA5 *	rs117730008	116795625	A	G	0.0457629	0.1195880	0.0147013	4.60E-17
11	APOA5 *	rs7123666	116796367	A	G	0.1577380	0.2962670	0.0084473	3.20E-273
11	APOA5 *	rs75919952	116796829	T	C	0.0412881	-0.1331040	0.0153650	8.10E-18
11	APOA5 *	rs35606865	116798127	C	T	0.0538690	-0.1570790	0.0135375	2.50E-32
11	APOA5 *	rs11216137	116799112	A	G	0.0508981	-0.1560610	0.0139279	2.50E-30
11	APOA5 *	rs11600380	116799466	C	T	0.0539323	-0.1573190	0.0135307	2.00E-32
11	APOA5 *	rs12294065	116800824	C	G	0.0503864	-0.1576460	0.0140086	1.30E-30
11	APOA5 *	rs116852373	116800861	A	G	0.0228470	-0.1398720	0.0203216	9.80E-13
11	APOA5 *	rs188651594	116802375	A	G	0.0275682	0.2675110	0.0186362	8.90E-47
11	APOA5 *	rs12791103	116802599	T	G	0.0502515	-0.1587400	0.0140346	9.00E-31
11	APOA5 *	rs1263164	116804575	A	C	0.3023070	-0.0914265	0.0067624	2.00E-42
11	APOA5 *	rs7112988	116805725	A	G	0.0343835	-0.1041090	0.0168037	6.10E-10
11	APOA5 *	rs61499278	116806508	ATTT	A	0.0475571	-0.1065750	0.0143779	1.60E-13
11	APOA4 *	rs1729407	116806654	G	C	0.3048540	-0.0922303	0.0067088	9.00E-44
11	APOA4 *	rs1263168	116807283	T	C	0.3054340	-0.0865985	0.0066336	1.70E-39
11	APOA4 *	rs1263169	116807423	T	A	0.3075420	-0.0893962	0.0066371	6.40E-42
11	APOA4 *	rs61905133	116807475	G	A	0.0510391	-0.1090480	0.0138764	2.80E-15
11	APOA4 *	rs11398704	116807533	CA	C	0.3523230	-0.1019290	0.0064832	6.10E-56
11	APOA4 *	rs1263170	116807697	C	T	0.3087550	-0.0881693	0.0066087	3.60E-41
11	APOA4 *	rs1729405	116808044	T	C	0.3083350	-0.0880814	0.0066073	4.20E-41
11	APOA4 *	rs75542613	116808439	A	G	0.0405294	-0.1782250	0.0154800	1.80E-32
11	APOA4 *	rs1263171	116809614	A	G	0.3053860	-0.0833523	0.0065907	6.10E-37
11	APOA4 *	rs6589571	116809702	T	C	0.1945080	0.1661730	0.0077999	1.00E-101
11	APOA4 *	rs1263172	116810202	A	G	0.3584200	-0.1005370	0.0063588	1.10E-56
11	APOA4 *	rs80220270	116810245	C	A	0.0515252	-0.1087630	0.0137927	2.60E-15
11	APOA4 *	rs1263173	116810292	A	G	0.3055430	-0.0832778	0.0065868	6.50E-37
11	APOA4 *	rs1263174	116810527	T	G	0.3093890	-0.0834806	0.0065790	3.00E-37
11	APOA4 *	rs75145979	116810778	A	C	0.0502824	-0.1020940	0.0139719	2.80E-13
11	APOA4 *	rs6589572	116810847	G	A	0.3057330	0.1987930	0.0065977	2.10E-204
11	APOA4 *	rs79538491	116811203	G	A	0.0607166	0.1692290	0.0128173	6.10E-42
11	APOA4 *	rs7927820	116811440	G	A	0.3045750	0.1993270	0.0065942	1.30E-205
11	APOA4 *	rs35180165	116811633	C	CAG	0.3042300	-0.0831385	0.0066074	1.10E-36
11	APOA4 *	rs76636922	116812279	A	G	0.3351230	-0.0850894	0.0064619	2.70E-41
11	APOA4 *	rs2727793	116812658	T	C	0.3043080	-0.0816977	0.0066183	2.20E-35
11	APOA4 *	rs75318540	116813146	T	C	0.2190540	-0.0746230	0.0074157	5.10E-25
11	APOA4 *	rs7396835	116813312	T	C	0.3051710	0.1978270	0.0065787	1.10E-203
11	APOA4 *	rs7396851	116813448	T	C	0.3048240	0.1985000	0.0065846	1.20E-204
11	APOA4 *	rs79841374	116813844	T	C	0.3342660	-0.0857185	0.0064637	9.00E-42
11	APOA4 *	rs2727791	116813846	G	C	0.3068670	-0.0840536	0.0066039	1.00E-37
11	APOA4 *	rs2849167	116814028	A	G	0.3067650	-0.0841768	0.0066072	9.70E-38
11	APOA4 *	rs2542063	116814051	A	G	0.3072160	-0.0841052	0.0066040	1.10E-37
11	APOA4 *	rs77535577	116814675	A	G	0.3333510	-0.0866746	0.0064897	2.70E-42
11	APOA4 *	rs6589573	116815050	C	G	0.3072350	0.2013110	0.0066447	1.90E-206
11	APOA4 *	rs7107757	116815572	T	C	0.3566990	0.1637010	0.0063861	3.00E-149
11	APOA4 *	chr11:116816190_CT_C	116816190	C	CT	0.3141790	-0.0796097	0.0066613	1.60E-34
11	APOA4 *	rs9735326	116818049	C	A	0.3262530	0.1843020	0.0065492	6.50E-179
11	APOA4 *	rs184316726	116818292	C	A	0.0472400	-0.1035540	0.0143839	7.00E-13
11	APOA4 *	rs1263176	116819407	T	C	0.3682880	0.1560570	0.0063442	8.70E-138
11	APOA4 *	rs1268354	116819862	C	T	0.3686390	0.1556910	0.0063427	2.50E-137
11	APOA4 *	rs1263177	116819996	C	T	0.3670940	0.1568120	0.0063552	8.90E-139
11	APOA4	rs2234669	116820795	G	GGACA	0.3036530	-0.0850487	0.0066878	9.10E-38
11	APOA4	rs5104	116821618	C	T	0.3197880	0.1908020	0.0065521	1.60E-191
11	APOA4	rs6413456	116821733	A	G	0.0332944	-0.1671960	0.0169604	3.50E-24
11	APOA4	rs5103	116821836	G	A	0.0487213	-0.1063240	0.0141637	8.60E-14
11	APOA4	rs5100	116821978	G	A	0.3724650	0.1546420	0.0063343	4.90E-136
11	APOA4	rs5096	116822379	G	A	0.3724350	0.1544810	0.0063343	1.10E-135
11	APOA4	rs2239013	116822637	T	C	0.0408422	-0.1744590	0.0154103	2.70E-31
11	APOA4	rs5093	116822638	A	G	0.2173790	-0.0758749	0.0074757	1.90E-25
11	APOA4	rs5092	116822748	C	T	0.3720600	0.1543960	0.0063399	3.10E-135
11	APOA4 *	rs1268833	116824150	G	A	0.3722770	0.1539420	0.0063367	1.40E-134

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	APOA4 *	rs10892035	116824222	A	G	0.3716720	0.1540020	0.0063392	1.60E-134
11	APOA4 *	rs182352602	116824894	A	G	0.2114420	-0.0760441	0.0075599	5.00E-25
11	APOA4 *	rs7111242	116825064	A	G	0.3205720	0.1872550	0.0065770	7.80E-183
11	APOA4 *	rs2216311	116825327	G	A	0.3721740	0.1545380	0.0063389	2.40E-135
11	APOA4 *	rs2098453	116825964	C	T	0.3716610	0.1550540	0.0063427	6.80E-136
11	APOA4 *	rs7123326	116825965	A	G	0.0488112	-0.1059110	0.0141468	9.00E-14
11	APOA4 *	rs2727789	116826171	G	T	0.3732220	0.1547150	0.0063399	1.90E-135
11	APOA4 *	rs2849176	116826205	T	C	0.3722550	0.1549820	0.0063419	6.80E-136
11	APOA4 *	rs2849174	116826350	A	G	0.0494058	-0.1055860	0.0140657	8.60E-14
11	APOA4 *	rs2542050	116826401	C	A	0.3716720	0.1552900	0.0063416	2.30E-136
11	APOC3 *	rs2849173	116826605	G	C	0.3717060	0.1552320	0.0063418	3.10E-136
11	APOC3 *	rs2071523	116826628	C	T	0.3717310	0.1552210	0.0063414	2.80E-136
11	APOC3 *	rs2071522	116826822	T	C	0.3717270	0.1550500	0.0063419	6.30E-136
11	APOC3 *	rs2542051	116827022	C	A	0.3718760	0.1548400	0.0063420	1.50E-135
11	APOC3 *	rs2071521	116827132	G	A	0.3718270	0.1549840	0.0063408	7.00E-136
11	APOC3 *	rs7101528	116827949	A	G	0.0490415	-0.1062700	0.0141190	6.20E-14
11	APOC3 *	rs2727788	116828247	A	C	0.0496147	-0.1059830	0.0140407	5.80E-14
11	APOC3 *	rs595049	116828729	C	A	0.3735650	0.1553400	0.0063200	3.40E-137
11	APOC3	rs734104	116830144	C	T	0.2928900	0.1398870	0.0067296	3.60E-98
11	APOC3	rs5128	116832924	G	C	0.2906650	0.1409010	0.0066936	1.60E-100
11	APOA1 *	rs10750098	116834852	G	T	0.2901420	0.1402320	0.0067152	8.90E-99
11	APOA1 *	rs12718462	116835003	C	T	0.0443757	-0.1566570	0.0147966	1.00E-27
11	APOA1 *	rs12721025	116835331	A	G	0.0477181	-0.1486410	0.0143958	2.30E-26
11	APOA1 *	rs12721026	116835452	G	T	0.0431155	-0.1557710	0.0150036	1.30E-26
11	APOA1 *	rs12718463	116835627	C	T	0.0422002	-0.1031900	0.0151156	5.30E-12
11	APOA1	rs5076	116836474	A	G	0.0416065	-0.1024270	0.0152226	1.10E-11
11	APOA1	rs12718464	116836685	A	G	0.0430442	-0.1558640	0.0150117	1.10E-26
11	APOA1	rs5069	116837538	A	G	0.0416509	-0.1018820	0.0152263	1.50E-11
11	APOA1 *	rs12718466	116837947	G	T	0.0414865	-0.1023220	0.0152475	1.30E-11
11	APOA1 *	rs368405969	116839577	T	C	0.0119502	-0.1878700	0.0280239	4.90E-12
11	APOA1 *	rs613808	116840252	G	A	0.2767020	-0.0994550	0.0069098	1.40E-47
11	APOA1 *	rs2727784	116840425	T	C	0.2577470	-0.1085260	0.0070799	4.10E-54
11	SIK3 *	rs480009	116841258	T	C	0.2495360	-0.0443123	0.0070932	1.60E-10
11	SIK3 *	rs370143719	116841590	C	T	0.0135894	-0.1780620	0.0262892	2.50E-12
11	SIK3 *	rs591592	116842850	T	C	0.2218350	-0.0734651	0.0074273	7.30E-23
11	SIK3 *	rs200408997	116842862	A	ACCC	0.0494313	0.1590910	0.0140238	8.60E-31
11	SIK3 *	rs579163	116842914	G	C	0.2222550	-0.0736541	0.0074236	4.90E-23
11	SIK3	rs371090973	116844640	T	TTA	0.0496193	0.1508660	0.0140152	5.30E-28
11	SIK3	rs201579941	116844674	A	ATAT	0.0485650	0.1566330	0.0141435	1.20E-29
11	SIK3	rs142174850	116845068	A	G	0.0818362	-0.1516980	0.0111113	7.00E-45
11	SIK3	rs143120617	116846722	T	C	0.0368530	-0.1581720	0.0161583	1.20E-23
11	SIK3	rs61905145	116847699	A	G	0.0501969	0.1537020	0.0139009	1.80E-29
11	SIK3	rs1145206	116847805	C	G	0.1301920	0.0574897	0.0090422	5.00E-11
11	SIK3	rs149318234	116847838	G	C	0.0389211	-0.0884884	0.0156978	6.80E-09
11	SIK3	rs7127590	116848086	G	T	0.4049100	-0.0455072	0.0062176	6.30E-13
11	SIK3	rs532815	116848142	A	G	0.2346150	-0.0779543	0.0072060	4.30E-27
11	SIK3	rs112030791	116848208	ATT	A	0.4040990	-0.0450053	0.0062252	1.20E-12
11	SIK3	rs145730196	116848209	A	G	0.4040990	-0.0450053	0.0062252	1.20E-12
11	SIK3	rs61905155	116848213	T	G	0.0500565	0.1528680	0.0139244	4.80E-29
11	SIK3	rs2289893	116849373	C	T	0.3499060	-0.0767886	0.0063889	6.00E-33
11	SIK3	rs660083	116850113	G	C	0.2313790	-0.0728943	0.0072212	8.80E-24
11	SIK3	rs11216161	116850485	C	T	0.4007890	-0.0423564	0.0062119	2.10E-11
11	SIK3	rs10047459	116851110	T	C	0.4003130	-0.0415828	0.0062051	4.70E-11
11	SIK3	rs10047462	116851325	T	G	0.4832940	-0.0846989	0.0060769	7.60E-45
11	SIK3	rs689243	116851977	C	G	0.2309390	-0.0706114	0.0072252	2.30E-22
11	SIK3	rs139952838	116852044	T	C	0.0281376	0.2421330	0.0183351	2.00E-40
11	SIK3	rs888245	116853021	G	C	0.0502861	0.1543040	0.0138806	1.00E-29
11	SIK3	rs77462380	116853121	T	C	0.0389264	-0.0882129	0.0156940	7.30E-09
11	SIK3	rs888246	116853516	T	C	0.0502741	0.1553630	0.0138806	4.10E-30
11	SIK3	rs75771311	116853517	A	G	0.0389230	-0.0883945	0.0156947	6.70E-09
11	SIK3	rs12099358	116855332	A	C	0.0504256	0.1535400	0.0138608	1.40E-29
11	SIK3	rs112618266	116855993	T	C	0.0791592	-0.1494830	0.0112336	6.90E-43
11	SIK3	rs640621	116856053	G	C	0.2348470	-0.0768259	0.0071737	1.60E-26
11	SIK3	rs78857232	116856749	T	C	0.0502383	0.1536530	0.0138826	2.00E-29
11	SIK3	rs117910440	116856831	C	T	0.0383510	-0.0858216	0.0158239	2.40E-08
11	SIK3	rs1035237	116857134	C	G	0.4845700	-0.0860675	0.0061005	5.30E-46
11	SIK3	rs78816728	116857155	C	T	0.0383521	-0.0858342	0.0158239	2.40E-08
11	SIK3	rs75385236	116857544	T	C	0.0383546	-0.0858662	0.0158240	2.30E-08
11	SIK3	rs6589574	116859922	A	G	0.3117620	0.1156290	0.0066244	9.70E-70
11	SIK3	rs567312	116860022	A	G	0.2336190	-0.0767110	0.0071891	2.20E-26
11	SIK3	rs4938315	116860489	A	G	0.4831850	-0.0855185	0.0061017	2.30E-45
11	SIK3	rs3056855	116860745	CCAA	A	0.0413219	-0.0859130	0.0155063	1.30E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs75501351	116861028	G	T	0.0383454	-0.0855727	0.0158281	2.60E-08
11	SIK3	rs2075292	116861796	T	G	0.4825200	-0.0867671	0.0061103	9.70E-47
11	SIK3	rs117010832	116861803	A	G	0.1385700	-0.0660625	0.0088924	7.60E-15
11	SIK3	rs484646	116862140	G	A	0.2349550	-0.0771772	0.0071727	8.10E-27
11	SIK3	rs6589575	116862594	T	C	0.4838720	-0.0857745	0.0060986	1.10E-45
11	SIK3	rs2080586	116862600	C	T	0.0500669	0.1556520	0.0139055	3.40E-30
11	SIK3	rs476399	116863012	C	T	0.2349200	-0.0769748	0.0071719	1.10E-26
11	SIK3	rs718847	116863430	T	C	0.4832460	-0.0855705	0.0060991	1.40E-45
11	SIK3	rs17120099	116864744	C	A	0.0792167	-0.1486890	0.0112294	1.80E-42
11	SIK3	rs6589576	116865072	G	C	0.4837490	-0.0860189	0.0060975	5.90E-46
11	SIK3	rs573549	116865963	G	A	0.2355180	-0.0779014	0.0071749	2.70E-27
11	SIK3	chr11:116866441_C_CTTTA	116866441	CTTTA	C	0.0400211	0.1668170	0.0155943	1.10E-27
11	SIK3	rs139447106	116866586	T	C	0.0383741	-0.0847200	0.0158239	3.40E-08
11	SIK3	rs77009426	116867798	T	C	0.0321518	-0.1220950	0.0173157	1.30E-12
11	SIK3	rs17120101	116867872	T	C	0.0325830	-0.1548660	0.0171378	2.50E-20
11	SIK3	rs11216168	116870837	A	G	0.0502358	0.1539750	0.0138827	1.40E-29
11	SIK3	rs533556	116870856	C	A	0.2358340	-0.0769291	0.0071581	9.90E-27
11	SIK3	rs17120111	116873302	T	C	0.0497596	0.1587840	0.0139540	4.80E-31
11	SIK3	rs11216169	116873673	C	T	0.0497643	0.1558180	0.0139564	6.90E-30
11	SIK3	rs9919599	116874768	G	C	0.4832380	-0.0847296	0.0061107	3.10E-44
11	SIK3	rs17120119	116876566	G	C	0.0772114	-0.1450750	0.0113679	5.70E-40
11	SIK3	rs77682889	116876596	T	C	0.0303550	0.2177580	0.0176436	1.70E-35
11	SIK3	rs12278117	116877453	A	G	0.0772072	-0.1452970	0.0113681	4.50E-40
11	SIK3	rs12279433	116877505	T	G	0.0785641	-0.1471930	0.0112695	1.30E-41
11	SIK3	rs12279464	116877766	T	C	0.0772072	-0.1452970	0.0113681	4.50E-40
11	SIK3	rs112867178	116877768	TCTAT	C	0.4819440	-0.0842048	0.0061184	1.10E-43
11	SIK3	rs12292614	116877799	G	A	0.0772072	-0.1452970	0.0113681	4.50E-40
11	SIK3	rs12286581	116878028	C	T	0.0772067	-0.1453050	0.0113681	4.40E-40
11	SIK3	rs61907566	116878189	G	C	0.2333610	-0.0764559	0.0072095	5.30E-26
11	SIK3	rs75294699	116878356	A	C	0.0772067	-0.1453050	0.0113681	4.40E-40
11	SIK3	rs76523703	116878793	G	T	0.0498117	0.1546440	0.0139507	2.00E-29
11	SIK3	rs6589577	116879261	T	C	0.4832140	-0.0850384	0.0061123	1.60E-44
11	SIK3	rs543819	116879357	G	A	0.0833170	-0.1461660	0.0109974	3.80E-43
11	SIK3	rs7396061	116880158	C	A	0.3167450	-0.0701551	0.0065717	7.60E-26
11	SIK3	rs74341458	116880833	A	G	0.0496683	0.1556810	0.0139696	8.20E-30
11	SIK3	rs482371	116881447	C	T	0.2289650	-0.0749868	0.0072545	1.10E-24
11	SIK3	rs7124741	116881503	T	A	0.4828590	-0.0850000	0.0061069	1.20E-44
11	SIK3	rs12275565	116882836	G	A	0.0822077	-0.1442630	0.0110701	1.20E-41
11	SIK3	rs12416987	116883549	C	T	0.0786008	-0.1472570	0.0112664	1.10E-41
11	SIK3	rs1269329	116884325	C	T	0.2348760	-0.0765841	0.0071967	3.90E-26
11	SIK3	rs139733873	116884844	G	A	0.0123661	0.2865620	0.0275000	2.80E-25
11	SIK3	rs11827828	116884868	A	G	0.0498171	0.1545050	0.0139498	2.20E-29
11	SIK3	rs2044426	116885467	A	G	0.0765484	-0.1461800	0.0114184	3.10E-40
11	SIK3	rs35378097	116886122	G	GT	0.0341375	-0.1554420	0.0167148	1.10E-21
11	SIK3	rs10892040	116886270	A	G	0.0768294	-0.1454750	0.0113929	3.90E-40
11	SIK3	rs11216174	116886532	G	A	0.0768336	-0.1452520	0.0113927	5.00E-40
11	SIK3	rs11216175	116886682	T	C	0.0768294	-0.1454750	0.0113929	3.90E-40
11	SIK3	chr11:116886752_T_TA	116886752	TA	T	0.2342000	-0.0767737	0.0071999	3.00E-26
11	SIK3	rs12284346	116887077	C	T	0.0777238	-0.1474890	0.0113295	1.60E-41
11	SIK3	rs12292278	116887977	C	A	0.0832172	-0.1461440	0.0109998	3.50E-43
11	SIK3	rs1473177	116888616	C	T	0.0497056	0.1558860	0.0139631	6.20E-30
11	SIK3	rs17174502	116888939	G	A	0.4833790	-0.0852655	0.0061135	7.60E-45
11	SIK3	rs12294191	116889108	G	A	0.0833684	-0.1463980	0.0109909	1.80E-43
11	SIK3	rs10892042	116889829	A	G	0.0497056	0.1558860	0.0139631	6.20E-30
11	SIK3	rs660443	116889977	C	T	0.2291550	-0.0749234	0.0072534	1.10E-24
11	SIK3	rs12285074	116891312	G	A	0.4830980	-0.0857733	0.0061283	3.20E-45
11	SIK3	rs72645459	116891441	C	A	0.4823590	-0.0860571	0.0061208	1.30E-45
11	SIK3	chr11:116891662_AAG_A	116891662	AAG	A	0.4815040	-0.0861984	0.0061139	7.80E-46
11	SIK3	rs144010715	116891837	AG	A	0.0833200	-0.1465080	0.0109948	1.70E-43
11	SIK3	rs75158858	116892113	A	G	0.0497056	0.1558860	0.0139631	6.20E-30
11	SIK3	rs672058	116893305	T	C	0.4000950	-0.0824543	0.0062366	7.00E-41
11	SIK3	rs74885676	116894221	T	G	0.1364160	-0.0653997	0.0089487	3.40E-14
11	SIK3	rs77349713	116894760	C	T	0.0838912	-0.1468520	0.0109513	5.70E-44
11	SIK3	rs11820814	116894984	C	T	0.0496587	0.1564270	0.0139746	4.40E-30
11	SIK3	rs74881320	116895209	C	A	0.0838874	-0.1469250	0.0109501	5.30E-44
11	SIK3	rs149874218	116895594	TTG	T	0.0840992	-0.1472390	0.0109465	3.30E-44
11	SIK3	rs11216178	116895674	T	G	0.0496126	0.1562560	0.0139829	5.90E-30
11	SIK3	rs10892044	116896183	C	T	0.0496485	0.1564340	0.0139764	4.50E-30
11	SIK3	rs376638077	116896662	C	CT	0.0155274	-0.1348750	0.0247234	7.50E-09
11	SIK3	rs2270392	116896972	C	T	0.1215260	-0.1316320	0.0093079	1.50E-48
11	SIK3	chr11:116897883_CA_C	116897883	C	CA	0.0741971	-0.1506190	0.0116224	3.90E-41
11	SIK3	rs111884008	116898027	C	G	0.1166600	-0.1313900	0.0094628	8.20E-47

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs190051172	116898198	G	C	0.0838929	-0.1469030	0.0109497	5.60E-44
11	SIK3	rs609177	116899801	G	A	0.2354380	-0.0775194	0.0071986	9.50E-27
11	SIK3	rs72645460	116900659	A	G	0.4804410	-0.0861065	0.0061227	1.40E-45
11	SIK3	rs188999199	116900812	T	C	0.0155274	-0.1344580	0.0247234	8.20E-09
11	SIK3	rs1076485	116901725	C	T	0.4431910	-0.0762057	0.0061505	1.70E-35
11	SIK3	rs17120131	116901770	C	T	0.0841943	-0.1477140	0.0109395	1.50E-44
11	SIK3	rs518181	116902071	A	C	0.2279700	-0.0762936	0.0072735	2.00E-25
11	SIK3	rs17120132	116902602	A	T	0.0842858	-0.1476910	0.0109320	1.20E-44
11	SIK3	rs11216180	116902662	T	A	0.0496687	0.1574400	0.0139727	1.90E-30
11	SIK3	rs17120136	116903045	G	T	0.0822451	-0.1456880	0.0110699	1.00E-42
11	SIK3	rs17120139	116903485	G	A	0.4801070	-0.0864986	0.0061245	5.20E-46
11	SIK3	rs78694306	116903528	T	G	0.0778740	-0.1467990	0.0113174	2.00E-41
11	SIK3	rs11216181	116903758	T	A	0.0463013	0.1653860	0.0144836	3.50E-31
11	SIK3	rs78832854	116903759	A	T	0.0808915	-0.1335390	0.0111452	1.70E-35
11	SIK3	rs115971514	116903783	C	G	0.0778740	-0.1467990	0.0113174	2.00E-41
11	SIK3	rs12280030	116904480	A	T	0.0840686	-0.1472340	0.0109360	2.30E-44
11	SIK3	rs7111854	116906110	T	A	0.1217240	-0.1319840	0.0092982	5.50E-49
11	SIK3	rs12273762	116906347	A	T	0.0840686	-0.1472340	0.0109360	2.30E-44
11	SIK3	rs9651681	116907349	C	T	0.0842840	-0.1476770	0.0109320	1.20E-44
11	SIK3	rs4938317	116907559	C	T	0.0496651	0.1574690	0.0139731	1.90E-30
11	SIK3	rs35184536	116908097	G	A	0.0841390	-0.1474550	0.0109404	2.30E-44
11	SIK3	rs10790166	116908783	G	A	0.2461080	-0.0407827	0.0070717	2.60E-09
11	SIK3	rs200905431	116909318	G	GA	0.0940899	-0.1242780	0.0106322	3.40E-34
11	SIK3	rs75920871	116909379	T	A	0.0497466	0.1590170	0.0139918	6.00E-31
11	SIK3	rs11216183	116910829	A	C	0.0751412	-0.1512420	0.0114843	2.10E-42
11	SIK3	rs191330880	116911276	A	G	0.0209624	-0.1248170	0.0213861	9.20E-10
11	SIK3	rs7123336	116912103	C	T	0.1629590	-0.0429797	0.0082232	3.50E-08
11	SIK3	rs11216185	116912258	G	T	0.0793403	-0.1476720	0.0112129	1.80E-42
11	SIK3	rs983567	116912884	C	T	0.1629570	-0.0432457	0.0082255	3.00E-08
11	SIK3	rs142195028	116913525	A	AG	0.0750439	-0.1515050	0.0114948	1.90E-42
11	SIK3	rs11357208	116913587	C	CT	0.0496401	0.1568230	0.0139793	3.50E-30
11	SIK3	rs7115583	116913660	T	G	0.1168940	-0.1322320	0.0094571	1.70E-47
11	SIK3	rs149566815	116913905	T	TAAAC	0.0750590	-0.1516540	0.0114955	1.60E-42
11	SIK3	rs11216186	116913976	C	T	0.0988354	-0.1398930	0.0101655	2.40E-46
11	SIK3	rs10892045	116914108	A	C	0.0463506	0.1580580	0.0144666	1.40E-28
11	SIK3	rs1838757	116914367	G	C	0.1281200	0.0531641	0.0091061	1.20E-09
11	SIK3	rs79711490	116914625	T	C	0.0988347	-0.1398920	0.0101655	2.40E-46
11	SIK3	rs11216187	116916432	T	C	0.0496307	0.1568170	0.0139806	3.60E-30
11	SIK3	rs12277181	116916604	A	G	0.0989665	-0.1391600	0.0101665	8.10E-46
11	SIK3	rs12277092	116916611	T	C	0.0988405	-0.1399280	0.0101652	2.30E-46
11	SIK3	rs7928298	116916811	T	A	0.0734951	-0.1200450	0.0117751	8.30E-26
11	SIK3	rs12418208	116916917	T	C	0.0961314	-0.1414040	0.0103125	6.00E-46
11	SIK3	rs12418209	116916925	T	C	0.0961314	-0.1414040	0.0103125	6.00E-46
11	SIK3	rs1006176	116917417	C	T	0.0990467	-0.1397710	0.0101528	2.80E-46
11	SIK3	chr11:116917733_AAGAG_A	116917733	A	AAGAG	0.0962194	-0.1357500	0.0103139	2.30E-42
11	SIK3	rs76136280	116917775	T	C	0.0496572	0.1569990	0.0139767	3.00E-30
11	SIK3	rs1135663	116918121	T	C	0.0856420	-0.1349660	0.0109543	2.90E-37
11	SIK3	rs79530380	116918472	A	T	0.0410664	0.1779850	0.0154519	2.40E-31
11	SIK3	rs78692246	116920591	A	G	0.0996346	-0.1390550	0.0101230	6.70E-46
11	SIK3	rs141203891	116921220	C	T	0.0101956	-0.2112150	0.0302238	7.70E-13
11	SIK3	rs7934763	116921641	G	T	0.0499761	0.1530020	0.0139373	5.00E-29
11	SIK3	rs7948838	116922245	G	A	0.1368300	-0.1289420	0.0088348	1.70E-51
11	SIK3	rs12225187	116922515	A	G	0.2030890	-0.0654261	0.0075755	1.60E-17
11	SIK3	rs12288386	116922907	T	C	0.0993171	-0.1390470	0.0101354	8.30E-46
11	SIK3	rs10892047	116922977	T	C	0.0992280	-0.1393950	0.0101447	5.40E-46
11	SIK3	rs117287138	116924163	A	G	0.0498858	0.1528350	0.0139511	7.20E-29
11	SIK3	rs56314469	116924187	A	G	0.0498858	0.1528350	0.0139511	7.20E-29
11	SIK3	rs12292371	116925232	C	G	0.0994169	-0.1390330	0.0101316	7.70E-46
11	SIK3	rs12292434	116925349	A	G	0.0993417	-0.1391430	0.0101341	7.10E-46
11	SIK3	rs7121898	116926130	T	A	0.2034290	-0.0648788	0.0075705	2.90E-17
11	SIK3	rs61907591	116926139	A	T	0.0499761	0.1530020	0.0139373	5.00E-29
11	SIK3	rs12285956	116926759	A	G	0.0993446	-0.1391510	0.0101340	7.10E-46
11	SIK3	rs11216190	116926968	C	T	0.1360460	-0.1295990	0.0088613	1.40E-51
11	SIK3	chr11:116927081_AT_A	116927081	A	AT	0.0968553	-0.1335720	0.0102898	2.00E-41
11	SIK3	rs1446105	116927828	T	C	0.2034370	-0.0647760	0.0075674	2.80E-17
11	SIK3	rs579890	116928247	G	A	0.4715960	-0.0817385	0.0061218	4.30E-41
11	SIK3	rs79157715	116929554	A	G	0.0994576	-0.1390420	0.0101274	8.30E-46
11	SIK3	rs10790167	116930227	C	T	0.2032980	-0.0645978	0.0075693	3.80E-17
11	SIK3	rs75776964	116930345	G	C	0.0994337	-0.1392980	0.0101282	5.70E-46
11	SIK3	rs645258	116930485	A	C	0.3136680	0.1005670	0.0065762	1.80E-53
11	SIK3	rs76690043	116930813	G	C	0.0499786	0.1529510	0.0139368	5.10E-29
11	SIK3	rs61907594	116931095	T	C	0.0499790	0.1529660	0.0139368	5.00E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs79974099	116931865	A	T	0.0499790	0.1529660	0.0139368	5.00E-29
11	SIK3	rs74615346	116932256	C	A	0.0995479	-0.1392140	0.0101241	6.20E-46
11	SIK3	chr11:116933137_CTT_C	116933137	C	CTT	0.0509608	-0.0848049	0.0139723	2.70E-10
11	SIK3	rs12270974	116933289	T	C	0.0994309	-0.1392970	0.0101284	5.80E-46
11	SIK3	rs7107702	116933428	C	T	0.1871720	-0.0530479	0.0077823	9.20E-13
11	SIK3	rs12272491	116933654	T	C	0.0994309	-0.1392970	0.0101284	5.80E-46
11	SIK3	rs12418735	116934046	G	T	0.0994337	-0.1393120	0.0101282	5.70E-46
11	SIK3	rs77204473	116934348	G	T	0.0647636	-0.1171050	0.0123244	4.50E-23
11	SIK3	rs562179	116934488	C	T	0.4365870	-0.0606297	0.0061582	8.20E-23
11	SIK3	rs79207844	116934725	A	G	0.0642944	-0.1194140	0.0123661	9.40E-24
11	SIK3	rs12274590	116934980	A	G	0.0642944	-0.1194140	0.0123661	9.40E-24
11	SIK3	rs144015791	116935158	T	G	0.0499790	0.1529660	0.0139368	5.00E-29
11	SIK3	rs2513095	116935553	C	T	0.4719850	-0.0811639	0.0061223	1.40E-40
11	SIK3	rs2513094	116935696	C	T	0.2662460	-0.0496163	0.0068845	1.10E-13
11	SIK3	rs2513093	116935971	G	A	0.4717820	-0.0817312	0.0061204	3.70E-41
11	SIK3	rs12273769	116936457	G	T	0.0994324	-0.1393650	0.0101279	5.20E-46
11	SIK3	rs12294657	116936652	C	G	0.0994352	-0.1393260	0.0101278	5.40E-46
11	SIK3	rs77920516	116936711	C	T	0.0885665	0.0885605	0.0107594	2.60E-16
11	SIK3	rs473172	116937254	G	A	0.4717900	-0.0817176	0.0061203	3.80E-41
11	SIK3	rs77136879	116937737	T	C	0.0994505	-0.1393120	0.0101267	5.40E-46
11	SIK3	chr11:116938204_AGAGGGGAGGGGAGGG_A	116938204	A	3GAGGG	0.1147150	-0.0819797	0.0095991	3.40E-19
11	SIK3	rs868771531	116938233	A	G	0.0116909	-0.1566520	0.0287531	9.30E-09
11	SIK3	rs142440762	116938378	A	G	0.1434210	-0.0512895	0.0087412	6.60E-10
11	SIK3	rs61907600	116938632	G	A	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs7480278	116939073	G	T	0.0994555	-0.1392690	0.0101265	5.70E-46
11	SIK3	rs61624438	116939229	A	C	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs80015203	116940190	G	A	0.0994555	-0.1392690	0.0101265	5.70E-46
11	SIK3	rs117877581	116940238	G	T	0.0995860	-0.1394390	0.0101255	4.40E-46
11	SIK3	rs116597701	116940771	G	C	0.0979498	-0.1384410	0.0102026	1.30E-44
11	SIK3	rs145705809	116940967	A	C	0.0130939	0.4273360	0.0267420	4.60E-58
11	SIK3	rs139127609	116940986	T	TTTTG	0.0994555	-0.1392690	0.0101265	5.70E-46
11	SIK3	rs473188	116941313	G	C	0.4714920	-0.0814173	0.0061187	6.90E-41
11	SIK3	rs78066444	116941342	C	A	0.0983352	-0.1367860	0.0101883	3.80E-44
11	SIK3	chr11:116941408_TA_T	116941408	T	TA	0.4802630	-0.0866569	0.0061867	8.70E-45
11	SIK3	rs17120157	116941912	C	T	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs75410648	116942722	T	C	0.0994664	-0.1390730	0.0101255	7.20E-46
11	SIK3	rs510988	116943088	T	C	0.4714640	-0.0814691	0.0061187	6.00E-41
11	SIK3	rs12292858	116943263	C	A	0.1367240	-0.1298420	0.0088329	3.90E-52
11	SIK3	rs10892048	116943880	G	A	0.2014510	-0.0637294	0.0076033	1.40E-16
11	SIK3	rs12421902	116943930	G	A	0.0976583	-0.1391220	0.0102242	3.40E-45
11	SIK3	chr11:116944465_GCAAT_G	116944465	G	GCAAT	0.4714600	-0.0814529	0.0061187	6.30E-41
11	SIK3	rs11216193	116944883	T	C	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	chr11:116944965_C_CTT	116944965	CTT	C	0.0795700	-0.1319800	0.0114336	1.30E-33
11	SIK3	rs11216194	116945022	C	G	0.0991425	-0.1389020	0.0101616	2.70E-45
11	SIK3	rs11216195	116945175	A	G	0.0973509	-0.1383250	0.0102450	2.60E-44
11	SIK3	rs11216196	116945176	G	T	0.0973509	-0.1383250	0.0102450	2.60E-44
11	SIK3	rs35485516	116945411	C	CAG	0.0994584	-0.1392590	0.0101267	5.90E-46
11	SIK3	rs10892049	116945500	C	G	0.1367130	-0.1298650	0.0088336	3.80E-52
11	SIK3	rs10892050	116945678	A	C	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs75958227	116945875	A	G	0.1397000	-0.0636332	0.0088408	5.60E-14
11	SIK3	rs7924318	116945914	G	C	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs11216197	116946062	G	A	0.0996988	-0.1385540	0.0101214	1.40E-45
11	SIK3	rs191655881	116946939	C	A	0.1367130	-0.1298650	0.0088336	3.80E-52
11	SIK3	rs111327557	116947068	T	C	0.0497173	0.1503580	0.0139878	5.30E-28
11	SIK3	rs1565486994	116947173	ATATT	T	0.0118521	-0.2091810	0.0284237	3.60E-14
11	SIK3	rs146056222	116947627	G	A	0.1367130	-0.1298650	0.0088336	3.80E-52
11	SIK3	rs61907604	116947691	G	A	0.1874500	-0.0533131	0.0077799	7.30E-13
11	SIK3	rs112704540	116947811	G	A	0.1871870	-0.0532428	0.0077813	7.50E-13
11	SIK3	rs146503809	116948352	G	A	0.0272677	0.2057640	0.0186356	8.30E-29
11	SIK3	rs4316540	116948525	T	C	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs12293755	116948548	T	A	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs1241658	116948901	A	G	0.4708670	-0.0802093	0.0061232	1.10E-39
11	SIK3	rs139552563	116949016	CAAAT	C	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs112297132	116949116	GA	G	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs6589580	116949157	A	G	0.1871870	-0.0532428	0.0077813	7.50E-13
11	SIK3	rs12419047	116949190	A	G	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs12421834	116949307	C	A	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs61907605	116949355	A	T	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs12420518	116949372	C	T	0.1367130	-0.1298650	0.0088336	3.80E-52
11	SIK3	rs142344418	116949918	C	CAG	0.0858273	0.0966183	0.0109189	7.70E-19
11	SIK3	rs12419437	116949974	A	G	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs1473324	116951202	G	T	0.0499822	0.1528890	0.0139364	5.30E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs1473325	116951318	T	C	0.0499822	0.1528890	0.0139364	5.30E-29
11	SIK3	rs76538122	116951618	G	A	0.0318231	-0.1637580	0.0173153	1.20E-22
11	SIK3	rs12286405	116951812	T	C	0.1367110	-0.1297770	0.0088335	4.50E-52
11	SIK3	rs11605327	116952346	A	G	0.2027770	-0.0646028	0.0075797	4.20E-17
11	SIK3	rs77467134	116952391	C	T	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs76654964	116952805	A	G	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs76146269	116952901	G	A	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs1473326	116952956	C	T	0.0499826	0.1528840	0.0139364	5.40E-29
11	SIK3	rs143550540	116953197	G	T	0.0648356	0.0758019	0.0124975	6.40E-09
11	SIK3	rs1473327	116953280	T	A	0.0500087	0.1528390	0.0139340	5.40E-29
11	SIK3	rs12275355	116953446	G	A	0.0994823	-0.1392740	0.0101255	4.90E-46
11	SIK3	rs12289974	116953570	T	C	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs2289890	116953904	A	G	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs511676	116954168	G	T	0.4718770	-0.0819755	0.0061211	2.20E-41
11	SIK3	rs2289892	116954524	A	G	0.0993621	-0.1391260	0.0101309	6.90E-46
11	SIK3	rs12291040	116955901	C	T	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs12270837	116955927	C	A	0.0994534	-0.1393270	0.0101264	5.30E-46
11	SIK3	rs10502221	116956154	T	C	0.2026140	-0.0642615	0.0075795	6.00E-17
11	SIK3	rs17120177	116956653	C	T	0.0994420	-0.1391000	0.0101323	7.90E-46
11	SIK3	rs1940626	116957405	C	T	0.1871370	-0.0529855	0.0077841	9.70E-13
11	SIK3	rs682048	116957604	G	T	0.2662100	-0.0495107	0.0068862	1.20E-13
11	SIK3	rs193291566	116957830	G	T	0.0102347	-0.2147500	0.0301560	3.40E-13
11	SIK3	rs878692	116958223	A	C	0.0993889	-0.1393960	0.0101377	6.30E-46
11	SIK3	rs6589582	116958484	C	A	0.2045830	-0.0654042	0.0075521	1.70E-17
11	SIK3	rs12420857	116958726	T	G	0.0993773	-0.1393780	0.0101383	6.80E-46
11	SIK3	rs7120706	116959371	C	T	0.2045780	-0.0654250	0.0075520	1.70E-17
11	SIK3	rs7120963	116959545	C	T	0.2045780	-0.0654250	0.0075520	1.70E-17
11	SIK3	rs11216199	116960300	T	C	0.0993418	-0.1390710	0.0101402	1.10E-45
11	SIK3	rs145400227	116960788	AGTAA	C	0.0993389	-0.1391300	0.0101403	1.00E-45
11	SIK3	rs11216200	116961127	T	C	0.1366760	-0.1297800	0.0088387	4.50E-52
11	SIK3	rs7112967	116961196	T	C	0.0499884	0.1527730	0.0139356	6.00E-29
11	SIK3	rs10892051	116962002	A	C	0.0993302	-0.1392220	0.0101407	9.00E-46
11	SIK3	rs117157737	116962297	T	G	0.0171782	-0.1885780	0.0235158	1.10E-16
11	SIK3	rs56134734	116962339	A	G	0.0499942	0.1525820	0.0139347	6.90E-29
11	SIK3	rs61905677	116962939	G	T	0.0499942	0.1525820	0.0139347	6.90E-29
11	SIK3	rs493134	116962963	T	C	0.4712360	-0.0814193	0.0061203	5.40E-41
11	SIK3	rs10502222	116963014	T	C	0.1849130	-0.0750601	0.0078584	2.10E-21
11	SIK3	rs145388534	116963492	T	C	0.0127499	0.1512110	0.0271551	8.00E-09
11	SIK3	rs10892052	116963597	A	G	0.1849010	-0.0750065	0.0078587	2.20E-21
11	SIK3	rs61905678	116964069	T	C	0.0499975	0.1524780	0.0139343	7.50E-29
11	SIK3	rs61905679	116964071	T	C	0.0499975	0.1524780	0.0139343	7.50E-29
11	SIK3	rs1815789	116964237	C	T	0.1869790	-0.0528158	0.0077897	1.30E-12
11	SIK3	rs1815788	116964255	C	T	0.1869450	-0.0527816	0.0077890	1.40E-12
11	SIK3	rs201165469	116964853	G	GC	0.0994432	-0.1394660	0.0101352	4.80E-46
11	SIK3	rs61905680	116965315	A	G	0.0499975	0.1524780	0.0139343	7.50E-29
11	SIK3	rs76930628	116965385	T	A	0.0206123	-0.1566110	0.0214612	1.30E-13
11	SIK3	rs61905681	116965493	C	A	0.0499975	0.1524780	0.0139343	7.50E-29
11	SIK3	rs2513097	116965496	G	A	0.2656150	-0.0503553	0.0068942	4.40E-14
11	SIK3	rs77320801	116965633	T	C	0.0499909	0.1525390	0.0139351	7.50E-29
11	SIK3	rs761823852	116965753	A	AT	0.0426077	0.1552780	0.0152292	3.30E-25
11	SIK3	rs78044162	116966373	T	C	0.1365600	-0.1295300	0.0088437	9.30E-52
11	SIK3	rs9971422	116966657	C	T	0.1360420	-0.1291080	0.0088638	1.80E-51
11	SIK3	rs113224863	116966687	G	GT	0.1864980	-0.0525520	0.0078016	1.50E-12
11	SIK3	rs1241655	116967092	T	G	0.2662130	-0.0496806	0.0068918	8.80E-14
11	SIK3	rs12281729	116967414	C	A	0.0993487	-0.1392750	0.0101425	8.50E-46
11	SIK3	rs7941927	116968188	G	A	0.1870190	-0.0529291	0.0077892	1.00E-12
11	SIK3	rs149144614	116968288	A	G	0.0450944	0.1624330	0.0146856	1.20E-29
11	SIK3	rs12417152	116968577	C	G	0.0991685	-0.1394620	0.0101540	8.80E-46
11	SIK3	rs11823013	116968819	C	T	0.0499851	0.1527330	0.0139371	6.00E-29
11	SIK3	rs11216204	116968898	A	G	0.0991496	-0.1396840	0.0101550	6.40E-46
11	SIK3	rs1241657	116969045	T	C	0.3123350	0.1006160	0.0065893	1.70E-53
11	SIK3	rs12272305	116969222	A	G	0.0958312	-0.1395310	0.0103376	2.50E-44
11	SIK3	rs12279266	116969317	C	T	0.0985669	-0.1384120	0.0101877	6.50E-45
11	SIK3	rs201227770	116969542	T	GCAATT	0.0359933	0.1561070	0.0165030	3.80E-22
11	SIK3	rs59294170	116970730	T	A	0.0499768	0.1530870	0.0139374	4.60E-29
11	SIK3	rs12418324	116971960	T	C	0.0991033	-0.1395360	0.0101559	8.50E-46
11	SIK3	rs11216206	116972709	G	C	0.3131670	-0.0662896	0.0065597	2.20E-25
11	SIK3	rs17120197	116974388	C	T	0.0501235	0.1531380	0.0139136	3.40E-29
11	SIK3	chr11:116974556_C_CTGTT	116974556	CTGTT	C	0.0992631	-0.1397390	0.0101472	6.20E-46
11	SIK3	rs74927399	116975550	C	T	0.0992718	-0.1398080	0.0101468	5.50E-46
11	SIK3	rs76949321	116975627	A	G	0.0992718	-0.1398080	0.0101468	5.50E-46
11	SIK3	rs11216209	116977470	C	T	0.0992834	-0.1399090	0.0101463	4.70E-46

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs11216210	116977613	T	G	0.1368120	-0.1291690	0.0088295	1.50E-51
11	SIK3	rs7109876	116977932	A	C	0.0501460	0.1528970	0.0139107	3.80E-29
11	SIK3	rs509171	116978141	T	C	0.2663460	-0.0491216	0.0068731	1.70E-13
11	SIK3	chr11:116978213_C_CA	116978213	CA	C	0.1699130	-0.0901581	0.0081955	1.40E-29
11	SIK3	rs11216212	116979635	A	T	0.0992834	-0.1399090	0.0101463	4.70E-46
11	SIK3	rs146178826	116980651	G	A	0.0992834	-0.1399090	0.0101463	4.70E-46
11	SIK3	rs7358350	116980892	C	T	0.1368120	-0.1291690	0.0088295	1.50E-51
11	SIK3	rs4938321	116981791	T	C	0.1873140	-0.0526620	0.0077754	1.30E-12
11	SIK3	rs11216215	116981971	A	T	0.0992834	-0.1399090	0.0101463	4.70E-46
11	SIK3	rs3863304	116982407	A	G	0.2013680	-0.0701899	0.0076142	8.90E-20
11	SIK3	rs3863305	116982408	T	C	0.2013680	-0.0701899	0.0076142	8.90E-20
11	SIK3	rs3863306	116982497	T	C	0.2026790	-0.0636339	0.0075865	1.40E-16
11	SIK3	rs7131351	116982890	A	G	0.2021880	-0.0626468	0.0075931	4.70E-16
11	SIK3	rs7117123	116982970	A	T	0.1926860	-0.0587662	0.0077635	9.60E-14
11	SIK3	rs10128690	116983206	A	G	0.0937084	-0.1361210	0.0104731	3.70E-41
11	SIK3	rs10128570	116983305	G	A	0.0992834	-0.1399090	0.0101463	4.70E-46
11	SIK3	rs10128571	116983465	G	A	0.0992834	-0.1399090	0.0101463	4.70E-46
11	SIK3	rs113184611	116984048	A	C	0.0501452	0.1529570	0.0139102	3.80E-29
11	SIK3	chr11:116984050_C_CAAA	116984050	CAAA	C	0.0248898	0.1323290	0.0199619	1.90E-11
11	SIK3	rs374519262	116984705	A	AC	0.1181930	-0.1300890	0.0095324	8.30E-45
11	SIK3	rs146725667	116985530	A	G	0.0338190	-0.1627610	0.0168098	2.40E-23
11	SIK3	rs12287768	116985606	C	A	0.0992833	-0.1397860	0.0101466	5.60E-46
11	SIK3	rs588918	116985926	C	T	0.4716580	-0.0797055	0.0061101	1.90E-39
11	SIK3	rs12274771	116985982	G	C	0.0992826	-0.1397760	0.0101466	5.60E-46
11	SIK3	rs12274773	116985993	T	C	0.0992826	-0.1397760	0.0101466	5.60E-46
11	SIK3	rs75212922	116986276	A	T	0.0992826	-0.1397760	0.0101466	5.60E-46
11	SIK3	rs10892053	116986287	T	C	0.2034880	-0.0629446	0.0075591	2.50E-16
11	SIK3	rs11216217	116986936	A	G	0.0992826	-0.1397760	0.0101466	5.60E-46
11	SIK3	chr11:116987321_TAA_T	116987321	T	TAA	0.1010190	-0.1326710	0.0100946	5.00E-42
11	SIK3	rs201445271	116987332	AC	A	0.0498844	0.1461780	0.0139723	2.00E-26
11	SIK3	rs143958391	116988214	T	C	0.0184221	0.1570630	0.0226792	8.50E-12
11	SIK3	rs10160754	116988278	C	A	0.1368010	-0.1290770	0.0088304	1.70E-51
11	SIK3	rs10160755	116988287	G	A	0.1368010	-0.1290770	0.0088304	1.70E-51
11	SIK3	rs11406946	116988385	CA	C	0.2065190	-0.0681438	0.0075382	3.10E-19
11	SIK3	rs190231637	116988547	A	G	0.0184221	0.1570630	0.0226792	8.50E-12
11	SIK3	rs519794	116988737	C	T	0.4721730	-0.0808477	0.0061124	1.70E-40
11	SIK3	rs10706688	116989575	T	TA	0.2026910	-0.0622521	0.0075834	6.70E-16
11	SIK3	rs7939934	116990552	T	A	0.1884420	-0.0536747	0.0077711	4.70E-13
11	SIK3	rs61905687	116991428	C	T	0.0501746	0.1528050	0.0139059	4.30E-29
11	SIK3	rs80242245	116991529	G	C	0.0992797	-0.1397950	0.0101467	5.50E-46
11	SIK3	rs11216218	116991945	T	C	0.0992797	-0.1397950	0.0101467	5.50E-46
11	SIK3	rs11216219	116992039	T	C	0.0992797	-0.1397950	0.0101467	5.50E-46
11	SIK3	rs607273	116992102	A	T	0.3115170	0.1029850	0.0065688	8.10E-56
11	SIK3	rs12272973	116992331	C	A	0.0998724	-0.1409850	0.0101519	1.10E-46
11	SIK3	rs10128682	116992742	T	C	0.0994168	-0.1401130	0.0101387	2.40E-46
11	SIK3	rs6589583	116993050	T	C	0.2665590	-0.0491944	0.0068681	1.60E-13
11	SIK3	rs7130531	116993117	T	C	0.0501746	0.1528050	0.0139059	4.30E-29
11	SIK3	rs11216220	116993272	C	T	0.1368160	-0.1289120	0.0088294	2.20E-51
11	SIK3	rs11375002	116993436	CA	C	0.4725960	-0.0809847	0.0061070	1.20E-40
11	SIK3	rs75826529	116994384	A	T	0.0994168	-0.1401130	0.0101387	2.40E-46
11	SIK3	rs74460214	116994491	C	T	0.0994168	-0.1401130	0.0101387	2.40E-46
11	SIK3	rs79349393	116994651	G	A	0.0994168	-0.1401130	0.0101387	2.40E-46
11	SIK3	rs7931665	116995524	G	A	0.1369290	-0.1293350	0.0088256	7.80E-52
11	SIK3	rs7931770	116995574	T	C	0.4713820	-0.0795451	0.0061055	2.50E-39
11	SIK3	rs7121347	116996493	T	G	0.4713820	-0.0795451	0.0061055	2.50E-39
11	SIK3	rs11604866	116996798	T	C	0.0994168	-0.1401130	0.0101387	2.40E-46
11	SIK3	rs10892054	116997505	T	C	0.1873490	-0.0527489	0.0077743	1.20E-12
11	SIK3	rs10892055	116997655	A	G	0.1873490	-0.0527489	0.0077743	1.20E-12
11	SIK3	rs7950213	116997938	A	C	0.0501843	0.1527210	0.0139046	4.60E-29
11	SIK3	chr11:116999579_G_GTTTTC	116999579	GTTTTC	G	0.0501843	0.1527210	0.0139046	4.60E-29
11	SIK3	rs10892056	116999695	C	G	0.0994168	-0.1401130	0.0101387	2.40E-46
11	SIK3	rs10502224	116999764	G	A	0.1369460	-0.1292140	0.0088266	9.70E-52
11	SIK3	rs7930264	117000050	A	G	0.2666340	-0.0488804	0.0068666	2.30E-13
11	SIK3	rs17120233	117000507	G	A	0.0501843	0.1527210	0.0139046	4.60E-29
11	SIK3	rs10892057	117001318	C	A	0.1375430	-0.1300970	0.0088229	1.50E-52
11	SIK3	chr11:117001505_C_CA	117001505	CA	C	0.2809300	-0.0576928	0.0068066	8.60E-17
11	SIK3	rs75858236	117001547	G	A	0.0501876	0.1525840	0.0139042	5.10E-29
11	SIK3	rs12278943	117003642	C	T	0.0992826	-0.1398350	0.0101466	5.20E-46
11	SIK3	rs7946390	117004436	G	A	0.1369290	-0.1292770	0.0088254	8.30E-52
11	SIK3	rs6589587	117004622	G	T	0.1873670	-0.0525594	0.0077738	1.40E-12
11	SIK3	rs11216224	117005208	C	T	0.1356900	-0.1286770	0.0088677	7.80E-51
11	SIK3	rs7114963	117005267	C	T	0.4671010	-0.0799064	0.0061341	1.70E-39

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs1940625	117005726	G	A	0.1369280	-0.1292680	0.0088254	8.40E-52
11	SIK3	rs10892058	117005905	T	C	0.2028860	-0.0628290	0.0075634	2.80E-16
11	SIK3	rs10790169	117006443	C	A	0.4716790	-0.0800909	0.0061023	6.60E-40
11	SIK3	rs77250716	117006637	C	T	0.0496857	0.1529970	0.0139780	6.50E-29
11	SIK3	rs11216225	117007298	G	A	0.1369280	-0.1292680	0.0088254	8.40E-52
11	SIK3	rs11216226	117007350	G	C	0.0994176	-0.1401290	0.0101387	2.30E-46
11	SIK3	rs11216227	117007881	G	C	0.2030580	-0.0634682	0.0075657	1.40E-16
11	SIK3	rs12276805	117008043	C	T	0.0973475	-0.1446480	0.0102546	7.50E-48
11	SIK3	rs57278884	117008464	AAAAGz	C	0.1874310	-0.0527992	0.0077721	1.10E-12
11	SIK3	chr11:117008471_G_GAAAAGAT	117008471	AAAAGz	G	0.1872480	-0.0535627	0.0077808	5.90E-13
11	SIK3	rs12271319	117008508	T	C	0.1369310	-0.1292650	0.0088253	8.40E-52
11	SIK3	rs12284696	117008803	G	A	0.1360500	-0.1295280	0.0088580	1.30E-51
11	SIK3	rs7931398	117008960	C	T	0.2672250	-0.0491353	0.0068626	1.70E-13
11	SIK3	rs117901629	117008963	A	G	0.0992905	-0.1398550	0.0101470	4.90E-46
11	SIK3	rs138181556	117009007	A	G	0.0992862	-0.1398720	0.0101465	4.90E-46
11	SIK3	rs7112937	117009740	C	T	0.1369490	-0.1292810	0.0088246	8.10E-52
11	SIK3	rs61905691	117009987	G	A	0.0501876	0.1525840	0.0139042	5.10E-29
11	SIK3	rs7127881	117010082	A	G	0.2068330	-0.0646845	0.0075602	3.30E-17
11	SIK3	rs58176010	117010731	A	G	0.0191077	0.2392870	0.0222703	2.30E-28
11	SIK3	rs10892059	117010929	A	G	0.2031160	-0.0628041	0.0075571	2.70E-16
11	SIK3	rs10892060	117010946	A	C	0.2027640	-0.0626674	0.0075647	3.40E-16
11	SIK3	rs4245168	117011922	A	C	0.4712740	-0.0799432	0.0060981	8.30E-40
11	SIK3	rs35123861	117012098	CA	C	0.2038520	-0.0636799	0.0075506	1.10E-16
11	SIK3	rs7125788	117012680	C	T	0.0501843	0.1525390	0.0139046	5.30E-29
11	SIK3	rs1442498591	117012824	AG	A	0.1651720	-0.0637756	0.0083422	1.30E-14
11	SIK3	chr11:117012827_G_GTT	117012827	GTT	G	0.0993713	-0.1401240	0.0101407	2.30E-46
11	SIK3	rs10790170	117012828	G	T	0.2041130	-0.0640500	0.0075730	9.00E-17
11	SIK3	rs61905705	117013060	T	A	0.0501883	0.1524610	0.0139042	5.70E-29
11	SIK3	rs61905706	117013061	T	G	0.0501883	0.1524610	0.0139042	5.70E-29
11	SIK3	rs140947361	117013808	A	AC	0.0501883	0.1524610	0.0139042	5.70E-29
11	SIK3	rs374772197	117013968	C	T	0.0500840	0.1527330	0.0139184	5.20E-29
11	SIK3	rs11216230	117014073	A	G	0.1738170	-0.0574707	0.0081018	4.40E-12
11	SIK3	rs35190172	117014597	T	TC	0.0501883	0.1524610	0.0139042	5.70E-29
11	SIK3	rs7119185	117015380	T	C	0.1873900	-0.0530200	0.0077728	8.30E-13
11	SIK3	rs10892061	117015398	T	C	0.2036290	-0.0637776	0.0075566	1.00E-16
11	SIK3	chr11:117015578_AT_A	117015578	A	AT	0.2666930	-0.0491916	0.0068646	1.50E-13
11	SIK3	rs79870586	117016005	A	G	0.0993858	-0.1399500	0.0101391	2.60E-46
11	SIK3	rs66751419	117017528	T	TG	0.2038510	-0.0637680	0.0075587	1.10E-16
11	SIK3	rs7128772	117018695	A	T	0.2621560	-0.0488366	0.0069369	4.00E-13
11	SIK3	rs80054374	117019951	G	A	0.0993887	-0.1399820	0.0101390	2.50E-46
11	SIK3	rs12808524	117020277	C	T	0.2037530	-0.0635711	0.0075574	1.30E-16
11	SIK3	rs17120237	117020330	C	T	0.0501916	0.1523590	0.0139038	6.10E-29
11	SIK3	rs77955134	117021652	A	G	0.0992545	-0.1397040	0.0101469	5.40E-46
11	SIK3	rs77594377	117021730	A	G	0.0992357	-0.1398610	0.0101481	4.50E-46
11	SIK3	rs112619870	117021940	C	A	0.0269237	0.1392230	0.0190595	2.70E-13
11	SIK3	rs142310263	117022278	C	ATCTC	0.0983508	-0.1403670	0.0101971	5.80E-46
11	SIK3	rs4936359	117023008	A	T	0.0501898	0.1523450	0.0139037	6.20E-29
11	SIK3	rs4936360	117023053	C	G	0.0501894	0.1523520	0.0139037	6.20E-29
11	SIK3	rs10466590	117023697	G	C	0.2606010	-0.0485085	0.0069541	5.30E-13
11	SIK3	rs143791312	117024639	T	C	0.0629186	-0.1145910	0.0125185	1.10E-21
11	SIK3	rs11216239	117024796	G	C	0.2666300	-0.0495947	0.0068646	1.00E-13
11	SIK3	rs10892063	117025439	C	A	0.2043510	-0.0629460	0.0075448	2.60E-16
11	SIK3	rs111860754	117025569	C	CA	0.0501846	0.1528440	0.0139017	3.90E-29
11	SIK3	rs10892064	117025837	C	G	0.2038660	-0.0628145	0.0075439	2.70E-16
11	SIK3	rs2186844	117026197	T	C	0.0992603	-0.1397100	0.0101467	5.40E-46
11	SIK3	rs10892065	117026308	C	T	0.2038660	-0.0628145	0.0075439	2.70E-16
11	SIK3	rs61905709	117027118	T	C	0.0501871	0.1528650	0.0139013	3.90E-29
11	SIK3	rs4936361	117027438	C	T	0.1816060	-0.0499212	0.0079130	5.70E-11
11	SIK3	rs4938325	117027763	A	G	0.0501926	0.1530700	0.0139004	3.20E-29
11	SIK3	rs7950364	117028170	G	C	0.4710380	-0.0802387	0.0060993	4.70E-40
11	SIK3	rs11216240	117028532	T	A	0.2666440	-0.0492661	0.0068625	1.40E-13
11	SIK3	rs11216241	117028533	C	A	0.2666700	-0.0493114	0.0068619	1.40E-13
11	SIK3	rs12289032	117028864	T	C	0.0992690	-0.1397620	0.0101463	4.80E-46
11	SIK3	rs141750997	117028962	CTGGA	A	0.1864440	-0.0533943	0.0077962	7.40E-13
11	SIK3	rs7926104	117029066	A	G	0.2035660	-0.0633275	0.0075513	1.70E-16
11	SIK3	rs112120205	117029070	A	G	0.0501926	0.1530700	0.0139004	3.20E-29
11	SIK3	rs146943088	117029109	C	A	0.0992690	-0.1397620	0.0101463	4.80E-46
11	SIK3	rs11600552	117030231	C	T	0.2666660	-0.0494109	0.0068621	1.20E-13
11	SIK3	rs11216242	117030833	A	G	0.2035770	-0.0633595	0.0075510	1.60E-16
11	SIK3	rs7112191	117031340	A	G	0.0501875	0.1527950	0.0139019	4.20E-29
11	SIK3	chr11:117031495_C_CATTTT	117031495	CATTTT	C	0.4710470	-0.0803005	0.0060992	4.10E-40
11	SIK3	rs199986368	117031627	C	T	0.0152296	0.4418270	0.0249106	3.40E-71

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs7481286	117031656	T	G	0.0993902	-0.1396130	0.0101391	3.90E-46
11	SIK3	rs12804122	117031900	G	C	0.2035600	-0.0626671	0.0075508	3.10E-16
11	SIK3	rs4548653	117032600	A	G	0.1873670	-0.0529588	0.0077715	8.80E-13
11	SIK3	rs7941428	117032668	G	C	0.2649960	-0.0458415	0.0068904	7.10E-12
11	SIK3	chr11:117032674_CTT_C	117032674	C	CTT	0.1054720	-0.1373820	0.0099230	8.50E-47
11	SIK3	rs4575311	117033641	A	G	0.2036190	-0.0634192	0.0075497	1.40E-16
11	SIK3	rs4938326	117034748	C	G	0.0501875	0.1527950	0.0139019	4.20E-29
11	SIK3	rs187437651	117034813	A	G	0.0184986	0.2262780	0.0227258	5.00E-23
11	SIK3	rs147518949	117035258	A	G	0.0184988	0.2262650	0.0227258	5.00E-23
11	SIK3	rs4938327	117036012	C	T	0.1874230	-0.0530258	0.0077690	7.90E-13
11	SIK3	rs3181	117036327	A	G	0.1874380	-0.0529590	0.0077690	8.60E-13
11	SIK3	rs10732856	117036397	C	T	0.4714440	-0.0799320	0.0060955	7.50E-40
11	SIK3	rs721783	117036733	T	C	0.1874840	-0.0530953	0.0077684	7.20E-13
11	SIK3	rs75216569	117036999	G	A	0.0994084	-0.1397440	0.0101382	3.90E-46
11	SIK3	rs7115242	117037567	A	G	0.3129540	0.1005440	0.0065364	3.20E-54
11	SIK3	rs7118591	117037741	A	C	0.1874440	-0.0530359	0.0077686	7.90E-13
11	SIK3	chr11:117037793_AAC_A	117037793	A	AAC	0.1874440	-0.0530359	0.0077686	7.90E-13
11	SIK3	rs80273401	117037990	C	T	0.0994084	-0.1397440	0.0101382	3.90E-46
11	SIK3	rs61905712	117038577	A	G	0.0502306	0.1522100	0.0138977	7.50E-29
11	SIK3	rs112870705	117038708	T	TCAC	0.0499786	0.1505820	0.0139352	2.90E-28
11	SIK3	rs61905713	117038713	T	C	0.0499786	0.1505820	0.0139352	2.90E-28
11	SIK3	rs147501797	117038982	A	G	0.0345580	-0.0896599	0.0166671	1.70E-08
11	SIK3	rs12273536	117040255	T	C	0.0966585	-0.1417540	0.0102672	5.10E-46
11	SIK3	rs12273545	117040296	T	C	0.0966585	-0.1417540	0.0102672	5.10E-46
11	SIK3	rs59266239	117040361	T	C	0.1293110	0.0506513	0.0090530	5.60E-09
11	SIK3	rs77999164	117041401	T	C	0.0966686	-0.1418460	0.0102672	4.50E-46
11	SIK3	rs58194633	117041909	C	CT	0.2633980	-0.0496800	0.0068927	1.40E-13
11	SIK3	rs11216244	117042014	T	C	0.2639480	-0.0489098	0.0068835	3.00E-13
11	SIK3	rs11216245	117042486	T	C	0.2639480	-0.0489098	0.0068835	3.00E-13
11	SIK3	rs80143284	117042854	A	C	0.0967989	-0.1419780	0.0102590	2.60E-46
11	SIK3	rs12279066	117043193	G	C	0.2638010	-0.0488376	0.0068860	3.30E-13
11	SIK3	rs17120241	117044304	C	T	0.0502153	0.1524870	0.0138980	5.50E-29
11	SIK3	rs11351498	117044488	T	TA	0.2636330	-0.0490038	0.0068904	2.90E-13
11	SIK3	rs2155583	117044501	G	A	0.4711960	-0.0803879	0.0060996	2.90E-40
11	SIK3	chr11:117044615_GA_G	117044615	G	GA	0.2199780	-0.0595648	0.0074836	5.20E-15
11	SIK3	rs2000614	117045026	T	C	0.4711070	-0.0803173	0.0060988	3.40E-40
11	SIK3	rs2000615	117045103	T	C	0.4711070	-0.0803173	0.0060988	3.40E-40
11	SIK3	rs2000616	117045813	T	C	0.4711040	-0.0803093	0.0060987	3.50E-40
11	SIK3	rs76972960	117045962	C	T	0.0502153	0.1524870	0.0138980	5.50E-29
11	SIK3	rs10750100	117046528	C	T	0.4711010	-0.0802939	0.0060987	3.60E-40
11	SIK3	rs61905716	117048351	T	C	0.0502157	0.1524970	0.0138980	5.50E-29
11	SIK3	rs12280172	117048557	A	G	0.0973882	-0.1382810	0.0102350	5.20E-44
11	SIK3	rs112151056	117048652	A	G	0.0502157	0.1524970	0.0138980	5.50E-29
11	SIK3	rs61905718	117048961	T	C	0.0502157	0.1524970	0.0138980	5.50E-29
11	SIK3	rs75890305	117049253	G	A	0.0966911	-0.1417390	0.0102656	5.20E-46
11	SIK3	rs142341972	117049453	T	C	0.1404000	-0.0667994	0.0088048	3.20E-15
11	SIK3	chr11:117049961_T_TA	117049961	TA	T	0.4735570	-0.0814657	0.0061295	9.60E-41
11	SIK3	rs11826651	117049977	A	T	0.0502218	0.1523850	0.0138961	6.00E-29
11	SIK3	rs10892066	117050211	T	C	0.2639490	-0.0488276	0.0068834	3.20E-13
11	SIK3	rs4938328	117050503	T	G	0.2067950	-0.0637354	0.0075074	4.60E-17
11	SIK3	rs1815786	117050674	T	C	0.3128000	0.1008860	0.0065579	3.20E-54
11	SIK3	rs1815787	117050681	C	T	0.4714220	-0.0804755	0.0060976	2.30E-40
11	SIK3	rs138470332	117051591	T	C	0.0187335	-0.1375340	0.0224303	2.90E-10
11	SIK3	rs111530588	117051870	A	G	0.0966904	-0.1417370	0.0102656	5.20E-46
11	SIK3	rs61905719	117051998	T	C	0.0502218	0.1523850	0.0138961	6.00E-29
11	SIK3	rs564325746	117052134	TG	T	0.0925093	0.0822484	0.0107431	6.40E-15
11	SIK3	rs78442878	117052138	G	A	0.1295850	0.0514961	0.0090510	3.10E-09
11	SIK3	rs17120251	117052772	C	T	0.1293930	0.0505742	0.0090509	5.60E-09
11	SIK3	rs7130297	117053154	T	C	0.4697880	-0.0839645	0.0061014	8.60E-44
11	SIK3	rs11216250	117053284	T	C	0.0959382	-0.1412370	0.0103069	2.20E-45
11	SIK3	rs80259223	117053602	A	G	0.0510992	0.1475490	0.0137949	9.40E-28
11	SIK3	rs11826742	117053650	G	C	0.1302040	0.0493064	0.0090339	1.10E-08
11	SIK3	rs723953	117054262	C	A	0.1294700	0.0500196	0.0090496	8.00E-09
11	SIK3	rs3886960	117054274	T	G	0.2639050	-0.0487467	0.0068839	3.60E-13
11	SIK3	rs723955	117054326	A	G	0.2639050	-0.0487467	0.0068839	3.60E-13
11	SIK3	rs7108912	117055280	A	G	0.2639070	-0.0487516	0.0068839	3.60E-13
11	SIK3	rs201829635	117056603	T	TC	0.0495429	0.1508560	0.0139903	4.50E-28
11	SIK3	rs117091722	117056884	A	G	0.0627833	-0.1690190	0.0125660	5.20E-42
11	SIK3	rs10790172	117057024	T	G	0.4732450	-0.0818080	0.0061273	5.60E-41
11	SIK3	rs10892067	117057046	C	G	0.0967888	-0.1420470	0.0102598	2.50E-46
11	SIK3	rs7124872	117057235	G	A	0.2640190	-0.0487559	0.0068832	3.60E-13
11	SIK3	rs7124996	117057290	T	C	0.2640190	-0.0487559	0.0068832	3.60E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs4938329	117057396	T	C	0.2640080	-0.0488403	0.0068830	3.30E-13
11	SIK3	rs11216252	117057507	A	G	0.0966838	-0.1417770	0.0102663	5.10E-46
11	SIK3	rs11216253	117057509	C	A	0.0966838	-0.1417770	0.0102663	5.10E-46
11	SIK3	rs10892068	117057830	T	C	0.0967874	-0.1420280	0.0102598	2.50E-46
11	SIK3	rs9943680	117058538	C	T	0.1873570	-0.0580384	0.0079574	8.30E-13
11	SIK3	rs11216255	117059279	G	A	0.2640850	-0.0487449	0.0068844	3.70E-13
11	SIK3	rs34992009	117059421	G	GC	0.2062390	-0.0643579	0.0075241	2.80E-17
11	SIK3	rs4938331	117059966	A	C	0.2061430	-0.0640344	0.0075244	3.90E-17
11	SIK3	rs4938332	117060082	G	A	0.2062380	-0.0643129	0.0075242	3.00E-17
11	SIK3	rs4938333	117060172	G	A	0.0502374	0.1525790	0.0138934	5.10E-29
11	SIK3	rs4938334	117060326	C	G	0.2064100	-0.0639935	0.0075247	4.50E-17
11	SIK3	rs61903394	117061182	A	G	0.0502345	0.1526020	0.0138938	5.00E-29
11	SIK3	rs61903395	117061191	G	A	0.1294700	0.0507379	0.0090498	5.00E-09
11	SIK3	rs6589590	117065365	C	A	0.2071400	-0.0636361	0.0075088	4.90E-17
11	SIK3	rs56751865	117066155	T	C	0.1156370	-0.1320330	0.0095531	5.20E-46
11	SIK3	rs112895963	117066443	T	A	0.0496376	0.1535060	0.0139810	4.50E-29
11	SIK3	rs79955870	117066645	T	C	0.0975100	-0.1434630	0.0102510	3.30E-47
11	SIK3	rs35187263	117067811	AC	A	0.2054070	-0.0693493	0.0075291	5.30E-20
11	SIK3	rs368388328	117069182	T	TTTG	0.0408263	0.1397440	0.0154278	9.10E-21
11	SIK3	rs11216261	117069494	C	T	0.0965779	-0.1417510	0.0102732	6.00E-46
11	SIK3	rs12280210	117069733	C	T	0.1342020	-0.1301700	0.0089041	1.70E-51
11	SIK3	rs9971421	117070824	T	C	0.0952943	-0.1410690	0.0103500	4.30E-45
11	SIK3	rs61903398	117070897	T	C	0.0500800	0.1529520	0.0139168	4.30E-29
11	SIK3	rs144942164	117071184	C	T	0.0392811	0.1609600	0.0157351	9.50E-26
11	SIK3	rs202154722	117071196	AT	A	0.0965537	-0.1412380	0.0102808	1.40E-45
11	SIK3	rs7101763	117071269	T	G	0.1843260	-0.0522636	0.0078264	2.70E-12
11	SIK3	rs17120280	117071416	A	G	0.0514196	0.1470560	0.0137611	2.70E-27
11	SIK3	rs77182215	117071650	A	C	0.0852930	0.1014160	0.0109411	1.30E-20
11	SIK3	rs61903399	117071759	T	A	0.0496310	0.1538800	0.0139833	3.30E-29
11	SIK3	chr11:117071926_G_GTGTT	117071926	GTGTT	G	0.2007480	-0.0709700	0.0076315	3.70E-20
11	SIK3	rs116582417	117072350	A	G	0.0964346	-0.1420660	0.0102814	4.90E-46
11	SIK3	rs1351452	117072638	C	A	0.4716300	-0.0801618	0.0061050	4.40E-40
11	SIK3	rs7109649	117072828	T	C	0.2638000	-0.0483452	0.0068913	5.70E-13
11	SIK3	rs1531706	117073236	A	C	0.2638000	-0.0483452	0.0068913	5.70E-13
11	SIK3	rs77400241	117073331	T	C	0.0171914	-0.1838850	0.0234890	9.10E-16
11	SIK3	rs7935913	117073632	A	G	0.2638000	-0.0483452	0.0068913	5.70E-13
11	SIK3	rs7935834	117073721	G	C	0.2638000	-0.0483452	0.0068913	5.70E-13
11	SIK3	rs1531707	117073996	A	G	0.2637960	-0.0483351	0.0068913	5.80E-13
11	SIK3	rs17120293	117074130	C	T	0.0964528	-0.1417560	0.0102801	7.10E-46
11	SIK3	rs4620758	117075002	A	G	0.1841510	-0.0518833	0.0078305	4.10E-12
11	SIK3	rs12274388	117075522	T	C	0.2615630	-0.0466699	0.0069261	4.30E-12
11	SIK3	rs7130213	117075936	A	C	0.1837390	-0.0522267	0.0078388	3.00E-12
11	SIK3	rs12274725	117076137	T	C	0.0964281	-0.1421080	0.0102821	4.60E-46
11	SIK3	rs7484045	117076174	T	C	0.2638140	-0.0484079	0.0068911	5.40E-13
11	SIK3	rs11216265	117076464	C	T	0.0964281	-0.1421080	0.0102821	4.60E-46
11	SIK3	rs12418036	117076590	A	G	0.0964281	-0.1421080	0.0102821	4.60E-46
11	SIK3	rs4938335	117076645	C	A	0.4712570	-0.0800654	0.0061065	6.00E-40
11	SIK3	rs4938336	117077726	G	A	0.0500695	0.1524640	0.0139190	6.60E-29
11	SIK3	rs10082609	117078358	T	C	0.2560630	-0.0447173	0.0069799	4.80E-11
11	SIK3	rs11216266	117079434	C	T	0.2637930	-0.0483145	0.0068913	5.90E-13
11	SIK3	rs10736487	117079516	G	A	0.4726220	-0.0787890	0.0061040	8.70E-39
11	SIK3	rs56777911	117080329	C	CT	0.2637950	-0.0483266	0.0068913	5.80E-13
11	SIK3	rs7106662	117080669	C	T	0.2637950	-0.0483266	0.0068913	5.80E-13
11	SIK3	rs10892070	117080817	A	G	0.2203320	-0.0656968	0.0073840	1.20E-18
11	SIK3	rs10082561	117080868	C	A	0.0913837	-0.1370880	0.0105300	6.80E-41
11	SIK3	rs4936362	117081484	T	C	0.0500678	0.1517150	0.0139213	1.20E-28
11	SIK3	rs11216267	117081676	T	C	0.2079360	-0.0612244	0.0074961	5.90E-16
11	SIK3	rs144977225	117082379	C	CCCA	0.2637950	-0.0483262	0.0068914	5.80E-13
11	SIK3	rs11216270	117082928	A	C	0.0964207	-0.1421920	0.0102825	4.30E-46
11	SIK3	rs1871756	117082929	A	G	0.1842760	-0.0521592	0.0078274	2.90E-12
11	SIK3	rs10892071	117083849	T	C	0.2637970	-0.0482473	0.0068914	6.30E-13
11	SIK3	rs61903416	117084333	C	T	0.2670720	-0.0493303	0.0068720	1.50E-13
11	SIK3	rs2368149	117085218	A	G	0.0963283	-0.1423550	0.0102884	3.90E-46
11	SIK3	rs61903417	117085441	G	T	0.0500619	0.1521110	0.0139208	9.10E-29
11	SIK3	rs61903418	117085949	A	G	0.0500583	0.1521450	0.0139212	9.00E-29
11	SIK3	rs12281358	117086274	C	T	0.0963218	-0.1423360	0.0102887	4.00E-46
11	SIK3	rs12274465	117086473	T	C	0.2634950	-0.0485554	0.0068973	4.80E-13
11	SIK3	rs6589592	117087191	C	G	0.3086200	0.1023070	0.0066122	5.20E-55
11	SIK3	rs12277910	117087817	A	C	0.1646770	-0.0515739	0.0082498	2.00E-10
11	SIK3	rs111901638	117089132	A	G	0.0501069	0.1523460	0.0139144	7.40E-29
11	SIK3	rs10892072	117089597	A	G	0.2076230	-0.0610307	0.0075044	7.70E-16
11	SIK3	rs11823918	117089781	C	G	0.0501098	0.1522690	0.0139140	8.10E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs77431162	117090820	T	C	0.0685849	0.0889799	0.0120035	3.20E-14
11	SIK3	rs61903421	117091086	T	A	0.0501094	0.1522640	0.0139139	8.10E-29
11	SIK3	rs116861530	117091945	A	G	0.0949985	-0.1442400	0.0103587	9.20E-47
11	SIK3	rs74420345	117092561	A	C	0.0949983	-0.1444890	0.0103589	6.40E-47
11	SIK3	rs7950093	117092803	T	G	0.2625490	-0.0488188	0.0069066	3.90E-13
11	SIK3	rs7950381	117093181	A	C	0.0500898	0.1526400	0.0139174	5.70E-29
11	SIK3	rs7950501	117093249	T	C	0.0500898	0.1526400	0.0139174	5.70E-29
11	SIK3	rs57383565	117093678	AG	A	0.0504835	0.1518140	0.0138884	9.20E-29
11	SIK3	rs900012	117095719	A	G	0.4683810	-0.0781351	0.0061187	3.20E-38
11	SIK3	rs1320668	117096950	T	C	0.4733710	-0.0749026	0.0061147	1.20E-35
11	SIK3	rs61903426	117097552	T	C	0.0543753	0.1554670	0.0134058	1.10E-31
11	SIK3	rs7128071	117098082	A	G	0.0528946	0.1513680	0.0135959	3.40E-29
11	SIK3 *	rs10892073	117098674	T	C	0.2031830	-0.0577294	0.0075790	1.90E-14
11	SIK3 *	rs76567973	117100045	G	C	0.0962288	-0.1440530	0.0102911	5.20E-47
11	SIK3 *	chr11:117100110_GT_G	117100110	G	GT	0.4761660	-0.0731424	0.0061211	4.60E-34
11	SIK3 *	rs78135964	117100961	T	G	0.0962571	-0.1439270	0.0102879	5.40E-47
11	SIK3 *	rs148233183	117101511	A	G	0.0962936	-0.1435890	0.0102854	8.20E-47
11	SIK3 *	rs4938338	117102178	A	C	0.0545433	0.1551240	0.0133758	1.20E-31
11	SIK3 *	rs4936363	117102219	T	C	0.0545441	0.1551170	0.0133759	1.20E-31
11	SIK3 *	rs76942203	117102531	A	G	0.0963224	-0.1437480	0.0102832	6.50E-47
11	SIK3 *	chr11:117103138_A_AAAT	117103138	AAAT	A	0.0961972	-0.1428280	0.0102975	3.80E-46
11	SIK3 *	rs12269901	117103213	C	G	0.2689200	-0.0444591	0.0068430	1.90E-11
11	SIK3 *	rs149576335	117104420	A	G	0.0962987	-0.1437780	0.0102847	6.00E-47
11	SIK3 *	rs11216275	117104988	G	T	0.0919449	0.0636623	0.0105055	1.50E-09
11	SIK3 *	rs142395187	117105293	G	A	0.0956929	-0.1439930	0.0103163	6.30E-47
11	SIK3 *	chr11:117105573_A_AT	117105573	AT	A	0.2025030	-0.0768432	0.0076861	8.90E-24
11	SIK3 *	rs4388921	117106062	C	T	0.1884810	-0.0474538	0.0077703	1.30E-10
11	SIK3 *	rs145671645	117106195	A	G	0.0290428	-0.1669790	0.0181254	8.40E-22
11	SIK3 *	rs10160799	117107172	A	G	0.4735170	-0.0733698	0.0061207	4.40E-34
11	SIK3 *	rs181104223	117107559	C	A	0.0292845	0.2085020	0.0180185	3.60E-32
11	SIK3 *	rs12416941	117108647	A	G	0.0968927	-0.1402110	0.0102627	5.70E-45
11	SIK3 *	rs113784559	117108649	G	C	0.0568148	0.1359360	0.0131151	8.70E-26
11	SIK3 *	rs10750101	117108973	C	T	0.4736550	-0.0734754	0.0061161	3.30E-34
11	SIK3 *	rs138783935	117109002	A	G	0.0183301	0.1463250	0.0227367	2.20E-10
11	SIK3 *	rs12271169	117109305	G	C	0.1778140	-0.0436486	0.0079587	8.40E-09
11	SIK3 *	rs4938339	117109878	T	C	0.0568253	0.1358990	0.0131141	8.90E-26
11	SIK3 *	rs4938340	117109906	A	G	0.0571815	0.1340900	0.0131097	3.60E-25
11	SIK3 *	rs10892074	117109925	T	G	0.2028120	-0.0555076	0.0075847	2.60E-13
11	SIK3 *	rs114221654	117109963	T	C	0.0968927	-0.1402110	0.0102627	5.70E-45
11	SIK3 *	rs35172278	117110063	CCTG	C	0.4853810	-0.0782469	0.0061272	1.60E-38
11	SIK3 *	rs61903427	117110070	C	G	0.0568253	0.1358990	0.0131141	8.90E-26
11	SIK3 *	rs7112111	117110142	G	T	0.1908920	-0.0495118	0.0077407	2.30E-11
11	SIK3 *	rs4635117	117110285	A	G	0.2984060	0.0965971	0.0067096	1.90E-48
11	SIK3 *	rs6589595	117110619	A	G	0.0568253	0.1358990	0.0131141	8.90E-26
11	SIK3 *	rs116770907	117110799	T	C	0.0968934	-0.1402030	0.0102627	5.80E-45
11	SIK3 *	rs2127907	117110864	G	A	0.4882270	-0.0783352	0.0061178	1.20E-38
11	SIK3 *	rs111677878	117111718	T	C	0.0968740	-0.1404170	0.0102646	4.50E-45
11	SIK3 *	rs7104023	117111886	T	A	0.1908430	-0.0495272	0.0077422	2.30E-11
11	SIK3 *	rs59700451	117112212	A	G	0.0568225	0.1357950	0.0131149	9.60E-26
11	SIK3 *	rs113979111	117112300	A	G	0.0568217	0.1357860	0.0131149	9.70E-26
11	SIK3 *	rs111560312	117112840	A	G	0.0568213	0.1357850	0.0131149	9.70E-26
11	SIK3 *	rs55703909	117114150	A	G	0.0568193	0.1358390	0.0131153	9.30E-26
11	SIK3 *	rs74882651	117114475	A	G	0.0968700	-0.1404850	0.0102653	4.30E-45
11	SIK3 *	rs60834024	117115141	A	C	0.0968824	-0.1403420	0.0102643	4.90E-45
11	SIK3 *	rs61903429	117115968	A	C	0.0568300	0.1359800	0.0131150	8.20E-26
11	SIK3 *	rs11216277	117116330	A	G	0.2937810	-0.0554526	0.0066969	1.30E-16
11	SIK3 *	rs145335872	117116511	A	C	0.0551228	-0.1138660	0.0133067	1.40E-18
11	SIK3 *	rs61903430	117116626	C	G	0.0568300	0.1360000	0.0131150	8.10E-26
11	SIK3 *	rs75904569	117117597	G	A	0.0568272	0.1360610	0.0131154	7.70E-26
11	SIK3 *	rs80197460	117118074	G	C	0.0968993	-0.1402210	0.0102635	6.20E-45
11	SIK3 *	rs10892076	117118220	A	G	0.2925740	-0.0553645	0.0067086	1.60E-16
11	SIK3 *	rs74428560	117119266	T	C	0.0568340	0.1361760	0.0131147	7.10E-26
11	SIK3 *	rs117300172	117119795	C	A	0.0156226	0.2037640	0.0244765	2.70E-17
11	SIK3 *	chr11:117120044_G_GAAAC	117120044	GAAAC	G	0.4293230	-0.1090720	0.0061742	8.80E-72
11	SIK3 *	rs200802441	117120056	C	A	0.4149810	-0.1064580	0.0062799	2.20E-66
11	SIK3 *	rs12366015	117120135	G	A	0.4290210	-0.1088330	0.0061720	1.40E-71
11	SIK3 *	rs138720977	117120356	ATAAG	A	0.2889070	-0.0524863	0.0067540	8.50E-15
11	SIK3 *	rs142756367	117120357	TAAGA	T	0.2935060	-0.0556186	0.0066979	1.10E-16
11	PAFAH1B2	rs74955808	117121969	A	G	0.0971479	-0.1392190	0.0102513	2.10E-44
11	PAFAH1B2	rs71037454	117122203	AGAAA	G	0.4867910	-0.0776388	0.0061028	3.70E-38
11	PAFAH1B2	rs6589596	117122465	C	T	0.4869570	-0.0774742	0.0061018	5.60E-38
11	PAFAH1B2	rs76868258	117122576	T	C	0.0568651	0.1368690	0.0131096	3.90E-26

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PAFAH1B2	rs12420361	117123072	A	G	0.0969668	-0.1406350	0.0102573	3.10E-45
11	PAFAH1B2	rs10892078	117123213	T	A	0.2034680	-0.0559342	0.0075638	1.30E-13
11	PAFAH1B2	rs11344600	117123743	C	CA	0.4868980	-0.0774397	0.0060966	5.00E-38
11	PAFAH1B2	rs35722128	117124277	C	CA	0.0568904	0.1363450	0.0131068	5.50E-26
11	PAFAH1B2	chr11:117125062_TAA_T	117125062	T	TAA	0.4871730	-0.0770908	0.0060880	7.60E-38
11	PAFAH1B2	rs17120344	117125629	A	G	0.0972031	-0.1388960	0.0102413	2.30E-44
11	PAFAH1B2	rs17120347	117125823	A	G	0.0569731	0.1354440	0.0130959	9.70E-26
11	PAFAH1B2	rs12419454	117125915	T	C	0.0972148	-0.1390130	0.0102408	2.10E-44
11	PAFAH1B2	rs12419459	117125995	T	C	0.0982604	-0.1341910	0.0101946	1.20E-41
11	PAFAH1B2	rs12416691	117126067	T	A	0.0972527	-0.1390640	0.0102390	1.80E-44
11	PAFAH1B2	rs6589597	117127082	T	C	0.4878780	-0.0765508	0.0060812	1.80E-37
11	PAFAH1B2	rs78302396	117127400	G	A	0.0843081	0.0856088	0.0109547	1.50E-15
11	PAFAH1B2	rs12420200	117127590	A	G	0.0972673	-0.1392350	0.0102384	1.50E-44
11	PAFAH1B2	rs182980806	117127672	T	G	0.0155596	0.2116090	0.0245295	9.60E-19
11	PAFAH1B2	rs145802214	117128196	C	A	0.0972673	-0.1392350	0.0102384	1.50E-44
11	PAFAH1B2	rs141250514	117128309	C	T	0.0972673	-0.1392350	0.0102384	1.50E-44
11	PAFAH1B2	rs4516002	117128343	G	A	0.4878630	-0.0765645	0.0060814	1.80E-37
11	PAFAH1B2	rs7131536	117128730	T	C	0.4880570	-0.0761942	0.0060826	4.40E-37
11	PAFAH1B2	rs7131686	117128843	T	C	0.4878710	-0.0765111	0.0060812	1.90E-37
11	PAFAH1B2	rs138039720	117128884	T	C	0.0972867	-0.1391830	0.0102392	1.50E-44
11	PAFAH1B2	chr11:117129006_TA_T	117129006	T	TA	0.4444860	-0.0689092	0.0061702	1.00E-29
11	PAFAH1B2	rs146067038	117129463	G	A	0.0972790	-0.1389950	0.0102402	2.10E-44
11	PAFAH1B2	rs10400366	117130239	A	G	0.2936210	-0.0548307	0.0066710	3.20E-16
11	PAFAH1B2	rs199498085	117130739	G	A	0.0905081	-0.1393770	0.0106305	6.60E-42
11	PAFAH1B2	rs12421425	117131244	T	C	0.0973104	-0.1391620	0.0102386	1.70E-44
11	PAFAH1B2	chr11:117131317_A_AT	117131317	AT	A	0.4420700	-0.0622475	0.0062084	2.10E-24
11	PAFAH1B2	rs142848583	117131334	AC	A	0.0114076	0.2666100	0.0286013	1.90E-20
11	PAFAH1B2	rs191044888	117131336	T	G	0.0114073	0.2665920	0.0286013	1.90E-20
11	PAFAH1B2	rs4938341	117131880	A	G	0.0572240	0.1351050	0.0130615	2.10E-25
11	PAFAH1B2	rs17120367	117132112	T	C	0.0973258	-0.1393360	0.0102375	1.30E-44
11	PAFAH1B2	chr11:117132474_CA_C	117132474	C	CA	0.4880780	-0.0763739	0.0060909	3.70E-37
11	PAFAH1B2	rs17120370	117132672	C	T	0.0973258	-0.1393360	0.0102375	1.30E-44
11	PAFAH1B2	rs74735277	117132702	T	C	0.0973229	-0.1393330	0.0102375	1.30E-44
11	PAFAH1B2	rs4938342	117132704	G	C	0.0573427	0.1338220	0.0130261	4.70E-25
11	PAFAH1B2	rs17120373	117132743	G	A	0.1352240	-0.1263110	0.0088753	2.10E-48
11	PAFAH1B2	rs4938343	117132812	C	G	0.4501050	-0.0665889	0.0061071	1.60E-28
11	PAFAH1B2	rs75208249	117132907	C	G	0.0975146	-0.1386400	0.0102268	2.80E-44
11	PAFAH1B2	rs114945429	117133485	T	G	0.0974170	-0.1398080	0.0102319	7.30E-45
11	PAFAH1B2	rs12417098	117134137	A	G	0.0967971	-0.1395750	0.0102629	1.80E-44
11	PAFAH1B2	rs141936239	117134911	C	T	0.1018570	-0.1394050	0.0101179	4.20E-45
11	PAFAH1B2	rs143261386	117135035	C	T	0.1018580	-0.1394230	0.0101179	4.10E-45
11	PAFAH1B2	rs2735181	117139073	T	C	0.2814450	-0.0575237	0.0068552	6.50E-17
11	PAFAH1B2	rs115991973	117139375	A	G	0.0967899	-0.1386200	0.0102627	6.30E-44
11	PAFAH1B2	rs116384608	117139407	G	A	0.0967899	-0.1386200	0.0102627	6.30E-44
11	PAFAH1B2	rs2471884	117139604	C	T	0.4875170	-0.0766812	0.0060898	2.10E-37
11	PAFAH1B2	rs77661993	117139758	C	A	0.0967950	-0.1386600	0.0102625	6.10E-44
11	PAFAH1B2	rs7934690	117140583	A	T	0.0570326	0.1357990	0.0130924	1.50E-25
11	PAFAH1B2	rs1555026168	117143445	AAG	A	0.4846530	-0.0676770	0.0061170	2.30E-29
11	PAFAH1B2	rs2622934	117144146	T	G	0.2946820	-0.0559120	0.0066710	7.30E-17
11	PAFAH1B2	rs76904522	117144147	A	G	0.0575817	0.1343730	0.0130335	2.00E-25
11	PAFAH1B2	rs113560866	117144473	C	G	0.0579184	0.1307890	0.0130098	3.10E-24
11	PAFAH1B2	rs2735183	117144479	T	C	0.2960390	-0.0539967	0.0066819	1.40E-15
11	PAFAH1B2	rs12419227	117144522	A	C	0.0995253	-0.1143060	0.0101380	2.20E-31
11	PAFAH1B2	rs149188200	117144559	T	G	0.0373636	0.1652320	0.0161497	1.60E-25
11	PAFAH1B2	rs118113112	117145374	A	G	0.0183761	0.1433850	0.0226820	4.30E-10
11	PAFAH1B2	rs11420191	117145447	CG	C	0.4956460	-0.0726298	0.0060859	9.20E-34
11	PAFAH1B2	rs2306471	117145734	T	C	0.1010280	-0.1148540	0.0100677	5.40E-32
11	PAFAH1B2	rs78270178	117146132	G	T	0.3159580	-0.0596722	0.0066875	4.50E-19
11	PAFAH1B2	rs12419436	117146739	G	T	0.1008230	-0.1139680	0.0100761	1.90E-31
11	PAFAH1B2	rs12420725	117146814	G	A	0.1012160	-0.1125580	0.0100577	7.90E-31
11	PAFAH1B2	rs117592676	117146994	T	C	0.0193645	0.3813050	0.0221405	3.80E-68
11	PAFAH1B2	rs12417984	117146998	A	G	0.1010600	-0.1143140	0.0100657	1.00E-31
11	PAFAH1B2	rs139864910	117147046	C	A	0.1010600	-0.1143140	0.0100657	1.00E-31
11	PAFAH1B2	rs139146464	117149151	G	A	0.1001290	-0.1125860	0.0101173	1.50E-30
11	PAFAH1B2	rs71037463	117149256	A	AT	0.4944990	-0.0728770	0.0060840	8.90E-34
11	PAFAH1B2	rs1461576929	117149430	T	G	0.0211732	0.1897370	0.0213587	9.00E-20
11	PAFAH1B2	rs7115562	117149754	G	A	0.4585200	-0.0630911	0.0060969	1.10E-25
11	PAFAH1B2	rs7116454	117150418	T	A	0.4585170	-0.0631069	0.0060968	1.10E-25
11	PAFAH1B2	rs45625638	117150710	C	G	0.0578109	0.1333220	0.0130068	3.00E-25
11	PAFAH1B2	chr11:117150989_GAA_G	117150989	G	GAA	0.1010900	-0.1117350	0.0101024	4.30E-30
11	PAFAH1B2	rs4938347	117151043	A	T	0.4570900	-0.0633116	0.0061268	1.60E-25
11	PAFAH1B2	rs4938348	117151161	C	G	0.4556110	-0.0610287	0.0061149	5.80E-24

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PAFAH1B2	rs4938350	117151560	G	A	0.4555410	-0.0609910	0.0061159	6.00E-24
11	PAFAH1B2	rs79831695	117151612	G	A	0.0300533	-0.1797010	0.0178714	1.50E-24
11	PAFAH1B2	rs4938351	117151636	C	A	0.2964570	-0.0567803	0.0066642	2.80E-17
11	PAFAH1B2	rs146629336	117152290	C	G	0.0201721	-0.1484220	0.0216346	2.30E-12
11	PAFAH1B2	rs7128382	117152771	C	A	0.4555730	-0.0604327	0.0061099	1.30E-23
11	PAFAH1B2	rs143494314	117152990	T	C	0.1010630	-0.1143500	0.0100656	9.80E-32
11	PAFAH1B2	rs7950633	117153586	T	C	0.4944410	-0.0703435	0.0060908	1.30E-31
11	PAFAH1B2	rs7940310	117153765	C	T	0.4934070	-0.0711671	0.0060856	2.30E-32
11	PAFAH1B2	chr11:117154119_G_GA	117154119	GA	G	0.4539550	-0.0624826	0.0061228	4.90E-25
11	PAFAH1B2	rs78123099	117154123	G	A	0.0177815	0.1520300	0.0230784	4.20E-12
11	PAFAH1B2	rs35500922	117154603	AT	A	0.0976028	-0.1136460	0.0102523	3.20E-30
11	PAFAH1B2	rs68137714	117154641	G	A	0.0578109	0.1333220	0.0130068	3.00E-25
11	PAFAH1B2	rs12418349	117155216	G	A	0.1010630	-0.1143500	0.0100656	9.80E-32
11	PAFAH1B2	rs2127905	117155658	C	A	0.4989690	-0.0739205	0.0060769	6.10E-35
11	PAFAH1B2	rs4936366	117156169	A	G	0.4585340	-0.0630750	0.0060965	1.10E-25
11	PAFAH1B2	rs4938352	117156765	A	G	0.4585340	-0.0630750	0.0060965	1.10E-25
11	PAFAH1B2	rs199763004	117157038	A	AG	0.5002530	-0.0693111	0.0061143	1.30E-30
11	PAFAH1B2	rs7123517	117157039	A	G	0.5005420	-0.0691574	0.0061126	1.50E-30
11	PAFAH1B2	rs117588325	117157577	T	A	0.0279327	0.2077830	0.0184593	1.70E-30
11	PAFAH1B2	rs12420250	117158011	A	G	0.1007800	-0.1143160	0.0100803	1.30E-31
11	PAFAH1B2	rs78166985	117159069	T	A	0.1008870	-0.1143300	0.0100754	1.20E-31
11	PAFAH1B2	rs1871757	117159865	A	T	0.4583660	-0.0629099	0.0060982	1.50E-25
11	PAFAH1B2	rs200545029	117159917	C	T	0.1009710	-0.1141080	0.0100686	1.40E-31
11	PAFAH1B2	rs142017584	117160647	A	G	0.1010660	-0.1143700	0.0100654	9.40E-32
11	PAFAH1B2	rs3736120	117161409	T	G	0.3304760	-0.0455248	0.0064663	2.50E-12
11	PAFAH1B2	rs12281009	117162243	G	A	0.1010660	-0.1143700	0.0100654	9.40E-32
11	PAFAH1B2	chr11:117162461_TC_T	117162461	T	TC	0.0118730	-0.1609170	0.0284904	3.60E-09
11	PAFAH1B2	rs71037468	117163187 CTGAGT	C	C	0.4559970	-0.0620661	0.0061184	9.30E-25
11	PAFAH1B2	rs7122944	117163903	T	G	0.4948180	-0.0748277	0.0060799	9.10E-36
11	PAFAH1B2	rs150984554	117164300	A	G	0.1001790	-0.1160290	0.0101109	2.10E-32
11	PAFAH1B2	rs12420127	117164603	G	A	0.1010660	-0.1143700	0.0100654	9.40E-32
11	PAFAH1B2	rs10892080	117164786	G	A	0.2976790	-0.0584887	0.0066524	2.00E-18
11	PAFAH1B2	rs149378955	117164863	A	G	0.0459487	0.1570280	0.0145340	3.60E-28
11	PAFAH1B2	rs7931335	117166089	T	C	0.4585450	-0.0630418	0.0060966	1.20E-25
11	PAFAH1B2	rs6589602	117166349	C	T	0.2987790	-0.0589507	0.0066393	9.60E-19
11	PAFAH1B2	rs7112513	117166645	G	A	0.4956910	-0.0729788	0.0060754	4.30E-34
11	PAFAH1B2	rs77171490	117168025	A	T	0.1010660	-0.1143700	0.0100654	9.40E-32
11	PAFAH1B2	rs190482111	117168438	A	G	0.1010600	-0.1144380	0.0100657	8.90E-32
11	PAFAH1B2	rs10892082	117168609	G	T	0.4955380	-0.0738116	0.0060779	7.80E-35
11	PAFAH1B2	rs116773440	117168745	C	A	0.1006680	-0.1153430	0.0100937	3.40E-32
11	PAFAH1B2	rs1060211	117169081	A	G	0.4585070	-0.0630305	0.0060970	1.30E-25
11	PAFAH1B2	rs45628435	117169482	GT	G	0.2987600	-0.0591198	0.0066397	7.70E-19
11	PAFAH1B2	rs77678768	117169789	C	G	0.1010600	-0.1144380	0.0100657	8.90E-32
11	PAFAH1B2	rs10750103	117171522	T	C	0.2981120	-0.0590118	0.0066471	1.10E-18
11	PAFAH1B2	rs4936367	117171661	A	G	0.4957080	-0.0730501	0.0060757	3.60E-34
11	PAFAH1B2	rs10892083	117171864	C	G	0.2082570	-0.0609175	0.0074910	3.90E-16
11	PAFAH1B2	rs7120309	117172100	A	T	0.4585460	-0.0630528	0.0060968	1.20E-25
11	PAFAH1B2	rs7120449	117172183	C	T	0.4582840	-0.0629594	0.0060979	1.40E-25
11	PAFAH1B2	rs7120565	117172233	C	T	0.2987650	-0.0590989	0.0066398	7.90E-19
11	PAFAH1B2	rs56371319	117172251	A	C	0.0578153	0.1333130	0.0130064	3.10E-25
11	PAFAH1B2	rs4604928	117173487	A	C	0.4957080	-0.0730502	0.0060757	3.60E-34
11	PAFAH1B2	chr11:117174484_A_AT	117174484	AT	A	0.0957003	-0.1132060	0.0103568	9.60E-30
11	PAFAH1B2	chr11:117174494_CT_C	117174494	C	CT	0.2970510	-0.0591970	0.0066717	1.20E-18
11	PAFAH1B2	rs7925256	117174619	T	C	0.2856200	0.0935683	0.0067738	9.60E-45
11	PAFAH1B2	rs146228126	117175016	T	G	0.0154608	0.1811140	0.0247017	1.60E-13
11	PAFAH1B2	rs10535646	117175444	T	TTGC	0.2989240	-0.0589814	0.0066410	9.50E-19
11	PAFAH1B2	rs4938353	117175481	A	G	0.4585280	-0.0631512	0.0060969	1.00E-25
11	PAFAH1B2	rs10790176	117177136	T	G	0.4585530	-0.0630125	0.0060969	1.30E-25
11	PAFAH1B2	rs80353869	117177406	A	G	0.1008430	-0.1146660	0.0100777	8.20E-32
11	SIDT2	rs12419178	117180202	T	C	0.1007320	-0.1147120	0.0100838	8.30E-32
11	SIDT2	rs34783152	117180423	A	AG	0.1007360	-0.1146620	0.0100835	8.60E-32
11	SIDT2	rs76883864	117181009	T	C	0.1007360	-0.1146590	0.0100835	8.70E-32
11	SIDT2	rs35248926	117181353	G	GTCTCT	0.4585700	-0.0632617	0.0061058	8.90E-26
11	SIDT2	rs2046150	117182717	A	C	0.1029250	-0.1133460	0.0099898	9.70E-32
11	SIDT2	rs4938355	117182959	G	A	0.0563983	0.1346340	0.0131633	4.40E-25
11	SIDT2	rs34033077	117183654	CT	C	0.0957986	-0.1078370	0.0103662	4.70E-27
11	SIDT2	rs2046149	117183993	G	C	0.1029280	-0.1133650	0.0099896	9.40E-32
11	SIDT2	rs6589603	117185123	C	T	0.4953130	-0.0747817	0.0061003	1.50E-35
11	SIDT2	rs11606672	117185343	T	C	0.1027150	-0.1127450	0.0100020	2.10E-31
11	SIDT2	rs2306472	117187346	T	C	0.1007230	-0.1138520	0.0100840	1.90E-31
11	SIDT2	rs546506427	117188416	C	T	0.1027220	-0.1127540	0.0100010	2.00E-31
11	SIDT2	rs775148500	117188417	TCA	T	0.1009430	-0.1145660	0.0100707	8.00E-32

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIDT2	rs90192	117188631	T	C	0.4609930	-0.0600156	0.0061015	1.90E-23
11	SIDT2	rs7933134	117189078	C	G	0.1029380	-0.1134380	0.0099882	8.40E-32
11	SIDT2	rs12419470	117191059	T	C	0.1027190	-0.1127540	0.0100009	2.00E-31
11	SIDT2	rs61703672	117191109	T	C	0.1027190	-0.1127540	0.0100009	2.00E-31
11	SIDT2	rs140056851	117191110	G	T	0.0459899	0.1566660	0.0145308	4.70E-28
11	SIDT2	rs499713	117191245	C	T	0.4584810	-0.0635480	0.0061129	6.90E-26
11	SIDT2	rs1242230	117191467	C	T	0.4975870	-0.0734174	0.0060768	1.40E-34
11	SIDT2	rs1242229	117191654	C	T	0.4979060	-0.0735093	0.0060758	1.10E-34
11	SIDT2	rs3213459	117191773	C	T	0.1029370	-0.1134320	0.0099880	8.40E-32
11	SIDT2	rs2301174	117192993	G	C	0.1027270	-0.1126870	0.0100003	2.10E-31
11	SIDT2	rs11605883	117194060	G	C	0.1009390	-0.1145660	0.0100707	8.10E-32
11	SIDT2	rs73008568	117194291	G	C	0.0563331	0.1349430	0.0131723	4.30E-25
11	SIDT2	rs3781985	117194350	C	G	0.1009390	-0.1145660	0.0100707	8.10E-32
11	SIDT2	rs80183569	117194437	A	G	0.1009390	-0.1145660	0.0100707	8.10E-32
11	SIDT2	rs1784042	117194760	A	G	0.2094480	-0.0609615	0.0074776	3.70E-16
11	SIDT2	rs11606480	117194817	A	G	0.1009390	-0.1145660	0.0100707	8.10E-32
11	SIDT2	rs112712475	117195056	A	C	0.0997053	-0.1154080	0.0101428	5.10E-32
11	LOC100652'	rs2269399	117195637	C	G	0.1009390	-0.1145650	0.0100707	8.10E-32
11	LOC100652'	rs74385934	117197728	A	G	0.1009390	-0.1146110	0.0100705	7.80E-32
11	LOC100652'	rs588534	117197788	G	A	0.4582200	-0.0634297	0.0060981	5.80E-26
11	LOC100652'	rs2075547	117197818	A	C	0.0563226	0.1345440	0.0131743	6.00E-25
11	LOC100652'	rs147581841	117197929	T	C	0.0247767	0.1883880	0.0195488	6.10E-23
11	LOC100652'	rs474488	117198261	G	A	0.4582070	-0.0635109	0.0060983	5.10E-26
11	LOC100652'	rs7112573	117198307	C	T	0.1029320	-0.1135830	0.0099881	7.40E-32
11	LOC100652'	rs2269398	117199072	T	C	0.1009270	-0.1148890	0.0100741	5.70E-32
11	LOC100652'	rs373143677	117199121	A	G	0.0168693	-0.1257630	0.0237887	1.30E-08
11	LOC100652'	rs17523113	117199185	A	G	0.0442545	0.1560400	0.0148023	5.10E-27
11	LOC100652'	rs2239678	117199880	T	C	0.1009090	-0.1150290	0.0100740	5.00E-32
11	LOC100652'	rs2170317	117200024	C	A	0.1009580	-0.1151350	0.0100743	4.60E-32
11	LOC100652'	rs494356	117201254	C	T	0.4698170	-0.0622457	0.0061371	1.10E-24
11	TAGLN	rs145613978	117202393	A	G	0.0292807	0.1965150	0.0180719	2.20E-28
11	TAGLN	rs12970	117203393	A	G	0.1012230	-0.1135300	0.0100554	2.00E-31
11	TAGLN	rs641620	117203513	T	C	0.4376550	-0.0547826	0.0061811	2.90E-19
11	TAGLN	rs2269397	117203583	C	T	0.1073530	-0.1051900	0.0098055	9.70E-29
11	PCSK7	rs659955	117209663	T	A	0.4988350	-0.0710996	0.0061046	2.20E-32
11	PCSK7	rs11216315	117209924	G	C	0.1030080	-0.1108420	0.0099815	1.10E-30
11	PCSK7	rs11216316	117210784	A	C	0.4967520	-0.0707784	0.0060935	3.70E-32
11	PCSK7	rs12417682	117211393	A	G	0.1033130	-0.1109360	0.0099677	9.20E-31
11	PCSK7	rs76169968	117212250	A	G	0.1034870	-0.1113600	0.0099555	4.60E-31
11	PCSK7	rs67201490	117212288	G	T	0.0551946	0.1316260	0.0132993	1.10E-23
11	PCSK7	rs4938357	117213324	A	G	0.0551913	0.1317110	0.0132996	1.00E-23
11	PCSK7	rs12418705	117213680	T	C	0.1013070	-0.1116090	0.0100509	1.50E-30
11	PCSK7	rs139694434	117213935	TTTTTC	T	0.4955750	-0.0709306	0.0060968	4.10E-32
11	PCSK7	rs77683187	117214494	C	A	0.1033720	-0.1110280	0.0099610	7.50E-31
11	PCSK7	rs236911	117214554	A	C	0.4960630	-0.0716260	0.0060912	9.50E-33
11	PCSK7	rs56081989	117214589	A	G	0.0553237	0.1315570	0.0132880	1.10E-23
11	PCSK7	rs36028244	117215198	C	CTTA	0.1031520	-0.1108990	0.0099752	1.20E-30
11	PCSK7	rs56061158	117216402	C	G	0.0553321	0.1310650	0.0132880	1.80E-23
11	PCSK7	rs150159690	117217269	TCACCT	A	0.1031070	-0.1105030	0.0099788	1.60E-30
11	PCSK7	rs2238005	117217366	T	C	0.1033530	-0.1110040	0.0099652	8.60E-31
11	PCSK7	rs236915	117217734	A	G	0.2984860	-0.0551839	0.0066561	2.20E-16
11	PCSK7	rs236916	117218912	G	A	0.4604470	-0.0602073	0.0061094	1.70E-23
11	PCSK7	rs2239009	117219006	C	G	0.1030720	-0.1102560	0.0099837	2.00E-30
11	PCSK7	rs74830	117219842	C	T	0.3032730	-0.0550908	0.0066350	1.60E-16
11	PCSK7	rs35590772	117220535	TG	T	0.4630270	-0.0608097	0.0061099	6.20E-24
11	PCSK7	rs236918	117220893	G	C	0.4984020	-0.0699154	0.0060786	1.60E-31
11	PCSK7	rs7941150	117221105	A	G	0.0553829	0.1305740	0.0132795	2.50E-23
11	PCSK7	rs78628783	117221335	T	C	0.1031280	-0.1103450	0.0099829	1.90E-30
11	PCSK7	rs80351364	117221678	T	A	0.1035180	-0.1107480	0.0099628	1.10E-30
11	PCSK7	rs6589606	117222170	T	C	0.1031310	-0.1103720	0.0099829	1.80E-30
11	PCSK7	rs17120523	117223875	G	A	0.0735741	-0.0920119	0.0117257	6.10E-16
11	PCSK7	rs146871029	117225450	T	C	0.0115799	0.2632950	0.0283844	7.10E-20
11	PCSK7	rs75519898	117226533	A	G	0.0255140	0.1801680	0.0193380	4.30E-21
11	PCSK7	chr11:117226836_T_TGGGAGCTG	117226836	GGAGC	T	0.4946770	0.0547049	0.0061089	6.30E-20
11	PCSK7	rs2306473	117227236	T	C	0.0598315	0.1079610	0.0128025	1.30E-17
11	PCSK7	rs111809212	117228821	C	T	0.0549243	0.1034060	0.0134249	4.90E-15
11	PCSK7	rs4938361	117229225	C	G	0.0583683	0.1067670	0.0130049	1.20E-16
11	PCSK7	rs4938362	117229313	A	G	0.0590119	0.1076560	0.0129338	3.50E-17
11	PCSK7	rs11542139	117229541	T	C	0.0435509	0.1128520	0.0150456	2.00E-14
11	RNF214	rs200694867	117244658	C	CTTTA	0.0249409	0.1956950	0.0196075	1.30E-23
11	RNF214	rs144580263	117253710	T	C	0.0488904	-0.1072990	0.0141118	3.50E-14
11	RNF214	rs145918995	117256488	T	C	0.0153341	0.2481360	0.0249412	1.90E-23

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	RNF214	rs188834389	117268913	A	G	0.0129155	0.1635310	0.0270221	2.70E-09
11	RNF214	rs142500562	117285352	T	C	0.0123265	0.1678840	0.0276756	2.40E-09
11	BACE1, BAI1	rs28989505	117291956	G	C	0.0293599	0.1030930	0.0180606	1.40E-08
11	BACE1	rs3741288	117315499	T	C	0.0307459	-0.1342030	0.0177329	2.80E-15
11	BACE1 *	rs1038851424	117317566	C	T	0.0147497	0.2466760	0.0254628	3.40E-22
11	CEP164	rs73014327	117325867	C	T	0.0326670	-0.1333550	0.0172196	7.90E-16
11	CEP164	rs559260586	117329862	A	T	0.0115459	0.1532170	0.0283570	3.50E-08
11	CEP164	rs1261791	117329922	A	T	0.0182876	0.1355640	0.0226170	3.00E-10
11	CEP164	rs11216357	117330037	G	T	0.0341868	-0.1314420	0.0167511	2.40E-16
11	CEP164	rs515756	117330449	G	T	0.1574780	0.0637758	0.0084785	2.20E-14
11	CEP164	chr11:117330649_CA_C	117330649	C	CA	0.1363790	0.0781894	0.0088847	6.50E-19
11	CEP164	rs609663	117331033	G	C	0.1520600	0.0558401	0.0084865	3.20E-11
11	CEP164	rs144584200	117332064	G	A	0.0317850	0.2021480	0.0175096	2.50E-30
11	CEP164	rs371259597	117332128	T	C	0.0152690	0.2641440	0.0250169	1.80E-26
11	CEP164	rs527347	117332917	G	A	0.1518770	0.0797164	0.0084808	9.10E-22
11	CEP164	rs576190	117335050	C	T	0.1518100	0.0795573	0.0084826	1.10E-21
11	CEP164	rs487298	117335128	T	G	0.1518100	0.0795573	0.0084826	1.10E-21
11	CEP164	rs138604381	117336091	T	G	0.0156348	0.1424890	0.0244283	9.70E-10
11	CEP164	rs524914	117336406	C	G	0.0156348	0.1424890	0.0244283	9.70E-10
11	CEP164	rs520315	117336910	C	T	0.1555220	0.0785391	0.0084459	2.10E-21
11	CEP164	rs620848	117336912	G	C	0.1555220	0.0785391	0.0084459	2.10E-21
11	CEP164	rs875209	117337554	A	G	0.1526640	0.0779978	0.0084604	6.80E-21
11	CEP164	rs645305	117338031	C	T	0.1531640	0.0796330	0.0084442	7.40E-22
11	CEP164	rs948181	117338233	T	C	0.1531640	0.0796330	0.0084442	7.40E-22
11	CEP164	rs140826677	117338449	T	C	0.0156591	0.1407920	0.0244095	1.40E-09
11	CEP164	rs573801	117338552	T	C	0.1531640	0.0795651	0.0084441	8.00E-22
11	CEP164	rs12221726	117339622	A	G	0.0321308	-0.1347870	0.0172393	7.10E-16
11	CEP164	rs578781	117339991	A	G	0.1521780	0.0796428	0.0084715	1.20E-21
11	CEP164	rs536021	117340185	C	T	0.1531960	0.0793701	0.0084429	1.00E-21
11	CEP164	rs610749	117340524	T	G	0.1535250	0.0805680	0.0084252	2.40E-22
11	CEP164	rs474891	117341621	T	G	0.1729390	0.0687689	0.0081312	9.10E-18
11	CEP164	rs561473	117341924	C	T	0.1504540	0.0824469	0.0085320	9.70E-23
11	CEP164	rs475385	117342176	T	C	0.1528840	0.0792770	0.0084545	1.50E-21
11	CEP164	rs495473	117342192	G	A	0.1369240	0.0688699	0.0084409	4.00E-15
11	CEP164	rs493516	117342444	A	G	0.1528540	0.0793731	0.0084556	1.30E-21
11	CEP164	rs11216360	117342473	A	G	0.0356164	-0.1315230	0.0164326	6.80E-17
11	CEP164	rs10892095	117343177	G	A	0.0343452	-0.1333080	0.0166829	8.70E-17
11	CEP164	rs573827	117343375	A	G	0.1530100	0.0795813	0.0084506	1.00E-21
11	CEP164	rs580119	117345497	G	T	0.1529330	0.0802139	0.0084587	5.30E-22
11	CEP164	rs143939925	117345621	A	G	0.0144933	-0.1447550	0.0254754	3.30E-09
11	CEP164	rs652346	117345883	T	C	0.1369710	0.0698841	0.0088451	1.70E-15
11	CEP164	rs494722	117345887	T	A	0.1369710	0.0698841	0.0088451	1.70E-15
11	CEP164	rs138869088	117346455	T	C	0.0108861	0.3554280	0.0294961	7.30E-33
11	CEP164	rs1242696	117346675	G	T	0.4224690	0.0360595	0.0062193	1.50E-08
11	CEP164	rs1261744	117347744	C	T	0.1508270	0.0796866	0.0085090	1.90E-21
11	CEP164	rs592828	117348589	C	G	0.1516430	0.0799441	0.0084871	9.50E-22
11	CEP164	rs508871	117349054	A	G	0.1505580	0.0784334	0.0085200	7.20E-21
11	CEP164	rs376718804	117349884	T	C	0.0156481	0.1399750	0.0244175	1.80E-09
11	CEP164	rs77261413	117350667	C	G	0.0156482	0.1399740	0.0244175	1.80E-09
11	CEP164	rs688207	117351423	T	C	0.1513720	0.0808194	0.0084969	3.10E-22
11	CEP164	rs490262	117351876	A	G	0.1378100	0.0938595	0.0089374	7.20E-27
11	CEP164	rs111820395	117352113	A	G	0.0158000	0.1354600	0.0243115	5.20E-09
11	CEP164	rs514806	117352226	T	G	0.1513790	0.0807067	0.0084966	3.60E-22
11	CEP164	rs118181839	117353290	T	C	0.0156482	0.1399740	0.0244175	1.80E-09
11	CEP164	rs657666	117353644	A	G	0.1513810	0.0807464	0.0084966	3.50E-22
11	CEP164	rs67060142	117353997	T	CTTCT	0.1452670	0.0776855	0.0086828	1.70E-19
11	CEP164	rs553303	117354102	T	C	0.1494660	0.0804271	0.0085582	1.00E-21
11	CEP164	rs655389	117354162	A	G	0.1513820	0.0807383	0.0084966	3.50E-22
11	CEP164	rs553506	117354171	T	C	0.1500280	0.0801142	0.0085379	1.20E-21
11	CEP164	rs654479	117354418	A	G	0.1513820	0.0807383	0.0084966	3.50E-22
11	CEP164	rs542176	117354725	T	G	0.1511600	0.0809711	0.0085038	2.70E-22
11	CEP164	rs542869	117354739	A	T	0.1340920	0.0719635	0.0089369	3.50E-16
11	CEP164	rs542900	117354751	A	T	0.1500820	0.0824875	0.0085367	6.10E-23
11	CEP164	rs535366	117355900	C	T	0.1513840	0.0805879	0.0084968	4.10E-22
11	CEP164	rs11216364	117355903	T	C	0.0862388	0.1395160	0.0110060	2.30E-37
11	CEP164	chr11:117355999_G_GAGCAGCAGC	117355999	GCAGC	G	0.1492330	0.0772011	0.0085643	3.20E-20
11	CEP164	rs537323	117356133	T	C	0.1513840	0.0805879	0.0084968	4.10E-22
11	CEP164	rs564674	117356803	C	T	0.4037320	0.0377263	0.0062740	4.10E-09
11	CEP164	rs528720	117356970	A	G	0.1511130	0.0814438	0.0085057	1.80E-22
11	CEP164	rs595367	117356978	C	T	0.1351310	0.0703750	0.0089012	1.40E-15
11	CEP164	rs534296	117357579	G	A	0.1513830	0.0806909	0.0084978	3.80E-22
11	CEP164	rs12221818	117357803	G	A	0.0347290	-0.1346170	0.0165899	2.80E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	CEP164	rs558854	117357948	A	G	0.1513530	0.0805509	0.0084979	4.50E-22
11	CEP164	rs486366	117357993	G	A	0.1513550	0.0805377	0.0084979	4.50E-22
11	CEP164	rs17591711	117358133	G	A	0.0746673	-0.0623377	0.0115719	3.10E-08
11	CEP164	rs4018864	117358402	AAT	A	0.1513420	0.0806122	0.0084985	4.10E-22
11	CEP164	rs2508664	117359175	T	C	0.1354170	0.0698460	0.0088921	2.00E-15
11	CEP164	rs2510450	117359186	T	C	0.1513750	0.0805818	0.0084992	4.40E-22
11	CEP164	rs512730	117360341	A	T	0.1529920	0.0785958	0.0084837	3.10E-21
11	CEP164	rs11216366	117360895	T	G	0.1357580	0.0689144	0.0088956	4.40E-15
11	CEP164	rs12421205	117361440	G	C	0.1517120	0.0801055	0.0085035	7.20E-22
11	CEP164	rs12421494	117361517	A	G	0.1517120	0.0801055	0.0085035	7.20E-22
11	CEP164	rs12418678	117361544	G	A	0.1357420	0.0689199	0.0088955	4.40E-15
11	CEP164	rs17500548	117361675	G	A	0.1357420	0.0689199	0.0088955	4.40E-15
11	CEP164	rs2305825	117361776	T	C	0.1514160	0.0801491	0.0085137	7.20E-22
11	CEP164	rs7934067	117362238	G	A	0.1517120	0.0801055	0.0085035	7.20E-22
11	CEP164	rs11828506	117362711	T	C	0.1513770	0.0805742	0.0084992	4.50E-22
11	CEP164	rs141670078	117363962	A	C	0.0156519	0.1400810	0.0244148	1.70E-09
11	CEP164	rs180742426	117364649	A	G	0.0156519	0.1400810	0.0244148	1.70E-09
11	CEP164	rs7945704	117364652	A	G	0.1088930	-0.0909732	0.0097707	5.60E-22
11	CEP164	rs7124084	117364696	T	C	0.1513680	0.0805468	0.0084996	4.50E-22
11	CEP164	rs10892097	117365344	T	C	0.1354160	0.0698371	0.0088921	2.00E-15
11	CEP164	chr11:117365567_A_ATTTC	117365567	ATTTC	A	0.1326790	0.0753909	0.0089908	2.90E-17
11	CEP164	rs10790179	117365603	T	G	0.1354170	0.0698286	0.0088921	2.00E-15
11	CEP164	rs11606575	117366491	G	C	0.0352786	-0.1367190	0.0164655	6.00E-18
11	CEP164	rs147121071	117366620	A	G	0.0156521	0.1403290	0.0244148	1.60E-09
11	CEP164	rs7109923	117366771	G	A	0.1507240	0.0796642	0.0085243	1.30E-21
11	CEP164	rs10892098	117367775	T	C	0.1506610	0.0793614	0.0085267	1.90E-21
11	CEP164	rs7115177	117368457	C	A	0.1513140	0.0763038	0.0085134	6.00E-20
11	CEP164	rs7115526	117368474	T	G	0.1513140	0.0763038	0.0085134	6.00E-20
11	CEP164	rs9651682	117369641	A	G	0.1517700	0.0772618	0.0085020	1.50E-20
11	CEP164	rs12417440	117370713	T	C	0.1339350	0.0685860	0.0089498	7.90E-15
11	CEP164	rs2305826	117371044	A	T	0.4054930	0.0358207	0.0062485	2.00E-08
11	CEP164	rs10790180	117375434	C	T	0.3458010	0.0526523	0.0064235	2.70E-16
11	CEP164	rs7952470	117377552	A	G	0.1345360	0.0686820	0.0089272	5.50E-15
11	CEP164	rs2305828	117380427	G	A	0.3416340	0.0535598	0.0064496	1.20E-16
11	CEP164	rs59763167	117381775	G	C	0.0158393	0.1334730	0.0242768	6.50E-09
11	CEP164	rs76663730	117389464	T	G	0.0157399	0.1371830	0.0243507	3.70E-09
11	CEP164	rs897837	117390772	G	C	0.1389850	0.0645011	0.0088370	1.10E-13
11	CEP164	rs34114773	117397967	C	T	0.0844864	-0.0627497	0.0109978	6.00E-09
11	CEP164	rs151275902	117406338	G	A	0.0157197	0.1393130	0.0243778	2.60E-09
11	CEP164	rs61995733	117408996	T	C	0.0163633	0.1317830	0.0239476	1.00E-08
11	CEP164	rs2279013	117412375	T	C	0.4778370	-0.0467864	0.0061711	8.60E-15
11	CEP164	rs9163	117413092	T	C	0.1545420	0.0610719	0.0084776	2.10E-13
11	CEP164	rs59415378	117413105	G	A	0.0156256	0.1415570	0.0244502	1.50E-09
11	CEP164 *	rs140869507	117413784	G	A	0.0156256	0.1415570	0.0244502	1.50E-09
11	CEP164 *	rs141853402	117413887	T	C	0.0156256	0.1415570	0.0244502	1.50E-09
11	CEP164 *	rs10736488	117414341	G	A	0.1550460	0.0602666	0.0084655	4.60E-13
11	CEP164 *	rs59114541	117419236	A	G	0.0117270	0.3104450	0.0281897	3.70E-28
11	CEP164 *	rs74523946	117420199	A	G	0.0337709	-0.1415670	0.0168426	5.60E-18
11	CEP164 *	rs11603208	117420247	T	G	0.0352661	-0.1377530	0.0165024	8.20E-18
11	CEP164 *	rs180850158	117420250	T	C	0.0148048	0.2549050	0.0251152	1.60E-24
11	DSCAML1	*rs11216379	117421040	G	A	0.0557524	-0.1075760	0.0134620	1.40E-16
11	DSCAML1	*rs75493192	117422143	G	A	0.0119147	0.2966270	0.0280159	3.60E-26
11	DSCAML1	*rs11607141	117423306	G	T	0.0331355	-0.1485580	0.0170717	1.90E-19
11	DSCAML1	*chr11:117423756_AAAAC_A	117423756	AAAAC	A	0.0115302	0.3835660	0.0287134	7.20E-40
11	DSCAML1	*rs7115491	117424434	G	T	0.0317322	-0.1533230	0.0174839	1.10E-19
11	DSCAML1	*rs117229433	117426594	A	C	0.0236932	-0.1295400	0.0200058	1.60E-11
11	DSCAML1	rs78890707	117632761	T	C	0.0483513	-0.0803920	0.0141545	1.20E-09
11	DSCAML1	rs11216484	117651629	A	G	0.0471090	-0.0762359	0.0145479	2.90E-08
12	PDE3A *	rs149437831	20310419	A	AG	0.0753003	-0.0654411	0.0116343	7.80E-09
12	PDE3A *	rs75293976	20310515	T	C	0.0753003	-0.0654411	0.0116343	7.80E-09
12	PDE3A *	rs59436957	20315489	A	G	0.0736853	-0.0666841	0.0117636	4.60E-09
12	PDE3A *	rs79719909	20321772	G	A	0.0711217	-0.0667814	0.0119785	7.70E-09
12	ACACB	rs2284684	109249140	A	G	0.2531420	-0.0352454	0.0071147	1.50E-08
12	ACACB	rs1013746	109250784	C	T	0.2510860	-0.0373986	0.0071145	2.50E-09
12	ACACB	rs10744776	109255001	A	G	0.2509240	-0.0370317	0.0071022	3.10E-09
12	ACACB	rs2075260	109259033	G	A	0.2566160	-0.0345517	0.0070454	1.60E-08
12	ACACB	rs2075261	109259991	A	G	0.2522930	-0.0364297	0.0070742	3.60E-09
12	ACACB	rs7298135	109260761	T	A	0.2529710	-0.0357872	0.0070854	7.10E-09
12	ACACB	rs9788220	109261811	T	C	0.2524270	-0.0357598	0.0070985	7.40E-09
12	ACACB	rs2075263	109266520	C	T	0.2569350	-0.0346470	0.0070226	1.40E-08
12	ACACB	rs12013	109267806	A	G	0.2523270	-0.0358641	0.0070570	5.50E-09
12	ACACB *	rs61510729	109271352	A	G	0.2553960	-0.0348078	0.0070112	9.80E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
12	ACACB *	rs12316300	109271875	T	G	0.2552610	-0.0348303	0.0070134	9.90E-09
12	FOXN4 *	rs7309513	109274417	A	T	0.2548530	-0.0353543	0.0070231	6.50E-09
12	FOXN4 *	rs7299775	109274549	T	C	0.2548440	-0.0353748	0.0070232	6.40E-09
12	FOXN4 *	rs146736814	109276891	A	AAG	0.2532360	-0.0355621	0.0070512	7.80E-09
12	IFT81	rs117624317	110194076	T	C	0.0970378	0.0570776	0.0104219	3.30E-08
12	HCAR2 *	rs644626	122682591	T	C	0.4718190	0.0341377	0.0061574	8.10E-09
12	HCAR2 *	rs535010	122697763	C	G	0.4717520	0.0339661	0.0061591	1.00E-08
12	HCAR2 *	rs586573	122701054	G	A	0.4721850	0.0335649	0.0061622	1.30E-08
12	HCAR2 *	rs6489222	122704952	A	G	0.4715120	0.0342667	0.0061513	7.40E-09
12	HCAR2 *	rs488391	122705131	C	T	0.4719520	0.0338711	0.0061668	1.40E-08
12	HCAR2 *	rs9668547	122706153	A	T	0.4733580	0.0340142	0.0061761	8.30E-09
12	HCAR2 *	rs9668559	122706398	A	C	0.4720590	0.0338131	0.0061550	1.20E-08
12	HCAR2 *	chr12:122706658_GA_G	122706658	GA	G	0.4651550	0.0353786	0.0062535	3.20E-09
12	HCAR2 *	rs2454718	122706828	T	C	0.4715490	0.0342015	0.0061508	7.70E-09
12	HCAR2 *	rs1798184	122707365	C	T	0.4715170	0.0343154	0.0061511	6.80E-09
12	HCAR3 *	rs602293	122710089	C	T	0.4813400	0.0335029	0.0062008	2.10E-08
12	HCAR3 *	rs574413	122710126	A	G	0.4813400	0.0335029	0.0062008	2.10E-08
12	HCAR3 *	rs600501	122710467	A	G	0.4704860	0.0342325	0.0061476	8.40E-09
12	HCAR3 *	rs588293	122710880	G	A	0.4706980	0.0340924	0.0061448	8.60E-09
12	HCAR3 *	rs681317	122711927	A	G	0.4708240	0.0341231	0.0061435	8.40E-09
12	HCAR3 *	rs680934	122711961	T	C	0.4708250	0.0341220	0.0061435	8.40E-09
12	HCAR3 *	rs680838	122712025	T	C	0.4708220	0.0341263	0.0061434	8.40E-09
12	HCAR3 *	rs2256936	122714389	C	T	0.4758870	0.0347332	0.0061765	8.00E-09
12	HCAR3	rs2550	122714930	T	C	0.4704080	0.0347708	0.0061471	4.50E-09
12	HCAR3	rs493623	122715208	A	G	0.4809970	0.0334442	0.0061892	1.90E-08
12	HCAR3	rs1798192	122716221	T	G	0.4716310	0.0344835	0.0061352	6.20E-09
12	HCAR3	rs1696352	122716390	T	G	0.4713200	0.0343458	0.0061382	6.80E-09
12	HCAR3 *	rs2256572	122716961	A	G	0.4725990	0.0340842	0.0061491	9.70E-09
12	HCAR3 *	rs2257405	122717501	A	C	0.4710230	0.0346760	0.0061439	5.00E-09
12	HCAR3 *	rs2264447	122717958	A	G	0.4712890	0.0341732	0.0061395	7.90E-09
12	HCAR3 *	rs2454703	122719184	T	C	0.4715900	0.0339655	0.0061417	1.00E-08
14	C14orf166 *	rs36016197	51987660	C	A	0.1477940	-0.0548350	0.0086918	1.30E-10
14	C14orf166	rs56877201	51992899	A	G	0.1474490	-0.0527735	0.0086921	4.90E-10
14	C14orf166	rs57358451	51993112	C	CAGTA	0.1474670	-0.0528001	0.0086919	4.90E-10
14	C14orf166	rs8014455	51994981	C	T	0.1585410	-0.0451797	0.0084741	3.70E-08
14	C14orf166	rs61971506	51996807	A	G	0.1484980	-0.0535214	0.0086851	2.20E-10
14	C14orf166	rs60016017	51997952	C	T	0.1590170	-0.0455079	0.0084560	2.60E-08
14	C14orf166	rs144834676	52001241	A	AGT	0.1491950	-0.0534071	0.0086413	2.10E-10
14	C14orf166	rs769017991	52003798	GCA	G	0.1451450	-0.0533517	0.0087658	5.10E-10
14	C14orf166	rs560019909	52003801	A	T	0.1356850	-0.0591590	0.0090985	8.00E-11
14	C14orf166	rs748469662	52003804	A	AAG	0.1356850	-0.0591590	0.0090985	8.00E-11
14	C14orf166	rs570077227	52003810	CCT	C	0.1356850	-0.0591590	0.0090985	8.00E-11
14	C14orf166	rs545434094	52003814	A	T	0.1356850	-0.0591590	0.0090985	8.00E-11
14	C14orf166	rs201511063	52003816	T	TTG	0.1356850	-0.0591590	0.0090985	8.00E-11
14	NID2	rs2029984	52007011	G	A	0.1589070	-0.0513173	0.0084372	2.60E-10
14	NID2	rs61971548	52009821	T	G	0.1538140	-0.0459711	0.0085288	2.50E-08
14	NID2	rs61971549	52011823	G	A	0.1663390	-0.0444204	0.0083537	2.70E-08
14	NID2	rs61971550	52011951	G	T	0.1571350	-0.0470360	0.0084495	7.50E-09
14	NID2	rs61971551	52013257	G	C	0.1566020	-0.0485961	0.0084498	2.50E-09
14	NID2	rs61971552	52014806	T	G	0.1564410	-0.0480907	0.0084384	3.30E-09
14	NID2	rs71422049	52016737	G	A	0.1564040	-0.0492533	0.0084364	1.50E-09
14	NID2	rs77091361	52020243	T	C	0.1552900	-0.0496004	0.0084669	1.60E-09
14	NID2	rs61971553	52020797	G	A	0.1623490	-0.0473837	0.0083326	5.40E-09
14	NID2	rs17124901	52021291	T	C	0.1611090	-0.0462175	0.0083570	9.80E-09
14	NID2	rs2073626	52021667	G	A	0.1609380	-0.0461375	0.0083609	9.90E-09
14	NID2	rs2073625	52021970	T	C	0.1679200	-0.0443327	0.0082405	2.40E-08
14	NID2	rs2073624	52022695	A	G	0.1673140	-0.0449734	0.0082450	1.80E-08
14	NID2	rs78670328	52023396	C	A	0.1602920	-0.0461503	0.0083954	1.00E-08
14	NID2	rs112195968	52023436	C	T	0.1670860	-0.0448315	0.0082542	2.10E-08
14	NID2	rs4901180	52023851	A	G	0.1670910	-0.0451668	0.0082551	1.60E-08
14	NID2	rs8020559	52023972	G	T	0.1602480	-0.0461686	0.0083969	1.00E-08
14	NID2	rs61971554	52024865	G	A	0.1583370	-0.0487358	0.0084578	2.70E-09
14	NID2	rs61971555	52025585	A	G	0.1678470	-0.0442556	0.0082440	3.10E-08
14	NID2	rs17124920	52026443	C	T	0.1679410	-0.0443433	0.0082441	2.90E-08
14	NID2	rs77101097	52027582	T	C	0.1591020	-0.0465628	0.0084276	8.90E-09
14	NID2	rs140170580	52027589	TA	T	0.1672360	-0.0449746	0.0082601	2.00E-08
14	NID2	rs74049344	52028636	G	T	0.1679130	-0.0449670	0.0082484	2.20E-08
14	NID2	rs61971558	52029306	A	G	0.1593340	-0.0465793	0.0084276	9.70E-09
14	NID2	rs8013745	52030027	T	G	0.1594000	-0.0464084	0.0084320	1.10E-08
14	NID2	rs3783632	52031393	A	C	0.1629680	-0.0494463	0.0083666	6.80E-10
14	NID2	rs2073620	52033610	C	T	0.1621600	-0.0495638	0.0083869	6.10E-10
14	NID2	rs11415769	52035018	C	CA	0.1569490	-0.0497388	0.0085126	1.70E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
14	NID2	rs2645750	52036074	C	A	0.1534030	-0.0519253	0.0085452	3.00E-10
14	NID2	rs2645749	52036077	C	A	0.1534030	-0.0519652	0.0085452	2.80E-10
14	NID2	rs2516593	52036651	T	C	0.1680620	-0.0476065	0.0082199	2.80E-09
14	NID2	rs2749875	52036678	G	A	0.1680760	-0.0475417	0.0082193	3.00E-09
14	NID2	rs2516592	52036827	T	C	0.1539030	-0.0527376	0.0085194	1.60E-10
14	NID2	rs71121678	52036872	A	AG	0.1540680	-0.0528054	0.0085215	1.50E-10
14	NID2	rs2749876	52037679	T	G	0.1543440	-0.0518619	0.0084994	2.80E-10
14	NID2	rs904061	52037906	T	C	0.1543880	-0.0519949	0.0084968	2.60E-10
14	NID2	rs753051	52038642	A	G	0.1544870	-0.0517963	0.0084927	3.00E-10
14	NID2	rs753050	52038657	A	G	0.1545390	-0.0521205	0.0084932	2.20E-10
14	NID2	rs2029976	52039093	C	T	0.1545300	-0.0518589	0.0084903	2.60E-10
14	NID2	rs2029975	52039352	C	T	0.1545970	-0.0520888	0.0084874	2.10E-10
14	NID2	rs10139288	52039768	T	C	0.1547930	-0.0524785	0.0084775	1.50E-10
14	NID2	rs3742536	52040711	A	G	0.1548850	-0.0528024	0.0084730	1.20E-10
14	NID2	rs1982963	52042383	G	A	0.1550190	-0.0536545	0.0084605	6.20E-11
14	NID2	rs3841694	52042541	TA	T	0.1550140	-0.0536498	0.0084609	6.20E-11
14	NID2	rs4898729	52042765	T	C	0.1546380	-0.0536158	0.0084722	7.50E-11
14	NID2	rs4901186	52042766	G	A	0.1550180	-0.0537302	0.0084629	6.50E-11
14	NID2	rs3818187	52043070	G	A	0.1548880	-0.0539660	0.0084668	5.40E-11
14	NID2	rs61973203	52043849	G	A	0.1513500	-0.0555107	0.0085648	2.20E-11
14	NID2	chr14:52044610_CT_C	52044610	CT	C	0.1548430	-0.0542107	0.0084789	4.80E-11
14	NID2	rs1566132	52045118	C	T	0.1548310	-0.0540978	0.0084720	4.50E-11
14	NID2	rs75766425	52045193	C	G	0.1184460	-0.0696829	0.0094731	3.80E-14
14	NID2	rs79823890	52045251	T	G	0.1187820	-0.0698331	0.0094619	3.10E-14
14	NID2	rs2516589	52045892	A	G	0.1525140	-0.0525507	0.0085371	2.50E-10
14	NID2	rs33921845	52045899	C	CTG	0.1546610	-0.0536111	0.0084826	7.00E-11
14	NID2	rs2749880	52046151	G	A	0.1543410	-0.0544575	0.0084868	3.70E-11
14	NID2	rs2645738	52046484	G	A	0.1543170	-0.0542438	0.0084867	4.40E-11
14	NID2	rs1566131	52047966	G	A	0.1543190	-0.0540270	0.0084881	4.80E-11
14	AKT1	rs2498787	104790244	C	T	0.3204630	0.0334030	0.0065643	4.20E-08
14	AKT1	rs2494749	104792556	G	A	0.3228780	0.0332190	0.0065556	4.70E-08
15	TLE3 *	rs4776482	69851564	G	C	0.4058850	-0.0341986	0.0063232	4.90E-09
15	TLE3 *	rs305006	69851871	T	C	0.3273620	-0.0361959	0.0065431	1.20E-09
15	TLE3 *	rs10468044	69852097	C	A	0.4057960	-0.0344628	0.0063211	3.70E-09
15	TLE3 *	rs305007	69853073	G	C	0.3628990	-0.0343068	0.0063931	4.50E-09
15	TLE3 *	rs305008	69853301	A	G	0.3629250	-0.0343033	0.0063923	4.50E-09
15	TLE3 *	rs305009	69853419	A	G	0.3274010	-0.0365741	0.0065174	5.90E-10
15	TLE3 *	rs305010	69853872	G	A	0.3629020	-0.0343051	0.0063926	4.40E-09
15	TLE3 *	rs480441	69855220	C	T	0.3271520	-0.0365141	0.0065229	5.60E-10
15	TLE3 *	rs442652	69856555	C	A	0.3270520	-0.0369698	0.0065280	3.80E-10
15	TLE3 *	rs428823	69856745	C	T	0.3271400	-0.0370876	0.0065272	3.30E-10
15	TLE3 *	rs28669171	69857361	T	G	0.3092960	-0.0363581	0.0067692	2.60E-09
15	TLE3 *	rs435315	69857677	A	T	0.3249210	-0.0384669	0.0065545	1.00E-10
15	TLE3 *	rs442784	69857947	T	C	0.3249270	-0.0385568	0.0065560	9.40E-11
15	TLE3 *	rs446721	69858754	T	C	0.3249060	-0.0384439	0.0065621	1.10E-10
15	TLE3 *	rs12594366	69860568	C	T	0.3165780	-0.0364147	0.0066171	9.90E-10
15	TLE3 *	rs59650813	69863741	C	G	0.3139530	-0.0373929	0.0066567	4.40E-10
15	TLE3 *	rs13380008	69867183	C	T	0.3414840	-0.0368722	0.0065522	3.10E-09
15	TLE3 *	rs13379513	69867218	A	G	0.3375570	-0.0380761	0.0065665	1.20E-09
15	TLE3 *	rs12593720	69868843	T	C	0.2379190	-0.0532939	0.0072384	4.70E-15
15	TLE3 *	rs304975	69869121	G	C	0.3471020	-0.0377733	0.0064950	9.50E-10
15	TLE3 *	rs304979	69870936	C	G	0.3464220	-0.0379880	0.0064984	7.30E-10
15	TLE3 *	rs4777205	69872486	A	C	0.3678320	-0.0354989	0.0064030	7.70E-09
15	TLE3 *	rs10162636	69875502	T	G	0.2416780	-0.0532334	0.0072501	4.60E-15
15	TLE3 *	rs78943073	69876104	A	G	0.2385190	-0.0540874	0.0072644	1.70E-15
15	TLE3 *	rs78385799	69878325	A	G	0.2706810	-0.0470894	0.0069821	7.90E-13
15	TLE3 *	rs304959	69878607	G	C	0.4051280	-0.0336793	0.0063130	4.70E-08
15	TLE3 *	rs6494835	69879436	A	T	0.2715100	-0.0488372	0.0069491	9.00E-14
15	TLE3 *	rs8035009	69879649	G	C	0.2719780	-0.0489551	0.0069395	7.90E-14
15	TLE3 *	rs75327024	69880728	A	G	0.2397960	-0.0547777	0.0072420	4.90E-16
15	TLE3 *	rs7166273	69881625	C	T	0.2395890	-0.0557674	0.0072242	1.50E-16
15	TLE3 *	rs304948	69884491	A	G	0.3481160	-0.0418922	0.0064557	1.40E-11
15	TLE3 *	rs1349680	69886868	C	T	0.3763720	-0.0419786	0.0063316	1.20E-11
15	TLE3 *	rs1349679	69887061	C	T	0.3760400	-0.0423211	0.0063285	7.80E-12
15	TLE3 *	rs304941	69887624	T	C	0.3469760	-0.0429208	0.0064521	4.60E-12
15	TLE3 *	rs7175768	69888636	C	T	0.3760960	-0.0422081	0.0063293	8.70E-12
15	TLE3 *	rs80287865	69889112	T	G	0.2302300	-0.0602347	0.0073045	1.70E-18
15	TLE3 *	rs77648222	69890512	G	A	0.2352270	-0.0598914	0.0072240	1.20E-18
15	TLE3 *	rs17756181	69891852	G	A	0.2446730	-0.0598291	0.0071213	6.30E-19
15	TLE3 *	rs28521935	69892800	C	A	0.2395780	-0.0597953	0.0071991	1.50E-18
15	TLE3 *	rs881053	69894413	A	G	0.3744550	-0.0426714	0.0063380	4.50E-12
15	TLE3 *	rs1452725	69895764	T	C	0.3719050	-0.0431687	0.0063580	2.10E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	TLE3 *	rs8041139	69896404	G	T	0.3473180	-0.0431712	0.0064506	2.60E-12
15	TLE3 *	rs1155996	69897006	C	T	0.3471490	-0.0426795	0.0064445	4.40E-12
15	TLE3 *	rs12591142	69897251	C	A	0.2308010	-0.0593196	0.0072913	4.60E-18
15	TLE3 *	rs12440731	69899052	A	G	0.3566200	-0.0426910	0.0064179	7.10E-12
15	TLE3 *	rs80039904	69901814	T	C	0.2293640	-0.0571538	0.0073551	8.00E-17
15	TLE3 *	rs2601882	69902992	T	G	0.2997320	-0.0402352	0.0067695	2.20E-10
15	TLE3 *	rs2679629	69903547	C	T	0.3238470	-0.0381564	0.0066187	1.40E-09
15	TLE3 *	rs2601883	69903678	C	G	0.2372110	-0.0574749	0.0072963	6.60E-17
15	TLE3 *	rs2601885	69904439	T	C	0.2926580	-0.0378010	0.0068174	2.70E-09
16	MT1G *	rs148823159	56666037	G	GCTGT	0.0265436	-0.1142840	0.0192799	5.30E-10
16	MT1G *	rs140661464	56666360	A	G	0.0200710	-0.1446540	0.0219936	2.50E-11
16	NUP93 *	rs150859494	56716207	A	G	0.0225648	-0.1732600	0.0206443	6.40E-18
16	NUP93	rs75745425	56749204	T	A	0.0254728	-0.1456460	0.0194260	7.00E-15
16	NUP93	rs185085605	56809107	G	A	0.0241749	-0.1415910	0.0199628	3.00E-13
16	MIR138-2 *	rs117678160	56855359	T	C	0.0230380	-0.1676990	0.0204153	2.90E-17
16	SLC12A3	rs551794976	56878467	C	T	0.0195898	-0.1219650	0.0221863	2.40E-08
16	SLC12A3 *	rs9925265	56916298	A	G	0.2290740	0.0422671	0.0073189	2.20E-09
16	HERPUD1	rs9938413	56938338	T	C	0.0691654	-0.0799948	0.0121176	1.10E-10
16	HERPUD1 *	rs76656725	56951859	T	C	0.0593855	0.0733643	0.0131109	5.30E-09
16	HERPUD1 *	rs76277974	56952295	A	G	0.0441313	0.1072480	0.0149626	3.90E-14
16	HERPUD1 *	rs75148450	56952891	C	T	0.0213498	0.1178230	0.0213702	2.30E-08
16	CETP *	rs12446515	56953103	T	C	0.1581010	-0.1676170	0.0084489	2.90E-92
16	CETP *	rs56156922	56953457	C	T	0.1642670	-0.1633990	0.0082958	9.70E-92
16	CETP *	rs56228609	56953853	T	C	0.1633340	-0.1650010	0.0082818	9.30E-94
16	CETP *	rs173539	56954132	T	C	0.2228040	-0.0901606	0.0073525	4.90E-36
16	CETP *	rs247616	56955678	T	C	0.1620460	-0.1651970	0.0082974	1.10E-93
16	CETP *	rs247617	56956804	A	C	0.1599420	-0.1658040	0.0083393	6.10E-93
16	CETP *	rs183130	56957451	T	C	0.1595510	-0.1668700	0.0083500	8.60E-94
16	CETP *	rs572564758	56957698	C	T	0.0210822	0.1564850	0.0213579	1.50E-13
16	CETP *	rs28888131	56957712	A	G	0.0565773	0.0749674	0.0132822	6.90E-09
16	CETP *	rs12934632	56957829	T	C	0.0565776	0.0751519	0.0132814	6.20E-09
16	CETP *	rs12149545	56959249	A	G	0.1600550	-0.1660140	0.0083360	4.40E-93
16	CETP *	rs12708967	56959299	C	T	0.0571014	0.0753406	0.0131994	4.30E-09
16	CETP *	rs3764261	56959412	A	C	0.1617030	-0.1658370	0.0083030	7.20E-94
16	CETP *	rs821840	56959974	G	A	0.1347110	-0.1693950	0.0091359	3.40E-81
16	CETP *	rs36229491	56960332	TA	T	0.1626160	-0.1654040	0.0082839	4.80E-94
16	CETP *	rs17231506	56960616	T	C	0.1626670	-0.1657380	0.0082846	2.50E-94
16	CETP *	rs36229485	56960824	T	C	0.0234928	0.1381620	0.0202426	2.00E-12
16	CETP *	rs4783961	56960982	A	G	0.2206390	-0.1073360	0.0073785	7.40E-51
16	CETP *	rs1800775	56961324	C	A	0.4966960	0.0598471	0.0061158	5.30E-25
16	CETP	rs3816117	56962246	T	C	0.4998840	0.0572252	0.0061325	4.90E-23
16	CETP	rs711752	56962299	A	G	0.4035380	-0.0930928	0.0062330	7.10E-56
16	CETP	rs708272	56962376	A	G	0.4033560	-0.0932511	0.0062349	4.70E-56
16	CETP	chr16:56962733_GCC_G	56962733	G	GCC	0.4032710	-0.0927291	0.0062642	7.50E-55
16	CETP	rs34620476	56962737	A	C	0.4032720	-0.0927545	0.0062643	7.10E-55
16	CETP	rs1864163	56963321	A	G	0.1356770	0.1087050	0.0089222	2.20E-36
16	CETP	rs5817082	56963437	CA	C	0.1347630	0.1100560	0.0089549	6.10E-37
16	CETP	rs7194225	56963744	C	G	0.0658225	0.0719598	0.0123909	1.40E-09
16	CETP	rs1331958145	56964034	A	TTATTI	0.0401720	-0.1186020	0.0158691	2.50E-14
16	CETP	rs9929488	56964660	C	G	0.1538460	0.1025500	0.0085194	5.60E-36
16	CETP	rs12720926	56965006	G	A	0.3040010	-0.1050020	0.0066781	3.30E-61
16	CETP	rs7203984	56965346	C	A	0.2750860	0.0877472	0.0068986	9.10E-39
16	CETP	rs11508026	56965416	T	C	0.2998050	-0.1016480	0.0066748	2.40E-57
16	CETP	rs71383212	56965440	T	TC	0.0611369	0.0842675	0.0128096	1.40E-12
16	CETP	rs17231569	56965866	C	CG	0.1372160	0.1148940	0.0089094	1.80E-40
16	CETP	rs34602471	56966330	G	A	0.0442988	0.1167420	0.0148613	1.20E-16
16	CETP	rs12720922	56966973	A	G	0.1378430	0.1159730	0.0088974	2.90E-41
16	CETP	rs4784741	56967304	T	C	0.3008770	-0.1031770	0.0066953	4.20E-59
16	CETP	chr16:56967342_T_TCACA	56967342	TCACA	T	0.1365270	0.1155390	0.0089309	1.10E-40
16	CETP	rs1555505859	56967345	CACAC	C	0.1372210	0.1152610	0.0089068	1.00E-40
16	CETP	rs12444012	56967526	A	G	0.3021480	-0.1038540	0.0066807	5.60E-60
16	CETP	rs118089749	56967882	A	G	0.0340798	-0.1321390	0.0170604	8.60E-17
16	CETP	rs9936680	56968240	C	T	0.0439622	0.1192210	0.0149162	2.70E-17
16	CETP	rs9924087	56968330	T	C	0.0445799	0.1178960	0.0148158	4.30E-17
16	CETP	rs9939224	56968820	T	G	0.1433230	0.1102670	0.0087276	1.10E-38
16	CETP	rs11076174	56969234	C	T	0.1197300	0.1002220	0.0094375	2.60E-28
16	CETP	rs7205804	56970977	A	G	0.3141510	-0.0936265	0.0065999	2.30E-50
16	CETP	rs1532625	56971389	T	C	0.2960710	-0.1047870	0.0067103	1.60E-60
16	CETP	rs1532624	56971567	A	C	0.2962880	-0.1046860	0.0067111	2.60E-60
16	CETP	rs11076175	56972466	G	A	0.1261820	0.1075150	0.0092162	1.60E-33
16	CETP	rs7499892	56972678	T	C	0.1715730	0.1210670	0.0081098	2.50E-54
16	CETP	rs289713	56972917	T	A	0.2782790	0.0824678	0.0069462	2.30E-34

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
16	CETP	rs11076176	56973534	G	T	0.2908470	0.0829446	0.0068288	1.80E-35
16	CETP	rs289714	56973539	G	A	0.2910840	0.0821122	0.0068259	6.80E-35
16	CETP	rs158477	56973698	G	A	0.4875920	0.0382166	0.0062306	8.70E-10
16	CETP	rs158478	56973822	A	C	0.4671770	0.0357905	0.0062083	1.10E-08
16	CETP	rs188149780	56974075	C	G	0.0168914	-0.2581710	0.0238606	9.80E-29
16	CETP	rs158479	56974136	G	A	0.4686330	0.0352325	0.0061987	2.00E-08
16	CETP	rs289715	56974596	A	T	0.1917420	-0.0423328	0.0077618	1.20E-08
16	CETP	rs736274	56975857	A	T	0.0699749	-0.0865149	0.0122205	2.40E-12
16	CETP	rs289718	56976020	C	T	0.3098470	-0.0470195	0.0066867	1.40E-13
16	CETP	rs289719	56976029	T	C	0.3098100	-0.0471567	0.0066860	1.20E-13
16	CETP	rs2033254	56976073	C	T	0.1325830	0.1100190	0.0090326	6.40E-36
16	CETP	rs11860407	56976916	G	A	0.1323830	0.1106980	0.0090412	3.40E-36
16	CETP	rs12708980	56978467	G	T	0.1405870	0.1056420	0.0088125	1.70E-34
16	CETP	rs1800774	56981633	T	C	0.1405970	0.1036040	0.0088052	3.00E-33
16	CETP	rs2303790	56983380	G	A	0.0300554	-0.2448450	0.0179914	1.40E-44
16	CETP	rs289741	56983562	G	A	0.3044730	-0.0489170	0.0067111	2.40E-14
16	CETP *	rs289742	56983850	C	G	0.1923780	-0.0418447	0.0078190	2.60E-08
16	CETP *	rs289743	56983884	G	A	0.3042880	-0.0489762	0.0067149	2.30E-14
16	CETP *	rs118153730	56985194	A	G	0.0169323	-0.2530330	0.0238757	2.60E-27
16	CMIP	chr16:81462504_TA_T	81462504	T	TA	0.3003430	0.0372248	0.0068078	4.80E-08
16	CMIP	rs11150389	81467942	A	G	0.3569410	-0.0336044	0.0064523	3.80E-08
16	CMIP	rs12596482	81469935	T	C	0.3599910	-0.0343534	0.0064701	1.80E-08
16	CMIP	rs12596548	81470272	T	C	0.3615130	-0.0341236	0.0064629	2.20E-08
16	CMIP	rs117424567	81471205	T	C	0.2706460	0.0395650	0.0070049	2.80E-08
16	CMIP	chr16:81471415_C_CAT	81471415	CAT	C	0.3610890	-0.0351987	0.0064865	8.80E-09
16	CMIP	rs34994024	81471550	C	CAT	0.3606280	-0.0359393	0.0064717	5.00E-09
16	CMIP	rs34659764	81471747	T	G	0.3607910	-0.0353818	0.0064776	7.90E-09
16	CMIP	rs9928008	81483993	A	G	0.2379690	0.0448716	0.0072905	1.60E-09
16	CMIP	rs7193307	81492697	A	G	0.3619000	-0.0339646	0.0064806	1.70E-08
16	CMIP	rs12932649	81493231	T	C	0.3619230	-0.0350665	0.0064521	5.90E-09
16	CMIP	chr16:81493350_GCGTTACCTGT_G	81493350	G	TTTACC	0.3634310	-0.0337410	0.0064536	1.50E-08
16	CMIP	rs35144862	81493439	C	CTT	0.2752900	-0.0367282	0.0069964	2.20E-08
16	CMIP	rs66710707	81495016	G	A	0.3640800	-0.0342016	0.0064507	1.10E-08
16	CMIP	rs2925994	81495569	G	A	0.3651980	-0.0335216	0.0064493	2.20E-08
16	CMIP	rs2966090	81495814	C	T	0.3671480	-0.0339449	0.0064289	1.20E-08
16	CMIP	rs2925995	81497424	T	A	0.3666810	-0.0373961	0.0064073	3.80E-10
16	CMIP	rs2927311	81497625	G	C	0.3668840	-0.0377033	0.0064014	2.70E-10
16	CMIP	rs4889326	81500057	T	C	0.3544580	-0.0383759	0.0064855	1.50E-10
16	CMIP	rs2966091	81500878	G	C	0.3681680	-0.0389718	0.0063946	6.80E-11
16	CMIP	rs2925979	81501185	T	C	0.4290000	0.0521362	0.0061712	1.10E-18
16	CMIP	rs12920728	81505237	A	G	0.3615420	-0.0407813	0.0064974	1.60E-11
16	CMIP	rs3803656	81517901	C	A	0.2577860	0.0443833	0.0070414	2.00E-10
17	CD300LG *	rs543019052	43846502	C	G	0.0111248	0.1612940	0.0293775	4.60E-09
17	CD300LG	rs200210430	43861775	G	A	0.0101417	0.1835870	0.0306762	1.50E-10
17	MPP2 *	rs566655597	43870054	A	C	0.0101969	0.1821270	0.0305961	2.10E-10
17	GPATCH8	rs146959348	44433528	A	G	0.0123288	0.1511020	0.0277811	4.10E-08
17	GPATCH8 *	rs929786922	44518409	A	G	0.0108083	0.1599400	0.0296056	3.50E-08
17	NSF	rs77162940	46750119	G	A	0.4153740	0.0305110	0.0062099	3.70E-08
17	WNT3	rs199526	46770341	G	C	0.4159180	0.0304468	0.0061931	3.80E-08
17	WNT3	rs199523	46771151	A	C	0.4176480	0.0303555	0.0061928	3.70E-08
17	WNT3	rs72628337	46773055	G	A	0.4166320	0.0302117	0.0061918	4.40E-08
17	WNT3	rs199521	46776090	C	G	0.4154370	0.0304578	0.0061845	3.40E-08
17	WNT3	rs199520	46776506	A	G	0.4151860	0.0302815	0.0061850	3.70E-08
17	WNT3	rs199519	46776558	A	G	0.4153750	0.0299572	0.0061866	4.90E-08
17	WNT3	rs4141293	46778317	G	A	0.4178410	0.0304065	0.0062141	4.80E-08
17	CLTC	rs60164173	59645912	A	G	0.4456330	0.0324587	0.0062007	4.50E-08
17	CLTC	rs2877975	59653444	T	C	0.4450320	0.0324271	0.0062038	4.60E-08
17	CLTC	rs57592560	59684662	T	C	0.4499640	0.0322482	0.0062042	4.70E-08
17	CLTC	rs2271303	59685510	C	T	0.4493900	0.0328243	0.0062040	3.00E-08
17	CLTC	rs7212825	59691837	G	A	0.4492250	0.0324520	0.0062052	4.00E-08
17	CLTC	rs139136427	59695672	C	CAAAA	0.4462710	0.0322365	0.0061917	4.10E-08
17	VMP1	rs111723017	59710070	C	G	0.4361040	0.0322808	0.0061998	3.50E-08
17	VMP1	rs9903626	59713266	G	A	0.4363090	0.0325094	0.0061978	2.50E-08
17	VMP1	rs76856339	59723605	A	G	0.4352400	0.0330616	0.0061779	1.20E-08
17	VMP1	rs8080483	59724061	C	A	0.4357300	0.0332619	0.0061834	1.10E-08
17	VMP1	rs72840511	59728650	T	G	0.4352840	0.0331569	0.0061779	1.10E-08
17	VMP1	rs9901606	59734046	C	A	0.4351010	0.0332063	0.0061703	1.10E-08
17	VMP1	rs9910518	59734706	C	T	0.4351460	0.0332544	0.0061703	1.10E-08
17	VMP1	rs2271304	59737280	G	A	0.4351610	0.0332544	0.0061687	9.90E-09
17	VMP1	rs28516945	59739217	C	T	0.4264650	0.0327832	0.0062127	1.70E-08
17	VMP1	rs56236317	59744764	T	C	0.4351070	0.0331514	0.0061709	1.10E-08
17	VMP1	rs7215180	59744993	G	A	0.4351070	0.0331514	0.0061709	1.10E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	VMP1	rs9907923	59747566	T	C	0.4340530	0.0326727	0.0061824	1.90E-08
17	VMP1	rs60451858	59749244	G	A	0.4355630	0.0332946	0.0061715	9.00E-09
17	VMP1	rs72840522	59752631	A	G	0.4351630	0.0331878	0.0061708	1.10E-08
17	VMP1	rs9899611	59754829	G	A	0.4354050	0.0331852	0.0061762	9.40E-09
17	VMP1	rs72838857	59759406	G	A	0.4341420	0.0336448	0.0061813	7.60E-09
17	VMP1	rs16943838	59762243	T	C	0.4352180	0.0331286	0.0061701	1.10E-08
17	VMP1	rs1874548	59763996	G	A	0.4348960	0.0328940	0.0061734	1.30E-08
17	VMP1	rs2777886	59767960	G	A	0.4352360	0.0332395	0.0061700	9.90E-09
17	VMP1	rs201444735	59774421	A	AAGAA	0.4302910	0.0357687	0.0062282	1.30E-09
17	VMP1	rs2645467	59777422	T	C	0.4355980	0.0338432	0.0061732	6.50E-09
17	VMP1	rs2132715	59781013	T	A	0.4353920	0.0338406	0.0061764	6.50E-09
17	VMP1	rs2173119	59782344	T	C	0.4354000	0.0337947	0.0061763	6.80E-09
17	VMP1	rs35519306	59782796	A	AG	0.4334430	0.0345866	0.0062024	4.20E-09
17	VMP1	rs2645474	59791240	A	G	0.4281660	0.0338063	0.0062471	8.70E-09
17	VMP1	rs2777900	59795133	A	G	0.4334600	0.0352706	0.0061698	1.60E-09
17	VMP1	rs2645492	59798193	A	G	0.4334240	0.0352079	0.0061693	1.70E-09
17	VMP1	rs2102507	59798546	G	A	0.4333060	0.0352333	0.0061698	1.70E-09
17	VMP1	rs2645491	59799688	T	C	0.4334540	0.0351286	0.0061695	1.80E-09
17	VMP1	rs2665400	59802840	A	G	0.4366740	0.0361589	0.0061703	6.10E-10
17	VMP1	rs34890976	59803949	AT	A	0.3986310	-0.0315992	0.0062887	4.50E-08
17	VMP1	rs2645489	59806010	G	T	0.4318200	0.0352961	0.0061853	1.30E-09
17	VMP1	rs2645486	59808540	A	T	0.4334980	0.0352787	0.0061696	1.60E-09
17	VMP1	rs2645487	59808764	G	T	0.4334970	0.0352818	0.0061696	1.60E-09
17	VMP1	rs11079389	59810591	A	G	0.4335030	0.0352735	0.0061697	1.60E-09
17	VMP1	rs2665403	59812624	A	G	0.4339880	0.0352201	0.0061659	1.60E-09
17	VMP1	rs2173120	59815279	T	A	0.4339280	0.0350476	0.0061662	2.00E-09
17	VMP1	chr17:59815464_ATTT_A	59815464	A	ATTT	0.4324070	0.0353177	0.0061837	1.70E-09
17	VMP1	rs115869798	59815468	A	T	0.4324070	0.0353177	0.0061837	1.70E-09
17	VMP1	rs71145576	59815855	C	AAAAA	0.4351770	0.0351086	0.0061755	1.90E-09
17	VMP1	rs147970496	59817246	TGGGC	C	0.4339660	0.0352409	0.0061662	1.60E-09
17	VMP1	rs7223793	59818661	G	T	0.4339720	0.0352410	0.0061662	1.60E-09
17	VMP1	rs2526352	59827462	A	G	0.4318360	0.0342206	0.0061831	5.10E-09
17	VMP1	rs1292063	59830407	T	A	0.4351910	0.0350103	0.0061765	2.00E-09
17	MIR21 *	rs1292037	59841547	C	T	0.4339470	0.0353669	0.0061660	1.40E-09
17	MIR21 *	rs13137	59841670	T	A	0.4339470	0.0353669	0.0061660	1.40E-09
17	MIR21 *	rs1292072	59848288	G	A	0.4337500	0.0348699	0.0061850	2.90E-09
17	MIR21 *	rs79417738	59850363	G	A	0.3729900	0.0351507	0.0064474	4.00E-08
17	TUBD1 *	rs1292067	59853285	T	G	0.4486520	0.0338491	0.0061812	1.90E-08
17	TUBD1 *	rs1292066	59854953	A	T	0.3871820	0.0341163	0.0063324	3.30E-08
17	TUBD1 *	rs1292043	59856808	G	A	0.3844140	0.0344887	0.0063185	2.90E-08
17	TUBD1 *	rs1292042	59857634	G	A	0.3829550	0.0345689	0.0063206	2.40E-08
17	TUBD1	rs2526358	59865224	G	A	0.3804600	0.0338024	0.0063197	4.80E-08
17	BPTF	rs3833111	67826457	CAG	C	0.3402260	-0.0376175	0.0066019	4.60E-09
17	BPTF	chr17:67829112_TTTG_T	67829112	TTTG	T	0.3442310	-0.0377297	0.0065704	3.10E-09
17	BPTF	rs12603589	67829132	T	C	0.3436310	-0.0381246	0.0065527	2.00E-09
17	BPTF	rs12601921	67829238	C	T	0.3425250	-0.0388437	0.0065973	1.20E-09
17	BPTF	rs12601919	67829258	A	G	0.3440580	-0.0384659	0.0065490	1.60E-09
17	BPTF	rs9915591	67829974	C	G	0.3441780	-0.0379374	0.0065506	2.40E-09
17	BPTF	rs12602556	67830745	A	G	0.3435160	-0.0380814	0.0065438	1.80E-09
17	BPTF	rs62084208	67831327	C	T	0.3439320	-0.0384089	0.0065384	1.30E-09
17	BPTF	rs2080090	67832255	T	A	0.3472450	-0.0374949	0.0065857	3.40E-09
17	BPTF	rs62084210	67832594	A	G	0.3436620	-0.0388913	0.0065369	7.60E-10
17	BPTF	rs12449312	67833242	A	C	0.3501490	-0.0372123	0.0065657	3.50E-09
17	BPTF	rs7223643	67834166	A	G	0.3445830	-0.0387874	0.0065007	6.60E-10
17	BPTF	rs1976052	67834462	C	T	0.3447530	-0.0390008	0.0064933	5.20E-10
17	BPTF	rs7209675	67835142	A	T	0.3445470	-0.0389466	0.0064617	4.50E-10
17	BPTF	chr17:67835212_T_TA	67835212	T	TA	0.3459550	-0.0393932	0.0064663	3.00E-10
17	BPTF	rs75873575	67835625	GT	G	0.3446820	-0.0393086	0.0064499	2.90E-10
17	BPTF	rs142633440	67835663	TTTTTT	A	0.3445090	-0.0390617	0.0064564	3.90E-10
17	BPTF	rs7218014	67835900	T	C	0.3436820	-0.0397279	0.0064658	2.00E-10
17	BPTF	rs7221651	67836274	G	A	0.3446560	-0.0393319	0.0064490	2.90E-10
17	BPTF	rs12452511	67836460	A	G	0.3446560	-0.0393319	0.0064490	2.90E-10
17	BPTF	rs1976053	67836886	C	G	0.3374160	-0.0402781	0.0064986	1.90E-10
17	BPTF	rs1976054	67837108	T	G	0.3446560	-0.0393319	0.0064490	2.90E-10
17	BPTF	rs7208909	67837430	T	C	0.3476440	-0.0382407	0.0064610	7.10E-10
17	BPTF	rs2052187	67838621	T	C	0.3446560	-0.0393319	0.0064490	2.90E-10
17	BPTF	rs11079705	67839336	A	T	0.3482000	-0.0378318	0.0064623	1.10E-09
17	BPTF	rs11079706	67839354	G	T	0.3449530	-0.0389147	0.0064628	4.20E-10
17	BPTF	rs11079707	67839501	G	A	0.3448910	-0.0392838	0.0064506	2.90E-10
17	BPTF	rs80135947	67839885	A	C	0.3446540	-0.0393407	0.0064489	2.80E-10
17	BPTF	chr17:67840458_CTTG_C	67840458	CTTG	C	0.3460270	-0.0387949	0.0064616	6.20E-10
17	BPTF	rs59252707	67840471	T	C	0.3570170	-0.0382102	0.0065064	1.40E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	BPTF	rs6504542	67840526	T	C	0.3446440	-0.0392986	0.0064491	2.90E-10
17	BPTF	rs8082512	67840943	T	C	0.3446440	-0.0392986	0.0064491	2.90E-10
17	BPTF	rs1599859	67841077	C	G	0.3444910	-0.0390101	0.0064511	3.90E-10
17	BPTF	rs1966410	67841099	T	C	0.3444910	-0.0390101	0.0064511	3.90E-10
17	BPTF	rs58551145	67841119	A	G	0.3446260	-0.0388622	0.0064516	4.80E-10
17	BPTF	rs6504543	67841543	T	C	0.3388380	-0.0402292	0.0064786	1.50E-10
17	BPTF	rs8067892	67841867	A	G	0.3446440	-0.0392986	0.0064491	2.90E-10
17	BPTF	rs8074078	67842627	T	G	0.3446440	-0.0392986	0.0064491	2.90E-10
17	BPTF	rs8073510	67843094	A	G	0.3458280	-0.0386814	0.0064526	5.80E-10
17	BPTF	rs12450363	67843992	T	C	0.3451910	-0.0385631	0.0064586	6.40E-10
17	BPTF	rs62084212	67844128	G	A	0.3551420	-0.0360622	0.0065409	8.00E-09
17	BPTF	rs112222385	67844408	T	C	0.3440620	-0.0392564	0.0064562	2.80E-10
17	BPTF	rs11871285	67844693	G	T	0.3464140	-0.0392528	0.0064487	3.30E-10
17	BPTF	rs11868959	67844694	T	C	0.3464140	-0.0392528	0.0064487	3.30E-10
17	BPTF	rs2365466	67845013	G	A	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs3029927	67845167	A	AAGT	0.3399920	-0.0402470	0.0064810	1.70E-10
17	BPTF	rs2365467	67845169	A	T	0.3399920	-0.0402470	0.0064810	1.70E-10
17	BPTF	rs2365468	67845202	C	T	0.3392820	-0.0401907	0.0064742	1.50E-10
17	BPTF	rs62084213	67845900	A	G	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs7223930	67846070	G	A	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs7224923	67846149	T	G	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs62084214	67847209	C	G	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	chr17:67848171_CT_C	67848171	CT	C	0.3335340	-0.0423000	0.0065716	3.00E-11
17	BPTF	rs8081517	67849581	A	T	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs8081856	67849802	A	G	0.3450640	-0.0397270	0.0064529	1.80E-10
17	BPTF	rs62084234	67850944	A	G	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs7212293	67851209	A	G	0.3394950	-0.0401672	0.0064752	1.50E-10
17	BPTF	chr17:67851919_CT_C	67851919	CT	C	0.3272180	-0.0380349	0.0066129	1.10E-09
17	BPTF	rs34733047	67852002	T	TA	0.3460470	-0.0398353	0.0064536	1.70E-10
17	BPTF	rs78452260	67852406	G	T	0.3451870	-0.0391837	0.0064454	3.20E-10
17	BPTF	rs79993364	67852461	C	CCT	0.3392820	-0.0401907	0.0064742	1.50E-10
17	BPTF	rs4791048	67852878	G	A	0.3392820	-0.0401907	0.0064742	1.50E-10
17	BPTF	rs2086744	67853159	C	G	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs2046323	67853811	T	G	0.3450980	-0.0393252	0.0064450	2.80E-10
17	BPTF	rs4791046	67855857	G	A	0.3457850	-0.0395562	0.0064483	1.70E-10
17	BPTF	rs4790908	67856791	T	G	0.3450870	-0.0392490	0.0064449	3.00E-10
17	BPTF	rs11079709	67857247	C	T	0.3446710	-0.0396854	0.0064642	2.40E-10
17	BPTF	rs62084235	67857321	C	T	0.3429480	-0.0395256	0.0064710	3.00E-10
17	BPTF	rs12450072	67857401	C	G	0.3452090	-0.0393713	0.0064448	2.70E-10
17	BPTF	rs74541577	67857535	C	T	0.3460610	-0.0392968	0.0064550	2.70E-10
17	BPTF	rs74561219	67857643	T	A	0.3451550	-0.0392227	0.0064451	3.10E-10
17	BPTF	rs28609796	67858988	T	A	0.3424940	-0.0384662	0.0064930	1.10E-09
17	BPTF	rs62084238	67860457	T	A	0.3453360	-0.0389833	0.0064498	4.10E-10
17	BPTF	rs2128792	67861061	C	T	0.3451040	-0.0392398	0.0064450	3.00E-10
17	BPTF	rs2365764	67861598	G	A	0.3450840	-0.0392339	0.0064448	3.00E-10
17	BPTF	rs62084240	67863117	C	A	0.3450770	-0.0392852	0.0064447	2.90E-10
17	BPTF	rs75352663	67863943	AT	A	0.3449560	-0.0391043	0.0064463	3.50E-10
17	BPTF	rs60432293	67864291	T	C	0.3451060	-0.0393502	0.0064450	2.60E-10
17	BPTF	rs59950564	67864743	A	G	0.3450770	-0.0392852	0.0064447	2.90E-10
17	BPTF	rs8077872	67864943	G	T	0.3392710	-0.0402155	0.0064741	1.50E-10
17	BPTF	rs34739687	67865998	TA	T	0.3392710	-0.0402155	0.0064741	1.50E-10
17	BPTF	rs4790905	67867234	C	A	0.3450780	-0.0392859	0.0064447	2.90E-10
17	BPTF	rs34872586	67867350	T	C	0.3453190	-0.0391685	0.0064475	3.40E-10
17	BPTF	rs58141639	67868786	C	T	0.3451030	-0.0392818	0.0064455	2.80E-10
17	BPTF	rs61067468	67869919	G	A	0.3488800	-0.0393528	0.0064687	3.10E-10
17	BPTF	rs62084246	67871795	G	C	0.3450470	-0.0391952	0.0064448	3.10E-10
17	BPTF	rs9912084	67871919	A	C	0.3450740	-0.0392735	0.0064447	2.90E-10
17	BPTF	rs9912770	67872117	C	T	0.3450740	-0.0392735	0.0064447	2.90E-10
17	BPTF	rs11869819	67872553	A	C	0.3450490	-0.0391986	0.0064448	3.10E-10
17	BPTF	rs55939964	67873181	G	A	0.3456380	-0.0395449	0.0064455	2.40E-10
17	BPTF	rs12602912	67873957	C	T	0.3452600	-0.0390864	0.0064408	3.20E-10
17	BPTF	rs12450907	67874528	T	G	0.3450490	-0.0391986	0.0064448	3.10E-10
17	BPTF	rs9890629	67875443	G	A	0.3450490	-0.0391986	0.0064448	3.10E-10
17	BPTF	rs12451707	67875482	G	A	0.3450490	-0.0391986	0.0064448	3.10E-10
17	BPTF	rs4569324	67876634	C	T	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs62084247	67876787	C	T	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs112651248	67876819	AAG	A	0.3392700	-0.0402194	0.0064740	1.40E-10
17	BPTF	rs9915108	67878347	T	C	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs9913471	67878379	C	T	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs62084248	67878425	C	T	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs12451511	67878745	T	G	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs62084249	67878882	A	G	0.3450750	-0.0392768	0.0064447	2.90E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	BPTF	rs73352808	67879041	G	A	0.3592010	-0.0367023	0.0065195	6.30E-09
17	BPTF	rs11867517	67879210	C	T	0.3457860	-0.0395714	0.0064584	2.10E-10
17	BPTF	rs11867537	67879376	A	G	0.3460640	-0.0397594	0.0064462	2.00E-10
17	BPTF	rs11867618	67879471	G	A	0.3463920	-0.0384430	0.0064450	6.70E-10
17	BPTF	rs35243555	67880361	G	C	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs58122682	67880799	T	C	0.3458440	-0.0391989	0.0064516	3.10E-10
17	BPTF	rs8074644	67882101	G	C	0.3451460	-0.0393431	0.0064448	2.70E-10
17	BPTF	rs62084251	67882620	G	A	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs9892803	67883127	T	G	0.3450750	-0.0392768	0.0064447	2.90E-10
17	BPTF	rs140912776	67883456	TA	T	0.3468720	-0.0394584	0.0064479	2.80E-10
17	BPTF	rs62084252	67883462	G	C	0.3468720	-0.0394584	0.0064479	2.80E-10
17	BPTF	rs9897982	67883476	G	T	0.3403960	-0.0403389	0.0064791	1.40E-10
17	BPTF	rs6504545	67884251	A	G	0.3457280	-0.0391812	0.0064529	2.80E-10
17	BPTF	rs6504546	67884269	A	C	0.3459280	-0.0397710	0.0064460	1.50E-10
17	BPTF	rs7213292	67884327	A	G	0.3457620	-0.0397494	0.0064454	1.80E-10
17	BPTF	rs115210018	67884423	T	C	0.3579790	-0.0357024	0.0065298	1.10E-08
17	BPTF	rs3935969	67885843	A	G	0.3450630	-0.0393494	0.0064448	2.70E-10
17	BPTF	rs4318247	67886056	A	G	0.3450630	-0.0393494	0.0064448	2.70E-10
17	BPTF	rs75360723	67886426	A	AT	0.3448020	-0.0401166	0.0064497	1.40E-10
17	BPTF	rs8082661	67888585	G	A	0.3454350	-0.0383390	0.0065384	1.50E-09
17	BPTF	rs7208663	67889055	T	C	0.3450630	-0.0393494	0.0064448	2.70E-10
17	BPTF	rs75231441	67889369	A	G	0.3450630	-0.0393494	0.0064448	2.70E-10
17	BPTF	rs12452823	67889667	G	A	0.3450620	-0.0393420	0.0064449	2.70E-10
17	BPTF	rs11079710	67889795	C	T	0.3144640	-0.0347206	0.0066053	2.50E-08
17	BPTF	rs6504548	67889932	T	C	0.3392280	-0.0402717	0.0064745	1.40E-10
17	BPTF	rs8079291	67891506	A	G	0.3441170	-0.0393205	0.0064557	2.60E-10
17	BPTF	rs8079754	67891780	A	G	0.3450460	-0.0392924	0.0064451	2.80E-10
17	BPTF	rs6504549	67892668	A	G	0.3392070	-0.0402229	0.0064748	1.50E-10
17	BPTF	rs61676547	67896391	G	C	0.3343270	-0.0416159	0.0065512	7.70E-11
17	BPTF	rs56148300	67896636	T	C	0.3266890	-0.0425314	0.0065403	2.60E-11
17	BPTF	rs3206817	67896718	A	G	0.3327490	-0.0413297	0.0065088	6.70E-11
17	BPTF	rs56404791	67896903	T	G	0.3273160	-0.0426835	0.0065347	2.30E-11
17	BPTF	rs145606454	67897173	AC	A	0.3318970	-0.0418025	0.0065124	4.10E-11
17	BPTF	rs60477798	67897174	C	A	0.3556670	-0.0416449	0.0065327	7.80E-11
17	BPTF	rs6504550	67898426	A	G	0.2945540	-0.0382893	0.0067300	3.20E-09
17	BPTF	chr17:67898661_CT_C	67898661	CT	C	0.3304770	-0.0413339	0.0065926	7.60E-11
17	BPTF	rs7216064	67902693	G	A	0.3339520	-0.0412136	0.0064976	8.40E-11
17	BPTF	rs8065906	67906529	G	A	0.3459090	-0.0387014	0.0064483	4.40E-10
17	BPTF	rs6504551	67907210	T	G	0.2946030	-0.0376901	0.0067294	5.10E-09
17	BPTF	rs12602655	67913326	A	G	0.3446620	-0.0382415	0.0064583	6.70E-10
17	BPTF	rs8072225	67916844	A	G	0.3260580	-0.0423129	0.0065458	3.50E-11
17	BPTF	rs55896768	67917242	T	C	0.3265090	-0.0422777	0.0065479	3.60E-11
17	BPTF	rs12600941	67922691	A	G	0.3452450	-0.0388081	0.0064542	3.90E-10
17	BPTF	rs62085991	67924392	G	A	0.3459050	-0.0385453	0.0064493	4.70E-10
17	BPTF	rs62085992	67926967	T	A	0.3463250	-0.0386617	0.0064508	4.70E-10
17	BPTF	rs62085993	67927036	T	C	0.3329720	-0.0416009	0.0065021	5.10E-11
17	BPTF	rs73338706	67930488	T	C	0.3317240	-0.0410363	0.0065177	1.10E-10
17	BPTF	rs4271626	67934017	G	A	0.3327760	-0.0417601	0.0065033	4.60E-11
17	BPTF	rs4791300	67934656	A	G	0.3276330	-0.0431044	0.0065704	2.20E-11
17	BPTF	rs4791299	67934821	A	G	0.3269900	-0.0437118	0.0065688	8.70E-12
17	BPTF	rs56393562	67937802	C	T	0.3321220	-0.0422392	0.0065138	2.90E-11
17	BPTF	rs5821447	67940063	TATTA ^A	T	0.3328220	-0.0424891	0.0065156	2.80E-11
17	BPTF	rs8071463	67942539	A	G	0.3317490	-0.0415282	0.0065119	5.90E-11
17	BPTF	rs12451721	67942959	G	A	0.3457030	-0.0386165	0.0064496	4.70E-10
17	BPTF	rs6504555	67944611	G	A	0.3290610	-0.0423879	0.0065668	4.10E-11
17	BPTF	rs11870068	67948399	A	C	0.3316560	-0.0408646	0.0065134	1.20E-10
17	BPTF	rs7223357	67949420	C	G	0.3324160	-0.0402835	0.0065067	2.20E-10
17	BPTF	rs7223813	67949724	A	G	0.3324160	-0.0402835	0.0065067	2.20E-10
17	BPTF	rs12449442	67951524	G	A	0.3433740	-0.0404482	0.0064992	2.00E-10
17	BPTF	rs11867401	67951854	A	G	0.3267530	-0.0415447	0.0065396	8.30E-11
17	BPTF	rs9907491	67953877	A	G	0.3267360	-0.0417105	0.0065390	7.20E-11
17	BPTF	rs71142114	67954174	G	GT	0.3241320	-0.0407644	0.0065780	2.80E-10
17	BPTF	rs4790974	67954991	T	A	0.3268270	-0.0417450	0.0065400	6.90E-11
17	BPTF	rs4790973	67955017	C	T	0.3328160	-0.0407993	0.0065039	1.30E-10
17	BPTF	rs77706698	67957232	G	A	0.3458950	-0.0377317	0.0064556	1.20E-09
17	BPTF	rs12601759	67959168	A	G	0.3323150	-0.0410074	0.0065100	1.20E-10
17	BPTF	rs9899520	67961452	G	A	0.3226620	-0.0420307	0.0065896	6.60E-11
17	BPTF	rs146879804	67961470	C	CT	0.3470340	-0.0377592	0.0064737	1.40E-09
17	BPTF	chr17:67961971_CA_C	67961971	CA	C	0.2940640	-0.0381631	0.0067402	4.00E-09
17	BPTF	rs148803332	67962134	C	AAAGA	0.3138220	-0.0421586	0.0067231	1.40E-10
17	BPTF	rs60626066	67965117	G	A	0.3523450	-0.0426445	0.0065023	3.50E-11
17	BPTF	rs10445361	67966122	T	G	0.3336240	-0.0446239	0.0065090	3.20E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	BPTF	rs5821446	67966422	AT	A	0.3322770	-0.0445809	0.0065084	3.70E-12
17	BPTF	rs77596502	67968054	TAGG	T	0.3410730	-0.0385114	0.0064832	6.20E-10
17	BPTF	rs62086042	67971327	T	C	0.2864420	-0.0360078	0.0067958	2.10E-08
17	BPTF	rs62086043	67971887	A	G	0.3280100	-0.0415529	0.0065634	8.50E-11
17	BPTF	rs62086044	67974721	G	T	0.3281380	-0.0406381	0.0065481	1.50E-10
17	BPTF	rs62086045	67977615	G	A	0.3270490	-0.0416199	0.0065553	6.50E-11
17	BPTF	rs4791212	67979269	C	T	0.3394500	-0.0385434	0.0065069	6.50E-10
17	BPTF	rs7210027	67980937	T	C	0.3265390	-0.0417127	0.0065631	6.50E-11
17	BPTF	rs4790941	67981016	G	A	0.3269450	-0.0416263	0.0065574	6.20E-11
17	BPTF	rs11656743	67984173	A	G	0.3251680	-0.0417233	0.0065728	5.70E-11
17	BPTF *	rs62086046	67986827	C	T	0.3278160	-0.0415865	0.0065584	5.90E-11
17	C17orf58 *	rs75772932	67988421	G	A	0.3429160	-0.0369019	0.0064981	2.40E-09
17	C17orf58	rs5821444	67991393	T	TTAA	0.3234360	-0.0425127	0.0066400	3.30E-11
17	C17orf58	rs9891146	67991933	C	T	0.2850650	-0.0373424	0.0068714	7.10E-09
17	C17orf58 *	rs7502307	67993845	C	G	0.3427900	-0.0387086	0.0065929	6.30E-10
17	C17orf58 *	rs113985803	67993855	A	G	0.3263350	-0.0420448	0.0066591	5.60E-11
17	C17orf58 *	rs56305452	67994384	A	C	0.3247650	-0.0413837	0.0066579	1.10E-10
17	C17orf58 *	rs56315139	67994455	G	C	0.2835870	-0.0364682	0.0069156	1.80E-08
17	C17orf58 *	rs62086884	67998284	G	C	0.3458010	-0.0388448	0.0065343	4.40E-10
17	C17orf58 *	rs4791295	68001201	G	A	0.3373980	-0.0407870	0.0065163	6.10E-11
17	C17orf58 *	rs28855509	68002051	T	C	0.3376690	-0.0397399	0.0065109	1.70E-10
17	C17orf58 *	rs74564337	68003451	C	T	0.3373640	-0.0413198	0.0065301	4.40E-11
17	C17orf58 *	rs6504568	68003532	T	C	0.3370030	-0.0408223	0.0065206	6.30E-11
17	C17orf58 *	rs75756093	68004462	TAGTC	T	0.3398740	-0.0398966	0.0065313	1.90E-10
17	C17orf58 *	rs62086889	68004487	C	T	0.3388190	-0.0403492	0.0065270	1.20E-10
17	C17orf58 *	rs8081714	68005014	G	A	0.3377480	-0.0405733	0.0065178	9.20E-11
17	C17orf58 *	chr17:68007425_G_GT	68007425	G	GT	0.3093030	-0.0401488	0.0067819	2.20E-09
17	C17orf58 *	rs28437386	68008555	T	A	0.3495760	-0.0385620	0.0065650	8.70E-10
17	C17orf58 *	rs78186330	68008599	G	A	0.3427190	-0.0384790	0.0065473	9.30E-10
17	C17orf58 *	chr17:68011432_TTTTG_T	68011432	TTTTG	T	0.3393690	-0.0406876	0.0065300	8.80E-11
17	C17orf58 *	rs62086897	68011928	A	C	0.3348030	-0.0394650	0.0065193	3.50E-10
17	C17orf58 *	rs62086898	68013004	A	G	0.3348030	-0.0394650	0.0065193	3.50E-10
17	C17orf58 *	rs62086899	68013018	C	T	0.3348030	-0.0394650	0.0065193	3.50E-10
17	KPNA2 *	rs7225959	68018993	T	A	0.3391280	-0.0402977	0.0065065	1.60E-10
17	KPNA2 *	rs62086903	68019890	T	C	0.3229380	-0.0405640	0.0065671	2.10E-10
17	KPNA2 *	rs62086904	68019980	C	T	0.3372100	-0.0384721	0.0064958	6.10E-10
17	KPNA2 *	rs62086906	68023810	T	C	0.3362010	-0.0384771	0.0064986	6.40E-10
17	KPNA2 *	rs145520076	68024495	G	A	0.3428030	-0.0390938	0.0065448	5.70E-10
17	KPNA2 *	rs189628481	68024502	C	T	0.3439710	-0.0385340	0.0065489	9.00E-10
17	KPNA2 *	rs192988621	68024504	C	T	0.3421200	-0.0384879	0.0065294	1.00E-09
17	KPNA2 *	rs183763906	68024506	C	T	0.3421200	-0.0384879	0.0065294	1.00E-09
17	KPNA2 *	rs200026262	68024507	A	G	0.3439710	-0.0385340	0.0065489	9.00E-10
17	KPNA2 *	rs62086907	68025051	A	G	0.3345400	-0.0371302	0.0065874	2.20E-09
17	KPNA2 *	rs62086908	68025098	G	C	0.3362040	-0.0381247	0.0065197	9.10E-10
17	KPNA2 *	rs7405987	68025278	A	G	0.3367380	-0.0387279	0.0064995	4.80E-10
17	KPNA2 *	rs8076753	68026725	G	A	0.3364650	-0.0385080	0.0064977	6.20E-10
17	KPNA2 *	rs79778350	68027670	C	T	0.3241850	-0.0379160	0.0066922	5.10E-09
17	KPNA2 *	rs62084669	68028054	A	G	0.3363420	-0.0386204	0.0064979	5.50E-10
17	KPNA2 *	rs77536355	68032115	T	A	0.3447930	-0.0369764	0.0064711	2.70E-09
17	KPNA2 *	chr17:68032921_CT_C	68032921	CT	C	0.3529480	-0.0370741	0.0064988	2.30E-09
17	KPNA2 *	rs35229997	68033474	T	G	0.3384150	-0.0384410	0.0064862	8.30E-10
17	KPNA2 *	rs7226002	68034719	T	C	0.3381520	-0.0384145	0.0064875	8.00E-10
17	KPNA2 *	rs62084681	68034876	G	A	0.3381520	-0.0384145	0.0064875	8.00E-10
17	KPNA2 *	rs62084682	68035405	G	C	0.3402000	-0.0371335	0.0064768	2.30E-09
17	KPNA2	rs7214119	68036182	G	A	0.3382190	-0.0383888	0.0064884	8.40E-10
17	KPNA2	rs8075764	68036993	C	A	0.3381520	-0.0384145	0.0064875	8.00E-10
17	KPNA2	rs146286181	68039012	CTA	C	0.3378030	-0.0383914	0.0064944	8.10E-10
17	KPNA2	rs62084689	68039173	T	C	0.3379780	-0.0380128	0.0064996	1.10E-09
17	KPNA2	rs62084692	68039728	C	T	0.3388570	-0.0388985	0.0065004	5.70E-10
17	KPNA2	chr17:68040078_C_CA	68040078	C	CA	0.3473060	-0.0380821	0.0065281	1.10E-09
17	KPNA2	chr17:68040818_A_AT	68040818	A	AT	0.2963690	-0.0347862	0.0067105	4.20E-08
17	KPNA2	rs62084694	68041478	G	T	0.3375020	-0.0383403	0.0064903	8.30E-10
17	KPNA2	rs62084697	68042440	G	A	0.3375020	-0.0383403	0.0064903	8.30E-10
17	KPNA2	chr17:68045755_AT_A	68045755	AT	A	0.3408230	-0.0370589	0.0065502	3.00E-09
17	KPNA2 *	rs62084703	68047268	C	T	0.3375700	-0.0378929	0.0064890	1.30E-09
17	KPNA2 *	rs78496681	68049047	C	CA	0.3365000	-0.0385763	0.0065041	7.30E-10
17	KPNA2 *	rs74354868	68049715	G	A	0.3375480	-0.0383903	0.0064904	7.90E-10
17	KPNA2 *	rs7503050	68052346	G	T	0.3374040	-0.0384555	0.0064914	7.50E-10
17	KPNA2 *	rs7503810	68053415	G	A	0.3332320	-0.0394234	0.0065100	4.00E-10
17	KPNA2 *	rs62084708	68053591	G	A	0.3331090	-0.0391237	0.0065113	5.20E-10
17	KPNA2 *	rs72318931	68058249	CTCTT	C	0.3363190	-0.0374132	0.0066267	6.70E-09
17	KPNA2 *	rs35040337	68060566	A	G	0.3330720	-0.0392802	0.0065120	4.30E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	KPNA2 *	rs200647245	68062663	A	AT	0.3404080	-0.0364521	0.0065351	8.50E-09
17	KPNA2 *	rs74976757	68064790	G	T	0.3374700	-0.0385801	0.0064932	6.40E-10
17	KPNA2 *	rs62084740	68065068	C	T	0.3374700	-0.0385801	0.0064932	6.40E-10
17	KPNA2 *	rs74900486	68066757	C	T	0.3374700	-0.0385801	0.0064932	6.40E-10
17	KPNA2 *	rs28850355	68068281	T	C	0.2913870	-0.0354597	0.0067617	4.20E-08
17	KPNA2 *	chr17:68069522_AT_A	68069522	AT	A	0.2949820	-0.0345690	0.0067202	4.90E-08
17	KPNA2 *	rs75544834	68070322	T	C	0.3337250	-0.0384486	0.0065247	1.20E-09
17	KPNA2 *	rs184478609	68071576	T	C	0.3351880	-0.0386298	0.0065271	5.90E-10
17	KPNA2 *	rs147170518	68079918	T	AATCC1	0.3395510	-0.0378386	0.0064981	1.50E-09
17	KPNA2 *	rs78352159	68082103	C	G	0.3393330	-0.0378610	0.0064948	1.90E-09
17	KPNA2 *	rs62084744	68082412	T	C	0.3404850	-0.0383970	0.0065057	1.10E-09
17	KPNA2 *	rs869223723	68082741	T	TTA	0.3401430	-0.0380508	0.0064989	1.70E-09
17	KPNA2 *	rs76877263	68092945	G	C	0.3381470	-0.0380069	0.0065103	1.90E-09
17	KPNA2 *	rs62084752	68093252	G	C	0.3386550	-0.0376236	0.0065099	2.90E-09
17	KPNA2 *	rs28512206	68093732	A	T	0.3384300	-0.0377170	0.0065183	2.60E-09
17	KPNA2 *	rs62084755	68099765	G	A	0.3431080	-0.0362664	0.0064984	7.60E-09
17	LINC00674	rs75868869	68102013	G	A	0.3440050	-0.0363914	0.0064928	6.90E-09
19	INSR	rs12461909	7145620	G	C	0.4882490	-0.0343552	0.0061569	3.80E-08
19	INSR	rs12460478	7145951	T	C	0.4883730	-0.0345097	0.0061555	3.30E-08
19	INSR	rs16994221	7147505	G	C	0.4882110	-0.0351781	0.0061799	1.60E-08
19	ANGPTL4 *	rs12974291	8353724	G	A	0.0761029	-0.0692523	0.0116066	5.60E-09
19	ANGPTL4 *	rs73497430	8355170	G	T	0.0758140	-0.0668630	0.0116362	4.70E-08
19	ANGPTL4 *	rs11881114	8356174	C	T	0.0161917	-0.1744110	0.0242839	7.20E-12
19	ANGPTL4 *	rs113472294	8356384	A	G	0.0161952	-0.1743170	0.0242813	7.50E-12
19	ANGPTL4 *	rs111651803	8356534	G	A	0.0161987	-0.1735630	0.0242787	9.30E-12
19	ANGPTL4 *	rs62117487	8359176	G	A	0.0293277	-0.1317190	0.0182843	1.10E-11
19	ANGPTL4 *	rs112090257	8359426	A	G	0.0162407	-0.1739480	0.0242476	7.90E-12
19	ANGPTL4 *	rs112365616	8360096	T	C	0.0158145	-0.1760260	0.0245723	1.40E-11
19	ANGPTL4 *	rs111500536	8360674	A	G	0.0318285	-0.1359000	0.0175183	1.50E-13
19	ANGPTL4 *	rs112634335	8361765	C	G	0.0163745	-0.1739690	0.0241393	6.90E-12
19	ANGPTL4 *	rs112822112	8363947	A	G	0.0152499	-0.1755310	0.0250463	1.70E-11
19	ANGPTL4	rs113446232	8368117	T	C	0.0166263	-0.1719840	0.0239579	6.70E-12
19	ANGPTL4	rs7255436	8368312	A	C	0.0828471	-0.0669132	0.0111188	8.50E-09
19	ANGPTL4	rs77439987	8369178	A	G	0.0169025	-0.1690670	0.0237535	8.20E-12
19	ANGPTL4	rs10410586	8370135	G	A	0.0821253	-0.0681986	0.0111666	4.30E-09
19	ANGPTL4	rs35061979	8371316	A	G	0.0167807	-0.1714610	0.0238386	4.80E-12
19	ANGPTL4	rs112625532	8372050	A	G	0.0167332	-0.1724980	0.0238680	3.80E-12
19	RAB11B-AS	rs111313909	8374409	C	T	0.0167276	-0.1748620	0.0238729	2.00E-12
19	RAB11B-AS	rs113896502	8375087	G	C	0.0167275	-0.1748530	0.0238729	2.00E-12
19	RAB11B-AS	rs11910861	8376434	A	T	0.0167275	-0.1748530	0.0238729	2.00E-12
19	RAB11B-AS	rs113687395	8377181	A	C	0.0167275	-0.1748530	0.0238729	2.00E-12
19	RAB11B-AS	rs112381844	8380361	T	C	0.0167282	-0.1748460	0.0238729	2.00E-12
19	RAB11B-AS	rs7249520	8381172	A	G	0.0813462	-0.0681996	0.0112299	5.60E-09
19	RAB11B-AS	rs7249624	8381251	A	G	0.0813492	-0.0681653	0.0112297	5.70E-09
19	RAB11B-AS	rs1834953	8382280	C	T	0.0813417	-0.0678959	0.0112313	6.60E-09
19	RAB11B-AS	rs149784573	8382281	A	G	0.0167318	-0.1751230	0.0238705	1.90E-12
19	RAB11B-AS	rs4350678	8382482	G	A	0.0813423	-0.0679068	0.0112313	6.60E-09
19	RAB11B-AS	rs4044436	8383150	C	T	0.0813378	-0.0679530	0.0112322	6.30E-09
19	RAB11B-AS	rs4044435	8383293	C	T	0.0813293	-0.0680170	0.0112327	6.30E-09
19	RAB11B-AS	rs113937955	8385469	C	T	0.0165427	-0.1776140	0.0240047	1.00E-12
19	RAB11B-AS	rs11668346	8385970	T	A	0.0809445	-0.0691373	0.0112604	5.00E-09
19	RAB11B-AS	rs12981318	8386546	A	G	0.0809197	-0.0694457	0.0112629	4.20E-09
19	RAB11B-AS	rs7351098	8386787	C	G	0.0808799	-0.0694565	0.0112674	4.50E-09
19	RAB11B-AS	rs11666233	8387161	A	C	0.0808741	-0.0701038	0.0112684	3.30E-09
19	RAB11B-AS	rs11666003	8387218	A	G	0.0807909	-0.0703251	0.0112761	2.70E-09
19	RAB11B-AS	rs71175847	8387366	T	TG	0.0805250	-0.0697841	0.0112962	3.80E-09
19	RAB11B-AS	rs62117510	8387729	G	T	0.0798672	-0.0703325	0.0113497	3.20E-09
19	RAB11B-AS	rs28729307	8387858	G	A	0.0802629	-0.0706614	0.0113193	2.70E-09
19	RAB11B-AS	rs10413136	8387995	C	T	0.0801399	-0.0707998	0.0113306	2.80E-09
19	RAB11B-AS	rs7250870	8388798	T	C	0.0797884	-0.0694943	0.0113654	5.60E-09
19	RAB11B-AS	rs7254882	8388938	C	T	0.0796871	-0.0685044	0.0113746	9.70E-09
19	RAB11B-AS	rs10421495	8389639	G	A	0.0788651	-0.0687007	0.0114513	1.10E-08
19	RAB11B	rs112981054	8390708	A	G	0.0160101	-0.1780330	0.0244503	1.70E-12
19	RAB11B	rs113090151	8390816	A	G	0.0160101	-0.1780200	0.0244503	1.70E-12
19	RAB11B	rs3786624	8391350	G	T	0.0780638	-0.0697550	0.0115462	7.00E-09
19	RAB11B	rs3786623	8391496	G	A	0.0779947	-0.0693734	0.0115530	8.90E-09
19	RAB11B	rs4267458	8392270	T	C	0.0777823	-0.0697290	0.0115845	7.40E-09
19	RAB11B	rs10403402	8401621	A	G	0.0151586	-0.1794950	0.0251055	3.20E-12
19	RAB11B *	rs10426486	8405069	A	G	0.0152030	-0.1774110	0.0250500	4.10E-12
19	RAB11B *	rs6603067	8405680	C	T	0.0154498	-0.1783940	0.0248399	1.90E-12
19	MARCH2 *	rs71175850	8409899	CA	C	0.0154205	-0.1785990	0.0248650	1.80E-12
19	MARCH2 *	rs62117520	8411923	A	G	0.0154218	-0.1788320	0.0248651	1.80E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	MARCH2 *	rs368688811	8413049	T	C	0.0151576	-0.1767300	0.0250903	5.10E-12
19	MARCH2	rs532604082	8415733	C	A	0.0114020	-0.1691920	0.0289938	2.50E-08
19	MARCH2	rs62117522	8416119	A	G	0.0154193	-0.1785790	0.0248680	1.80E-12
19	MARCH2	rs112826244	8422486	G	A	0.0151698	-0.1784140	0.0250817	3.10E-12
19	MARCH2	rs77968216	8422767	C	T	0.0142315	-0.1842430	0.0258938	1.70E-12
19	MARCH2	rs199582202	8425619	A	AT	0.0158939	-0.1482490	0.0246901	5.90E-09
19	MARCH2	rs61499007	8428930	T	C	0.0133726	-0.1807560	0.0266160	2.10E-11
19	MARCH2	rs17159300	8429250	T	C	0.0133462	-0.1805520	0.0266440	2.30E-11
19	MARCH2	rs34344658	8430227	C	G	0.0133590	-0.1803590	0.0266301	2.30E-11
19	MARCH2	rs34350946	8430231	T	C	0.0133938	-0.1814250	0.0266347	1.60E-11
19	MARCH2	rs113550925	8435655	G	C	0.0133818	-0.1806580	0.0266059	1.90E-11
19	MARCH2	rs60748247	8435690	CACCTC	C	0.0136403	-0.1826240	0.0263395	6.30E-12
19	MARCH2	rs6603071	8435751	T	G	0.0133818	-0.1806580	0.0266059	1.90E-11
19	MARCH2	rs112363339	8437217	C	T	0.0132253	-0.1763400	0.0267519	7.80E-11
19	MARCH2	rs7408526	8437225	A	C	0.0132252	-0.1763360	0.0267519	7.80E-11
19	MARCH2	rs7408547	8437349	A	T	0.0132251	-0.1763460	0.0267519	7.80E-11
19	MARCH2	rs12976614	8437541	T	C	0.0133078	-0.1742690	0.0266824	1.10E-10
19	MARCH2	rs11259981	8438690	A	G	0.0132343	-0.1765920	0.0267413	7.50E-11
19	MARCH2 *	rs7251323	8440340	T	C	0.0132412	-0.1762450	0.0267343	7.80E-11
19	MARCH2 *	rs6603074	8440448	C	T	0.0135134	-0.1768700	0.0264503	3.70E-11
19	MARCH2 *	rs11259982	8441103	T	C	0.0132687	-0.1748980	0.0267098	1.00E-10
19	HNRNPM *	rs10796330	8442955	A	G	0.0132796	-0.1703060	0.0266958	3.20E-10
19	HNRNPM	rs11881939	8445260	T	C	0.0132900	-0.1701540	0.0266852	3.20E-10
19	HNRNPM	rs7245737	8445529	T	G	0.0132935	-0.1685310	0.0266818	4.80E-10
19	HNRNPM	rs6603078	8446441	C	G	0.0135674	-0.1679290	0.0264246	3.50E-10
19	HNRNPM	rs78136847	8447444	T	A	0.0132970	-0.1687870	0.0266782	4.30E-10
19	HNRNPM	rs76586439	8448918	A	G	0.0132967	-0.1688090	0.0266782	4.30E-10
19	HNRNPM	rs11259984	8450593	T	G	0.0132967	-0.1688090	0.0266782	4.30E-10
19	HNRNPM	rs113420240	8450730	A	T	0.0107071	-0.1868950	0.0297724	2.20E-09
19	HNRNPM	rs7253907	8452130	G	A	0.0133040	-0.1682940	0.0266713	4.60E-10
19	HNRNPM	rs6603081	8454016	C	T	0.0133425	-0.1672880	0.0266331	5.90E-10
19	HNRNPM	rs10420411	8455165	T	G	0.0121397	-0.1652040	0.0279415	7.60E-09
19	HNRNPM	rs151032440	8458266	C	A	0.0133426	-0.1672800	0.0266331	5.90E-10
19	HNRNPM	rs372974746	8460844	CTA	C	0.0133426	-0.1672780	0.0266331	5.90E-10
19	HNRNPM	rs1057253	8461561	C	G	0.0135938	-0.1693080	0.0263726	2.20E-10
19	HNRNPM	rs8102587	8463426	A	G	0.0133427	-0.1672860	0.0266331	5.90E-10
19	HNRNPM	rs11878480	8465813	C	T	0.0133423	-0.1672510	0.0266331	6.00E-10
19	HNRNPM	rs11259987	8467885	G	A	0.0136179	-0.1694160	0.0263490	2.00E-10
19	HNRNPM	rs11259988	8468021	T	C	0.0133669	-0.1674010	0.0266088	5.40E-10
19	HNRNPM	rs7258281	8468620	T	C	0.0133669	-0.1674010	0.0266088	5.40E-10
19	HNRNPM	rs10421511	8469041	A	G	0.0140373	-0.1697460	0.0259359	1.30E-10
19	HNRNPM	rs113957806	8470495	G	T	0.0133669	-0.1674010	0.0266088	5.40E-10
19	HNRNPM	rs7507730	8470498	T	G	0.0133857	-0.1670990	0.0266022	6.30E-10
19	HNRNPM	rs145645068	8471306	G	T	0.0143713	-0.1593610	0.0257003	4.30E-10
19	HNRNPM	rs77540833	8472481	G	A	0.0133668	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs7507621	8475376	T	C	0.0133668	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs7408534	8476906	G	T	0.0136178	-0.1694120	0.0263490	2.00E-10
19	HNRNPM	rs126111110	8477456	A	G	0.0136178	-0.1694120	0.0263490	2.00E-10
19	HNRNPM	rs7255548	8477853	C	T	0.0133668	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs58043469	8480627	T	C	0.0130272	-0.1689130	0.0269621	8.30E-10
19	HNRNPM	rs111364559	8481241	C	T	0.0134503	-0.1674080	0.0265403	4.80E-10
19	HNRNPM	rs6603083	8482573	A	G	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs7508561	8483613	A	T	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs7409317	8483991	C	T	0.0136177	-0.1694120	0.0263490	2.00E-10
19	HNRNPM	rs6603084	8484333	T	C	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs7250951	8484576	A	T	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs10412549	8485223	G	C	0.0136177	-0.1694120	0.0263490	2.00E-10
19	HNRNPM	rs2230647	8486210	T	C	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs55635857	8486649	CTGAT	C	0.0136177	-0.1694120	0.0263490	2.00E-10
19	HNRNPM	rs11669139	8486968	A	G	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs12608524	8487283	C	T	0.0133667	-0.1673980	0.0266088	5.40E-10
19	HNRNPM	rs7507526	8488438	C	T	0.0136247	-0.1695490	0.0263423	2.00E-10
19	HNRNPM	rs6992	8488746	C	T	0.0133789	-0.1673390	0.0265985	5.00E-10
19	PRAM1	rs58034536	8493082	A	G	0.0133561	-0.1687860	0.0266191	3.90E-10
19	DOCK6	rs4804575	11218965	A	G	0.2603110	0.0477446	0.0070293	1.20E-10
19	DOCK6	rs4804576	11220678	T	G	0.2623440	0.0475245	0.0069798	1.10E-10
19	DOCK6	rs4804153	11220855	T	C	0.2591500	0.0508469	0.0070198	7.30E-12
19	DOCK6	rs3826815	11221829	T	C	0.2623440	0.0474397	0.0069796	1.20E-10
19	DOCK6	rs12971537	11222682	T	G	0.2621430	0.0475522	0.0069823	1.00E-10
19	DOCK6	rs12974173	11222683	T	A	0.2621430	0.0475522	0.0069823	1.00E-10
19	DOCK6	rs3810308	11222920	C	T	0.2663360	0.0473524	0.0069216	8.70E-11
19	DOCK6	rs4804154	11223503	T	C	0.2661560	0.0476912	0.0069210	6.10E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	DOCK6	rs4804155	11223619	G	C	0.2667580	0.0473022	0.0069126	9.40E-11
19	DOCK6	rs8101801	11224801	A	C	0.2667400	0.0472264	0.0069133	9.80E-11
19	DOCK6	rs66466742	11225768	T	C	0.2667960	0.0473607	0.0069143	8.40E-11
19	DOCK6	rs1865063	11230353	T	C	0.2639040	0.0512509	0.0069512	2.20E-12
19	DOCK6	rs34757881	11230786	T	C	0.1305450	0.0544316	0.0091528	4.40E-08
19	DOCK6	rs12463177	11231004	C	G	0.2628970	0.0514619	0.0069591	2.60E-12
19	DOCK6	rs17766692	11231923	T	C	0.2666890	0.0483229	0.0069150	4.50E-11
19	DOCK6	chr19:11232871_T_TG	11232871	TG	T	0.2663220	0.0487418	0.0069323	3.50E-11
19	DOCK6	rs17699089	11233119	G	A	0.2636640	0.0520219	0.0069481	1.50E-12
19	DOCK6	rs80068988	11234639	GA	G	0.2731360	0.0470469	0.0068971	1.10E-10
19	DOCK6	rs56322906	11235479	A	G	0.2616370	0.0517339	0.0069618	2.60E-12
19	DOCK6	rs3760782	11235874	T	C	0.2626250	0.0513537	0.0069481	3.30E-12
19	DOCK6	rs737337	11236817	C	T	0.2682620	0.0482705	0.0068969	4.70E-11
19	DOCK6	rs737338	11236981	T	C	0.2603870	0.0513179	0.0069726	3.50E-12
19	DOCK6	rs3745683	11237845	A	G	0.2603370	0.0509838	0.0069842	7.80E-12
19	C19orf80, D	rs2278426	11239812	T	C	0.2616950	0.0490081	0.0069755	5.00E-11
19	NCAN	rs145876852	19248021	C	A	0.0146324	-0.1461410	0.0254234	2.50E-08
19	HAPLN4	rs150641967	19259531	T	TGACA	0.0607602	-0.1347740	0.0128291	1.90E-26
19	TM6SF2	rs58542926	19268740	T	C	0.0665326	-0.1407040	0.0122519	1.00E-31
19	SUGP1	rs8107974	19277691	T	A	0.0960514	-0.0768462	0.0103407	1.50E-14
19	SUGP1	rs200210321	19283081	AG	A	0.1025540	-0.0724047	0.0100893	2.00E-13
19	SUGP1	rs10401969	19296909	C	T	0.0963898	-0.0749149	0.0103319	5.40E-14
19	SUGP1	rs739846	19308262	A	G	0.0960179	-0.0747978	0.0103427	8.70E-14
19	SUGP1	rs57962361	19314216	T	C	0.1645810	-0.0466218	0.0082222	3.10E-09
19	SUGP1	rs11668104	19315372	A	G	0.1645800	-0.0466262	0.0082222	3.00E-09
19	SUGP1	rs186896134	19318143	T	G	0.0124637	-0.1586660	0.0276105	1.60E-08
19	MAU2	rs111234557	19325420	G	C	0.1642790	-0.0470064	0.0082296	2.40E-09
19	MAU2	rs11411903	19329255	TA	T	0.1672080	-0.0488811	0.0081786	5.20E-10
19	MAU2	rs58489806	19346108	T	C	0.1649840	-0.0488130	0.0082184	7.30E-10
19	MAU2	rs11672355	19351893	C	G	0.1625790	-0.0493136	0.0083088	8.10E-10
19	MAU2	rs2285626	19356736	T	C	0.1741460	-0.0543357	0.0080547	2.20E-12
19	MAU2	rs117970794	19357846	T	C	0.0908042	-0.0668558	0.0106048	6.40E-11
19	MAU2 *	rs56255430	19367068	C	A	0.0662729	-0.1124290	0.0122830	1.00E-20
19	GATAD2A †	rs59148799	19373199	G	A	0.1363860	-0.0588335	0.0088900	4.60E-12
19	GATAD2A †	rs12052117	19374296	T	C	0.1363630	-0.0581363	0.0088900	8.20E-12
19	GATAD2A	rs10408875	19392764	C	T	0.1364910	-0.0591238	0.0088857	3.00E-12
19	GATAD2A	rs56241616	19395283	T	C	0.1364850	-0.0591368	0.0088858	2.90E-12
19	GATAD2A	rs10408596	19401848	T	A	0.1364670	-0.0592584	0.0088867	2.60E-12
19	GATAD2A	rs34324111	19402759	G	T	0.1406260	-0.0555225	0.0089050	9.90E-11
19	GATAD2A	rs113460678	19402771	G	T	0.1290160	-0.0593073	0.0091204	1.30E-11
19	GATAD2A	rs188552254	19406360	G	A	0.1341500	-0.0577468	0.0089696	1.10E-11
19	GATAD2A	rs2965185	19414983	C	T	0.1604080	-0.0628757	0.0083138	4.10E-15
19	GATAD2A	rs11668386	19421101	G	A	0.1366030	-0.0587940	0.0088796	3.60E-12
19	GATAD2A	rs8182472	19429082	C	T	0.1367180	-0.0593390	0.0088767	2.50E-12
19	GATAD2A	rs79954596	19437834	G	T	0.1366210	-0.0587458	0.0088796	3.70E-12
19	GATAD2A	rs28720066	19461411	T	G	0.1358250	-0.0593826	0.0089081	2.80E-12
19	GATAD2A	rs73002956	19467934	G	A	0.0701922	-0.1063630	0.0119498	9.50E-20
19	GATAD2A	rs145702982	19468917	T	A	0.0663682	-0.1044300	0.0122643	1.90E-18
19	GATAD2A	rs73002960	19472183	T	C	0.1398150	-0.0578495	0.0088022	6.00E-12
19	GATAD2A	rs3794991	19499787	T	C	0.0732811	-0.1120620	0.0117018	1.70E-22
19	GATAD2A	rs57009615	19502813	G	A	0.1480770	-0.0662321	0.0085853	1.20E-15
19	GATAD2A	chr19:19507571_C_CCCCCAG	19507571	'CCCCA	C	0.0243623	-0.1155780	0.0198031	3.70E-09
19	GATAD2A	rs148458424	19507589	T	G	0.0248260	-0.1145160	0.0196118	3.60E-09
19	GATAD2A †	rs56273306	19510195	C	T	0.1389030	-0.0577707	0.0088220	7.20E-12
19	GATAD2A †	rs113365218	19510388	A	G	0.1383510	-0.0566848	0.0088433	2.00E-11
19	YJEFN3	rs56397647	19531986	T	C	0.1367190	-0.0573967	0.0088928	1.30E-11
19	CILP2 *	rs16996148	19547663	T	G	0.0693622	-0.1133790	0.0120096	5.40E-22
19	CILP2 *	rs17216525	19551411	T	C	0.0755190	-0.1055260	0.0115441	1.00E-20
19	CILP2 *	rs17216588	19553268	T	C	0.0739215	-0.0870255	0.0117337	2.60E-14
19	PBX4 *	rs143988316	19556445	T	C	0.0763415	-0.0916047	0.0115459	3.00E-16
19	PBX4 *	rs78916915	19558399	A	G	0.0757788	-0.0858772	0.0115559	3.50E-14
19	PBX4 *	rs150824230	19559801	A	G	0.0748925	-0.0856376	0.0116293	3.30E-14
19	PBX4 *	rs73004926	19560457	T	C	0.0748925	-0.0856376	0.0116293	3.30E-14
19	PBX4	rs73004933	19564887	T	C	0.0744150	-0.0875983	0.0116551	1.40E-14
19	PBX4	rs141756246	19574661	GT	G	0.0709033	-0.0928406	0.0119930	8.80E-15
19	PBX4	rs73004951	19584419	T	C	0.0947370	-0.0781296	0.0104737	2.30E-14
19	PBX4	rs12608729	19589743	T	C	0.0922184	-0.0796693	0.0105654	1.90E-14
19	PBX4	rs73004959	19600330	T	C	0.0922449	-0.0797207	0.0105606	2.10E-14
19	PBX4	rs73004962	19602260	T	A	0.0844836	-0.0831268	0.0109827	1.60E-14
19	PBX4	rs73004966	19605749	T	C	0.0806244	-0.0908514	0.0112172	2.50E-16
19	PBX4	rs57504626	19609590	T	C	0.0842011	-0.0854808	0.0109995	2.40E-15
19	PBX4	rs16996185	19609979	G	T	0.0855585	-0.0841018	0.0109038	4.60E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	PBX4	rs12610185	19610913	A	G	0.0855206	-0.0840611	0.0109082	3.80E-15
19	PBX4	rs12610191	19611167	T	C	0.0855142	-0.0839889	0.0109095	4.10E-15
19	PBX4	rs10500212	19612406	T	C	0.0857973	-0.0834450	0.0109013	6.40E-15
19	PBX4	rs58847337	19615213	A	G	0.0788154	-0.0927724	0.0113323	8.10E-17
19	PBX4	rs73004975	19616343	G	A	0.0973389	-0.0749631	0.0103026	8.90E-14
19	GMIP	rs2304128	19635342	T	G	0.0537405	-0.0776512	0.0136362	3.20E-09
19	CEBPA *	rs11308479	33321108	C	CA	0.1641040	0.0498730	0.0083455	5.90E-09
19	CEBPA *	rs10403076	33322595	T	C	0.1590520	0.0509374	0.0084192	3.10E-09
19	CEBPA *	rs10403125	33322664	T	C	0.1592430	0.0508029	0.0084183	3.30E-09
19	CEBPA *	rs10402014	33322870	A	G	0.1702920	0.0519271	0.0081874	5.60E-10
19	CEBPA *	rs10411163	33323488	G	A	0.1660250	0.0511552	0.0082630	1.20E-09
19	CEBPA *	rs28885440	33323563	A	G	0.1658890	0.0507391	0.0082623	1.70E-09
19	CEBPA *	rs113811498	33323649	A	ATAT	0.1597040	0.0513283	0.0083785	1.80E-09
19	CEBPA *	rs7254869	33323787	C	T	0.1598190	0.0515105	0.0083734	1.50E-09
19	CEBPA *	rs7253713	33324221	A	G	0.1663200	0.0511774	0.0082411	1.20E-09
19	CEBPA *	rs10415737	33324300	C	G	0.1663270	0.0511326	0.0082410	1.20E-09
19	CEBPA *	rs10415770	33324336	A	G	0.1663310	0.0511337	0.0082408	1.20E-09
19	CEBPA *	rs60656848	33325591	C	T	0.1601690	0.0512397	0.0083599	2.00E-09
19	CEBPA *	rs12608723	33326227	G	A	0.1715310	0.0531262	0.0081235	1.60E-10
19	CEBPA *	rs112167957	33326622	GA	G	0.1715380	0.0531418	0.0081231	1.60E-10
19	CEBPA *	rs7251395	33327226	C	G	0.1650850	0.0530940	0.0082456	3.30E-10
19	CEBPA *	rs7256107	33327250	C	T	0.1713640	0.0530109	0.0081275	1.90E-10
19	CEBPA *	rs10413354	33327308	G	C	0.1715630	0.0528422	0.0081222	2.00E-10
19	CEBPA *	rs10414141	33327311	T	A	0.1650870	0.0530686	0.0082455	3.30E-10
19	CEBPA *	rs7251758	33327479	A	G	0.1716980	0.0529525	0.0081199	1.90E-10
19	CEBPA *	rs112432604	33328149	G	A	0.1695920	0.0546946	0.0082088	1.10E-10
19	CEBPA *	rs10421445	33328331	G	A	0.1717240	0.0528554	0.0081205	2.10E-10
19	CEBPA *	rs10426997	33328338	C	T	0.1646440	0.0531764	0.0082555	3.20E-10
19	CEBPA *	rs7253865	33330342	G	T	0.1670870	0.0511843	0.0082266	1.10E-09
19	CEBPA *	rs149222436	33336002	T	C	0.1590340	0.0511603	0.0083888	2.20E-09
19	CEBPA *	rs141706710	33336121	T	C	0.1590780	0.0511667	0.0083876	2.20E-09
19	CEBPG *	rs16967971	33339692	T	G	0.1596950	0.0506456	0.0083745	2.30E-09
19	CEBPG *	rs12610763	33350705	A	G	0.1594740	0.0482803	0.0083793	1.60E-08
19	CEBPG *	rs10417389	33350819	T	C	0.1594570	0.0483036	0.0083800	1.60E-08
19	CEBPG *	rs10409981	33358189	T	C	0.1594620	0.0478921	0.0083824	2.40E-08
19	CEBPG *	rs10416682	33358955	T	C	0.1806310	0.0457958	0.0080078	2.90E-08
19	CEBPG *	rs4805872	33358978	C	T	0.1814660	0.0450734	0.0079867	4.50E-08
19	CEBPG *	rs1423065	33359589	T	C	0.1726530	0.0488136	0.0080975	3.00E-09
19	CEBPG *	chr19:33360112_C_CT	33360112	CT	C	0.1634230	0.0552523	0.0083626	6.20E-11
19	CEBPG *	rs10425856	33361416	C	T	0.1753430	0.0489378	0.0080440	2.60E-09
19	CEBPG *	rs11878996	33366074	C	T	0.1725510	0.0506002	0.0081011	7.80E-10
19	CEBPG *	rs2112820	33371182	C	T	0.1725970	0.0509037	0.0080984	5.70E-10
19	CEBPG *	rs77592544	33372029	G	T	0.1719540	0.0503548	0.0081266	9.30E-10
19	CEBPG *	rs78230685	33372898	C	A	0.1717690	0.0504356	0.0081243	7.50E-10
19	CEBPG *	rs116494882	33374217	T	C	0.1722780	0.0495525	0.0081247	1.50E-09
19	CEBPG *	rs151086462	33376066	TG	T	0.1720780	0.0486273	0.0081391	2.90E-09
19	CEBPG *	rs77152611	33378116	T	C	0.1717780	0.0488107	0.0081353	3.20E-09
19	PVRL2 *	rs111371860	44842530	T	A	0.0243613	0.1138810	0.0199958	1.40E-08
19	PVRL2	rs11667610	44852338	T	C	0.0362242	0.1032140	0.0166360	4.40E-10
19	PVRL2	rs10421035	44853417	G	A	0.0366705	0.0998378	0.0165383	1.60E-09
19	PVRL2	rs12971462	44853638	A	G	0.0366037	0.0998461	0.0165525	1.70E-09
19	PVRL2	rs8105340	44864520	C	T	0.0637369	0.0821092	0.0125000	3.60E-11
19	PVRL2	rs3112439	44864715	G	C	0.0607563	0.0767004	0.0127917	2.70E-09
19	PVRL2	rs3112440	44864753	A	G	0.0633589	0.0812165	0.0125393	6.10E-11
19	PVRL2	rs12610605	44867581	G	A	0.4844720	0.0625314	0.0061233	4.50E-25
19	PVRL2	rs4803766	44867911	A	G	0.3708700	0.0518673	0.0063236	2.50E-17
19	PVRL2	rs184521142	44868404	A	G	0.0126283	0.1432300	0.0274229	6.70E-09
19	PVRL2	rs34165484	44868428	A	AT	0.4848750	0.0615485	0.0061905	7.00E-24
19	PVRL2	rs200149544	44868448	T	TTTTTT	0.4860950	0.0610388	0.0061935	1.60E-23
19	PVRL2	rs404935	44869537	A	G	0.1380840	0.0928129	0.0088797	6.00E-27
19	PVRL2	rs79954154	44870118	A	G	0.0218772	0.1745310	0.0209184	1.10E-17
19	PVRL2	rs395908	44870308	A	G	0.1316280	0.0888680	0.0090907	1.30E-23
19	PVRL2	rs148251724	44872787	TATTTA	G	0.4668850	0.0657718	0.0061722	1.90E-27
19	PVRL2	rs519113	44873027	G	C	0.1574410	0.0881173	0.0083777	1.40E-27
19	PVRL2	rs34278513	44874887	T	C	0.1336330	0.0915782	0.0089792	2.70E-26
19	PVRL2	rs412776	44876259	A	G	0.1306950	0.1161340	0.0090783	2.10E-39
19	PVRL2	rs3865427	44877704	A	C	0.1258270	0.1074650	0.0092344	8.40E-33
19	PVRL2	rs11668861	44877713	G	T	0.2088270	0.1088410	0.0075562	5.70E-48
19	PVRL2	rs6859	44878777	A	G	0.2969750	0.0780204	0.0066967	2.20E-32
19	PVRL2	rs406456	44879460	G	A	0.1042740	0.0656933	0.0100581	2.10E-10
19	PVRL2	rs3852860	44879709	C	T	0.2133790	0.1206550	0.0074967	2.30E-59
19	PVRL2	rs71352237	44879822	C	T	0.1186060	0.1189940	0.0094955	3.20E-38

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	PVRL2	rs71171301	44879834	AC	A	0.1185900	0.1189810	0.0094966	3.20E-38
19	PVRL2	rs34224078	44879858	G	A	0.1185730	0.1191070	0.0094975	3.10E-38
19	PVRL2	rs35879138	44879882	A	T	0.1185570	0.1192390	0.0094974	2.60E-38
19	PVRL2	rs11083749	44880848	C	T	0.0914273	0.0924122	0.0107320	4.90E-17
19	PVRL2	rs406315	44880859	G	A	0.0850823	0.0788955	0.0110835	4.60E-12
19	PVRL2	rs34994196	44881075	GC	G	0.0908271	0.0915367	0.0107529	8.10E-17
19	PVRL2	rs142042446	44883210	GTAA	G	0.0854889	0.1849980	0.0109094	2.50E-69
19	PVRL2	rs283808	44883777	C	A	0.0851852	0.1041040	0.0110171	1.70E-21
19	PVRL2	rs283809	44883800	G	A	0.0857484	0.1048190	0.0109758	4.60E-22
19	PVRL2	rs12972156	44884202	G	C	0.0807334	0.1978180	0.0112358	1.50E-75
19	PVRL2	rs12972970	44884339	A	G	0.0807531	0.1985790	0.0112337	4.00E-76
19	PVRL2	rs34342646	44884873	A	G	0.0808558	0.1979830	0.0112226	8.90E-76
19	PVRL2	rs283810	44884984	G	T	0.0871336	0.1051950	0.0108852	1.80E-22
19	PVRL2	rs283811	44885243	G	A	0.1685240	0.1656780	0.0081834	5.70E-97
19	PVRL2	rs283813	44885917	A	T	0.0876962	0.1067140	0.0108197	1.90E-23
19	PVRL2	rs7254892	44886339	A	G	0.0616460	0.1197720	0.0127467	7.70E-22
19	PVRL2	rs283815	44887076	G	A	0.1729170	0.1571930	0.0080804	2.80E-89
19	PVRL2	rs148665049	44887875	T	C	0.0223939	0.1884480	0.0206975	3.10E-21
19	PVRL2	rs6857	44888997	T	C	0.0825067	0.1934520	0.0111060	5.30E-74
19	TOMM40 *	rs71352238	44891079	C	T	0.0824238	0.1961380	0.0111117	6.90E-76
19	TOMM40	rs184017	44891712	G	T	0.1748960	0.1551040	0.0080521	1.20E-88
19	TOMM40	rs157580	44892009	A	G	0.4327530	0.0884159	0.0061506	4.30E-50
19	TOMM40	rs2075650	44892362	G	A	0.0827639	0.1938880	0.0110920	1.70E-74
19	TOMM40	rs34404554	44892652	G	C	0.0821089	0.1965430	0.0111273	6.30E-76
19	TOMM40	rs11556505	44892887	T	C	0.0821576	0.1979940	0.0111291	7.30E-77
19	TOMM40	rs157582	44892962	T	C	0.1730710	0.1627480	0.0080800	5.10E-96
19	TOMM40	rs157584	44893642	C	T	0.3151650	0.0394852	0.0065816	2.30E-09
19	TOMM40	rs1160983	44893972	A	G	0.0664373	0.1082600	0.0123485	3.60E-19
19	TOMM40	rs157585	44894255	C	A	0.3203820	0.0410405	0.0065636	3.90E-10
19	TOMM40	rs157588	44895007	T	C	0.3154020	0.0412127	0.0065774	4.50E-10
19	TOMM40	rs157590	44895459	C	A	0.3224550	0.0407058	0.0065324	3.00E-10
19	TOMM40	rs61679753	44897490	A	T	0.0739896	0.1213690	0.0117151	7.70E-26
19	TOMM40	rs111784051	44899005	G	T	0.0728835	0.1179020	0.0117991	2.60E-24
19	TOMM40	rs405697	44901434	G	A	0.4007330	0.1045690	0.0062443	1.50E-66
19	TOMM40	rs10119	44903416	A	G	0.0869311	0.2272840	0.0108798	1.00E-103
19	APOE *	rs769446	44905371	C	T	0.0703196	0.1217710	0.0120903	7.40E-25
19	APOE *	rs405509	44905579	G	T	0.2953370	0.0457768	0.0067035	1.40E-11
19	APOE	rs440446	44905910	G	C	0.3883890	0.1157740	0.0062772	1.30E-78
19	APOE	rs769449	44906745	A	G	0.0763714	0.2302230	0.0115045	1.00E-95
19	APOE	rs429358	44908684	C	T	0.0864235	0.2363640	0.0108879	7.90E-112
19	APOE	rs7412	44908822	T	C	0.0724838	0.1197170	0.0118156	9.40E-25
19	APOE *	rs1065853	44909976	T	G	0.0724429	0.1200440	0.0118178	6.90E-25
19	APOE *	rs376097536	44909977	G	GGT	0.0865834	0.2148620	0.0109779	1.60E-92
19	APOE *	rs75627662	44910319	T	C	0.1678100	0.1636300	0.0081974	5.60E-93
19	APOE *	rs72654473	44911142	A	C	0.0757807	0.1190700	0.0115682	9.70E-26
19	APOE *	rs439401	44911194	C	T	0.4063180	0.1109870	0.0062228	9.70E-73
19	APOC1 *	rs445925	44912383	A	G	0.0829483	0.1348980	0.0110886	5.70E-35
19	APOC1 *	rs10414043	44912456	A	G	0.0904787	0.1896230	0.0106561	4.70E-75
19	APOC1 *	rs7256200	44912678	T	G	0.0906723	0.1899190	0.0106547	3.20E-75
19	APOC1 *	rs483082	44912921	T	G	0.1736450	0.1804090	0.0080756	1.20E-115
19	APOC1 *	rs584007	44913221	G	A	0.4054570	0.1113250	0.0062317	2.70E-73
19	APOC1 *	rs438811	44913484	T	C	0.1736830	0.1803810	0.0080768	1.10E-115
19	APOC1 *	rs390082	44913574	G	T	0.0827384	0.1354420	0.0111103	3.20E-35
19	APOC1 *	rs11568822	44914381	CTTCG	C	0.1680800	0.1720710	0.0081862	6.80E-103
19	APOC1	rs5117	44915533	C	T	0.1686800	0.1707800	0.0082021	2.20E-101
19	APOC1	rs3826688	44915704	C	T	0.4102500	0.1116780	0.0062490	3.00E-73
19	APOC1	rs73052335	44916825	C	A	0.0921633	0.1889200	0.0106683	1.90E-73
19	APOC1	rs12721046	44917997	A	G	0.1007280	0.1890080	0.0101836	4.70E-80
19	APOC1	rs484195	44918620	G	A	0.4054260	0.1080620	0.0062908	2.10E-68
19	APOC1	rs12721051	44918903	G	C	0.1012680	0.1870320	0.0101412	9.50E-80
19	APOC1 *	rs56131196	44919589	A	G	0.1015580	0.1861810	0.0101226	2.00E-79
19	APOC1 *	rs4420638	44919689	G	A	0.1016030	0.1860310	0.0101204	2.30E-79
19	APOC1 *	rs117569256	44920073	G	A	0.0350045	0.1264870	0.0167062	4.70E-14
19	APOC1 *	chr19:44920730_C_CA	44920730	CA	C	0.0877809	0.1851080	0.0109839	6.30E-66
19	APOC1 *	rs199769815	44921765	A	G	0.0232238	0.1264050	0.0204422	1.20E-09
19	APOC1 *	rs190712692	44921921	A	G	0.0728880	0.1192510	0.0118276	5.00E-25
19	APOC1 *	rs141622900	44923535	A	G	0.0732397	0.1155200	0.0117632	7.70E-24
19	APOC1P1	rs114448690	44928196	A	G	0.2194230	0.0994620	0.0075416	3.10E-40
19	APOC1P1	rs113345881	44928379	G	A	0.2297550	0.0984324	0.0074017	3.60E-41
19	APOC1P1	rs112871012	44928640	A	G	0.2276860	0.0953755	0.0074051	1.20E-38
19	APOC1P1	rs111271293	44928832	C	T	0.2310600	0.0956760	0.0073273	6.90E-40
19	APOC1P1	chr19:44928869_AAAAAC_A	44928869	A	AAAAAC	0.2303470	0.0952743	0.0073376	1.90E-39

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	APOC1P1	rs7259350	44929021	C	T	0.2405780	0.0983051	0.0071588	8.20E-44
19	APOC1P1	rs7259004	44929300	C	G	0.2418100	0.0985099	0.0071325	1.60E-44
19	APOC1P1	chr19:44930070_T_TA	44930070	TA	T	0.2222110	0.0991365	0.0074709	1.40E-40
19	ZNF579 *	rs11084402	55581999	T	C	0.1582540	0.0425520	0.0083800	4.20E-08
19	ZNF579 *	rs11879347	55582190	T	A	0.1576890	0.0430199	0.0083956	3.40E-08
19	ZNF579 *	rs111702114	55582630	G	A	0.1581140	0.0426272	0.0083852	4.40E-08
19	ZNF579 *	rs12978375	55582847	T	C	0.1562100	0.0447118	0.0084338	1.60E-08
19	ZNF579 *	rs11669682	55583561	A	G	0.1577510	0.0427138	0.0084003	4.70E-08
19	ZNF579 *	rs34174244	55584189	A	G	0.1549020	0.0433871	0.0084877	3.60E-08
19	FIZ1 *	rs12610881	55586393	T	C	0.1567220	0.0435344	0.0084362	3.00E-08
19	FIZ1 *	rs12610709	55590996	A	G	0.1549190	0.0435977	0.0084920	3.30E-08
20	PLTP	rs6065904	45906012	A	G	0.2985510	0.0537047	0.0066787	3.20E-17
20	PLTP	rs148753678	45907567	C	CACA	0.0668791	0.1397490	0.0123308	6.10E-31
20	PLTP	rs3091649	45909058	G	A	0.4383010	-0.0475012	0.0061950	2.70E-15
20	PLTP	rs378114	45909788	T	C	0.4058230	-0.0544004	0.0062355	4.10E-19
20	PLTP	rs435306	45909845	G	T	0.4083750	-0.0540635	0.0062212	5.20E-19
20	PLTP	rs441346	45910853	G	C	0.4305630	-0.0461416	0.0062128	3.50E-14
20	PLTP	rs394643	45911539	A	G	0.4246330	-0.0448442	0.0062307	1.30E-13
20	PLTP	rs2294212	45911925	G	C	0.3541470	-0.0450981	0.0064390	6.50E-13
20	PLTP	rs2294213	45912053	G	C	0.3528220	-0.0450401	0.0064505	7.00E-13
20	PLTP	rs200238866	45912201	C	CCCT	0.0669734	0.1392470	0.0122600	3.80E-31
20	PLTP	rs3092096	45912327	A	AC	0.4619790	-0.0403333	0.0061682	1.10E-11
20	PLTP *	rs76083992	45916159	T	C	0.0674360	0.1373380	0.0122135	1.30E-30
20	PLTP *	rs4810479	45916409	T	C	0.3983030	-0.0542453	0.0062493	1.50E-19
20	PLTP *	rs4812975	45916821	A	G	0.3985130	-0.0544640	0.0062496	1.10E-19
20	PLTP *	rs6130967	45919050	A	G	0.0674474	0.1374660	0.0122118	1.20E-30
20	PLTP *	rs2868346	45919331	T	C	0.3976580	-0.0549287	0.0062659	7.20E-20
20	PLTP *	rs3843763	45919554	T	C	0.3973020	-0.0541791	0.0062703	1.90E-19
20	PLTP *	rs6130969	45920383	T	G	0.0673145	0.1366520	0.0122204	2.70E-30
20	PLTP *	rs6073958	45923216	C	T	0.1268160	0.1029130	0.0092272	5.30E-30
20	PCIF1 *	rs2903809	45924256	A	C	0.3957230	-0.0529437	0.0063163	1.80E-18
20	PCIF1 *	rs1810322	45925065	A	G	0.0652675	0.1361880	0.0124193	3.90E-29
20	PCIF1 *	rs111859808	45930210	A	G	0.0668967	0.1361630	0.0122654	7.20E-30
20	PCIF1 *	rs6032589	45930959	C	T	0.3610080	-0.0492150	0.0063887	1.50E-15
20	PCIF1 *	rs113232549	45931069	T	C	0.0668998	0.1361620	0.0122651	7.00E-30
20	PCIF1	rs74436333	45937405	G	A	0.0668971	0.1361270	0.0122648	7.50E-30
20	PCIF1	rs6032597	45938696	T	G	0.3599730	-0.0488044	0.0063888	2.20E-15
20	PCIF1	rs6094229	45941824	G	C	0.3604220	-0.0488877	0.0063887	1.90E-15
20	PCIF1	rs2297194	45945077	G	A	0.0669053	0.1362740	0.0122637	6.30E-30
20	PCIF1	rs1111750	45945599	C	T	0.0669297	0.1363570	0.0122619	5.50E-30
20	ZNF335 *	rs6130975	45948343	A	G	0.0669043	0.1362850	0.0122637	6.20E-30
20	ZNF335 *	rs6124759	45948363	G	C	0.3833060	-0.0459138	0.0063013	1.80E-14
20	ZNF335	rs3363	45948675	T	C	0.3599170	-0.0495706	0.0063773	7.70E-16
20	ZNF335	rs16990951	45950035	A	T	0.3838070	-0.0461952	0.0062997	1.30E-14
20	ZNF335	rs3746503	45950322	G	A	0.3828920	-0.0462731	0.0062956	1.30E-14
20	ZNF335	rs6130976	45950933	T	C	0.0667647	0.1360940	0.0122758	7.20E-30
20	ZNF335	rs34240177	45951651	C	G	0.0670457	0.1362430	0.0122494	4.80E-30
20	ZNF335	rs6124760	45952814	G	C	0.0672984	0.1372920	0.0122208	1.40E-30
20	ZNF335	rs6032601	45956315	A	G	0.3809780	-0.0464604	0.0063125	1.00E-14
20	ZNF335	rs3848718	45957124	A	G	0.0657152	0.1370590	0.0123581	7.20E-30
20	ZNF335	rs111434827	45958597	T	C	0.0671197	0.1373920	0.0122371	1.40E-30
20	ZNF335	rs6032602	45958731	C	T	0.3818250	-0.0460009	0.0063024	1.80E-14
20	ZNF335	rs6130977	45959191	A	C	0.0671197	0.1373920	0.0122371	1.40E-30
20	ZNF335	rs3746508	45959540	A	G	0.3850510	-0.0448345	0.0063005	8.20E-14
20	ZNF335	rs3746509	45959602	C	T	0.3817840	-0.0460280	0.0063033	1.60E-14
20	ZNF335	rs6130978	45959766	G	A	0.0671171	0.1374560	0.0122374	1.30E-30
20	ZNF335	rs79645412	45960177	C	G	0.0670498	0.1378990	0.0122451	1.10E-30
20	ZNF335	rs6104404	45961203	A	C	0.3821420	-0.0458585	0.0063061	2.20E-14
20	ZNF335	rs16990964	45962093	A	G	0.0671459	0.1376310	0.0122347	1.10E-30
20	ZNF335	rs147204976	45963071	A	G	0.0963345	0.1077570	0.0104194	7.60E-26
20	ZNF335	rs3746511	45963725	T	C	0.3805130	-0.0463388	0.0063250	1.60E-14
20	ZNF335	rs3746512	45963997	T	C	0.3803230	-0.0462497	0.0063290	1.80E-14
20	ZNF335	rs74880664	45965956	A	GT	0.0671368	0.1375390	0.0122358	1.20E-30
20	ZNF335	rs143167649	45966533	C	TCTGT	0.0652705	0.1366890	0.0124090	1.30E-29
20	ZNF335	rs3092073	45967010	A	G	0.4476880	-0.0433652	0.0062223	1.30E-13
20	ZNF335	rs76907877	45967688	T	C	0.0668941	0.1356260	0.0122613	1.00E-29
20	ZNF335	rs78558150	45970350	T	C	0.0528867	0.1319270	0.0137518	5.20E-23
20	ZNF335 *	rs16990971	45972654	G	A	0.0674371	0.1321710	0.0122380	1.20E-28
20	ZNF335 *	rs11469011	45973042	G	GCCTA1	0.3783660	-0.0470142	0.0063929	1.10E-14
20	ZNF335 *	rs6017717	45975324	C	G	0.3784130	-0.0460405	0.0063979	4.10E-14
20	MMP9 *	rs78295912	45993859	T	C	0.0657677	0.1306580	0.0124461	6.00E-26
20	MMP9 *	rs1888235	45995328	T	C	0.1172080	0.0750212	0.0096209	1.00E-14

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20	MMP9 *	rs145026700	45996044	T	C	0.0652517	0.1301290	0.0124914	1.10E-25
20	MMP9 *	rs6073984	46002014	G	A	0.1154260	0.0753674	0.0096693	1.20E-14
20	MMP9 *	rs73622643	46003887	T	C	0.2864430	0.0472807	0.0068878	6.00E-12
20	MMP9 *	rs3918241	46007096	A	T	0.1209520	0.0677971	0.0094473	1.00E-12
20	MMP9 *	rs3918242	46007337	T	C	0.1209580	0.0678193	0.0094464	1.00E-12
20	MMP9	rs79845319	46010332	C	A	0.3215050	0.0392737	0.0066528	5.90E-09
20	MMP9	rs2274755	46011053	T	G	0.1230410	0.0686861	0.0093385	3.90E-13
20	MMP9	rs2236416	46011936	G	A	0.1237100	0.0679518	0.0093041	7.60E-13
20	MMP9	rs17577	46014472	A	G	0.1258800	0.0667297	0.0092112	8.00E-13
20	MMP9	rs3918261	46014953	G	A	0.1258930	0.0667950	0.0092105	7.60E-13
20	MMP9	rs13925	46016326	A	G	0.1258920	0.0666630	0.0092099	8.40E-13
20	MMP9 *	rs3918270	46016700	A	G	0.1219890	0.0642421	0.0093868	1.10E-11
20	MMP9 *	rs8184490	46016794	G	C	0.0711332	0.1132170	0.0119397	1.60E-21
20	MMP9 *	rs3918271	46016954	A	G	0.1194110	0.0684370	0.0094746	7.50E-13
20	SLC12A5 *	rs66553311	46020003	G	C	0.3629090	0.0398213	0.0064172	2.20E-09
20	SLC12A5 *	rs10432735	46021679	T	A	0.1253730	0.0659135	0.0092183	1.60E-12
20	SLC12A5	rs7363950	46023753	C	T	0.3645250	0.0403417	0.0064005	1.40E-09
20	SLC12A5	rs62215576	46023758	T	C	0.1259230	0.0661886	0.0092075	1.10E-12
20	SLC12A5	rs6094238	46024468	G	C	0.3638400	0.0406023	0.0064024	1.10E-09
20	SLC12A5	rs6124764	46027498	A	T	0.1229020	0.0686281	0.0093608	1.90E-13
20	SLC12A5	rs11908352	46027501	A	C	0.1228990	0.0685898	0.0093610	1.90E-13
20	SLC12A5	rs6124765	46039572	T	C	0.1238590	0.0685818	0.0094598	1.20E-12
20	SLC12A5	rs116878061	46057452	T	G	0.0687517	0.1022410	0.0121248	1.50E-17
22	TTC28	rs6005795	28520936	T	C	0.2863370	-0.0372674	0.0067854	4.50E-08
22	PLA2G6	rs4820318	38174306	A	G	0.2652380	-0.0374861	0.0069288	4.80E-08
22	MAFF *	rs2413506	38197121	C	T	0.2607320	-0.0387460	0.0069923	1.80E-08
22	MAFF *	chr22:38197454_AT_A	38197454	A	AT	0.2558560	-0.0393889	0.0070576	1.80E-08
22	MAFF *	rs4821760	38198076	T	C	0.2580960	-0.0381449	0.0070009	3.40E-08
22	MAFF *	rs2899297	38198661	G	A	0.2607820	-0.0389955	0.0069613	1.80E-08
22	MAFF *	rs3761446	38199476	A	G	0.2623340	-0.0378605	0.0069464	4.20E-08
22	MAFF	rs2267372	38202227	A	G	0.2560620	-0.0385711	0.0070192	3.30E-08
22	MAFF	rs4821764	38203357	G	A	0.3652940	-0.0410924	0.0063522	1.60E-10
22	MAFF	rs4820323	38203760	C	G	0.3744910	-0.0408131	0.0063071	1.30E-10
22	MAFF	rs4820324	38203850	G	C	0.3744730	-0.0409216	0.0063063	1.10E-10
22	MAFF	rs4820325	38203971	G	A	0.3747330	-0.0410927	0.0063074	8.80E-11
22	MAFF	rs2267373	38204535	C	T	0.3743690	-0.0411540	0.0063084	8.80E-11
22	MAFF	rs2267375	38205224	G	T	0.3743220	-0.0411450	0.0063082	8.80E-11
22	MAFF	rs34364526	38205423	C	CCT	0.3720630	-0.0424821	0.0063169	2.30E-11
22	MAFF	rs11914181	38206133	T	C	0.3743370	-0.0418990	0.0063065	4.40E-11
22	MAFF	rs2899298	38207179	C	G	0.3745310	-0.0416190	0.0063075	5.40E-11
22	MAFF	rs11450220	38211527	T	TG	0.3689750	-0.0422800	0.0063428	3.20E-11
22	MAFF	rs2064103	38212220	T	C	0.3682890	-0.0424003	0.0063515	3.00E-11
22	MAFF	rs5995550	38216365	C	A	0.2544650	-0.0393843	0.0071094	2.60E-08
22	MAFF *	rs36116754	38216511	A	AT	0.2537020	-0.0404695	0.0071291	1.10E-08
22	MAFF *	rs5995551	38217191	C	A	0.2542340	-0.0387639	0.0071545	4.70E-08
22	TMEM184B	rs6001053	38218083	C	T	0.2540780	-0.0395757	0.0071639	2.30E-08
22	PPARA	rs1800234	46219983	C	T	0.0439651	-0.0827363	0.0149481	8.00E-09

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error
This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.
The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 7. Summary of variants exhibiting genome-wide significance for the glucose levels, identified within the Taiwan Biobank.

CHR	Gene	SNP	Pos (h38)	EA	NEA	EAf	BETA	SE	P
1	SYNC *	rs786459	32708643	G	A	0.2055500	0.0263129	0.0045162	4.5E-09
1	SYNC *	rs785797	32712148	T	C	0.2127830	0.0257652	0.0044252	4.7E-09
1	SYNC *	rs785798	32712569	T	G	0.2132850	0.0258864	0.0044223	3.6E-09
1	SYNC *	rs1085309	32712746	G	A	0.2127850	0.0258326	0.0044251	4.2E-09
1	SYNC *	rs403352	32713303	A	G	0.2127890	0.0258103	0.0044250	4.3E-09
1	SYNC *	rs419145	32713555	A	G	0.2128930	0.0256787	0.0044235	4.9E-09
1	SYNC *	rs810835	32713875	G	A	0.2638480	0.0224824	0.0041451	3.1E-08
1	SYNC *	rs785799	32713935	G	A	0.2128020	0.0257283	0.0044246	4.8E-09
1	SYNC *	rs785800	32714021	G	A	0.2129220	0.0258281	0.0044254	4.5E-09
1	SYNC *	rs451855	32714852	A	T	0.2118230	0.0260447	0.0044411	3.9E-09
1	SYNC *	rs785803	32715163	G	A	0.2122530	0.0260320	0.0044362	3.9E-09
1	SYNC *	rs1680969	32715340	A	T	0.2119750	0.0263339	0.0044526	2.6E-09
1	SYNC *	rs1680970	32715341	C	T	0.2119750	0.0263339	0.0044526	2.6E-09
1	SYNC *	rs702838	32716437	A	G	0.2167770	0.0254173	0.0044191	8.6E-09
1	SYNC *	rs412730	32716810	A	G	0.2385380	0.0238086	0.0042760	1.9E-08
1	SLC2A1-AS1	rs841839	42964413	C	A	0.4893840	0.0269668	0.0036480	1.7E-13
1	SLC2A1-AS1	rs4306169	42965762	A	G	0.4894150	0.0268672	0.0036482	2.1E-13
1	SLC2A1-AS1	rs2367159	42966918	C	T	0.4894560	0.0269202	0.0036485	1.9E-13
1	SLC2A1-AS1	rs841569	42968953	C	A	0.4882430	0.0272081	0.0036542	1.2E-13
1	SLC2A1-AS1	rs2005136	42969976	G	A	0.4883110	0.0272751	0.0036562	1.0E-13
1	SLC2A1-AS1	rs2367160	42969979	G	A	0.4883110	0.0272751	0.0036562	1.0E-13
1	SLC2A1-AS1	rs841572	42970380	G	A	0.4881900	0.0272351	0.0036568	1.2E-13
1	SLC2A1-AS1	rs841574	42970842	T	C	0.4881640	0.0271589	0.0036566	1.3E-13
1	SLC2A1-AS1	rs841575	42971859	C	T	0.4888710	0.0271497	0.0036598	1.5E-13
1	SLC2A1-AS1	rs4660693	42977254	G	A	0.4956090	0.0273093	0.0036897	1.2E-13
1	SLC2A1-AS1	rs11210771	42978889	T	C	0.3675590	-0.0223140	0.0038208	8.2E-09
1	SLC2A1-AS1	rs7413414	42981420	T	C	0.4785390	0.0272130	0.0036744	1.4E-13
1	SLC2A1-AS1	rs1890681	42981546	G	C	0.4956210	0.0279701	0.0036737	2.3E-14
1	SLC2A1-AS1	rs7525322	42981639	T	C	0.4956350	0.0280006	0.0036738	2.1E-14
1	SLC2A1-AS1	rs11210772	42982828	A	G	0.3671700	-0.0229948	0.0038089	2.1E-09
1	SLC2A1 *	rs4660694	42984511	C	T	0.4964280	0.0281351	0.0036752	1.4E-14
1	SLC2A1 *	rs11210774	42985058	T	C	0.4958370	0.0279289	0.0036730	2.5E-14
1	SLC2A1 *	rs11210775	42985133	C	A	0.4958340	0.0279724	0.0036730	2.3E-14
1	SLC2A1 *	rs12124652	42985544	T	C	0.4963020	0.0280559	0.0036743	2.0E-14
1	SLC2A1 *	rs12145014	42985998	G	T	0.4960390	0.0280796	0.0036762	2.1E-14
1	SLC2A1 *	rs7515271	42986230	A	G	0.4963130	0.0280885	0.0036743	1.8E-14
1	SLC2A1 *	rs12735957	42987351	A	G	0.4633340	0.0263137	0.0037285	2.3E-12
1	SLC2A1 *	rs6177742	42987641	G	A	0.4977560	0.0286177	0.0036788	5.9E-15
1	SLC2A1 *	rs12757571	42987759	C	A	0.4962850	0.0282245	0.0036790	1.4E-14
1	SLC2A1 *	rs12752348	42988388	T	C	0.4788430	0.0275714	0.0036785	7.4E-14
1	SLC2A1 *	rs12734089	42988655	G	A	0.4793610	0.0274755	0.0036836	9.1E-14
1	SLC2A1 *	rs10158845	42989612	G	A	0.4881930	0.0278344	0.0036833	2.9E-14
1	SLC2A1 *	chr1:42990228_C_CA	42990228	C	CA	0.3775500	-0.0219157	0.0038173	1.5E-08
1	SLC2A1 *	rs4660696	42990795	T	C	0.4970160	0.0260693	0.0036806	2.2E-12
1	SLC2A1 *	rs12029931	42991209	T	C	0.3652000	-0.0228142	0.0038203	2.6E-09
1	SLC2A1 *	rs11210776	42992268	A	G	0.4658810	-0.0264610	0.0037045	9.2E-13
1	PDE4B *	rs783063	66380080	G	A	0.0743855	-0.0388445	0.0069194	4.3E-08
1	PDE4B *	rs11374630	66380756	AG	A	0.0744609	-0.0391133	0.0069158	3.2E-08
1	PDE4B *	rs783061	66380859	G	C	0.0744609	-0.0391133	0.0069158	3.2E-08
1	PDE4B *	rs783060	66381083	C	A	0.0744705	-0.0391208	0.0069154	3.2E-08
1	PDE4B *	rs783058	66381577	T	C	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783057	66382260	A	G	0.0744787	-0.0391106	0.0069152	3.2E-08
1	PDE4B *	rs783056	66382293	G	A	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783055	66382609	G	A	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783054	66382807	G	A	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs4655840	66382911	C	T	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783052	66383434	A	G	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783051	66383727	A	C	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783050	66383765	G	T	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs2793367	66383905	G	A	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783048	66384222	T	C	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783047	66384331	G	A	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783046	66384693	T	G	0.0744543	-0.0391860	0.0069164	3.0E-08
1	PDE4B *	rs783044	66385769	A	C	0.0744068	-0.0391641	0.0069191	3.0E-08
1	PDE4B *	rs35858170	66385958	T	TC	0.0742956	-0.0393214	0.0069248	2.6E-08
1	PDE4B *	rs783041	66386552	G	A	0.0742829	-0.0393954	0.0069257	2.5E-08
1	PDE4B *	rs1194486	66389704	A	G	0.0742182	-0.0396995	0.0069289	2.0E-08
1	WDR78	rs1925408	66899351	C	T	0.1379650	-0.0286334	0.0052696	4.7E-09
1	WDR78	rs1118392	66900866	C	T	0.1451390	-0.0266866	0.0051605	2.9E-08
1	WDR78	rs1118393	66900985	A	G	0.1384150	-0.0284693	0.0052596	5.7E-09
1	WDR78	rs2985808	66902058	T	C	0.1384590	-0.0285593	0.0052583	5.0E-09
1	WDR78	rs3008888	66903282	C	T	0.1385720	-0.0285071	0.0052594	5.2E-09
1	WDR78	rs2104415	66903715	G	A	0.1453820	-0.0267161	0.0051589	2.6E-08
1	WDR78	rs1925411	66904609	C	T	0.1387310	-0.0286280	0.0052559	4.3E-09
1	WDR78	rs3008892	66907875	A	T	0.1388570	-0.0284163	0.0052525	5.2E-09
1	WDR78	rs2985810	66910479	T	C	0.1400150	-0.0286750	0.0052277	2.9E-09
1	WDR78	rs56165014	66911832	C	CACTGAC	0.1406400	-0.0283071	0.0052309	4.6E-09
1	WDR78	rs2985811	66912039	G	T	0.1400310	-0.0286876	0.0052269	2.8E-09
1	WDR78	rs3008894	66912056	A	G	0.1400310	-0.0286876	0.0052269	2.8E-09
1	WDR78	rs2182143	66913253	T	C	0.1400300	-0.0286774	0.0052269	2.8E-09
1	WDR78	rs3008848	66913601	C	T	0.1400300	-0.0286774	0.0052269	2.8E-09
1	WDR78	rs4388680	66915939	T	C	0.1382500	-0.0282204	0.0052676	6.6E-09
1	WDR78	rs3008852	66917733	G	A	0.1400320	-0.0288119	0.0052266	2.4E-09
1	WDR78	rs3008853	66919805	C	T	0.1400410	-0.0288015	0.0052263	2.4E-09
1	WDR78	rs3008854	66920268	T	C	0.1400410	-0.0288015	0.0052263	2.4E-09
1	WDR78	rs3008855	66920521	C	T	0.1400410	-0.0288015	0.0052263	2.4E-09
1	WDR78	rs2985816	66922067	G	T	0.1400410	-0.0287908	0.0052263	2.4E-09
1	WDR78	rs3008856	66922218	T	C	0.1400440	-0.0287699	0.0052262	2.5E-09
1	WDR78	rs10701425	66922332	T	TGA	0.1400980	-0.0286274	0.0052270	2.8E-09
1	WDR78	rs56707923	66922333	T	C	0.1400980	-0.0286274	0.0052270	2.8E-09
1	WDR78	rs4655658	66923925	C	T	0.1400400	-0.0287773	0.0052262	2.5E-09
1	WDR78	rs3008858	66924733	G	C	0.1397740	-0.0286443	0.0052291	2.9E-09
1	WDR78	rs1886686	66924785	C	G	0.1397740	-0.0286443	0.0052291	2.9E-09
1	MIER1	rs3008859	66925316	G	C	0.1397740	-0.0286443	0.0052291	2.9E-09
1	MIER1	rs3008860	66925320	G	C	0.1397740	-0.0286443	0.0052291	2.9E-09
1	MIER1	rs3008861	66930539	T	G	0.1396150	-0.0285040	0.0052292	3.5E-09
1	MIER1	rs2985817	66932924	G	C	0.1397300	-0.0285716	0.0052264	3.0E-09
1	MIER1	rs2985818	66933233	G	A	0.1397300	-0.0285716	0.0052264	3.0E-09
1	MIER1	rs2147838	66933783	T	C	0.1397250	-0.0286517	0.0052264	2.7E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	MIER1	chr1:66934572_C_CT	66934572	C	CT	0.1453180	-0.0289582	0.0052065	2.4E-09
1	MIER1	rs4655659	66936913	T	C	0.1417030	-0.0299618	0.0052082	3.9E-10
1	MIER1	rs3008865	66937155	T	C	0.1398430	-0.0287199	0.0052244	2.4E-09
1	MIER1	rs2985821	66938104	G	A	0.1397430	-0.0286924	0.0052263	2.6E-09
1	MIER1	rs2985822	66939227	T	G	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs1925412	66939374	G	A	0.1398050	-0.0287191	0.0052257	2.5E-09
1	MIER1	chr1:66943990_AT_A	66943990	AT	A	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs2985824	66944488	A	G	0.1398170	-0.0286604	0.0052272	2.7E-09
1	MIER1	rs2985825	66947139	T	G	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs2985826	66947235	G	C	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs912797	66947795	A	G	0.1398680	-0.0285556	0.0052259	3.0E-09
1	MIER1	rs76686883	66949936	AC	A	0.1397560	-0.0287486	0.0052266	2.4E-09
1	MIER1	rs58773947	66950709	A	AC	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs35686197	66950838	ATC	A	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs1925413	66951418	T	C	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	chr1:66951572_GT_G	66951572	GT	G	0.1448240	-0.0263024	0.0051976	3.6E-08
1	MIER1	rs3008870	66952344	C	T	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs3008871	66953406	G	A	0.1398010	-0.0286629	0.0052269	2.7E-09
1	MIER1	rs2985830	66954908	C	G	0.1397480	-0.0286550	0.0052263	2.7E-09
1	MIER1	rs2031495	66956031	G	T	0.1397490	-0.0286362	0.0052263	2.7E-09
1	MIER1	rs2025608	66956867	C	T	0.1397400	-0.0286148	0.0052266	2.7E-09
1	MIER1	rs71802222	66957631	AT	A	0.1397400	-0.0286148	0.0052266	2.7E-09
1	MIER1	rs3831089	66958314	T	TTCTC	0.1399030	-0.0286786	0.0052292	2.5E-09
1	MIER1	rs11322381	66958474	TA	T	0.1398320	-0.0287324	0.0052261	2.3E-09
1	MIER1	rs2985794	66959628	T	G	0.1398430	-0.0286273	0.0052257	2.6E-09
1	MIER1	chr1:66959811_A_AT	66959811	A	AT	0.1445050	-0.0274092	0.0052236	9.5E-09
1	MIER1	rs3008873	66960087	G	A	0.1397400	-0.0286148	0.0052266	2.7E-09
1	MIER1	rs2985795	66960540	A	G	0.1397400	-0.0286148	0.0052266	2.7E-09
1	MIER1	rs4655663	66964420	G	A	0.1390040	-0.0284562	0.0052416	4.0E-09
1	MIER1	rs7511948	66964744	A	G	0.1397400	-0.0286148	0.0052266	2.7E-09
1	MIER1	rs3008874	66965682	A	T	0.1415780	-0.0274746	0.0052081	9.0E-09
1	MIER1	rs2985797	66965816	T	C	0.1397390	-0.0286229	0.0052266	2.7E-09
1	MIER1	rs3008875	66966348	T	C	0.1397390	-0.0286229	0.0052266	2.7E-09
1	MIER1	rs11208976	66968728	G	A	0.1397390	-0.0286229	0.0052266	2.7E-09
1	MIER1	rs12041926	66968919	T	C	0.1397390	-0.0286229	0.0052266	2.7E-09
1	MIER1	rs72673725	66969581	C	G	0.1397410	-0.0285738	0.0052265	2.8E-09
1	MIER1	rs12137403	66971360	T	C	0.1396660	-0.0286046	0.0052278	2.8E-09
1	MIER1	rs67019224	66972050	G	GATA	0.1397410	-0.0285738	0.0052265	2.8E-09
1	MIER1	rs67779446	66972229	A	ACAC	0.1288150	-0.0308459	0.0054370	9.1E-10
1	MIER1	rs72158845	66972236	AC	A	0.1374820	-0.0287065	0.0052744	3.2E-09
1	MIER1	rs12131222	66972852	T	A	0.1397410	-0.0285738	0.0052265	2.8E-09
1	MIER1	rs35365746	66973217	A	G	0.1397440	-0.0286030	0.0052265	2.7E-09
1	MIER1	rs145267594	66975538	A	AAAAG	0.1340900	-0.0289914	0.0053440	4.3E-09
1	MIER1	rs201428899	66975989	TG	T	0.1335920	-0.0299943	0.0053416	1.6E-09
1	MIER1	rs72673729	66975990	G	T	0.1419480	-0.0287264	0.0052105	2.3E-09
1	MIER1	rs11208978	66976527	T	C	0.1397410	-0.0286002	0.0052264	2.7E-09
1	MIER1	rs11208979	66976592	T	C	0.1397410	-0.0286002	0.0052264	2.7E-09
1	MIER1	rs58680688	66978068	G	C	0.1397630	-0.0285275	0.0052270	3.0E-09
1	MIER1	rs59766514	66978286	A	ATAGG	0.1397010	-0.0285171	0.0052274	3.3E-09
1	MIER1	rs202040528	66978292	A	AGGTATC	0.1313840	-0.0299000	0.0053975	2.4E-09
1	MIER1	rs34367328	66979638	C	T	0.1397390	-0.0286122	0.0052264	2.7E-09
1	MIER1	rs12039172	66981767	G	A	0.1397390	-0.0286122	0.0052264	2.7E-09
1	MIER1	rs4620509	66984258	G	A	0.1397410	-0.0286114	0.0052264	2.7E-09
1	MIER1	rs1137656	66985919	C	A	0.1393200	-0.0276810	0.0052364	7.8E-09
1	MIER1	rs12117131	66986239	T	C	0.1397540	-0.0285119	0.0052262	3.0E-09
1	MIER1	rs12132068	66986241	T	G	0.1397540	-0.0285119	0.0052262	3.0E-09
1	MIER1	rs17497828	66986639	A	G	0.1397740	-0.0286113	0.0052269	2.7E-09
1	MIER1	rs142144569	66988113	TCGTATG	T	0.1397570	-0.0285087	0.0052261	3.0E-09
1	MIER1 *	rs12132532	66991332	T	G	0.1397540	-0.0285070	0.0052262	3.0E-09
1	MIER1 *	rs17497947	66991516	T	G	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1 *	rs12740884	66994172	A	C	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1 *	rs12143044	66994371	T	A	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1 *	rs12044278	66995294	C	T	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1 *	rs12044492	66995984	C	T	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1 *	rs6673462	66996174	C	A	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1 *	rs11208985	66998983	A	G	0.1397540	-0.0285070	0.0052262	3.0E-09
1	SLC35D1	rs2065000	67002441	C	G	0.1394320	-0.0281871	0.0052331	4.3E-09
1	SLC35D1	rs2755256	67006009	A	T	0.1401060	-0.0285193	0.0052381	3.9E-09
1	SLC35D1	rs2815348	67006482	G	C	0.1389680	-0.0291177	0.0052445	1.7E-09
1	SLC35D1	rs11313486	67006689	TG	T	0.1389680	-0.0291177	0.0052445	1.7E-09
1	SLC35D1	rs34882801	67007482	A	AG	0.1389680	-0.0291177	0.0052445	1.7E-09
1	SLC35D1	rs3048471	67009698	T	TCGG	0.1389680	-0.0291177	0.0052445	1.7E-09
1	SLC35D1	rs2815350	67011632	G	A	0.1391850	-0.0290584	0.0052480	1.7E-09
1	SLC35D1	rs2755240	67011656	T	G	0.1389680	-0.0291177	0.0052445	1.7E-09
1	SLC35D1	rs2815351	67012297	A	G	0.1389680	-0.0291177	0.0052445	1.7E-09
1	SLC35D1	rs975451	67014377	T	C	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs975452	67014507	A	T	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs2009319	67015387	G	T	0.1384770	-0.0298199	0.0052564	7.4E-10
1	SLC35D1	rs2009311	67015554	C	T	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs2815352	67016421	A	G	0.1394490	-0.0303739	0.0052431	4.6E-10
1	SLC35D1	rs2815353	67017689	A	G	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs2815354	67017959	A	T	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs2755244	67018787	T	C	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs2065001	67020826	C	G	0.1389700	-0.0290897	0.0052445	1.7E-09
1	SLC35D1	rs2755245	67022281	C	G	0.1389680	-0.0290763	0.0052445	1.7E-09
1	SLC35D1	rs2755246	67023301	A	G	0.1383820	-0.0291367	0.0052625	1.5E-09
1	SLC35D1	rs2815357	67026171	T	C	0.1387830	-0.0290691	0.0052581	1.6E-09
1	SLC35D1	rs2755248	67026941	A	G	0.1386130	-0.0292700	0.0052580	1.3E-09
1	SLC35D1	rs2755249	67027979	A	G	0.1386110	-0.0292897	0.0052580	1.3E-09
1	SLC35D1	rs2815359	67028691	T	C	0.1386110	-0.0292897	0.0052580	1.3E-09
1	SLC35D1	rs2815361	67028908	G	T	0.1386110	-0.0292897	0.0052580	1.3E-09
1	SLC35D1	rs2755250	67029600	A	G	0.1386110	-0.0292897	0.0052580	1.3E-09
1	SLC35D1	rs2815369	67035211	T	C	0.1385840	-0.0293202	0.0052587	1.2E-09
1	SLC35D1	rs2815370	67038044	G	A	0.1385860	-0.0292669	0.0052587	1.3E-09
1	SLC35D1	rs2815371	67038630	A	G	0.1377760	-0.0296744	0.0052822	9.8E-10
1	SLC35D1	rs2815373	67040097	C	T	0.1382500	-0.0297115	0.0052775	8.9E-10
1	FAM46C *	rs12406858	117598870	C	A	0.4431780	-0.0191762	0.0036768	3.8E-08
1	FAM46C *	rs1966228	117601710	G	A	0.4444120	-0.0194963	0.0036744	2.7E-08
1	PROX1 *	rs340883	213972363	T	C	0.3847100	0.0211412	0.0037625	8.2E-09
1	PROX1 *	rs340877	213983903	G	A	0.4948780	-0.0217326	0.0036568	9.7E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	PROX1 *	rs340876	213984789	C	T	0.4933560	-0.0224346	0.0036375	2.6E-10
1	PROX1 *	rs340875	213985643	G	C	0.4937570	-0.0220309	0.0036354	4.9E-10
1	PROX1 *	rs340874	213985913	C	T	0.3848400	0.0218358	0.0037220	1.5E-09
1	PROX1	rs340839	213988477	G	A	0.4922340	-0.0209890	0.0036252	4.4E-09
1	ACTA1 *	rs61042964	229429880	T	TC	0.3300110	-0.0201184	0.0038714	2.4E-08
1	ACTA1 *	rs499689	229429985	G	A	0.3160490	-0.0201302	0.0038995	2.5E-08
1	ACTA1 *	rs500639	229430081	G	A	0.3168220	-0.0199506	0.0038944	3.4E-08
1	NUP133	rs660198	229443047	C	G	0.3075040	-0.0211677	0.0039988	1.3E-08
1	ABCB10	rs348330	229537208	A	G	0.3146380	-0.0249500	0.0039638	1.2E-11
2	MAPRE3	rs80214805	26985753	T	C	0.0353473	-0.0549889	0.0099295	3.0E-08
2	TMEM214 *	rs118039822	27045514	C	T	0.0364281	-0.0539560	0.0097656	3.6E-08
2	TCF23 *	rs77748253	27165966	T	C	0.0350570	-0.0561808	0.0099311	3.2E-08
2	TCF23 *	rs76668651	27174494	A	G	0.0381250	-0.0553255	0.0095461	8.2E-09
2	SLC5A6 *	rs74684611	27191771	C	T	0.1046000	0.0366447	0.0060470	5.7E-09
2	TRIM54	rs76147177	27286115	C	T	0.0430196	-0.0505092	0.0090237	2.6E-08
2	GTF3C2	rs112796438	27348981	A	C	0.1390700	0.0294757	0.0052477	4.0E-08
2	PPM1G *	rs1728918	27412596	A	G	0.2089450	-0.0285490	0.0044530	5.2E-11
2	NRBP1 *	rs147530299	27419228	A	AGTGGC	0.1582700	-0.0271779	0.0050000	2.4E-08
2	IFT172	chr2:27475777_CT_C	27475777	C	CT	0.1409680	0.0296738	0.0052129	2.4E-08
2	GCKR	rs2293572	27505910	G	C	0.1442880	0.0287877	0.0051703	3.7E-08
2	GCKR	rs1260326	27508073	T	C	0.4935410	-0.0586768	0.0036201	6.8E-60
2	GCKR	rs3817588	27508345	C	T	0.3570120	0.0463964	0.0037792	1.4E-35
2	GCKR	rs35073769	27508509	T	C	0.1500490	0.0287293	0.0050644	1.9E-08
2	GCKR	rs148527487	27509703	AT	A	0.3525800	0.0460511	0.0038153	1.4E-34
2	GCKR	chr2:27509775_C_CAA	27509775	CAA	C	0.1535710	0.0285805	0.0050436	2.2E-08
2	GCKR	rs4425043	27510585	A	G	0.1484980	0.0283776	0.0050916	2.9E-08
2	GCKR	rs6547692	27512105	G	A	0.4922980	-0.0577023	0.0036291	6.1E-58
2	GCKR	rs8179225	27514314	G	A	0.1495920	0.0286803	0.0050755	1.8E-08
2	GCKR	rs8179229	27515033	T	A	0.1495910	0.0287172	0.0050755	1.7E-08
2	GCKR	rs12471703	27515987	T	C	0.1486290	0.0284225	0.0050904	2.5E-08
2	GCKR	rs12472643	27516439	T	C	0.1406460	0.0301888	0.0052192	5.6E-09
2	GCKR	rs11127044	27517537	G	C	0.1500450	0.0285577	0.0050684	1.9E-08
2	GCKR	rs780096	27518205	C	G	0.4915710	-0.0570731	0.0036220	6.0E-57
2	GCKR	rs780095	27518238	A	G	0.4902510	-0.0569230	0.0036251	1.5E-56
2	GCKR	rs780094	27518370	T	C	0.4812390	-0.0561237	0.0036215	7.8E-55
2	GCKR	rs780093	27519736	T	C	0.4839140	-0.0563913	0.0036223	1.0E-55
2	GCKR	rs780092	27520287	G	A	0.3594020	0.0465065	0.0037714	7.6E-36
2	GCKR	rs814295	27520348	G	A	0.3611600	0.0467519	0.0037667	2.6E-36
2	GCKR	rs74928908	27521222	G	A	0.3583020	0.0462912	0.0037763	2.2E-35
2	GCKR *	rs1260334	27525730	C	A	0.4873180	-0.0557344	0.0036395	5.6E-54
2	GCKR *	rs1260333	27525757	A	G	0.4865280	-0.0563404	0.0036162	9.4E-56
2	GCKR *	rs1313566	27526037	G	A	0.4841960	-0.0557534	0.0036436	1.1E-53
2	GCKR *	rs11336847	27526125	AT	A	0.4844880	-0.0563039	0.0036553	2.5E-54
2	GCKR *	rs6744393	27527272	T	C	0.3586540	0.0468111	0.0038200	3.9E-35
2	GCKR *	rs2950835	27527678	A	G	0.4858230	-0.0557761	0.0036711	9.9E-53
2	GCKR *	rs2911711	27527679	T	A	0.4858270	-0.0557791	0.0036711	9.7E-53
2	GCKR *	rs78680773	27528695	C	A	0.3567740	0.0458279	0.0038210	9.6E-34
2	GCKR *	rs6753534	27530004	C	T	0.4865450	-0.0485099	0.0036801	4.3E-40
2	GCKR *	rs74450311	27531758	C	CAT	0.3748900	0.0303678	0.0037451	1.6E-16
2	GCKR *	rs62131879	27532245	G	T	0.3756090	0.0307863	0.0037434	5.0E-17
2	GCKR *	rs7606605	27532849	T	A	0.2111190	-0.0300289	0.0045082	1.8E-11
2	GCKR *	rs4665987	27532958	A	G	0.4729930	-0.0420455	0.0036319	1.1E-31
2	GCKR *	rs10181342	27534476	G	A	0.3755010	0.0307828	0.0037433	5.4E-17
2	GCKR *	rs4665988	27538569	A	C	0.4731560	-0.0419819	0.0036310	1.3E-31
2	GCKR *	rs116443177	27541255	T	C	0.3772590	0.0306536	0.0037405	6.7E-17
2	GCKR *	rs62131881	27541914	T	G	0.3753730	0.0307819	0.0037426	5.2E-17
2	GCKR *	rs62131882	27542613	C	T	0.3769530	0.0308337	0.0037380	4.3E-17
2	GCKR *	rs12473139	27542720	C	T	0.4740610	-0.0419430	0.0036290	1.6E-31
2	GCKR *	rs4665991	27543417	A	G	0.4736390	-0.0421767	0.0036322	9.1E-32
2	GCKR *	rs67080990	27544621	G	GC	0.4742000	-0.0419201	0.0036300	1.8E-31
2	GCKR *	rs62141278	27545514	T	C	0.3777010	0.0306044	0.0037394	7.9E-17
2	GCKR *	rs59210625	27546607	C	A	0.2113290	-0.0301765	0.0045059	1.4E-11
2	GCKR *	rs62141279	27548548	T	C	0.3763760	0.0309259	0.0037418	3.9E-17
2	C2orf16 *	chr2:27550224_C_CT	27550224	CT	C	0.3722600	0.0318604	0.0037736	9.1E-18
2	C2orf16 *	rs2384627	27551582	A	G	0.3755600	0.0307533	0.0037413	5.5E-17
2	C2orf16 *	rs202103665	27553764	A	AT	0.4722300	-0.0413914	0.0036291	1.0E-30
2	C2orf16 *	rs62141281	27554784	T	G	0.3763550	0.0305581	0.0037368	7.3E-17
2	C2orf16 *	rs6751087	27555149	C	T	0.3763560	0.0305534	0.0037368	7.4E-17
2	C2orf16 *	rs12995461	27555300	C	A	0.4725640	-0.0414205	0.0036272	8.6E-31
2	C2orf16 *	rs10169065	27555693	G	A	0.4725640	-0.0414190	0.0036272	8.7E-31
2	C2orf16 *	rs10179872	27555705	A	G	0.4713590	-0.0412618	0.0036294	1.4E-30
2	C2orf16 *	rs79414972	27558930	G	A	0.3638870	0.0287223	0.0038046	1.3E-14
2	C2orf16 *	rs62141288	27560331	A	G	0.3544700	0.0294196	0.0038314	3.5E-15
2	C2orf16 *	rs200969564	27560335	GAC	G	0.3544700	0.0294196	0.0038314	3.5E-15
2	C2orf16 *	rs62141290	27560525	C	T	0.3746570	0.0310019	0.0037463	4.2E-17
2	C2orf16 *	rs4665382	27560934	C	T	0.4725750	-0.0414484	0.0036277	8.0E-31
2	C2orf16 *	rs62141291	27561167	T	C	0.3763800	0.0306228	0.0037363	6.5E-17
2	C2orf16 *	rs62141292	27561433	C	A	0.3763750	0.0306223	0.0037363	6.5E-17
2	C2orf16 *	rs7570476	27561791	T	C	0.4725020	-0.0415313	0.0036275	6.2E-31
2	C2orf16 *	rs10208529	27563321	T	A	0.4725100	-0.0415351	0.0036275	6.1E-31
2	C2orf16 *	rs60854669	27564062	C	T	0.3763540	0.0306009	0.0037364	6.8E-17
2	C2orf16 *	rs965813	27566994	A	T	0.3763300	0.0306553	0.0037367	5.9E-17
2	C2orf16 *	rs4665383	27568688	G	C	0.4725140	-0.0415180	0.0036275	6.4E-31
2	C2orf16 *	rs59876138	27569456	C	A	0.3763400	0.0306571	0.0037367	5.8E-17
2	C2orf16 *	rs7577311	27571054	T	G	0.4727190	-0.0415214	0.0036289	7.4E-31
2	C2orf16 *	rs6704596	27574060	G	A	0.3763480	0.0306152	0.0037367	6.3E-17
2	C2orf16	rs1919127	27578626	C	T	0.4724950	-0.0414715	0.0036263	7.2E-31
2	C2orf16	rs1919128	27578892	G	A	0.4725390	-0.0414851	0.0036259	6.9E-31
2	C2orf16	rs3811644	27579938	G	A	0.3763330	0.0305079	0.0037363	7.9E-17
2	ZNF512	rs6734059	27585287	C	T	0.3764330	0.0304461	0.0037362	9.2E-17
2	ZNF512	rs12478841	27588855	G	A	0.4733320	-0.0412781	0.0036261	1.4E-30
2	ZNF512	rs6760250	27589385	A	G	0.4733320	-0.0412781	0.0036261	1.4E-30
2	ZNF512	rs62138963	27591507	T	C	0.3763180	0.0305087	0.0037361	8.1E-17
2	ZNF512	rs62138964	27591571	T	C	0.3763180	0.0305087	0.0037361	8.1E-17
2	ZNF512	rs13022873	27592643	C	A	0.4732740	-0.0413248	0.0036276	1.3E-30
2	ZNF512	rs76013440	27593448	A	G	0.3753040	0.0305916	0.0037430	6.1E-17
2	ZNF512	rs62138965	27593726	C	T	0.3754890	0.0304334	0.0037415	1.1E-16
2	ZNF512	rs13010586	27594950	A	G	0.4733440	-0.0412992	0.0036260	1.3E-30
2	ZNF512	rs1919129	27595854	G	C	0.3763150	0.0305095	0.0037360	8.0E-17
2	ZNF512	rs62138966	27596305	A	G	0.3760600	0.0307247	0.0037370	5.2E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ZNF512	rs12989678	27598615	T	C	0.4727710	-0.0413741	0.0036377	1.5E-30
2	ZNF512	rs78378018	27599416	GAC	G	0.3764230	0.0304448	0.0037368	9.2E-17
2	ZNF512	rs56725354	27601301	C	G	0.3763140	0.0305104	0.0037361	8.0E-17
2	ZNF512	rs62138968	27601618	G	C	0.3763120	0.0305034	0.0037361	8.1E-17
2	ZNF512	rs112927528	27601644	TTTTTG	T	0.3751370	0.0305547	0.0037427	8.3E-17
2	ZNF512	rs12467475	27602848	C	T	0.4720040	-0.0412368	0.0036284	2.3E-30
2	ZNF512	rs12464616	27604225	T	C	0.4732900	-0.0413095	0.0036263	1.2E-30
2	ZNF512	rs2141372	27604329	T	G	0.3763390	0.0304339	0.0037365	9.5E-17
2	ZNF512	rs66497975	27604459	T	GTCATGT	0.4718790	-0.0407215	0.0036328	1.1E-29
2	ZNF512	rs6719960	27607200	G	A	0.3762950	0.0304687	0.0037364	9.0E-17
2	ZNF512	rs6547735	27608740	C	T	0.3762920	0.0304336	0.0037366	9.8E-17
2	ZNF512	rs2384656	27609188	G	A	0.4733040	-0.0412937	0.0036264	1.4E-30
2	ZNF512	rs1881397	27609418	G	A	0.3767370	0.0301923	0.0037385	1.7E-16
2	ZNF512	chr2:27609869_CA_C	27609869	C	CA	0.3956190	0.0291296	0.0037769	1.9E-15
2	ZNF512	rs112427483	27610460	T	TATATAT	0.3316630	0.0339102	0.0039220	2.1E-18
2	ZNF512	rs74175068	27610635	C	T	0.4597760	-0.0412063	0.0037047	2.9E-29
2	ZNF512	rs34016998	27610820	T	C	0.4726630	-0.0409503	0.0036262	3.6E-30
2	ZNF512	rs12987055	27611285	C	T	0.4729860	-0.0406811	0.0036264	8.2E-30
2	ZNF512	rs13405762	27611748	C	A	0.3739610	0.0305645	0.0037503	1.2E-16
2	ZNF512	rs78170284	27612215	A	G	0.3766180	0.0305596	0.0037371	7.6E-17
2	ZNF512	rs13020949	27613738	T	C	0.4727850	-0.0411084	0.0036281	2.5E-30
2	ZNF512	chr2:27614806_CT_C	27614806	C	CT	0.3763110	0.0307361	0.0037409	5.1E-17
2	ZNF512	rs1881395	27615682	A	G	0.3762540	0.0307219	0.0037413	5.4E-17
2	ZNF512	rs4666000	27616502	C	T	0.4726540	-0.0409371	0.0036296	5.0E-30
2	ZNF512	rs2068834	27616672	C	T	0.4722960	-0.0408265	0.0036301	6.8E-30
2	ZNF512	rs7571558	27616965	G	C	0.3763300	0.0307511	0.0037414	5.2E-17
2	ZNF512	rs4666002	27617773	C	G	0.4720670	-0.0411389	0.0036333	2.5E-30
2	ZNF512	rs62138971	27617887	A	G	0.3752100	0.0303748	0.0037603	1.7E-16
2	ZNF512	rs1881396	27621734	G	T	0.3711690	0.0298496	0.0037677	6.7E-16
2	GNP1	rs3749147	27629051	A	G	0.3142250	-0.0338526	0.0039052	4.2E-18
2	GNP1	rs146892484	27629283	C	CG	0.4177910	-0.0236581	0.0036846	7.0E-11
2	GNP1	rs34502053	27631657	A	G	0.3168580	-0.0335041	0.0038984	9.5E-18
2	GNP1	rs10173720	27632530	A	T	0.4192080	-0.0239474	0.0036758	4.1E-11
2	GNP1	rs6719175	27636484	A	T	0.3154140	-0.0333409	0.0039179	1.7E-17
2	GNP1	rs77350364	27643272	A	G	0.4186850	-0.0240052	0.0036864	3.3E-11
2	GNP1	rs12474585	27648726	C	T	0.4187070	-0.0241162	0.0036845	2.9E-11
2	GNP1	rs35605899	27649445	A	AATAT	0.3357220	-0.0307507	0.0038487	1.1E-15
2	GNP1	rs8731	27650459	C	G	0.4182680	-0.0238202	0.0036848	4.6E-11
2	SUPT7L	chr2:27652149_AAAAT_A	27652149	AAAAT	A	0.4175030	-0.0237055	0.0036929	6.3E-11
2	SUPT7L	rs67775899	27652169	TAAA	T	0.4181360	-0.0238867	0.0036966	4.6E-11
2	SUPT7L	rs10202364	27652175	T	A	0.4186480	-0.0239536	0.0036918	4.3E-11
2	SUPT7L	rs4666010	27655819	T	C	0.4181830	-0.0237088	0.0036847	5.7E-11
2	SLC4A1AP	rs2272406	27669156	T	A	0.3356610	-0.0307712	0.0038464	1.3E-15
2	SLC4A1AP	rs76586169	27674968	G	A	0.4178760	-0.0238260	0.0036842	5.1E-11
2	SLC4A1AP	rs13021208	27678861	T	C	0.3357260	-0.0304297	0.0038477	2.5E-15
2	SLC4A1AP	rs72613829	27680120	C	T	0.4170090	-0.0232337	0.0036866	1.6E-10
2	SLC4A1AP	rs13023094	27687839	C	A	0.3358000	-0.0308879	0.0038448	1.0E-15
2	SLC4A1AP	rs12998770	27690321	C	T	0.3360200	-0.0309806	0.0038451	8.3E-16
2	SLC4A1AP *	rs80322731	27697569	G	A	0.2085600	-0.0290649	0.0045294	1.5E-10
2	SLC4A1AP *	rs13030973	27705930	C	T	0.3329330	-0.0299973	0.0038456	6.4E-15
2	SLC4A1AP *	rs4665385	27707970	C	T	0.4135150	-0.0231127	0.0036827	2.0E-10
2	SLC4A1AP *	rs6727388	27709720	G	A	0.3321750	-0.0297529	0.0038486	1.1E-14
2	SLC4A1AP *	rs4616435	27710775	T	C	0.3328930	-0.0299966	0.0038461	6.4E-15
2	SLC4A1AP *	rs58199976	27711657	T	C	0.4126170	-0.0232859	0.0036838	1.6E-10
2	SLC4A1AP *	rs6727215	27711864	A	G	0.3321420	-0.0298008	0.0038488	9.9E-15
2	SLC4A1AP *	rs4665386	27712485	C	A	0.4140870	-0.0232958	0.0036820	1.4E-10
2	SLC4A1AP *	rs6742571	27719021	G	A	0.4197700	-0.0236629	0.0036837	8.1E-11
2	SLC4A1AP *	chr2:27724905_CT_C	27724905	C	CT	0.4121490	-0.0227901	0.0037370	6.9E-10
2	SLC4A1AP *	rs1881394	27726185	G	A	0.4158630	-0.0227166	0.0037141	7.5E-10
2	SLC4A1AP *	rs10432705	27727970	A	G	0.3320080	-0.0292604	0.0038889	6.4E-14
2	SLC4A1AP *	rs867282	27728791	C	T	0.4156830	-0.0228327	0.0037115	6.3E-10
2	SLC4A1AP *	rs2384655	27729368	T	A	0.4157290	-0.0227842	0.0037115	6.7E-10
2	SLC4A1AP *	rs12994085	27729539	T	C	0.4157380	-0.0227663	0.0037115	6.8E-10
2	SLC4A1AP *	rs12993377	27729900	C	G	0.4157330	-0.0227139	0.0037116	7.5E-10
2	MRPL33 *	rs12624148	27733614	C	T	0.4159170	-0.0229153	0.0037179	5.3E-10
2	MRPL33 *	rs6753736	27735988	G	C	0.4211010	-0.0227921	0.0037094	7.1E-10
2	MRPL33 *	rs75429814	27738747	T	C	0.4115430	-0.0220725	0.0037377	3.5E-09
2	MRPL33 *	rs111938697	27740266	C	T	0.4156930	-0.0211091	0.0037243	1.3E-08
2	MRPL33 *	rs12714223	27740463	A	G	0.4146960	-0.0215045	0.0037237	6.8E-09
2	MRPL33 *	rs36017854	27740804	AAT	A	0.4138460	-0.0216837	0.0037291	5.1E-09
2	MRPL33 *	rs9678824	27741461	G	C	0.4149070	-0.0215464	0.0037214	6.2E-09
2	MRPL33 *	rs13023194	27744393	C	G	0.3339210	-0.0271202	0.0038795	3.7E-12
2	MRPL33 *	rs9967838	27745587	C	A	0.4148780	-0.0213775	0.0036985	6.0E-09
2	MRPL33 *	chr2:27747209_A_AT	27747209	AT	A	0.4032370	-0.0221023	0.0037209	1.7E-09
2	MRPL33 *	rs9677663	27749578	A	G	0.4101070	-0.0222902	0.0036873	1.4E-09
2	MRPL33 *	rs57238885	27751393	C	G	0.4101900	-0.0225407	0.0036854	9.2E-10
2	MRPL33 *	rs10201247	27752104	G	A	0.4101900	-0.0225407	0.0036854	9.2E-10
2	MRPL33 *	rs6547796	27752527	C	T	0.4104870	-0.0224607	0.0036858	1.1E-09
2	MRPL33 *	rs4666011	27758045	G	C	0.4102220	-0.0225429	0.0036848	9.0E-10
2	MRPL33 *	rs10209020	27758077	T	C	0.4104680	-0.0225523	0.0036858	9.2E-10
2	MRPL33 *	rs12471347	27758788	G	C	0.4103080	-0.0225819	0.0036835	8.2E-10
2	MRPL33 *	rs77154381	27759252	A	G	0.4085080	-0.0230481	0.0036900	4.5E-10
2	MRPL33 *	rs12477908	27764179	C	A	0.4113760	-0.0221219	0.0036825	1.6E-09
2	MRPL33 *	rs13006480	27764354	G	C	0.3266500	-0.0296174	0.0038954	4.2E-14
2	MRPL33 *	rs13013484	27765954	A	G	0.4103480	-0.0225821	0.0036837	8.3E-10
2	MRPL33 *	rs4665390	27767042	C	T	0.4113860	-0.0224457	0.0036846	9.5E-10
2	MRPL33 *	rs74429612	27770976	C	T	0.4114770	-0.0221121	0.0036823	1.7E-09
2	MRPL33	rs3736594	27772914	C	A	0.4114800	-0.0220162	0.0036823	1.9E-09
2	MRPL33	rs3792252	27773064	A	G	0.4103120	-0.0226244	0.0036834	7.6E-10
2	MRPL33	rs35463245	27777857	C	G	0.4083950	-0.0223222	0.0036940	1.4E-09
2	MRPL33	rs17006242	27778184	C	A	0.4113260	-0.0221217	0.0036826	1.6E-09
2	MRPL33	rs3792253	27779135	T	C	0.4102150	-0.0225115	0.0036842	9.2E-10
2	MRPL33 *	rs13030345	27780307	T	G	0.3069730	-0.0283533	0.0039600	1.4E-12
2	RBKS	rs74327441	27784205	G	A	0.4042030	-0.0223368	0.0037412	2.1E-09
2	RBKS	rs7593136	27794925	A	G	0.4116540	-0.0227080	0.0036822	7.7E-10
2	RBKS	rs6744348	27795158	A	C	0.4116620	-0.0227633	0.0036818	7.1E-10
2	RBKS	rs36035825	27795264	T	G	0.4116600	-0.0227543	0.0036818	7.2E-10
2	RBKS	rs4666012	27795426	A	G	0.4116580	-0.0227642	0.0036818	7.1E-10
2	RBKS	rs11322614	27796225	AT	A	0.4103600	-0.0228816	0.0036912	6.2E-10
2	RBKS	rs4666013	27796239	C	T	0.4116600	-0.0227632	0.0036817	7.2E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	RBKS	rs4666014	27796308	G	A	0.4117520	-0.0228337	0.0036816	6.9E-10
2	RBKS	rs4666015	27796500	G	A	0.4116790	-0.0227697	0.0036815	7.2E-10
2	RBKS	rs34181670	27796989	T	C	0.4116800	-0.0227924	0.0036815	6.9E-10
2	RBKS	rs35679500	27797099	T	C	0.4116800	-0.0227924	0.0036815	6.9E-10
2	RBKS	rs12623170	27797290	C	T	0.4120990	-0.0225942	0.0036803	8.4E-10
2	RBKS	rs3935148	27798099	T	A	0.4088180	-0.0230514	0.0036877	5.6E-10
2	RBKS	rs71441095	27866981	A	G	0.4712280	0.0200345	0.0036707	2.4E-08
2	RBKS	rs10171517	27867192	T	C	0.4713830	0.0201675	0.0036702	1.9E-08
2	RBKS	rs898034	27867953	T	C	0.4714920	0.0202284	0.0036697	1.7E-08
2	SIX3 *	rs494904	44914041	T	C	0.3310750	0.0318517	0.0039191	2.3E-16
2	SIX3 *	rs1026061	44914872	G	C	0.3238390	0.0314877	0.0039361	1.5E-15
2	SIX3 *	rs1026062	44914939	A	G	0.3200480	0.0307542	0.0039292	6.1E-15
2	SIX3 *	rs17032710	44916600	C	G	0.3014680	0.0338038	0.0039862	2.1E-17
2	SIX3 *	rs483256	44918132	A	C	0.4974900	0.0293665	0.0036252	5.8E-16
2	SIX3 *	rs481223	44918368	T	C	0.4976200	0.0292727	0.0036246	6.2E-16
2	SIX3 *	rs480310	44918457	A	G	0.4975890	0.0293168	0.0036240	5.6E-16
2	SIX3 *	rs34438374	44918590	A	AC	0.4975770	0.0292633	0.0036215	6.3E-16
2	SIX3 *	rs477659	44918722	A	G	0.4975460	0.0293324	0.0036236	5.8E-16
2	SIX3 *	rs476710	44918830	A	G	0.4976140	0.0292827	0.0036236	6.2E-16
2	SIX3 *	rs476619	44918866	A	G	0.4976320	0.0292718	0.0036239	6.3E-16
2	SIX3 *	rs1798714	44919305	T	C	0.4976020	0.0295633	0.0036331	4.4E-16
2	SIX3 *	rs561400	44919373	G	T	0.4999710	-0.0294726	0.0036362	5.7E-16
2	SIX3 *	rs559503	44919407	A	C	0.4986400	-0.0294184	0.0036371	5.8E-16
2	SIX3 *	rs556151	44919896	T	C	0.4975060	0.0299764	0.0036375	1.8E-16
2	SIX3 *	rs533063	44920177	A	C	0.4975900	0.0300407	0.0036390	1.7E-16
2	SIX3 *	rs529438	44920554	T	C	0.4994910	0.0299687	0.0036411	2.0E-16
2	SIX3 *	rs480385	44920585	C	A	0.4996970	0.0300899	0.0036424	1.6E-16
2	SIX3 *	rs503982	44920996	T	C	0.4994010	0.0299225	0.0036427	2.3E-16
2	SIX3 *	rs503821	44921068	A	G	0.4994330	0.0299332	0.0036426	2.2E-16
2	SIX3 *	rs496467	44921864	C	T	0.4351010	-0.0391110	0.0036876	1.8E-26
2	SIX3 *	rs6748377	44922234	T	G	0.4188110	0.0341550	0.0037295	2.5E-20
2	SIX3 *	rs1992825	44923139	C	G	0.3645220	0.0403722	0.0037679	4.5E-27
2	SIX3 *	rs517055	44923338	A	T	0.4374930	-0.0414009	0.0036629	6.4E-30
2	SIX3 *	rs511704	44923916	T	C	0.4375260	-0.0411564	0.0036544	7.8E-30
2	SIX3 *	rs486389	44924018	C	T	0.4385770	-0.0413692	0.0036554	5.0E-30
2	SIX3 *	rs487260	44924103	A	G	0.4383120	-0.0411905	0.0036569	8.1E-30
2	SIX3 *	rs486917	44924302	G	A	0.4384970	-0.0411141	0.0036575	9.3E-30
2	SIX3 *	rs7340480	44924418	T	C	0.3512170	0.0391376	0.0037986	2.4E-25
2	SIX3 *	rs72794102	44924461	T	C	0.4283470	-0.0419956	0.0036695	3.1E-31
2	SIX3 *	rs485800	44924469	G	A	0.4381480	-0.0411960	0.0036587	6.5E-30
2	SIX3 *	rs491175	44924551	G	C	0.4380280	-0.0411112	0.0036596	8.9E-30
2	SIX3 *	rs4953148	44925383	T	A	0.4270570	-0.0426042	0.0036730	6.3E-32
2	SIX3 *	rs2342406	44925609	C	T	0.3692780	0.0409970	0.0037388	2.4E-28
2	SIX3 *	rs538543	44926148	C	G	0.4254320	-0.0421273	0.0036835	1.0E-30
2	SIX3 *	rs549814	44926369	T	C	0.4463400	-0.0428376	0.0036880	1.3E-31
2	SIX3 *	rs7568987	44927090	G	A	0.4503380	-0.0431627	0.0036929	3.6E-32
2	SIX3 *	rs7569203	44927279	C	A	0.4502700	-0.0431345	0.0036971	6.0E-32
2	SIX3 *	rs163518	44954013	T	C	0.1561410	-0.0570917	0.0050312	5.3E-31
2	SIX3 *	rs984494	44955829	T	C	0.1694440	-0.0544567	0.0048533	4.7E-30
2	SIX3 *	rs75399305	44956246	C	T	0.2928030	-0.0524525	0.0040324	1.5E-38
2	SIX3 *	rs163515	44956880	G	A	0.1679010	-0.0551647	0.0048412	1.4E-31
2	SIX3 *	rs11305873	44957266	G	GT	0.4575030	0.0797094	0.0036638	1.3E-104
2	SIX3 *	rs4952728	44957284	C	T	0.1791250	-0.0527241	0.0047308	1.2E-29
2	SIX3 *	rs79473174	44957495	T	C	0.2915760	-0.0531896	0.0040064	6.3E-40
2	SIX3 *	rs4953153	44957632	G	A	0.1776750	-0.0532018	0.0047442	5.4E-30
2	SIX3 *	rs163514	44958067	A	G	0.3005630	-0.0530391	0.0039747	8.5E-40
2	SIX3 *	rs163513	44958085	A	G	0.3010060	-0.0527547	0.0039723	1.9E-39
2	SIX3 *	rs163512	44958128	A	G	0.1903590	-0.0537515	0.0046330	1.0E-32
2	SIX3 *	rs163511	44958956	T	C	0.1891720	-0.0531276	0.0046463	6.8E-32
2	SIX3 *	chr2:44959755_A_AAAAAC	44959755	AAAAAC	A	0.2918810	-0.0544766	0.0039966	5.5E-42
2	SIX3 *	rs1983312	44959988	G	A	0.2686500	-0.0457255	0.0040905	2.8E-29
2	SIX3 *	rs9973503	44960431	T	G	0.3043220	-0.0569054	0.0039338	4.1E-47
2	SIX3 *	rs895636	44961214	T	C	0.4215810	0.0865108	0.0036556	9.2E-124
2	SIX3 *	rs340515	44961231	G	T	0.4372670	0.0853317	0.0036542	4.8E-122
2	SIX3 *	rs10205222	44961386	G	A	0.2062310	0.0679183	0.0044832	9.8E-51
2	SIX3 *	rs74262181	44961926	T	C	0.0919473	0.0564992	0.0062941	1.5E-20
2	SIX3 *	rs4953155	44962357	A	T	0.4957850	-0.0784099	0.0036462	1.6E-103
2	SIX3 *	rs2121564	44962886	G	C	0.2103650	0.0672640	0.0044643	1.7E-50
2	SIX3 *	rs5830819	44962917	AC	A	0.4278140	0.0869046	0.0036676	2.3E-124
2	SIX3 *	rs2164701	44963232	C	G	0.2099750	0.0671183	0.0044677	2.5E-50
2	SIX3 *	rs163510	44964087	A	G	0.1885310	-0.0518495	0.0046657	2.6E-30
2	SIX3 *	rs10191589	44964185	A	C	0.2065120	0.0665530	0.0044930	8.7E-49
2	SIX3 *	rs12712928	44964941	C	G	0.4332780	0.0880344	0.0036880	1.4E-126
2	SIX2 *	rs485348	44975928	G	C	0.1775890	-0.0342215	0.0048099	2.4E-12
2	SIX2 *	rs487117	44976084	A	G	0.4256980	-0.0359428	0.0037065	1.1E-21
2	SIX2 *	rs489083	44976311	T	A	0.4216440	-0.0347173	0.0036954	2.5E-20
2	SIX2 *	rs12612076	44976372	A	G	0.1614280	-0.0345521	0.0049720	7.3E-12
2	SIX2 *	rs34816609	44976443	GT	G	0.4261280	-0.0355626	0.0036969	2.0E-21
2	SIX2 *	rs4953159	44976598	T	C	0.4297940	0.0447795	0.0036760	9.5E-33
2	SIX2 *	rs526258	44977027	T	C	0.1620000	-0.0400686	0.0049673	8.6E-16
2	SIX2 *	rs521875	44977552	G	T	0.4733070	-0.0342059	0.0036380	1.5E-19
2	SIX2 *	rs532628	44977694	T	G	0.4716440	-0.0341933	0.0036363	1.8E-19
2	SIX2 *	rs12611664	44977724	C	T	0.1604430	-0.0330428	0.0049540	7.4E-11
2	SIX2 *	rs11690627	44977800	T	G	0.4287100	0.0446189	0.0036639	1.8E-32
2	SIX2 *	rs545851	44977917	C	G	0.4782430	-0.0352808	0.0036379	8.6E-21
2	SIX2 *	rs545880	44977923	C	G	0.4782430	-0.0352808	0.0036379	8.6E-21
2	SIX2 *	rs11680561	44977985	G	A	0.4360880	0.0436219	0.0036455	2.8E-31
2	SIX2 *	rs546698	44977994	C	T	0.4718870	-0.0342576	0.0036300	1.4E-19
2	SIX2 *	rs558110	44978156	A	G	0.1647630	-0.0390046	0.0048996	2.1E-15
2	SIX2 *	rs4953161	44978408	T	G	0.4358050	0.0433283	0.0036457	6.6E-31
2	SIX2 *	rs561078	44978527	A	G	0.3434630	-0.0243845	0.0038412	5.3E-10
2	SIX2 *	chr2:44979036_A_AAAAAC	44979036	AAAAAC	A	0.1620040	-0.0340522	0.0049427	1.3E-11
2	SIX2 *	rs477072	44979099	T	C	0.1645610	-0.0399735	0.0049090	3.9E-16
2	SIX2 *	rs578732	44979184	T	C	0.1650690	-0.0404260	0.0049041	1.7E-16
2	SIX2 *	rs478012	44979201	C	T	0.1650690	-0.0404260	0.0049041	1.7E-16
2	SIX2 *	rs478921	44979313	A	G	0.4742400	-0.0356207	0.0036691	8.0E-21
2	SIX2 *	rs57044027	44979712	G	C	0.1605650	-0.0331277	0.0049488	5.8E-11
2	SIX2 *	rs505935	44979962	G	C	0.1656270	-0.0403276	0.0048978	2.0E-16
2	SIX2 *	rs12053535	44980452	T	C	0.4285180	0.0426353	0.0036789	2.9E-29
2	SIX2 *	rs62130886	44980459	T	A	0.4778120	-0.0338412	0.0036554	7.4E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	SIX2 *	rs201959083	44980462	C	T	0.4801950	-0.0341111	0.0036657	4.0E-19
2	SIX2 *	rs501581	44980480	C	T	0.4759380	-0.0342189	0.0036477	2.1E-19
2	SIX2 *	rs510523	44980490	T	C	0.4750510	-0.0343558	0.0036426	1.4E-19
2	SIX2 *	rs503435	44980685	G	A	0.1667970	-0.0394545	0.0048747	5.9E-16
2	SIX2 *	rs1216887026	44980728	GT	G	0.4733020	-0.0345141	0.0036324	6.6E-20
2	SIX2 *	rs11381995	44980732	C	CG	0.4726420	-0.0343233	0.0036291	1.0E-19
2	SIX2 *	rs11419947	44981068	T	TA	0.4718120	-0.0344286	0.0036291	8.5E-20
2	SIX2 *	rs540627	44981467	A	G	0.4709080	-0.0339352	0.0036284	3.0E-19
2	SIX2 *	rs541473	44981553	A	C	0.1654490	-0.0391678	0.0048906	1.3E-15
2	SIX2 *	rs478918	44981814	G	T	0.4705870	-0.0339032	0.0036266	3.2E-19
2	SIX2 *	rs566941	44981999	A	C	0.1647120	-0.0385362	0.0048969	4.1E-15
2	SIX2 *	rs568094	44982168	T	G	0.4703560	-0.0334961	0.0036248	8.7E-19
2	SIX2 *	rs482536	44982175	G	C	0.4711750	-0.0334386	0.0036289	1.1E-18
2	SIX2 *	rs2921986	44982279	A	G	0.4869370	0.0416630	0.0036121	7.7E-30
2	SIX2 *	rs486930	44983030	T	C	0.1641950	-0.0377674	0.0048981	1.3E-14
2	SIX2 *	rs490731	44983447	T	C	0.4711680	-0.0343377	0.0036310	1.1E-19
2	SIX2 *	rs515713	44983502	A	G	0.4701120	-0.0337428	0.0036274	4.4E-19
2	SIX2 *	rs1657854	44983666	C	T	0.47000470	-0.0337263	0.0036284	4.7E-19
2	SIX2 *	rs2917758	44983704	G	C	0.4382480	0.0428746	0.0036393	2.6E-30
2	SIX2 *	rs2959238	44983760	T	C	0.4700260	-0.0337387	0.0036287	4.5E-19
2	SIX2 *	rs2959239	44983824	T	C	0.1643370	-0.0377604	0.0048967	1.4E-14
2	SIX2 *	rs2917759	44984049	A	C	0.4700550	-0.0337284	0.0036295	4.8E-19
2	SIX2 *	rs2917760	44984090	G	A	0.1653520	-0.0376807	0.0048859	1.5E-14
2	SIX2 *	rs2917761	44984145	A	G	0.4697090	-0.0333272	0.0036343	1.5E-18
2	SIX2 *	rs2917762	44984329	G	A	0.4699880	-0.0335034	0.0036348	1.0E-18
2	SIX2 *	rs2917763	44984481	G	C	0.4702460	-0.0334325	0.0036367	1.3E-18
2	SIX2 *	rs2917764	44984604	C	G	0.4721440	-0.0338394	0.0036370	4.0E-19
2	SIX2 *	rs2959240	44984764	A	T	0.4702130	-0.0334506	0.0036377	1.2E-18
2	SIX2 *	rs2959241	44984775	A	T	0.4702130	-0.0334506	0.0036377	1.2E-18
2	SIX2 *	rs2959242	44984953	T	C	0.4702150	-0.0334628	0.0036378	1.2E-18
2	SIX2 *	rs2922016	44984977	C	G	0.4708150	-0.0334979	0.0036384	1.0E-18
2	SIX2 *	rs2917765	44985119	G	A	0.4701330	-0.0335530	0.0036370	9.7E-19
2	SIX2 *	rs2922015	44985149	T	C	0.4374320	0.0424953	0.0036518	1.6E-29
2	SIX2 *	rs2917766	44985227	A	C	0.3289250	-0.0434237	0.0038660	1.1E-28
2	SIX2 *	rs2959243	44985382	T	C	0.4708960	-0.0334395	0.0036381	1.2E-18
2	SIX2 *	rs2922014	44985493	T	C	0.4377180	0.0423945	0.0036490	1.9E-29
2	SIX2 *	chr2:44985885_T_TAATAA	44985885	T	TAATAA	0.4711370	-0.0332983	0.0036411	2.0E-18
2	SIX2 *	rs2342409	44985987	T	C	0.1637260	-0.0372433	0.0049046	3.4E-14
2	SIX2 *	rs2342410	44986149	A	G	0.4694020	-0.0335340	0.0036379	1.1E-18
2	SIX2 *	rs1545371	44986338	C	T	0.0715648	-0.0436257	0.0071274	8.2E-10
2	SIX2 *	rs895633	44986552	A	T	0.1643890	-0.0370674	0.0048955	3.7E-14
2	SIX2 *	rs874576	44986884	A	G	0.4712330	-0.0334052	0.0036398	1.6E-18
2	SIX2 *	rs2959244	44987410	G	T	0.4356910	0.0425346	0.0036555	1.3E-29
2	SIX2 *	rs4143309	44988029	G	A	0.1653900	-0.0328244	0.0048804	3.8E-11
2	SIX2 *	rs2959245	44988731	C	G	0.3310730	-0.0429774	0.0038545	2.6E-28
2	SIX2 *	rs2959246	44988741	A	G	0.3310650	-0.0429892	0.0038545	2.5E-28
2	SIX2 *	rs2922013	44988798	C	A	0.3312430	-0.0431339	0.0038557	1.8E-28
2	SIX2 *	rs2959247	44988818	T	C	0.3305010	-0.0431601	0.0038568	1.8E-28
2	SIX2 *	rs2959248	44988948	T	C	0.4449330	0.0435254	0.0036671	7.2E-31
2	SIX2 *	rs2922012	44989007	C	G	0.1644030	-0.0369486	0.0048974	4.4E-14
2	SIX2 *	rs2917767	44989140	A	G	0.3310350	-0.0427870	0.0038548	4.4E-28
2	SIX2 *	rs2922011	44989567	A	G	0.3303540	-0.0429265	0.0038567	3.3E-28
2	SIX2 *	rs2922010	44989900	C	A	0.4512130	0.0427526	0.0036472	4.2E-30
2	SIX2 *	rs10201353	44989958	G	A	0.1667390	-0.0318718	0.0048553	1.2E-10
2	SIX2 *	rs10190453	44990006	C	T	0.1665260	-0.0320330	0.0048585	1.0E-10
2	SIX2 *	rs2917768	44990141	G	A	0.3365670	-0.0435099	0.0038494	3.7E-29
2	SIX2 *	rs2959249	44990190	A	T	0.3312910	-0.0426107	0.0038555	7.4E-28
2	SIX2 *	rs10179001	44990924	A	G	0.1665050	-0.0319187	0.0048591	1.2E-10
2	SIX2 *	rs10181483	44991102	T	G	0.1665060	-0.0319345	0.0048587	1.2E-10
2	SIX2 *	rs10711552	44991420	G	GT	0.1665980	-0.0316991	0.0048585	1.6E-10
2	SIX2 *	rs12622589	44991675	G	A	0.1664930	-0.0319701	0.0048595	1.1E-10
2	SIX2 *	rs13404503	44992491	A	G	0.1656270	-0.0323079	0.0048766	7.8E-11
2	SIX2 *	rs10188145	44992996	A	G	0.1656120	-0.0323047	0.0048770	7.9E-11
2	SIX2 *	rs2959250	44993130	T	C	0.3311250	-0.0425168	0.0038795	1.8E-27
2	SIX2 *	rs2917769	44993209	T	C	0.4749270	-0.0474098	0.0036546	2.5E-37
2	SIX2 *	rs767492	44993940	G	T	0.2580180	-0.0361099	0.0041653	2.6E-18
2	SIX2 *	rs767491	44994077	C	A	0.2588490	-0.0360252	0.0041619	2.4E-18
2	SIX2 *	rs767493	44994166	C	T	0.1658700	-0.0352102	0.0048950	4.5E-13
2	SIX2 *	rs76450452	44994259	G	T	0.1650820	-0.0323248	0.0048868	8.3E-11
2	SIX2 *	rs34375457	44994403	AG	A	0.4349650	0.0421949	0.0036726	2.7E-29
2	SIX2 *	rs2922008	44994808	T	C	0.4323990	0.0419873	0.0036789	5.2E-29
2	SIX2 *	rs2917770	44995773	T	C	0.1648460	-0.0358108	0.0049029	2.4E-13
2	SIX2 *	rs2959251	44996132	C	G	0.4775770	-0.0475107	0.0036664	2.2E-37
2	SIX2 *	rs2922007	44996370	C	G	0.4296890	0.0438285	0.0036814	2.0E-31
2	SIX2 *	rs75858902	44998598	C	T	0.1880000	-0.0356493	0.0046853	3.5E-14
2	SIX2 *	rs9917268	44999161	T	C	0.1879630	-0.0354051	0.0046865	5.5E-14
2	SIX2 *	rs80188420	44999591	G	A	0.1879380	-0.0356128	0.0046863	4.0E-14
2	SIX2 *	rs2959252	45002286	A	C	0.4181530	0.0437715	0.0037326	2.2E-30
2	SIX2 *	rs2959253	45002733	A	G	0.1394530	-0.0345832	0.0052955	6.9E-11
2	SIX2 *	rs35417092	45004250	AG	A	0.1463150	-0.0357440	0.0051976	4.4E-12
2	SIX2 *	rs77492481	45005622	C	A	0.1858940	-0.0335038	0.0047145	1.5E-12
2	SIX2 *	rs3738975	45006637	G	C	0.1871950	-0.0332818	0.0047027	1.7E-12
2	SIX2 *	rs1529973	45006922	C	G	0.1399490	-0.0356925	0.0052899	1.5E-11
2	SIX2 *	rs2959230	45006974	A	C	0.1403930	-0.0356352	0.0052839	1.5E-11
2	SIX2 *	rs2959229	45007224	T	C	0.2700870	-0.0355365	0.0041495	2.1E-17
2	SIX2 *	rs895631	45007871	T	C	0.1290940	-0.0348037	0.0054710	2.5E-10
2	SIX2 *	rs2959228	45009664	T	G	0.1377920	-0.0365377	0.0053215	8.1E-12
2	SIX2 *	rs2342412	45010857	T	G	0.4594830	-0.0484583	0.0036526	3.9E-39
2	SIX2 *	rs921118	45011034	G	A	0.4571670	-0.0490047	0.0036525	6.7E-40
2	SIX2 *	rs921117	45011072	T	C	0.4587830	-0.0489661	0.0036490	6.4E-40
2	SIX2 *	rs964992	45011571	G	A	0.4590670	-0.0485430	0.0036444	2.5E-39
2	SIX2 *	rs964991	45011582	T	G	0.4525020	0.0425753	0.0036620	6.7E-30
2	SIX2 *	rs1447106	45011882	T	C	0.4579860	-0.0478318	0.0036431	2.7E-38
2	SIX2 *	rs1447105	45011931	T	C	0.4582280	-0.0478467	0.0036430	2.5E-38
2	SIX2 *	rs1347660	45012035	A	G	0.3259380	-0.0414740	0.0038828	3.3E-26
2	SIX2 *	rs2922005	45012254	C	G	0.4583020	-0.0477400	0.0036399	2.8E-38
2	SIX2 *	rs2922004	45012255	A	G	0.2715990	-0.0346907	0.0041286	1.2E-16
2	SIX2 *	rs2917771	45012499	T	G	0.4576120	-0.0478899	0.0036424	1.5E-38
2	SIX2 *	rs2917772	45012569	T	C	0.4580640	-0.0474973	0.0036381	5.6E-38
2	SIX2 *	rs2917773	45012854	A	G	0.4582110	-0.0473160	0.0036340	9.5E-38

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	SIX2 *	rs2959227	45013665	T	C	0.3261730	-0.0410089	0.0038755	7.9E-26
2	SIX2 *	rs921116	45014191	A	G	0.4571200	-0.0478937	0.0036364	1.1E-38
2	SIX2 *	rs921115	45014477	C	G	0.4598210	-0.0470596	0.0036382	2.9E-37
2	SIX2 *	rs34898797	45014685	GC	G	0.4585460	-0.0476092	0.0036304	2.6E-38
2	SIX2 *	rs12712931	45014869	T	C	0.4584680	-0.0475616	0.0036298	3.0E-38
2	SIX2 *	rs2922002	45015062	G	C	0.4492040	-0.0473017	0.0036352	7.3E-38
2	SIX2 *	rs35242472	45015081	T	TTC	0.4492380	-0.0472485	0.0036347	8.4E-38
2	SIX2 *	rs2959226	45015488	C	T	0.4491830	-0.0472714	0.0036358	8.3E-38
2	SIX2 *	rs2922001	45015552	A	G	0.4329800	-0.0451138	0.0036714	3.9E-34
2	SIX2 *	rs2959225	45015584	A	G	0.4491490	-0.0472994	0.0036358	7.0E-38
2	SIX2 *	rs2959224	45015646	C	T	0.4482930	-0.0475553	0.0036407	3.7E-38
2	SIX2 *	rs2922000	45016636	A	G	0.3302910	-0.0417809	0.0038602	4.7E-27
2	SIX2 *	rs34667850	45016714	TG	T	0.4081070	-0.0471016	0.0036795	1.6E-37
2	SIX2 *	rs11356602	45016717	A	T	0.4081070	-0.0471016	0.0036795	1.6E-37
2	SIX2 *	rs12612323	45016939	C	G	0.1762750	-0.0330979	0.0048199	8.9E-12
2	SIX2 *	rs3064299	45017629	TGA	T	0.1434340	-0.0363192	0.0052346	3.1E-12
2	SIX2 *	rs35745300	45017658	A	AT	0.4494040	-0.0471500	0.0036388	1.1E-37
2	SIX2 *	rs735845	45017983	G	T	0.3306300	-0.0419747	0.0038586	2.7E-27
2	SIX2 *	rs2959223	45018026	A	G	0.4564600	0.0424043	0.0036389	3.4E-30
2	SIX2 *	rs2921998	45019362	A	G	0.3166290	-0.0250635	0.0039491	3.6E-10
2	SIX2 *	rs2921997	45019818	G	A	0.3172280	-0.0247909	0.0039510	5.8E-10
2	SIX2 *	rs2921996	45020631	A	G	0.1334730	-0.0344625	0.0053949	1.3E-10
2	SIX2 *	rs11389526	45023016	G	GT	0.1321880	-0.0350006	0.0054275	1.0E-10
2	SIX2 *	rs13392039	45031466	T	A	0.2294120	-0.0277937	0.0043813	5.4E-11
2	SIX2 *	rs60977305	45033870	G	C	0.2322770	-0.0271305	0.0043526	1.2E-10
2	SIX2 *	rs58759697	45034571	A	G	0.2310850	-0.0282244	0.0043600	2.8E-11
2	SIX2 *	rs111568822	45034984	A	G	0.2311040	-0.0280965	0.0043597	3.6E-11
2	SIX2 *	rs4261761	45035808	C	A	0.2302740	-0.0266227	0.0043678	4.0E-10
2	SIX2 *	rs113961175	45037186	T	C	0.2608500	-0.0233174	0.0042141	1.5E-08
2	SIX2 *	rs72797962	45045995	A	C	0.2198950	-0.0326532	0.0043616	2.4E-14
2	SIX2 *	rs72797964	45046892	T	G	0.2167630	-0.0321986	0.0043868	5.7E-14
2	SIX2 *	rs56272009	45047996	G	C	0.2170530	-0.0321474	0.0043854	5.9E-14
2	SIX2 *	rs10171794	45048564	T	G	0.2464490	-0.0293900	0.0042234	6.7E-13
2	SIX2 *	rs958197	45049361	A	T	0.2432200	-0.0300171	0.0042384	4.3E-13
2	SIX2 *	rs10198370	45049417	G	A	0.2984740	-0.0268730	0.0040208	3.2E-12
2	SIX2 *	rs72797967	45050199	T	C	0.2112780	-0.0330847	0.0044499	3.7E-14
2	SIX2 *	rs4952738	45050461	T	C	0.3255380	-0.0279087	0.0038957	3.8E-13
2	SIX2 *	rs4952739	45050495	A	G	0.3345580	-0.0281614	0.0038815	1.4E-13
2	SIX2 *	rs4953184	45050569	C	T	0.3340730	-0.0277572	0.0038832	3.3E-13
2	SIX2 *	rs4953185	45050614	G	C	0.3269080	-0.0271107	0.0039030	1.8E-12
2	SIX2 *	rs4953186	45050903	G	T	0.3262560	-0.0273311	0.0039014	1.2E-12
2	SIX2 *	rs13413865	45051262	C	T	0.2412430	-0.0292567	0.0042668	2.5E-12
2	MIR4432 *	rs243091	60338433	T	C	0.3335980	-0.0271682	0.0038446	5.3E-12
2	MIR4432 *	rs243090	60338844	T	C	0.3336500	-0.0272045	0.0038450	4.9E-12
2	MIR4432 *	rs243088	60341610	A	T	0.3362260	-0.0276666	0.0038341	1.8E-12
2	MIR4432 *	rs243086	60343930	A	G	0.3424680	-0.0303847	0.0038418	7.4E-15
2	MIR4432 *	rs243085	60345536	C	T	0.3416430	-0.0304302	0.0038519	8.0E-15
2	MIR4432 *	rs243083	60346735	A	G	0.3425660	-0.0308978	0.0038555	3.6E-15
2	MIR4432 *	rs34563342	60347678	T	TAA	0.2718680	-0.0239259	0.0041506	2.0E-08
2	MIR4432 *	rs12999494	60352489	T	C	0.3387590	-0.0305984	0.0038469	2.5E-15
2	MIR4432 *	rs10183568	60352636	C	T	0.2696220	-0.0255475	0.0041384	9.6E-10
2	MIR4432 *	rs968919	60352853	T	C	0.3387450	-0.0316981	0.0038451	2.5E-16
2	MIR4432 *	rs10174120	60353145	C	G	0.2615800	-0.0277092	0.0041666	5.3E-11
2	MIR4432 *	rs9309325	60353696	G	A	0.3339790	-0.0329345	0.0038423	1.9E-17
2	MIR4432 *	rs1912980	60354720	T	C	0.3321540	-0.0326289	0.0038530	3.5E-17
2	MIR4432 *	rs243024	60356530	G	A	0.3394260	-0.0340273	0.0038291	1.2E-18
2	MIR4432 *	chr2:60357552_GA_G	60357552	G	GA	0.3381110	-0.0322166	0.0038513	8.5E-17
2	MIR4432 *	rs243021	60357684	G	A	0.3383430	-0.0343039	0.0038247	5.1E-19
2	MIR4432 *	rs243020	60357893	A	G	0.3370770	-0.0338129	0.0038341	1.7E-18
2	MIR4432 *	rs243019	60358671	T	C	0.3347990	-0.0336127	0.0038486	3.2E-18
2	MIR4432 *	rs184837	60361715	A	G	0.3212600	-0.0231397	0.0038852	9.0E-10
2	MIR4432 *	rs243015	60361734	A	G	0.3213140	-0.0229644	0.0038849	1.2E-09
2	MIR4432 *	rs173371	60362149	T	C	0.3340780	-0.0221975	0.0038676	2.9E-09
2	GRB14	rs117368015	164619507	A	G	0.0214909	-0.0696977	0.0125153	9.3E-09
2	CERS6 *	rs75872726	168399647	A	G	0.0125090	0.0947754	0.0163484	7.9E-09
2	CERS6 *	rs148018619	168408162	C	T	0.0125753	0.0925339	0.0163009	1.6E-08
2	CERS6	rs183376905	168484891	C	T	0.0199155	-0.0847287	0.0129768	5.8E-11
2	CERS6	rs143013456	168494748	G	A	0.0208579	-0.0812707	0.0126897	1.9E-10
2	CERS6	rs145035633	168625032	C	T	0.0264761	-0.0959090	0.0114716	9.8E-17
2	CERS6	rs12613101	168631974	T	C	0.0234884	-0.0913446	0.0121713	1.2E-13
2	CERS6	rs75966854	168671361	A	G	0.0295399	-0.1058290	0.0108385	2.6E-22
2	CERS6	rs61415125	168679773	G	A	0.0438978	-0.0895853	0.0088349	7.4E-25
2	CERS6	chr2:168686451_C_CAAA	168686451	CAAA	C	0.0114201	-0.1193890	0.0173592	4.6E-12
2	CERS6	rs74744541	168710557	G	A	0.1588400	-0.0347531	0.0049919	1.1E-12
2	CERS6	rs13400900	168710964	G	C	0.1571590	-0.0353238	0.0050169	9.0E-13
2	CERS6	rs10439295	168713421	G	T	0.1549280	-0.0351682	0.0050139	8.2E-13
2	CERS6	rs73969937	168719578	C	T	0.1538300	-0.0354895	0.0050155	5.8E-13
2	CERS6	rs144622225	168722068	G	T	0.0369616	-0.1039900	0.0096178	3.1E-28
2	CERS6	rs55662783	168723335	G	T	0.1528170	-0.0354529	0.0050225	7.7E-13
2	CERS6	rs7609075	168724453	C	T	0.1517260	-0.0363585	0.0050372	2.6E-13
2	CERS6	rs75096535	168724948	A	G	0.1512780	-0.0360073	0.0050442	4.2E-13
2	CERS6	rs56012705	168725454	T	C	0.1451860	-0.0371763	0.0051349	2.7E-13
2	CERS6	rs6433089	168741009	A	G	0.1552310	0.0313969	0.0050626	6.6E-10
2	CERS6	rs113186009	168741014	G	T	0.0943466	0.0363762	0.0062217	5.2E-09
2	CERS6	rs577637175	168745246	ATT	A	0.0990762	0.0420118	0.0061700	1.3E-11
2	CERS6	rs28459000	168745247	T	A	0.1053350	0.0414373	0.0059859	5.4E-12
2	CERS6	rs115545608	168760437	T	G	0.1853220	0.0357874	0.0046608	1.2E-14
2	CERS6, CERS6-AS1	rs3814378	168773982	C	A	0.3831990	-0.0320210	0.0037839	4.3E-17
2	CERS6-AS1	rs4668107	168775917	A	T	0.4488220	-0.0243201	0.0036910	4.5E-11
2	CERS6-AS1	rs12993040	168777040	G	C	0.3822940	-0.0310510	0.0037691	1.7E-16
2	CERS6-AS1	rs10173825	168778339	A	G	0.0802267	0.0369513	0.0067139	3.5E-08
2	CERS6-AS1	rs10197320	168778453	G	A	0.0803862	0.0367556	0.0067092	4.0E-08
2	CERS6-AS1	rs13033513	168779015	C	T	0.3880530	-0.0306142	0.0037602	5.7E-16
2	CERS6-AS1	rs62175688	168779786	A	G	0.1439070	0.0288180	0.0052109	3.7E-08
2	CERS6-AS1	rs13412928	168780482	A	T	0.0790835	0.0375519	0.0067730	2.9E-08
2	NOSTRIN	rs829950	168797545	A	G	0.3250930	0.0446344	0.0038611	2.6E-31
2	NOSTRIN	rs830031	168812521	T	C	0.2895030	0.0487436	0.0040772	1.9E-33
2	NOSTRIN	rs35424978	168813014	A	AC	0.2896080	0.0488265	0.0040741	1.2E-33
2	NOSTRIN	rs17200300	168813451	C	T	0.2896080	0.0486111	0.0040733	2.4E-33
2	NOSTRIN	rs13002530	168820241	T	C	0.2984220	0.0536145	0.0039612	2.2E-42

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	NOSTRIN	rs150351649	168820264	A	ACT	0.0231031	-0.0778707	0.0121892	1.2E-10
2	NOSTRIN	rs1568550	168821687	T	C	0.2959770	0.0541153	0.0039749	8.8E-43
2	NOSTRIN	rs3732031	168824641	T	C	0.2890220	0.0562052	0.0040122	3.8E-45
2	NOSTRIN	rs487756	168830049	T	C	0.3206340	0.0603753	0.0039537	1.1E-53
2	NOSTRIN	rs519599	168831170	A	G	0.0433160	0.0480113	0.0089654	3.3E-08
2	NOSTRIN	rs472233	168832237	G	A	0.3225910	0.0601346	0.0039442	1.8E-53
2	NOSTRIN	rs9287904	168832837	G	A	0.2728280	0.0558660	0.0041572	2.5E-41
2	NOSTRIN	rs552445	168833261	G	C	0.3220930	0.0602654	0.0039453	1.4E-53
2	NOSTRIN	rs549582	168833579	C	T	0.0433711	0.0486302	0.0089598	2.3E-08
2	NOSTRIN	chr2:168833816_CA_C	168833816	CA	C	0.3221760	0.0602665	0.0039451	1.3E-53
2	NOSTRIN	rs522893	168834219	T	C	0.3219610	0.0601938	0.0039456	2.0E-53
2	NOSTRIN	rs75798003	168835460	A	C	0.0115660	0.1103330	0.0169066	1.2E-10
2	NOSTRIN	rs830194	168836132	C	T	0.3219600	0.0600780	0.0039466	3.1E-53
2	NOSTRIN	rs36083800	168836904	T	C	0.3215050	0.0604139	0.0039486	7.8E-54
2	NOSTRIN	rs12386224	168837921	C	G	0.2723820	0.0562061	0.0041618	6.6E-42
2	NOSTRIN	rs578521	168837951	T	C	0.3222720	0.0600220	0.0039475	2.6E-53
2	NOSTRIN	rs10930337	168838521	T	C	0.2719460	0.0563704	0.0041628	4.7E-42
2	NOSTRIN	rs474538	168838686	G	A	0.3220750	0.0603018	0.0039492	1.5E-53
2	NOSTRIN	rs2947934	168839020	G	A	0.3227990	0.0607038	0.0039467	2.3E-54
2	NOSTRIN	rs501303	168840918	T	C	0.3219780	0.0613827	0.0039486	1.4E-55
2	NOSTRIN	rs28675349	168841452	T	A	0.2719960	0.0575514	0.0041598	7.5E-44
2	NOSTRIN	rs2177076	168841869	A	C	0.3220010	0.0614137	0.0039484	1.2E-55
2	NOSTRIN	rs2685798	168843665	G	A	0.3223580	0.0613970	0.0039466	8.3E-56
2	NOSTRIN	rs508423	168844544	A	G	0.3219560	0.0614315	0.0039471	7.7E-56
2	NOSTRIN	rs2461386	168844686	C	G	0.3219530	0.0613663	0.0039479	1.0E-55
2	NOSTRIN	rs578797	168844845	A	C	0.3227600	0.0617386	0.0039500	2.4E-56
2	NOSTRIN	rs11424404	168845089	G	GA	0.3219440	0.0614015	0.0039471	8.7E-56
2	NOSTRIN	rs471087	168845128	G	T	0.3219280	0.0612565	0.0039466	1.5E-55
2	NOSTRIN	rs474751	168845527	A	G	0.3221060	0.0613591	0.0039460	9.6E-56
2	NOSTRIN	rs559113	168846419	A	T	0.3205740	0.0620653	0.0039562	7.5E-57
2	NOSTRIN	rs505283	168846524	A	G	0.3183980	0.0621445	0.0039615	9.7E-57
2	NOSTRIN	rs531864	168847150	C	T	0.3078400	0.0595562	0.0039343	5.4E-53
2	NOSTRIN	rs560952	168847977	T	C	0.4178830	0.0697522	0.0037351	1.3E-80
2	NOSTRIN	rs497808	168848527	T	G	0.4206150	0.0698145	0.0037202	2.8E-81
2	NOSTRIN	rs11354593	168848560	CA	C	0.4199880	0.0697865	0.0037195	3.4E-81
2	NOSTRIN	rs566465	168848594	A	T	0.3545240	0.0639075	0.0038421	2.1E-63
2	NOSTRIN	rs2140046	168849569	C	T	0.2497920	0.0685088	0.0042701	1.5E-57
2	NOSTRIN	rs199990125	168850024	T	TG	0.0631819	0.0387466	0.0074440	2.8E-08
2	NOSTRIN	rs5836209	168850752	A	ATTCTCT	0.2606880	0.0664596	0.0041964	1.9E-56
2	NOSTRIN	rs540652	168850918	C	T	0.4183270	0.0698731	0.0037225	3.2E-81
2	NOSTRIN	rs118103537	168850945	C	T	0.0635635	0.0385770	0.0074227	2.7E-08
2	NOSTRIN	rs488621	168851042	A	G	0.4181730	0.0697038	0.0037232	9.3E-81
2	NOSTRIN	rs16856030	168851503	C	A	0.0638984	0.0386388	0.0074071	2.4E-08
2	NOSTRIN	rs546146	168852687	C	G	0.3530140	0.0641198	0.0038445	1.5E-63
2	NOSTRIN	rs527393	168853247	G	A	0.4183290	0.0699665	0.0037211	1.8E-81
2	NOSTRIN	rs147001220	168854028	T	C	0.0638460	0.0394747	0.0074054	1.3E-08
2	NOSTRIN	rs11678685	168854097	A	G	0.2477990	0.0692563	0.0042838	1.3E-58
2	NOSTRIN	rs140979969	168854467	T	TC	0.0636179	0.0391504	0.0074187	1.7E-08
2	NOSTRIN	rs188584661	168854468	T	C	0.0633832	0.0390466	0.0074328	2.0E-08
2	NOSTRIN	rs75458689	168854608	G	T	0.0638558	0.0394167	0.0074044	1.3E-08
2	NOSTRIN	rs2685799	168854794	T	C	0.4147550	0.0715074	0.0037287	1.2E-84
2	NOSTRIN	rs79589372	168855995	T	C	0.0639627	0.0390578	0.0073985	1.8E-08
2	NOSTRIN	rs60615208	168856084	A	G	0.0640083	0.0393723	0.0073972	1.4E-08
2	NOSTRIN	rs2632380	168857840	T	C	0.4136620	0.0726090	0.0037307	3.1E-87
2	NOSTRIN	rs11893114	168858017	T	C	0.0638674	0.0394587	0.0074038	1.3E-08
2	NOSTRIN	rs16856059	168858072	T	C	0.0638674	0.0394587	0.0074038	1.3E-08
2	NOSTRIN	rs569997	168858383	T	C	0.4153400	0.0723915	0.0037260	4.1E-87
2	NOSTRIN	rs16823013	168859100	T	C	0.0639372	0.0390100	0.0074001	1.8E-08
2	NOSTRIN	rs576062	168859176	A	G	0.4140280	0.0726355	0.0037291	2.7E-87
2	NOSTRIN	rs11296225	168859357	A	AT	0.0639400	0.0389249	0.0074013	2.0E-08
2	NOSTRIN	rs16856061	168859371	T	C	0.0639286	0.0390666	0.0074012	1.8E-08
2	NOSTRIN	rs116841798	168860182	T	C	0.0625655	0.0407113	0.0074977	1.0E-08
2	NOSTRIN	rs2632372	168861031	T	C	0.3506520	0.0682585	0.0038094	4.9E-73
2	NOSTRIN	rs10497348	168861791	A	G	0.0623871	0.0404927	0.0075165	1.2E-08
2	NOSTRIN	rs580507	168862392	T	C	0.1643780	0.0342891	0.0049322	2.5E-13
2	NOSTRIN	rs67216045	168862543	T	TGTAA	0.2438760	0.0714348	0.0042566	4.5E-63
2	NOSTRIN	rs143166986	168862756	C	TTCTTTA	0.4154620	0.0737082	0.0037045	1.2E-90
2	NOSTRIN	rs16856065	168862819	T	C	0.0622292	0.0405124	0.0075248	1.2E-08
2	NOSTRIN	rs12993143	168862990	G	T	0.2509270	0.0690248	0.0042169	4.0E-60
2	NOSTRIN	rs62176769	168864640	G	T	0.0624698	0.0403203	0.0075154	1.5E-08
2	NOSTRIN	rs3931	168864871	G	A	0.2621250	0.0687747	0.0041181	6.1E-63
2	NOSTRIN *	rs7588452	168865434	T	A	0.2605530	0.0708099	0.0041351	6.8E-66
2	NOSTRIN *	rs10679511	168865777	AGAT	A	0.2631230	0.0687125	0.0041218	1.6E-62
2	SPC25 *	rs9751269	168869393	A	G	0.4194430	0.0720746	0.0036940	2.8E-87
2	SPC25	rs6734923	168871220	G	C	0.4187190	0.0723241	0.0036953	8.7E-88
2	SPC25	rs369597046	168871779	C	CTTTAAA	0.0621527	0.0407177	0.0075339	1.0E-08
2	SPC25	rs113891842	168871890	T	A	0.0621238	0.0407668	0.0075322	1.0E-08
2	SPC25	rs75601606	168872063	T	C	0.0621179	0.0407427	0.0075326	1.0E-08
2	SPC25	rs112075308	168872812	C	T	0.0621668	0.0403499	0.0075320	1.4E-08
2	SPC25	rs554494	168873053	G	A	0.4197790	0.0724498	0.0036947	4.4E-88
2	SPC25	rs3770567	168873143	T	C	0.2515100	0.0715718	0.0042096	1.3E-64
2	SPC25	rs3821116	168873339	T	G	0.2512240	0.0713391	0.0042085	2.2E-64
2	SPC25	rs16856071	168873834	G	A	0.2505070	0.0721268	0.0042247	3.8E-65
2	SPC25	rs75727050	168873882	G	A	0.0621632	0.0403923	0.0075324	1.4E-08
2	SPC25	rs117387626	168874140	T	C	0.0621156	0.0407829	0.0075330	1.0E-08
2	SPC25	rs506273	168875025	T	C	0.4131370	0.0734956	0.0037051	2.7E-90
2	SPC25	rs146168468	168875719	A	G	0.0585737	0.0402272	0.0077450	2.8E-08
2	SPC25	rs35792626	168877958	CAA	C	0.2815940	0.0743865	0.0040775	3.3E-74
2	SPC25	rs117646340	168879148	C	A	0.0585002	0.0395130	0.0077557	4.9E-08
2	SPC25	rs117127191	168879188	A	C	0.0584624	0.0397999	0.0077572	4.1E-08
2	SPC25	rs117442359	168879496	C	T	0.0584438	0.0397976	0.0077589	4.2E-08
2	SPC25	rs117223439	168879751	C	G	0.0584168	0.0398720	0.0077612	4.0E-08
2	SPC25	rs543727	168879788	A	T	0.4373270	0.0774914	0.0037155	2.8E-99
2	SPC25	rs76550195	168880415	G	T	0.0583603	0.0396248	0.0077658	4.8E-08
2	SPC25	rs524586	168881341	A	G	0.3739170	0.0720431	0.0037924	2.4E-81
2	SPC25	rs493816	168881727	C	T	0.4407320	0.0788304	0.0037154	2.2E-102
2	SPC25	rs11688437	168882029	C	T	0.2805550	0.0747266	0.0040868	1.7E-74
2	SPC25	rs141616568	168882099	T	C	0.0106043	0.1096290	0.0177011	9.5E-10
2	SPC25	rs79584371	168882231	A	G	0.0581452	0.0402295	0.0077829	2.9E-08
2	SPC25	rs113060280	168887255	C	T	0.0608812	0.0404358	0.0076195	1.8E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	SPC25	rs35962426	168887282	T	C	0.2762440	0.0779240	0.0041274	4.0E-79
2	SPC25	rs117715822	168887557	C	A	0.0607069	0.0405834	0.0076311	1.5E-08
2	SPC25	rs62176784	168888041	G	A	0.2801420	0.0766871	0.0041126	3.4E-77
2	SPC25	rs117836618	168888104	G	C	0.0604869	0.0400510	0.0076458	2.4E-08
2	G6PC2 *	rs12475693	168897085	G	A	0.1350090	-0.0748446	0.0053370	1.6E-44
2	G6PC2 *	rs12475700	168897166	G	A	0.1789580	-0.0673108	0.0047669	7.5E-45
2	G6PC2 *	rs111485380	168897613	C	T	0.0107238	-0.1588920	0.0176963	1.0E-19
2	G6PC2 *	rs532597188	168897620	TA	T	0.1016650	-0.1077620	0.0060657	2.2E-71
2	G6PC2 *	rs151057583	168897652	C	T	0.1090560	-0.0970542	0.0058479	1.6E-62
2	G6PC2 *	rs181340133	168897853	A	G	0.1106020	-0.0921874	0.0057897	2.3E-57
2	G6PC2 *	rs186545600	168897854	C	T	0.1106040	-0.0922256	0.0057896	2.0E-57
2	G6PC2 *	rs34177044	168897975	A	G	0.4075450	0.1034530	0.0037264	1.3E-171
2	G6PC2 *	rs1969376	168898253	G	A	0.1473280	-0.0789554	0.0051300	3.1E-53
2	G6PC2 *	rs13387347	168898336	C	T	0.4547100	0.0949841	0.0036791	1.6E-149
2	G6PC2 *	rs12623237	168899548	A	G	0.1116070	-0.0920368	0.0057538	6.9E-58
2	G6PC2 *	rs517413	168899598	G	T	0.1485480	-0.0781642	0.0051026	7.5E-53
2	G6PC2 *	rs540524	168900420	G	A	0.4004500	-0.0574215	0.0037018	5.4E-56
2	G6PC2 *	rs1402837	168900844	T	C	0.4040650	0.1049690	0.0036960	1.3E-179
2	G6PC2 *	rs573225	168901031	G	A	0.0554652	-0.0552558	0.0079267	8.3E-12
2	G6PC2 *	rs2232316	168901052	A	G	0.1378170	-0.0688268	0.0052499	4.2E-39
2	G6PC2	rs6715133	168901637	T	C	0.1109040	-0.0930351	0.0057645	1.1E-58
2	G6PC2	rs138969710	168901785	A	G	0.1065790	-0.0918562	0.0058871	8.6E-55
2	G6PC2	rs2740590	168901806	A	G	0.1228340	0.0427454	0.0056044	4.4E-14
2	G6PC2	rs6730651	168901847	C	T	0.1360110	-0.0720404	0.0052819	4.6E-42
2	G6PC2	rs117973553	168903679	T	A	0.1151030	-0.0907869	0.0056690	2.7E-58
2	G6PC2	rs560887	168906638	T	C	0.0334527	-0.1458930	0.0100707	4.8E-48
2	G6PC2	rs492594	168907666	C	G	0.4254290	-0.0537480	0.0036537	1.9E-50
2	G6PC2	rs2232326	168907981	C	T	0.0403894	-0.3005850	0.0092633	1.9E-235
2	G6PC2	rs570876	168908867	T	A	0.4239330	-0.0541249	0.0036581	5.1E-51
2	G6PC2	rs567243	168909227	G	A	0.4244840	-0.0537088	0.0036551	2.3E-50
2	G6PC2	rs3732033	168909936	C	T	0.1148540	-0.0913858	0.0056784	7.0E-59
2	G6PC2 *	rs12053049	168910638	C	T	0.2899220	0.1069160	0.0040538	2.3E-157
2	G6PC2 *	rs188687619	168911476	T	C	0.0276427	0.0647369	0.0112340	3.5E-09
2	G6PC2 *	rs519884	168911677	G	A	0.4254080	-0.0535053	0.0036677	8.5E-50
2	G6PC2 *	rs58898793	168912242	T	TAA	0.1253820	0.0436169	0.0055425	7.1E-15
2	G6PC2 *	rs491443	168912517	C	A	0.4257290	-0.0532304	0.0036675	2.5E-49
2	G6PC2 *	rs118182742	168913001	A	T	0.1126920	-0.0948991	0.0057363	9.3E-62
2	G6PC2 *	rs75578971	168913199	T	C	0.1103380	-0.0963238	0.0057944	3.2E-62
2	G6PC2 *	rs75578260	168913739	A	G	0.1106660	-0.0933443	0.0057962	9.6E-59
2	G6PC2 *	rs16856187	168913876	C	A	0.2934570	0.1052280	0.0040454	6.7E-153
2	G6PC2 *	rs60415045	168914614	C	A	0.2887000	0.1072750	0.0040617	8.1E-158
2	G6PC2 *	rs10497347	168914704	C	T	0.2845830	0.1069240	0.0040808	1.9E-155
2	G6PC2 *	rs66629516	168914874	T	TG	0.2830570	0.1071470	0.0040859	9.1E-156
2	G6PC2 *	rs13419326	168914910	C	A	0.2830690	0.1071650	0.0040859	8.2E-156
2	G6PC2 *	rs4144857	168914996	C	G	0.2830890	0.1071180	0.0040855	9.4E-156
2	G6PC2 *	rs4144858	168915008	T	C	0.2831010	0.1071540	0.0040854	7.1E-156
2	G6PC2 *	rs504979	168915349	T	C	0.3458330	0.0788785	0.0038654	1.5E-95
2	ABCB11 *	rs34174959	168917202	C	CA	0.0809212	-0.0505753	0.0066340	9.4E-14
2	ABCB11 *	rs563694	168917561	C	A	0.0422020	-0.1129800	0.0090025	2.1E-36
2	ABCB11 *	rs117326521	168917836	G	T	0.0959531	-0.1076090	0.0062091	1.8E-68
2	ABCB11 *	rs537183	168918136	C	T	0.0419265	-0.1148310	0.0090300	2.5E-37
2	ABCB11 *	rs502570	168918449	A	G	0.0558845	-0.0794981	0.0078710	1.2E-23
2	ABCB11 *	rs71676177	168919036	A	ATTTG	0.2886660	0.1067430	0.0040400	9.6E-158
2	ABCB11 *	rs71397674	168919186	ATCAG	A	0.0832688	-0.0477369	0.0065512	1.1E-12
2	ABCB11 *	rs73972707	168919250	G	A	0.2888050	0.1065800	0.0040392	2.2E-157
2	ABCB11 *	rs28819151	168919319	G	A	0.2888050	0.1065960	0.0040391	1.9E-157
2	ABCB11 *	rs580670	168919611	T	A	0.0567131	-0.0757655	0.0078176	5.9E-22
2	ABCB11 *	rs74870851	168919713	G	A	0.2888800	0.1065620	0.0040386	1.9E-157
2	ABCB11 *	rs578763	168919850	G	T	0.0562965	-0.0784043	0.0078524	2.7E-23
2	ABCB11 *	rs500432	168919904	G	T	0.0832527	-0.0477642	0.0065508	1.0E-12
2	ABCB11 *	rs475612	168920236	T	C	0.0559040	-0.0793092	0.0078697	1.5E-23
2	ABCB11 *	rs518598	168920404	T	C	0.0558852	-0.0791477	0.0078701	1.8E-23
2	ABCB11 *	rs66798250	168920493	T	C	0.1131500	0.0441313	0.0058086	3.9E-14
2	ABCB11 *	chr2:168920546_AT_A	168920546	AT	A	0.3485120	0.0752089	0.0038827	2.5E-85
2	ABCB11 *	rs78529720	168920787	G	A	0.2909030	0.1062130	0.0040255	3.2E-157
2	ABCB11 *	rs557462	168921085	C	T	0.0410422	-0.1175560	0.0091240	2.8E-38
2	ABCB11 *	rs147578319	168921847	TTTTC	T	0.3770380	0.0753495	0.0037967	2.3E-91
2	ABCB11 *	rs192788039	168922071	G	A	0.0396771	-0.2869460	0.0093907	3.0E-207
2	ABCB11 *	rs478333	168922646	G	A	0.3615780	0.0723992	0.0038220	5.2E-83
2	ABCB11 *	rs4148804	168922695	T	C	0.2787660	0.1016860	0.0040989	5.3E-139
2	ABCB11	rs496550	168923202	T	C	0.3732440	0.0741075	0.0037441	1.5E-90
2	ABCB11	rs495714	168923254	C	T	0.3733690	0.0741076	0.0037427	1.2E-90
2	ABCB11	rs473351	168923386	T	C	0.0794355	-0.0517369	0.0066778	3.5E-14
2	ABCB11	rs579275	168923856	T	C	0.3730660	0.0738900	0.0037451	4.9E-90
2	ABCB11	rs519887	168924375	T	C	0.3730480	0.0738725	0.0037453	5.4E-90
2	ABCB11	rs519035	168924451	T	C	0.3730470	0.0738718	0.0037453	5.4E-90
2	ABCB11	rs484066	168925971	A	T	0.3496840	0.0740491	0.0037993	2.2E-87
2	ABCB11	rs483234	168926064	T	C	0.4987120	0.0885072	0.0036925	1.5E-130
2	ABCB11	rs569829	168926359	T	C	0.0153316	-0.0867210	0.0147480	1.2E-08
2	ABCB11	rs7561903	168927055	G	T	0.1277850	0.0424206	0.0055244	1.7E-14
2	ABCB11	rs16856247	168927903	T	C	0.2912840	0.1020360	0.0039877	9.2E-148
2	ABCB11	rs17540154	168927983	G	A	0.1300850	0.0416939	0.0054800	3.9E-14
2	ABCB11	rs508506	168928445	A	C	0.0153637	-0.0887047	0.0147369	4.9E-09
2	ABCB11	rs503931	168928939	A	C	0.3727750	0.0730442	0.0037489	8.1E-88
2	ABCB11	rs34193789	168929777	A	G	0.1158260	0.0434589	0.0057681	5.2E-14
2	ABCB11	rs551754	168931176	C	T	0.3728700	0.0735728	0.0037450	2.6E-89
2	ABCB11	rs527150	168931529	A	G	0.3728160	0.0735694	0.0037447	2.5E-89
2	ABCB11	rs531772	168931964	T	C	0.0799168	-0.0513329	0.0066650	4.3E-14
2	ABCB11	rs497692	168932506	T	C	0.3732510	0.0735983	0.0037434	1.8E-89
2	ABCB11	rs494874	168932796	T	C	0.0150997	-0.0905424	0.0148616	2.7E-09
2	ABCB11	rs13389076	168933002	A	G	0.3153450	0.0819042	0.0039119	1.3E-99
2	ABCB11	rs16856252	168933210	C	T	0.3420990	0.0803704	0.0038272	1.1E-100
2	ABCB11	rs555975	168934425	G	A	0.3759600	0.0727140	0.0037580	1.2E-86
2	ABCB11	rs552976	168934928	A	G	0.0124944	-0.1339710	0.0162936	2.8E-16
2	ABCB11	rs3755157	168935661	T	C	0.3146240	0.0960105	0.0038998	2.9E-138
2	ABCB11	rs3755158	168935678	G	C	0.3448020	0.0785771	0.0038131	2.3E-97
2	ABCB11	rs472614	168935911	A	G	0.3723000	0.0708581	0.0037494	7.9E-83
2	ABCB11	rs11568379	168936458	T	C	0.0298258	0.0642964	0.0107357	1.5E-09
2	ABCB11	rs565412	168937773	A	G	0.3721470	0.0706041	0.0037594	6.6E-82
2	ABCB11	rs567074	168937921	T	C	0.3721050	0.0706710	0.0037597	4.8E-82

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ABCB11	rs479682	168938177	T	C	0.3699160	0.0705834	0.0037694	2.2E-81
2	ABCB11	rs480562	168938261	T	A	0.3719680	0.0705344	0.0037618	1.2E-81
2	ABCB11	rs482508	168938473	A	G	0.3703340	0.0707064	0.0037665	9.0E-82
2	ABCB11	rs508743	168938777	C	G	0.3707270	0.0709768	0.0037725	7.9E-82
2	ABCB11	rs58512362	168938957	G	A	0.3446520	0.0787098	0.0038313	3.6E-96
2	ABCB11	rs79933700	168939085	CTGTT	C	0.3710590	0.0709561	0.0037710	7.0E-82
2	ABCB11	rs2544360	168939677	T	C	0.3579230	0.0704927	0.0037973	3.8E-79
2	ABCB11	rs2685803	168939775	A	G	0.3718430	0.0708015	0.0037737	2.7E-81
2	ABCB11	rs2544367	168939778	T	C	0.3718430	0.0708015	0.0037737	2.7E-81
2	ABCB11	rs2685804	168940262	A	G	0.3714270	0.0710859	0.0037694	4.3E-82
2	ABCB11	rs2685805	168940550	A	G	0.3714650	0.0711441	0.0037711	3.4E-82
2	ABCB11	rs2685806	168940794	A	G	0.3713740	0.0710234	0.0037704	6.4E-82
2	ABCB11	rs2685807	168941016	C	T	0.3713580	0.0709810	0.0037706	7.5E-82
2	ABCB11	rs2685808	168941130	G	T	0.3715140	0.0709611	0.0037715	8.4E-82
2	ABCB11	rs1581397	168941142	T	C	0.3715900	0.0707204	0.0037721	2.9E-81
2	ABCB11	rs2685810	168941222	T	C	0.3713720	0.0709259	0.0037707	9.5E-82
2	ABCB11	rs2685811	168941417	A	G	0.3713580	0.0708830	0.0037708	1.1E-81
2	ABCB11	rs77601801	168941523	G	A	0.3218450	0.0807643	0.0039093	9.5E-97
2	ABCB11	rs2685812	168941661	A	G	0.3727210	0.0709264	0.0037717	5.4E-82
2	ABCB11	rs2685813	168941929	T	C	0.3727220	0.0710117	0.0037721	3.8E-82
2	ABCB11	rs2685814	168942109	T	C	0.3726940	0.0709424	0.0037726	5.6E-82
2	ABCB11	rs3084063	168942222	C	CATATTA	0.3775350	0.0712190	0.0037926	2.8E-81
2	ABCB11	rs2250677	168942778	C	T	0.3728990	0.0711616	0.0037741	2.1E-82
2	ABCB11	rs2307959	168943763	A	ACGTG	0.3741490	0.0712833	0.0037761	1.3E-82
2	ABCB11	rs5836215	168943792	G	GT	0.3729460	0.0711513	0.0037758	4.2E-82
2	ABCB11	rs853791	168943918	A	G	0.3729310	0.0711593	0.0037760	4.1E-82
2	ABCB11	rs853790	168943931	A	T	0.3743280	0.0710223	0.0037790	9.5E-82
2	ABCB11	chr2:168944282_TG_T	168944282	TG	T	0.3733640	0.0711815	0.0037780	4.3E-82
2	ABCB11	rs853789	168944978	A	G	0.0128537	-0.1270430	0.0160715	4.1E-15
2	ABCB11	rs860510	168945118	A	C	0.3729400	0.0711303	0.0037775	3.9E-82
2	ABCB11	rs853788	168945395	T	C	0.3729180	0.0711835	0.0037780	3.3E-82
2	ABCB11	rs853787	168945742	G	T	0.0442444	-0.1052580	0.0088229	2.2E-33
2	ABCB11	rs853786	168945800	G	A	0.3731880	0.0713968	0.0037808	1.9E-82
2	ABCB11	rs862662	168945819	C	A	0.3731720	0.0713846	0.0037809	2.0E-82
2	ABCB11	rs853785	168946084	C	T	0.3731360	0.0715635	0.0037855	1.6E-82
2	ABCB11	rs16856261	168947058	T	C	0.3105080	0.0964063	0.0039683	4.4E-134
2	ABCB11	rs853784	168947164	C	T	0.3726950	0.0714424	0.0038144	3.9E-81
2	ABCB11	rs853783	168949001	A	C	0.3681630	0.0705163	0.0038296	8.5E-79
2	ABCB11	rs55700007	168949511	G	T	0.3421290	0.0788527	0.0038941	1.4E-93
2	ABCB11	rs853782	168949788	C	T	0.3703290	0.0710675	0.0038266	6.5E-80
2	ABCB11	rs853781	168949811	A	G	0.3680770	0.0701821	0.0038339	8.9E-78
2	ABCB11	rs139014876	168950218	A	G	0.0372648	-0.2967150	0.0096923	1.8E-209
2	ABCB11	rs72886761	168950228	A	G	0.3411490	0.0789192	0.0038960	8.1E-94
2	ABCB11	rs853780	168950972	C	G	0.3703110	0.0709842	0.0038306	1.1E-79
2	ABCB11	rs853777	168955707	T	C	0.0469195	-0.1045760	0.0086104	4.5E-34
2	ABCB11	rs76527478	168956919	G	C	0.0413344	0.0543832	0.0091722	1.7E-09
2	ABCB11	rs4148798	168958465	A	G	0.0341600	0.0544024	0.0099882	4.4E-08
2	ABCB11	rs3821120	168960426	G	C	0.1127210	-0.0323903	0.0057065	4.5E-08
2	ITGA6	rs6721624	172429726	A	G	0.2800080	-0.0243641	0.0040850	3.0E-10
2	ITGA6	rs3108779	172430569	G	T	0.2914830	-0.0251995	0.0039886	1.7E-11
2	ITGA6	rs12053442	172430677	C	G	0.2843030	-0.0249439	0.0040161	4.3E-11
2	ITGA6	rs6757785	172431436	A	G	0.3426750	-0.0195104	0.0038214	4.5E-08
2	ITGA6	rs76264695	172431524	A	G	0.2836830	-0.0251294	0.0040203	3.3E-11
2	ITGA6	rs1920984	172432697	T	C	0.4470830	-0.0200835	0.0036442	8.0E-09
2	ITGA6	rs75166599	172433055	A	G	0.2647500	-0.0235534	0.0041061	9.5E-10
2	ITGA6	rs77282844	172433143	A	G	0.2781630	-0.0256617	0.0040524	3.0E-11
2	ITGA6	rs2077921	172433280	T	C	0.4178940	-0.0223060	0.0037113	3.5E-10
2	ITGA6	rs28464102	172433497	A	G	0.4382830	-0.0236450	0.0036577	2.1E-11
2	ITGA6	rs10171775	172434033	C	A	0.4958940	-0.0220440	0.0036457	4.4E-10
2	ITGA6	rs10184567	172434268	T	C	0.4549100	-0.0246121	0.0036475	4.3E-12
2	ITGA6	rs7604441	172434474	T	G	0.4543670	-0.0248582	0.0036448	2.5E-12
2	ITGA6	rs75979419	172434538	T	C	0.2870710	-0.0325713	0.0039999	4.5E-17
2	ITGA6	rs10195932	172434620	A	T	0.4964020	-0.0226645	0.0036230	1.2E-10
2	ITGA6	rs7567140	172435060	A	G	0.4642130	-0.0239565	0.0036427	1.7E-11
2	ITGA6	rs7567159	172435133	A	G	0.4556110	-0.0246765	0.0036394	3.3E-12
2	ITGA6	rs10175670	172435494	C	T	0.4975520	-0.0227397	0.0036232	9.7E-11
2	ITGA6	rs61479854	172435641	G	T	0.4931730	-0.0220158	0.0036589	5.4E-10
2	ITGA6	rs78341162	172436080	G	A	0.4982590	-0.0227563	0.0036235	8.2E-11
2	ITGA6	rs75689576	172436211	A	G	0.2884270	-0.0323773	0.0039923	4.7E-17
2	ITGA6	rs80002558	172436447	G	A	0.4984070	-0.0229336	0.0036256	5.5E-11
2	ITGA6	rs59454075	172436547	A	G	0.2884840	-0.0323647	0.0039920	4.7E-17
2	ITGA6	rs3934627	172436651	C	T	0.4990080	-0.0229001	0.0036256	5.3E-11
2	ITGA6	rs79160711	172437278	G	A	0.2892830	-0.0323761	0.0039887	3.8E-17
2	ITGA6	rs28485589	172438303	G	A	0.2876560	-0.0327272	0.0039958	3.1E-17
2	ITGA6	rs57878744	172438319	A	G	0.2877060	-0.0324426	0.0039953	5.7E-17
2	ITGA6	rs28540552	172438448	G	A	0.4559750	-0.0252828	0.0036414	9.2E-13
2	ITGA6	rs74483274	172438523	G	A	0.2882900	-0.0326930	0.0039936	2.9E-17
2	ITGA6	rs80010354	172438582	A	G	0.2875460	-0.0327498	0.0039971	3.2E-17
2	ITGA6	rs76837457	172438663	T	G	0.2876390	-0.0327003	0.0039953	3.4E-17
2	ITGA6	rs141195656	172438756	C	CTT	0.2876030	-0.0326844	0.0039955	3.3E-17
2	ITGA6	rs78181761	172438803	G	A	0.2875960	-0.0327837	0.0039955	2.8E-17
2	ITGA6	rs79416408	172439072	T	C	0.2874530	-0.0324781	0.0039984	5.3E-17
2	ITGA6	rs12469875	172439308	T	C	0.4950200	-0.0232841	0.0036236	2.8E-11
2	ITGA6	rs13414928	172439574	G	A	0.3296500	-0.0286074	0.0038483	1.4E-14
2	ITGA6	rs16860377	172440312	C	T	0.4972340	-0.0235333	0.0036249	1.4E-11
2	ITGA6	rs4405725	172440654	A	T	0.2887220	-0.0324394	0.0039932	3.9E-17
2	ITGA6	rs10497381	172440802	G	A	0.4972510	-0.0236810	0.0036252	1.1E-11
2	ITGA6	rs3762618	172441119	C	G	0.2888690	-0.0327324	0.0039909	2.1E-17
2	ITGA6	rs3762619	172441157	G	A	0.4972660	-0.0236425	0.0036249	1.2E-11
2	ITGA6	rs10207640	172442998	G	A	0.2889220	-0.0324750	0.0039894	3.4E-17
2	ITGA6	rs10207654	172443028	G	A	0.2886980	-0.0326627	0.0039905	2.5E-17
2	ITGA6	rs16860397	172443466	T	G	0.2526230	-0.0279276	0.0041634	2.4E-12
2	ITGA6	rs74994420	172443843	C	T	0.4982470	-0.0233881	0.0036245	2.6E-11
2	ITGA6	rs10187564	172443887	A	G	0.2875710	-0.0326558	0.0039954	3.5E-17
2	ITGA6	rs148644163	172444602	A	G	0.2830960	-0.0322551	0.0040357	1.5E-16
2	ITGA6	rs368148277	172444604	C	CA	0.2810590	-0.0317093	0.0040540	4.8E-16
2	ITGA6	rs80353656	172444674	C	T	0.2525960	-0.0279445	0.0041670	2.6E-12
2	ITGA6	rs13410475	172444890	A	C	0.2872540	-0.0329568	0.0040012	2.5E-17
2	ITGA6	rs146618443	172445075	T	G	0.2870200	-0.0327817	0.0039975	3.2E-17
2	ITGA6	chr2:172445338_CT_C	172445338	CT	C	0.4957560	-0.0235842	0.0036256	1.6E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ITGA6	rs9711634	172445372	G	A	0.4958210	-0.0235331	0.0036252	1.8E-11
2	ITGA6	rs4281870	172445747	A	G	0.4958170	-0.0235344	0.0036251	1.8E-11
2	ITGA6	rs4480959	172445817	C	T	0.4966450	-0.0235255	0.0036253	2.0E-11
2	ITGA6	rs76128279	172446275	T	C	0.4964040	-0.0235314	0.0036250	1.6E-11
2	ITGA6	rs75397932	172446361	A	G	0.4957280	-0.0235592	0.0036253	1.7E-11
2	ITGA6	rs12621278	172446825	G	A	0.2887760	-0.0327077	0.0039904	2.1E-17
2	ITGA6	rs12615596	172446954	A	G	0.2873450	-0.0325084	0.0039992	4.4E-17
2	ITGA6	rs76911281	172447953	C	T	0.4985300	-0.0232363	0.0036248	2.8E-11
2	ITGA6	rs1574259	172448725	T	C	0.2878520	-0.0329103	0.0039974	2.2E-17
2	ITGA6	rs1574256	172449237	C	G	0.2882270	-0.0327734	0.0039927	2.3E-17
2	ITGA6	rs10210544	172449611	G	A	0.3090910	-0.0321923	0.0039135	1.5E-17
2	ITGA6	rs12052250	172449942	G	A	0.2752590	-0.0354918	0.0041025	2.4E-19
2	ITGA6	rs12052253	172449985	T	A	0.2881910	-0.0331158	0.0039952	1.2E-17
2	ITGA6	rs6721597	172450817	T	A	0.4664470	-0.0222814	0.0036335	1.5E-10
2	ITGA6	rs13387602	172450989	G	A	0.3095580	-0.0321879	0.0039123	1.4E-17
2	ITGA6	rs12052385	172451489	G	A	0.2493940	-0.0289108	0.0041997	7.0E-13
2	ITGA6	rs16860416	172452060	A	G	0.3082510	-0.0325087	0.0039179	1.1E-17
2	ITGA6	rs10197251	172452682	C	A	0.4990050	-0.0230940	0.0036201	3.3E-11
2	ITGA6	rs16860419	172453098	C	G	0.2521810	-0.0285653	0.0041704	7.8E-13
2	ITGA6	rs115112210	172453451	T	G	0.2876050	-0.0330404	0.0039955	1.5E-17
2	ITGA6	rs114161133	172453516	T	G	0.2880880	-0.0329776	0.0039952	1.5E-17
2	ITGA6	rs13421350	172453843	A	G	0.3088390	-0.0322765	0.0039140	1.4E-17
2	ITGA6	rs12622044	172454139	A	G	0.4991520	0.0235479	0.0036628	2.7E-11
2	ITGA6	rs16860426	172454384	T	A	0.2865740	-0.0334122	0.0040046	6.1E-18
2	ITGA6	rs77167534	172455202	T	C	0.2677960	-0.0354777	0.0040837	2.3E-19
2	ITGA6	rs6726739	172455652	A	G	0.2882500	-0.0347526	0.0039927	1.8E-19
2	ITGA6	rs28595036	172456228	T	C	0.2889790	-0.0345548	0.0039885	2.3E-19
2	ITGA6	rs16860438	172456685	T	A	0.2676140	-0.0350680	0.0040853	6.3E-19
2	ITGA6	rs116532339	172457063	G	T	0.2673250	-0.0355263	0.0040938	2.7E-19
2	ITGA6	rs10208194	172457155	A	T	0.2882900	-0.0347203	0.0040006	2.0E-19
2	ITGA6	rs12473999	172457216	C	T	0.4685820	-0.0220767	0.0036496	2.6E-10
2	ITGA6	rs7564416	172457598	A	G	0.2878520	-0.0343798	0.0040082	5.8E-19
2	ITGA6	rs34679972	172457977	T	G	0.3108400	-0.0329772	0.0039431	5.2E-18
2	ITGA6	rs35783685	172458199	T	C	0.3039840	-0.0334889	0.0039495	2.0E-18
2	ITGA6	rs35821653	172458277	G	A	0.3053790	-0.0335375	0.0039491	2.0E-18
2	ITGA6	rs12464480	172459110	C	T	0.3104030	-0.0350288	0.0039186	2.5E-20
2	ITGA6	rs35180608	172459261	C	T	0.3100400	-0.0348653	0.0039216	4.4E-20
2	ITGA6	rs36040769	172459270	G	A	0.3100400	-0.0348900	0.0039216	4.1E-20
2	ITGA6	rs35700760	172459285	T	C	0.3104020	-0.0349559	0.0039180	2.9E-20
2	ITGA6	rs68069880	172459490	G	A	0.3104320	-0.0349404	0.0039201	2.8E-20
2	ITGA6	rs75888567	172459528	A	G	0.2775020	-0.0367941	0.0040484	6.6E-21
2	ITGA6	rs34526119	172459544	C	A	0.3105720	-0.0349377	0.0039160	3.1E-20
2	ITGA6	rs35861954	172459629	C	T	0.3106280	-0.0350192	0.0039155	2.6E-20
2	ITGA6	rs16860450	172460089	A	G	0.3104800	-0.0349631	0.0039079	2.9E-20
2	ITGA6	rs12622724	172460180	A	G	0.2772220	-0.0367274	0.0040426	7.0E-21
2	ITGA6	rs12616256	172460394	G	A	0.3104750	-0.0349146	0.0039080	3.3E-20
2	ITGA6	rs12622816	172460470	A	G	0.3104750	-0.0349146	0.0039080	3.3E-20
2	ITGA6	rs12613307	172460516	G	T	0.2772480	-0.0366919	0.0040425	7.4E-21
2	ITGA6	rs12477594	172460628	G	A	0.4992460	-0.0229083	0.0036296	3.5E-11
2	ITGA6	rs35288169	172461148	G	A	0.3110940	-0.0348148	0.0039068	3.6E-20
2	ITGA6	rs1076594	172461708	G	A	0.3296790	-0.0349717	0.0038521	5.2E-21
2	ITGA6	rs1076595	172461891	T	C	0.4969140	-0.0236876	0.0036313	7.5E-12
2	ITGA6	rs2357411	172462191	G	A	0.3457750	-0.0358294	0.0038189	1.5E-22
2	ITGA6	rs1076596	172462521	A	G	0.3109800	-0.0351858	0.0039112	1.9E-20
2	ITGA6	rs74461567	172463095	T	C	0.2764890	-0.0372673	0.0040715	5.9E-21
2	ITGA6	rs74819816	172465128	T	TTAC	0.4918570	0.0229231	0.0036245	3.5E-11
2	ITGA6	rs3749148	172465821	T	G	0.4817030	-0.0226948	0.0036222	7.4E-11
2	ITGA6	rs116108611	172466348	A	G	0.2871780	-0.0374312	0.0040011	8.7E-22
2	ITGA6	rs16860478	172469988	G	T	0.2883690	-0.0372073	0.0039954	1.3E-21
2	ITGA6	rs16860498	172472953	T	G	0.4928940	0.0234618	0.0036257	9.9E-12
2	ITGA6	rs3792257	172475470	C	A	0.4974160	0.0239601	0.0036238	4.1E-12
2	ITGA6	rs55867175	172475481	C	A	0.2869260	-0.0372613	0.0040050	1.5E-21
2	ITGA6	rs6730905	172477100	G	A	0.4151990	-0.0269696	0.0036760	1.7E-14
2	ITGA6	rs6759316	172477256	A	G	0.3667210	-0.0206598	0.0037558	3.6E-09
2	ITGA6	rs34094408	172477266	A	G	0.4953110	0.0233660	0.0036175	1.2E-11
2	ITGA6	rs6759557	172477436	A	G	0.4136290	-0.0272753	0.0036748	9.1E-15
2	ITGA6	rs16860513	172477639	A	T	0.2869690	-0.0374709	0.0040017	8.2E-22
2	ITGA6	rs16860515	172477688	T	C	0.2835450	-0.0359409	0.0040159	4.3E-20
2	ITGA6	rs12469958	172478608	A	G	0.4973490	0.0234743	0.0036248	1.3E-11
2	ITGA6	rs7587940	172479060	T	C	0.3767600	-0.0292530	0.0037322	8.7E-16
2	ITGA6	rs9636257	172479400	A	G	0.2858400	-0.0375191	0.0040044	9.0E-22
2	ITGA6	rs1920979	172479746	G	A	0.3770510	-0.0294403	0.0037310	5.9E-16
2	ITGA6	rs2293647	172479952	C	A	0.2392730	-0.0323976	0.0042438	1.8E-15
2	ITGA6	rs6718477	172481339	G	A	0.4962670	0.0236102	0.0036224	9.0E-12
2	ITGA6	rs79437690	172481633	T	C	0.4961830	0.0236592	0.0036230	8.3E-12
2	ITGA6	rs12465295	172481772	G	A	0.4964500	0.0235415	0.0036238	1.0E-11
2	ITGA6	rs58936375	172482610	T	TGCTGTG	0.3420840	-0.0295481	0.0038341	1.6E-15
2	ITGA6	rs16860543	172486448	A	G	0.4964080	0.0235048	0.0036199	9.5E-12
2	ITGA6	rs2701268	172486471	A	G	0.3427660	-0.0300966	0.0038124	4.3E-16
2	ITGA6	rs2293649	172487375	C	T	0.4704270	-0.0228689	0.0036295	2.9E-11
2	ITGA6	rs2293648	172487429	T	A	0.2861400	-0.0375209	0.0040037	5.7E-22
2	ITGA6	rs10930559	172488096	T	C	0.2854800	-0.0375395	0.0040061	7.5E-22
2	ITGA6	rs138348628	172488272	AT	A	0.2856060	-0.0376728	0.0040181	7.2E-22
2	ITGA6	rs1344272	172488590	G	A	0.4699530	-0.0229602	0.0036301	2.1E-11
2	ITGA6	rs7609465	172490229	C	T	0.4691340	-0.0229955	0.0036316	2.2E-11
2	ITGA6	rs7582972	172490283	A	G	0.4690810	-0.0230621	0.0036317	2.0E-11
2	ITGA6	rs60275829	172490331	G	C	0.4985600	0.0244295	0.0036226	1.7E-12
2	ITGA6	rs56084828	172491179	C	A	0.4969240	0.0237659	0.0036216	6.8E-12
2	ITGA6	rs78340400	172492538	G	A	0.4959520	0.0236173	0.0036208	7.8E-12
2	ITGA6	rs7564654	172492673	G	A	0.4692950	-0.0229266	0.0036308	2.5E-11
2	ITGA6	rs7564591	172492799	C	G	0.4663990	-0.0240094	0.0036346	3.9E-12
2	ITGA6	rs4619573	172493757	C	T	0.4698740	-0.0229971	0.0036309	2.0E-11
2	ITGA6	rs79474289	172497318	A	C	0.2854340	-0.0376549	0.0040071	6.0E-22
2	ITGA6	rs2293646	172502141	T	C	0.4978900	0.0242318	0.0036196	2.1E-12
2	ITGA6	rs2293645	172502232	T	C	0.2848530	-0.0372300	0.0040095	1.8E-21
2	ITGA6	rs3792260	172503073	G	A	0.4985480	0.0242585	0.0036187	2.3E-12
2	ITGA6	rs16860634	172503630	G	T	0.2860670	-0.0376227	0.0040059	6.8E-22
2	ITGA6	chr2:172505961_T_TA	172505961	TA	T	0.2355750	-0.0326223	0.0042829	2.0E-15
2	ITGA6 *	rs16860643	172506550	G	A	0.2861920	-0.0373485	0.0040043	9.4E-22
2	ITGA6 *	rs199505421	172506780	T	TATATAA	0.2695070	-0.0369729	0.0041081	5.9E-20

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ITGA6 *	rs76343634	172506812	T	C	0.4820840	-0.0215522	0.0036783	6.0E-10
2	ITGA6 *	rs78785265	172507381	A	G	0.4955110	0.0235527	0.0036199	8.1E-12
2	ITGA6 *	rs2357415	172508265	T	C	0.4980480	0.0240665	0.0036190	2.8E-12
2	ITGA6 *	rs114997784	172509103	G	C	0.2376060	-0.0326630	0.0042600	1.7E-15
2	ITGA6 *	rs200671136	172509305	A	AAAAT	0.4718270	0.0243647	0.0036918	8.3E-12
2	ITGA6 *	rs1574247	172509348	T	C	0.4979580	0.0240655	0.0036195	2.9E-12
2	ITGA6 *	rs78534109	172509696	G	C	0.2865500	-0.0372388	0.0040055	1.4E-21
2	ITGA6 *	rs34237921	172509705	G	A	0.4448680	-0.0280462	0.0036413	9.7E-16
2	ITGA6 *	rs7591883	172510134	C	G	0.4984970	0.0241034	0.0036194	3.0E-12
2	ITGA6 *	rs7565216	172510276	G	A	0.4985510	0.0241050	0.0036191	3.0E-12
2	ITGA6 *	rs60096331	172510663	G	C	0.2382360	-0.0327760	0.0042538	1.3E-15
2	ITGA6 *	rs2178474	172510744	G	A	0.4988100	0.0242323	0.0036211	2.6E-12
2	ITGA6 *	rs34387566	172511198	TG	T	0.4992830	0.0241894	0.0036189	2.9E-12
2	ITGA6 *	rs12622687	172511307	C	T	0.4991900	0.0241575	0.0036189	3.1E-12
2	ITGA6 *	rs12619242	172511352	T	G	0.4992930	0.0241790	0.0036188	2.9E-12
2	ITGA6 *	rs76262416	172511502	G	C	0.4993260	0.0242383	0.0036186	2.6E-12
2	ITGA6 *	rs59476799	172511591	C	T	0.2857650	-0.0374699	0.0040092	1.1E-21
2	ITGA6 *	rs60446415	172511756	T	C	0.4986150	0.0241832	0.0036189	2.6E-12
2	ITGA6 *	rs57404607	172512549	T	G	0.2374010	-0.0329477	0.0042623	1.1E-15
2	ITGA6 *	rs59374567	172512574	T	C	0.2374000	-0.0328924	0.0042622	1.2E-15
2	ITGA6 *	rs76258544	172513033	A	G	0.4983980	0.0243325	0.0036190	2.0E-12
2	ITGA6 *	rs12467358	172513310	G	A	0.4984980	0.0243820	0.0036190	1.8E-12
2	ITGA6 *	rs6755100	172513417	T	C	0.4979970	0.0243533	0.0036201	1.8E-12
2	ITGA6 *	rs59970483	172513616	A	G	0.2381270	-0.0328253	0.0042546	1.2E-15
2	ITGA6 *	rs78623829	172514502	A	G	0.2360150	-0.0326896	0.0042724	1.8E-15
2	ITGA6 *	rs58044442	172514530	C	A	0.4987870	0.0242812	0.0036185	2.2E-12
2	ITGA6 *	rs13402061	172515320	G	A	0.4988120	0.0242578	0.0036183	2.3E-12
2	ITGA6 *	rs79095690	172515424	T	C	0.4987190	0.0241975	0.0036185	2.6E-12
2	ITGA6 *	rs79346771	172516356	G	C	0.4986200	0.0241654	0.0036184	2.7E-12
2	ITGA6 *	rs79594061	172516367	T	A	0.4986200	0.0241654	0.0036184	2.7E-12
2	ITGA6 *	rs139428359	172516382	C	CT	0.4986200	0.0241654	0.0036184	2.7E-12
2	ITGA6 *	rs57957394	172516821	A	G	0.4985270	0.0241154	0.0036187	3.0E-12
2	ITGA6 *	rs12474168	172517676	A	G	0.4986690	0.0241850	0.0036185	2.6E-12
2	ITGA6 *	rs12474995	172517855	C	G	0.4986760	0.0241926	0.0036185	2.6E-12
2	ITGA6 *	rs115142421	172518049	A	T	0.2848180	-0.0375695	0.0040096	7.9E-22
2	ITGA6 *	rs7562753	172518060	T	C	0.4439050	-0.0281186	0.0036420	1.0E-15
2	ITGA6 *	rs7562865	172518137	T	C	0.4439130	-0.0281734	0.0036419	9.0E-16
2	ITGA6 *	rs76738244	172518258	A	G	0.2361440	-0.0325150	0.0042694	2.6E-15
2	ITGA6 *	rs12476126	172518939	A	C	0.4986730	0.0241707	0.0036188	2.7E-12
2	ITGA6 *	rs12477247	172519894	A	C	0.4986300	0.0240946	0.0036191	3.1E-12
2	ITGA6 *	rs12465442	172520013	C	T	0.4989190	0.0241293	0.0036195	3.2E-12
2	ITGA6 *	rs12478465	172521218	T	C	0.4986300	0.0241738	0.0036183	2.7E-12
2	ITGA6 *	rs10174809	172521806	T	C	0.4438750	-0.0282943	0.0036419	6.8E-16
2	ITGA6 *	rs13383151	172522632	A	C	0.4984190	0.0243634	0.0036197	2.0E-12
2	ITGA6 *	rs76246006	172523371	T	C	0.4986270	0.0241597	0.0036183	2.7E-12
2	ITGA6 *	rs77655885	172523420	A	C	0.4986300	0.0241738	0.0036183	2.7E-12
2	ITGA6 *	rs77546188	172523614	T	C	0.4987340	0.0242201	0.0036184	2.4E-12
2	ITGA6 *	rs77403951	172524917	G	T	0.4991720	0.0242744	0.0036192	2.0E-12
2	ITGA6 *	rs12052921	172525615	C	T	0.3190900	-0.0358606	0.0038841	2.9E-21
2	ITGA6 *	rs57121294	172525726	C	CA	0.2838960	-0.0370409	0.0040185	3.5E-21
2	ITGA6 *	rs4308101	172526047	T	C	0.4985300	0.0243891	0.0036184	1.8E-12
2	ITGA6 *	rs59300838	172526055	G	T	0.3190900	-0.0358606	0.0038841	2.9E-21
2	ITGA6 *	rs60442917	172526208	G	A	0.4663530	-0.0235625	0.0036331	9.3E-12
2	ITGA6 *	rs59524026	172526240	C	T	0.4662460	-0.0236263	0.0036332	8.2E-12
2	ITGA6 *	rs59610589	172526297	T	C	0.4984910	0.0243852	0.0036185	1.8E-12
2	ITGA6 *	rs58016698	172526398	T	C	0.4986520	0.0245098	0.0036176	1.4E-12
2	ITGA6 *	rs142975632	172527123	T	C	0.2350970	-0.0324695	0.0042814	3.6E-15
2	ITGA6 *	rs186345866	172527508	A	G	0.4985410	0.0244189	0.0036182	1.7E-12
2	ITGA6 *	rs78800266	172527672	T	C	0.4985340	0.0244145	0.0036185	1.7E-12
2	ITGA6 *	rs77055029	172527929	C	T	0.4985450	0.0244135	0.0036185	1.7E-12
2	ITGA6 *	rs183141927	172528214	A	T	0.2843050	-0.0372371	0.0040151	2.2E-21
2	ITGA6 *	rs57244773	172528877	C	G	0.2842030	-0.0373047	0.0040156	1.8E-21
2	ITGA6 *	rs147233048	172529175	C	T	0.2843050	-0.0372371	0.0040151	2.2E-21
2	ITGA6 *	rs142731545	172529473	C	T	0.2839480	-0.0369811	0.0040186	4.4E-21
2	ITGA6 *	rs12612087	172529559	C	T	0.4977580	0.0243253	0.0036194	1.9E-12
2	ITGA6 *	rs75669437	172530645	A	G	0.2847110	-0.0377527	0.0040108	5.2E-22
2	PDK1 *	rs12615584	172532962	C	T	0.2848130	-0.0375575	0.0040098	8.0E-22
2	PDK1 *	rs80350104	172533543	T	G	0.4978920	0.0242043	0.0036183	2.4E-12
2	PDK1 *	rs57587465	172535039	C	T	0.2849180	-0.0375203	0.0040093	8.6E-22
2	PDK1 *	rs145463827	172535428	T	TTAA	0.2847130	-0.0376506	0.0040103	6.6E-22
2	PDK1 *	rs6741759	172536395	C	T	0.2849160	-0.0375158	0.0040093	8.8E-22
2	PDK1 *	rs79481012	172536536	G	T	0.2373020	-0.0323873	0.0042577	2.5E-15
2	PDK1 *	rs56882727	172536620	G	A	0.2849160	-0.0375158	0.0040093	8.8E-22
2	PDK1 *	rs6730284	172536938	T	C	0.2846350	-0.0375859	0.0040113	7.2E-22
2	PDK1 *	rs12611902	172538119	T	C	0.2850450	-0.0374798	0.0040113	1.0E-21
2	PDK1 *	rs12611959	172538135	C	G	0.2848270	-0.0376650	0.0040096	6.2E-22
2	PDK1 *	rs373139898	172538163	T	C	0.4958580	0.0249462	0.0036293	6.3E-13
2	PDK1 *	rs189892835	172538372	C	T	0.4981020	0.0242970	0.0036184	2.0E-12
2	PDK1 *	rs181480655	172538373	A	G	0.2372040	-0.0325092	0.0042583	2.1E-15
2	PDK1 *	rs185475817	172538453	A	C	0.2848270	-0.0376650	0.0040096	6.2E-22
2	PDK1 *	rs182540392	172538468	T	C	0.4943030	0.0229851	0.0036634	4.9E-11
2	PDK1 *	rs188148040	172538602	A	G	0.2848270	-0.0376650	0.0040096	6.2E-22
2	PDK1 *	rs1482883845	172539105	TAATA	T	0.2355660	-0.0322432	0.0042727	3.3E-15
2	PDK1 *	rs7591769	172540158	A	G	0.3192820	-0.0359708	0.0038838	2.1E-21
2	PDK1 *	rs6743174	172540602	T	G	0.2848290	-0.0376609	0.0040096	6.3E-22
2	PDK1 *	rs74615753	172540717	C	G	0.4981800	0.0243623	0.0036192	1.8E-12
2	PDK1 *	rs79341997	172540859	T	C	0.4981800	0.0243623	0.0036192	1.8E-12
2	PDK1 *	rs75623910	172540993	C	G	0.4981760	0.0243727	0.0036192	1.8E-12
2	PDK1 *	rs147340898	172541290	A	G	0.2372110	-0.0325478	0.0042586	2.0E-15
2	PDK1 *	rs72894386	172541542	C	T	0.4676840	-0.0238647	0.0036323	4.9E-12
2	PDK1 *	rs79916089	172541668	C	A	0.4981690	0.0243994	0.0036193	1.7E-12
2	PDK1 *	rs7560501	172542553	T	C	0.4098060	-0.0284710	0.0036855	6.8E-16
2	PDK1 *	rs138935309	172542716	T	C	0.4970580	0.0242750	0.0036218	2.1E-12
2	PDK1 *	rs139429426	172542984	A	G	0.4982560	0.0245361	0.0036216	1.3E-12
2	PDK1 *	rs59020762	172544079	A	G	0.4981920	0.0251858	0.0036410	4.9E-13
2	PDK1 *	rs138822454	172544592	G	A	0.2353970	-0.0329818	0.0042903	1.5E-15
2	PDK1 *	rs76382989	172545435	C	G	0.4984020	0.0252839	0.0036498	4.9E-13
2	PDK1 *	rs74355465	172545440	A	G	0.2833330	-0.0379734	0.0040368	5.9E-22
2	PDK1 *	rs80176582	172546028	T	C	0.4973950	0.0252889	0.0036500	4.7E-13
2	PDK1 *	rs4972839	172546132	C	A	0.4676490	-0.0247183	0.0036612	1.4E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	PDK1 *	rs115160117	172546276	C	G	0.2835130	-0.0379883	0.0040353	5.1E-22
2	PDK1 *	rs75612195	172547435	A	G	0.4973400	0.0252515	0.0036547	5.4E-13
2	PDK1 *	rs4972841	172548750	T	C	0.4087870	-0.0288250	0.0037226	6.7E-16
2	PDK1 *	rs12475916	172549965	C	T	0.4986800	0.0254245	0.0036719	4.8E-13
2	PDK1 *	rs12151618	172550832	T	C	0.3315500	-0.0344929	0.0039264	1.0E-19
2	PDK1 *	rs78647569	172550978	G	C	0.2424300	-0.0448721	0.0042604	3.1E-27
2	PDK1 *	rs61542159	172552923	T	C	0.4603180	-0.0310240	0.0036380	5.7E-19
2	PDK1 *	rs35077188	172552943	AG	A	0.1892270	-0.0416798	0.0046385	1.1E-20
2	PDK1 *	rs10181851	172555077	G	A	0.2419630	-0.0444381	0.0042259	3.4E-27
2	PDK1 *	rs3835124	172555296	C	CATT	0.2279570	-0.0463348	0.0043166	2.8E-28
2	PDK1	rs3765065	172555526	A	T	0.2419710	-0.0443801	0.0042259	3.9E-27
2	PDK1	rs10930561	172556521	T	C	0.2280340	-0.0462612	0.0043154	3.2E-28
2	PDK1	rs77842539	172557137	C	T	0.4703780	-0.0316183	0.0036657	5.3E-19
2	PDK1	rs12465704	172557657	T	A	0.2373490	-0.0440454	0.0042821	4.4E-26
2	PDK1	rs79289120	172557731	C	T	0.4701660	-0.0316496	0.0036644	4.5E-19
2	PDK1	rs8179584	172558338	T	G	0.2280390	-0.0462780	0.0043153	3.0E-28
2	PDK1	rs78279758	172559347	T	A	0.2280880	-0.0463717	0.0043155	2.4E-28
2	PDK1	rs151175749	172559679	G	C	0.2280450	-0.0463010	0.0043153	2.9E-28
2	PDK1	rs6752386	172560621	G	A	0.2419140	-0.0446405	0.0042264	2.0E-27
2	PDK1	rs72296958	172564143	TCTC	T	0.4750830	-0.0314567	0.0036719	1.0E-18
2	PDK1	rs6433368	172564146	T	C	0.2455550	-0.0449068	0.0042458	1.7E-27
2	PDK1	rs10930562	172565979	T	C	0.2421620	-0.0445040	0.0042274	3.1E-27
2	PDK1	rs10930563	172566312	C	T	0.2280490	-0.0463534	0.0043154	2.5E-28
2	PDK1	rs3769321	172567626	G	A	0.2419690	-0.0446173	0.0042263	2.2E-27
2	PDK1	rs57418091	172570364	T	A	0.4593840	-0.0300918	0.0036327	4.7E-18
2	PDK1	rs12467086	172576217	T	C	0.1873510	-0.0416427	0.0046501	1.2E-20
2	PDK1	rs62167835	172576720	T	C	0.2420370	-0.0444935	0.0042252	2.9E-27
2	PDK1	rs6738196	172579734	T	C	0.2420160	-0.0443018	0.0042247	4.5E-27
2	PDK1	rs10930564	172581387	T	A	0.1865440	-0.0420776	0.0046604	6.2E-21
2	PDK1	rs139756689	172581622	GCAT	G	0.2280970	-0.0463483	0.0043150	2.6E-28
2	PDK1	rs74265086	172583655	G	T	0.2280970	-0.0463483	0.0043150	2.6E-28
2	PDK1	rs140037972	172584212	GT	G	0.2280970	-0.0463483	0.0043150	2.6E-28
2	PDK1	rs118107311	172587278	A	G	0.2360330	-0.0469121	0.0042739	2.2E-29
2	PDK1	rs74747026	172587626	G	T	0.4689230	-0.0318495	0.0036374	7.2E-20
2	PDK1	rs6710129	172588026	C	T	0.2500270	-0.0450735	0.0041905	2.9E-28
2	PDK1	rs16860693	172588550	C	T	0.2362550	-0.0467623	0.0042740	3.2E-29
2	PDK1	rs117897460	172588743	G	A	0.2355460	-0.0472407	0.0042836	9.7E-30
2	PDK1	rs10930565	172589507	G	A	0.2494350	-0.0452602	0.0042000	2.1E-28
2	PDK1	rs76624092	172589636	T	C	0.2355630	-0.0470525	0.0042856	1.8E-29
2	PDK1	rs79246370	172591150	T	G	0.2274940	-0.0465697	0.0043265	1.7E-28
2	PDK1	rs77843385	172591311	T	C	0.2274950	-0.0465695	0.0043265	1.7E-28
2	PDK1	rs34051646	172591951	G	T	0.2414570	-0.0448038	0.0042374	1.6E-27
2	PDK1	rs147018019	172592437	CT	C	0.4602370	-0.0311663	0.0036397	3.6E-19
2	PDK1	rs76751608	172592581	T	C	0.1868390	-0.0419894	0.0046623	6.8E-21
2	PDK1	rs1530864	172596075	G	A	0.2277400	-0.0464851	0.0043278	1.9E-28
2	PDK1	rs1530865	172596362	C	G	0.2273960	-0.0467586	0.0043284	1.1E-28
2	PDK1	rs70937083	172597071	A	G	0.2274200	-0.0467825	0.0043282	1.0E-28
2	PDK1	rs11904158	172597092	A	G	0.2412330	-0.0449043	0.0042407	1.1E-27
2	PDK1	rs70937084	172597865	G	C	0.2274550	-0.0468524	0.0043278	8.1E-29
2	PDK1	rs2357637	172598410	A	C	0.1867440	-0.0421804	0.0046638	4.5E-21
2	PDK1	rs1075638	172600468	C	G	0.2330190	-0.0442997	0.0043181	9.1E-26
2	PDK1	rs13019331	172602573	T	C	0.2415870	-0.0447555	0.0042364	1.8E-27
2	PDK1	rs7584769	172603556	C	G	0.2415800	-0.0446453	0.0042371	2.4E-27
2	PDK1	rs61505737	172604604	A	G	0.2274890	-0.0467414	0.0043279	1.2E-28
2	PDK1	rs77271607	172605458	A	G	0.2267870	-0.0468589	0.0043358	9.7E-29
2	PDK1	rs79037658	172606053	A	C	0.2283580	-0.0474036	0.0043239	1.3E-29
2	PDK1	rs13401676	172608553	A	G	0.2566510	-0.0453414	0.0041517	2.3E-29
2	PDK1	rs75202749	172609290	T	C	0.2414790	-0.0470349	0.0042432	3.0E-30
2	PDK1	rs12476204	172614243	T	C	0.2593930	-0.0458916	0.0041285	1.7E-30
2	PDK1	rs1133602	172614546	C	G	0.2595130	-0.0461067	0.0041272	9.0E-31
2	PDK1	rs1868901	172615069	C	G	0.2590220	-0.0462389	0.0041322	7.0E-31
2	PDK1	rs13024563	172615848	A	G	0.2595380	-0.0460842	0.0041269	9.1E-31
2	PDK1	rs78205119	172615985	C	A	0.2447310	-0.0475812	0.0042107	1.5E-31
2	PDK1	rs77511817	172615986	C	A	0.2429980	-0.0472511	0.0042294	5.7E-31
2	PDK1	rs78132475	172617380	A	G	0.2450270	-0.0477657	0.0042071	8.2E-32
2	PDK1	rs1010752	172617950	G	C	0.2442460	-0.0481059	0.0042158	4.4E-32
2	PDK1	rs13015260	172619555	T	G	0.2633660	-0.0448371	0.0041159	2.5E-29
2	PDK1	rs16860737	172619662	C	T	0.2632090	-0.0449365	0.0041147	1.7E-29
2	PDK1	rs35046889	172620955	C	CA	0.2631310	-0.0451303	0.0041190	1.1E-29
2	PDK1	rs187504991	172621894	A	G	0.2473730	-0.0462635	0.0042105	5.3E-30
2	PDK1	rs16860741	172621993	T	C	0.2459140	-0.0450379	0.0042778	1.8E-27
2	PDK1	rs12465512	172624318	A	G	0.2484590	-0.0468207	0.0042003	8.4E-31
2	PDK1 *	rs12693008	172625657	T	C	0.2650800	-0.0450133	0.0041277	2.5E-29
2	PDK1 *	rs10930566	172626751	A	C	0.2480460	-0.0469465	0.0042036	7.3E-31
2	PDK1 *	rs10930567	172626863	T	A	0.2484640	-0.0468445	0.0042005	8.1E-31
2	PDK1 *	rs836590	172628379	T	G	0.2557420	-0.0466778	0.0041586	4.2E-31
2	PDK1 *	rs1531150	172629151	G	A	0.2577680	-0.0468725	0.0041400	1.2E-31
2	PDK1 *	rs1531149	172629158	G	A	0.2431870	-0.0484991	0.0042222	1.1E-32
2	PDK1 *	rs1531148	172629164	T	G	0.2431870	-0.0484991	0.0042222	1.1E-32
2	PDK1 *	rs6733679	172629415	C	T	0.2577940	-0.0469152	0.0041388	1.2E-31
2	PDK1 *	rs6718681	172629486	T	C	0.2426580	-0.0485097	0.0042271	1.6E-32
2	PDK1 *	rs6719140	172629647	T	G	0.2432410	-0.0483285	0.0042202	2.0E-32
2	PDK1 *	rs2599268	172629694	G	A	0.2578590	-0.0466049	0.0041356	2.5E-31
2	PDK1 *	rs2606070	172629761	A	C	0.2578730	-0.0465971	0.0041355	2.6E-31
2	PDK1 *	rs1869923	172630004	G	C	0.2578810	-0.0466161	0.0041355	2.5E-31
2	PDK1 *	chr2:172630632_AT_A	172630632	AT	A	0.2624380	-0.0430762	0.0042114	2.7E-26
2	PDK1 *	rs2599266	172630901	T	A	0.2578870	-0.0466536	0.0041356	2.2E-31
2	PDK1 *	rs2606067	172630950	G	T	0.2578960	-0.0466170	0.0041355	2.5E-31
2	PDK1 *	rs2606066	172631140	A	G	0.2578980	-0.0466317	0.0041356	2.4E-31
2	PDK1 *	rs2606065	172631181	A	G	0.2578980	-0.0466317	0.0041356	2.4E-31
2	PDK1 *	rs2599265	172631255	C	T	0.2578980	-0.0466317	0.0041356	2.4E-31
2	PDK1 *	rs2599264	172631408	C	T	0.2579010	-0.0466189	0.0041355	2.5E-31
2	PDK1 *	rs2599263	172631417	C	T	0.2579010	-0.0466189	0.0041355	2.5E-31
2	PDK1 *	rs10661367	172631539	C	CTG	0.2584040	-0.0464455	0.0041365	4.1E-31
2	PDK1 *	rs11313460	172631540	CA	C	0.2584040	-0.0464455	0.0041365	4.1E-31
2	PDK1 *	rs2599262	172631829	T	G	0.2579070	-0.0466411	0.0041354	2.3E-31
2	PDK1 *	rs2599261	172632024	C	G	0.2578820	-0.0466867	0.0041357	2.1E-31
2	PDK1 *	rs147080643	172632025	G	C	0.2433010	-0.0482883	0.0042179	2.0E-32
2	PDK1 *	rs2606064	172632419	C	T	0.2580750	-0.0466640	0.0041353	2.3E-31
2	PDK1 *	rs2606063	172632668	A	C	0.2579100	-0.0466205	0.0041354	2.5E-31

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	PDK1 *	rs2599260	172632713	G	A	0.2580970	-0.0466558	0.0041361	2.3E-31
2	PDK1 *	rs2606062	172632764	A	G	0.2582460	-0.0464909	0.0041373	4.5E-31
2	PDK1 *	rs6731354	172632912	C	T	0.2597050	-0.0468820	0.0041440	1.9E-31
2	PDK1 *	rs142280784	172633211	TA	T	0.2626150	-0.0465112	0.0041376	2.8E-31
2	PDK1 *	rs836634	172633297	C	T	0.2571920	-0.0464798	0.0041426	5.3E-31
2	PDK1 *	rs10658682	172633575	T	TGTA	0.2590360	-0.0464354	0.0041414	6.0E-31
2	PDK1 *	rs836632	172634547	C	A	0.2578920	-0.0466936	0.0041364	2.1E-31
2	PDK1 *	chr2:172634772_CAA_C	172634772	CAA	C	0.2578880	-0.0467663	0.0041365	1.7E-31
2	PDK1 *	rs836631	172634844	A	T	0.2579690	-0.0466432	0.0041366	2.3E-31
2	PDK1 *	rs836630	172635320	C	G	0.2578820	-0.0467406	0.0041368	1.8E-31
2	PDK1 *	rs836629	172635497	A	G	0.2578840	-0.0467430	0.0041368	1.8E-31
2	PDK1 *	rs2606073	172635695	C	G	0.2578860	-0.0467424	0.0041368	1.8E-31
2	PDK1 *	rs2606074	172635698	T	C	0.2578860	-0.0467424	0.0041368	1.8E-31
2	PDK1 *	rs836628	172636341	A	G	0.2433350	-0.0483730	0.0042186	1.6E-32
2	PDK1 *	rs836626	172636840	T	A	0.2578840	-0.0467757	0.0041369	1.7E-31
2	PDK1 *	rs4972845	172639828	A	C	0.4830320	-0.0352861	0.0036261	3.7E-24
2	PDK1 *	rs60127617	172643739	C	T	0.2434470	-0.0481161	0.0042194	2.6E-32
2	PDK1 *	rs77437224	172645792	T	C	0.2430110	-0.0481838	0.0042233	2.7E-32
2	PDK1 *	rs57566649	172647095	A	C	0.4839680	-0.0349594	0.0036199	4.5E-24
2	PDK1 *	rs80158804	172647384	C	A	0.2433470	-0.0482048	0.0042224	2.5E-32
2	PDK1 *	rs836617	172647569	A	T	0.2579460	-0.0466109	0.0041400	2.4E-31
2	PDK1 *	rs2122833	172647821	T	A	0.2001120	-0.0433218	0.0045398	1.9E-23
2	PDK1 *	rs836616	172648028	G	A	0.2579490	-0.0465560	0.0041403	2.8E-31
2	PDK1 *	rs836614	172648642	A	C	0.2579440	-0.0466003	0.0041407	2.6E-31
2	PDK1 *	rs1097478	172649473	G	A	0.2579140	-0.0465058	0.0041415	3.5E-31
2	PDK1 *	rs12617037	172649627	A	G	0.2433020	-0.0481055	0.0042241	3.6E-32
2	PDK1 *	rs137897332	172650225	G	A	0.2432500	-0.0479814	0.0042255	5.6E-32
2	PDK1 *	rs28761282	172650880	C	T	0.2431060	-0.0479071	0.0042275	6.5E-32
2	PDK1 *	rs28867382	172651163	C	A	0.2430780	-0.0479467	0.0042279	5.8E-32
2	PDK1 *	rs9798439	172651888	T	C	0.4855900	-0.0347640	0.0036248	1.0E-23
2	PDK1 *	rs139763357	172652497	G	A	0.4837780	-0.0349897	0.0036186	4.1E-24
2	PDK1 *	rs144443538	172652600	T	C	0.4835860	-0.0348395	0.0036170	6.2E-24
2	PDK1 *	rs72662141	172652804	C	T	0.4839040	-0.0349641	0.0036170	4.1E-24
2	PDK1 *	rs78065659	172653192	A	G	0.4835400	-0.0348192	0.0036171	6.5E-24
2	PDK1 *	rs12620518	172653376	A	G	0.2430200	-0.0481050	0.0042289	3.8E-32
2	PDK1 *	rs79599856	172653487	T	C	0.4841780	-0.0353005	0.0036185	1.8E-24
2	PDK1 *	rs74698076	172653535	G	A	0.4842390	-0.0348997	0.0036184	4.9E-24
2	PDK1 *	rs11665243	172653956	G	A	0.4839810	-0.0350561	0.0036172	3.1E-24
2	PDK1 *	rs34043892	172655356	A	AG	0.2575740	-0.0466158	0.0041469	2.7E-31
2	PDK1 *	rs79060028	172655684	A	G	0.2429330	-0.0481725	0.0042299	3.1E-32
2	PDK1 *	rs6705827	172656127	G	C	0.4835600	-0.0348998	0.0036165	4.7E-24
2	PDK1 *	rs58308687	172656931	T	C	0.4835610	-0.0348994	0.0036165	4.7E-24
2	PDK1 *	rs61121406	172657316	A	G	0.2428360	-0.0481965	0.0042317	2.9E-32
2	PDK1 *	rs10930568	172657345	T	G	0.2428340	-0.0482048	0.0042317	2.9E-32
2	PDK1 *	rs836608	172657553	C	A	0.2577750	-0.0465389	0.0041476	3.7E-31
2	PDK1 *	rs58324965	172657797	A	AGC	0.2428290	-0.0483024	0.0042322	2.2E-32
2	PDK1 *	rs4972847	172659139	G	A	0.4835660	-0.0348649	0.0036164	5.0E-24
2	PDK1 *	rs73042937	172659317	T	C	0.4835640	-0.0348875	0.0036161	5.0E-24
2	PDK1 *	rs4972848	172659402	A	G	0.4835730	-0.0348834	0.0036163	4.7E-24
2	PDK1 *	rs7595971	172659799	A	C	0.4835650	-0.0348816	0.0036165	4.9E-24
2	PDK1 *	rs16860778	172660155	T	C	0.4835650	-0.0348742	0.0036165	5.1E-24
2	PDK1 *	chr2:172660231_T_TTC	172660231	T	TTC	0.4835790	-0.0348507	0.0036166	5.5E-24
2	PDK1 *	rs2198799	172661431	C	G	0.4877410	-0.0351982	0.0036309	3.4E-24
2	PDK1 *	rs2198800	172661466	T	C	0.4835840	-0.0349960	0.0036184	3.9E-24
2	PDK1 *	rs59547791	172661720	A	C	0.4835500	-0.0348356	0.0036167	5.6E-24
2	PDK1 *	rs59839960	172662188	A	G	0.4834400	-0.0351276	0.0036207	2.3E-24
2	PDK1 *	rs80152180	172663986	C	T	0.4835540	-0.0350869	0.0036256	2.9E-24
2	PDK1 *	rs79299771	172664090	T	C	0.4841040	-0.0351289	0.0036286	3.1E-24
2	PDK1 *	rs56750684	172664184	A	G	0.4871280	-0.0346165	0.0036462	1.8E-23
2	PDK1 *	rs73042954	172664216	T	C	0.4853810	-0.0345288	0.0036374	1.8E-23
2	PDK1 *	rs139394539	172664219	A	G	0.1979730	-0.0434119	0.0045805	2.2E-23
2	PDK1 *	rs16860781	172665481	A	C	0.2413810	-0.0487593	0.0042538	8.9E-33
2	PDK1 *	rs78587499	172665821	G	C	0.4836740	-0.0349025	0.0036285	4.6E-24
2	PDK1 *	rs2034854	172666038	T	C	0.4834470	-0.0349034	0.0036274	4.5E-24
2	PDK1 *	rs2122832	172666333	A	T	0.4838120	-0.0348832	0.0036285	5.1E-24
2	PDK1 *	rs836643	172666748	A	G	0.2426070	-0.0484439	0.0042513	2.0E-32
2	PDK1 *	rs78370943	172666993	G	A	0.2433540	-0.0485525	0.0042443	1.1E-32
2	PDK1 *	rs78373236	172667922	T	C	0.2000290	-0.0430042	0.0045595	4.0E-23
2	PDK1 *	rs2054163	172668460	G	A	0.4558550	-0.0358055	0.0036523	3.8E-25
2	PDK1 *	rs2054162	172668497	G	T	0.4738320	-0.0358391	0.0036360	1.8E-25
2	PDK1 *	rs16860789	172668594	G	A	0.2428470	-0.0479755	0.0042492	6.1E-32
2	PDK1 *	rs6733953	172668844	C	T	0.4566530	-0.0356502	0.0036575	7.2E-25
2	PDK1 *	rs4404239	172669121	G	A	0.4738580	-0.0358794	0.0036352	1.6E-25
2	PDK1 *	rs4482449	172669250	G	A	0.4738600	-0.0358417	0.0036352	1.8E-25
2	PDK1 *	rs4313941	172669531	T	C	0.4738340	-0.0358079	0.0036347	1.9E-25
2	PDK1 *	rs7590282	172670145	C	T	0.4556530	-0.0357515	0.0036496	4.1E-25
2	PDK1 *	rs12052531	172670857	A	G	0.2426770	-0.0479059	0.0042506	7.4E-32
2	PDK1 *	rs6716527	172671142	A	G	0.4600130	-0.0360823	0.0036647	2.7E-25
2	PDK1 *	rs59891077	172671463	CT	C	0.4740250	-0.0363874	0.0036458	5.9E-26
2	PDK1 *	rs16860794	172671791	G	A	0.4743610	-0.0359908	0.0036298	9.7E-26
2	PDK1 *	rs16860795	172672019	A	G	0.4744040	-0.0358906	0.0036292	1.4E-25
2	PDK1 *	chr2:172672620_C_CT	172672620	C	CT	0.4823320	-0.0355030	0.0036596	1.7E-24
2	PDK1 *	rs16860796	172672701	G	C	0.4565850	-0.0356285	0.0036461	5.7E-25
2	PDK1 *	rs16860798	172672814	G	A	0.4744470	-0.0358844	0.0036289	1.4E-25
2	PDK1 *	rs56412542	172672888	G	A	0.4564880	-0.0356998	0.0036452	4.4E-25
2	PDK1 *	rs80221871	172672889	A	G	0.4744440	-0.0358938	0.0036289	1.4E-25
2	PDK1 *	rs76262493	172672896	CA	C	0.2418880	-0.0474377	0.0042597	3.9E-31
2	PDK1 *	rs59103702	172672987	A	G	0.4564890	-0.0357007	0.0036452	4.4E-25
2	PDK1 *	rs78726056	172673061	AG	A	0.4744490	-0.0359221	0.0036288	1.3E-25
2	PDK1 *	rs78327151	172673292	G	A	0.4745690	-0.0359391	0.0036299	1.3E-25
2	PDK1 *	rs12622834	172673819	A	G	0.4570120	-0.0354724	0.0036478	9.2E-25
2	PDK1 *	rs2084732	172676126	T	C	0.4742560	-0.0360536	0.0036225	7.6E-26
2	PDK1 *	rs2084731	172676276	G	A	0.4742560	-0.0360536	0.0036225	7.6E-26
2	PDK1 *	rs4972514	172676708	G	C	0.4742530	-0.0360288	0.0036225	8.2E-26
2	PDK1 *	rs4972515	172676882	A	G	0.4742530	-0.0360288	0.0036225	8.2E-26
2	PDK1 *	rs4972849	172677035	C	T	0.4742490	-0.0360080	0.0036225	8.8E-26
2	PDK1 *	rs79888531	172677285	G	A	0.4743170	-0.0360841	0.0036229	7.3E-26
2	PDK1 *	rs78972754	172677433	C	G	0.4662070	-0.0360378	0.0036343	2.4E-25
2	PDK1 *	rs74695195	172677623	A	G	0.4741950	-0.0360518	0.0036222	7.8E-26
2	PDK1 *	rs12622335	172678095	A	G	0.4742230	-0.0360678	0.0036222	7.5E-26

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	PDK1 *	chr2:172679870_GT_G	172679870	G	GT	0.2429970	-0.0479560	0.0042442	5.8E-32
2	PDK1 *	rs836637	172679871	T	G	0.2429970	-0.0479560	0.0042442	5.8E-32
2	PDK1 *	rs201599279	172679872	G	T	0.2428140	-0.0476028	0.0042464	1.8E-31
2	PDK1 *	rs16860809	172680015	A	G	0.4718570	-0.0355440	0.0036211	3.7E-25
2	RAPGEF4 *	rs4972850	172681271	C	T	0.4721270	-0.0356495	0.0036224	2.8E-25
2	RAPGEF4 *	rs733331	172681585	G	A	0.4718520	-0.0355795	0.0036210	3.3E-25
2	RAPGEF4 *	rs144216493	172681939	A	G	0.2430910	-0.0479241	0.0042430	6.3E-32
2	RAPGEF4 *	rs4972516	172682653	A	G	0.4539130	-0.0353457	0.0036385	1.2E-24
2	RAPGEF4 *	rs142624099	172682865	C	CAA	0.2429490	-0.0478951	0.0042447	7.2E-32
2	RAPGEF4 *	rs4972851	172682906	A	G	0.4718420	-0.0356116	0.0036209	3.0E-25
2	RAPGEF4 *	rs112264349	172683156	C	A	0.4718420	-0.0356116	0.0036209	3.0E-25
2	RAPGEF4 *	rs61556691	172683833	C	A	0.4538210	-0.0351913	0.0036388	1.8E-24
2	RAPGEF4 *	rs13384307	172684247	T	C	0.4539550	-0.0353490	0.0036383	1.2E-24
2	RAPGEF4 *	rs78910115	172685102	T	C	0.4714520	-0.0355909	0.0036229	3.8E-25
2	RAPGEF4 *	rs10930569	172688839	C	A	0.2606070	-0.0467064	0.0041550	1.1E-31
2	RAPGEF4 *	rs12621044	172688881	C	G	0.2000340	-0.0439305	0.0045596	6.6E-24
2	RAPGEF4 *	rs72489033	172691730	A	G	0.2427210	-0.0478218	0.0042493	1.0E-31
2	RAPGEF4 *	rs77048077	172691795	C	A	0.2427080	-0.0478252	0.0042495	1.0E-31
2	RAPGEF4 *	rs59578456	172692476	T	C	0.2426770	-0.0477083	0.0042502	1.4E-31
2	RAPGEF4 *	rs74791596	172692928	T	G	0.2425840	-0.0478760	0.0042511	9.2E-32
2	RAPGEF4 *	rs12464110	172693389	T	C	0.2424410	-0.0478914	0.0042528	8.5E-32
2	RAPGEF4 *	rs75551158	172693939	C	T	0.4718830	-0.0356583	0.0036224	2.7E-25
2	RAPGEF4 *	rs6733671	172694340	G	T	0.2419480	-0.0476778	0.0042591	2.1E-31
2	RAPGEF4 *	rs77771090	172695948	A	G	0.2411090	-0.0475608	0.0042713	3.6E-31
2	RAPGEF4 *	rs6709144	172697303	A	G	0.2410210	-0.0474787	0.0042729	4.8E-31
2	RAPGEF4 *	rs146021188	172697789	GCC	G	0.2410080	-0.0474475	0.0042735	5.4E-31
2	RAPGEF4 *	rs201760103	172697790	C	G	0.2410080	-0.0474475	0.0042735	5.4E-31
2	RAPGEF4 *	rs141483353	172699726	CTTTT	C	0.4723910	-0.0355595	0.0036388	5.6E-25
2	RAPGEF4 *	rs763815265	172699728	TTTTTTC	T	0.4723430	-0.0354813	0.0036373	6.7E-25
2	RAPGEF4 *	rs149913877	172699759	T	TA	0.2290950	-0.0459654	0.0043974	9.0E-28
2	RAPGEF4 *	rs6433376	172699786	T	C	0.2585920	-0.0459983	0.0041819	1.3E-30
2	RAPGEF4 *	rs12465795	172699910	T	C	0.2409410	-0.0474375	0.0042752	6.1E-31
2	RAPGEF4 *	rs77170493	172701632	G	T	0.2363730	-0.0490012	0.0043194	4.1E-32
2	RAPGEF4 *	rs74265101	172702205	G	A	0.2407440	-0.0471342	0.0042813	1.8E-30
2	RAPGEF4 *	rs13423020	172702402	G	A	0.2582880	-0.0458285	0.0041895	3.0E-30
2	RAPGEF4 *	rs12469378	172703437	T	C	0.2405260	-0.0473446	0.0042858	1.2E-30
2	RAPGEF4 *	rs77143891	172704236	T	C	0.2395140	-0.0478913	0.0042953	4.2E-31
2	RAPGEF4 *	rs12617921	172704935	T	C	0.2403670	-0.0476375	0.0042901	6.9E-31
2	RAPGEF4 *	rs12618132	172705511	A	G	0.2402500	-0.0477971	0.0042924	4.4E-31
2	RAPGEF4 *	chr2:172708276_GA_G	172708276	GA	G	0.4721620	-0.0351702	0.0036804	4.6E-24
2	RAPGEF4 *	rs79542292	172709048	T	C	0.4689170	-0.0346802	0.0036693	1.1E-23
2	RAPGEF4 *	rs4395226	172709602	C	T	0.2583350	-0.0449720	0.0042117	3.9E-29
2	RAPGEF4 *	rs16860834	172714066	C	T	0.3820580	-0.0287386	0.0037224	2.2E-16
2	RAPGEF4 *	rs12613850	172718606	G	A	0.2448340	-0.0407659	0.0042043	2.2E-24
2	RAPGEF4 *	rs79134870	172720527	C	G	0.2343370	-0.0407448	0.0042832	2.3E-23
2	RAPGEF4-AS1	rs75792231	172725305	CA	C	0.4892540	-0.0466090	0.0036814	1.3E-40
2	RAPGEF4-AS1	rs6733277	172726125	G	A	0.4375550	-0.0400108	0.0037085	5.1E-30
2	RAPGEF4-AS1	rs6733278	172726126	C	A	0.4379510	-0.0402122	0.0037144	3.7E-30
2	RAPGEF4-AS1	rs11884105	172726470	A	G	0.4605020	-0.0472845	0.0036286	1.1E-42
2	RAPGEF4-AS1	rs11895028	172726537	G	A	0.4836700	-0.0485098	0.0036253	7.7E-45
2	RAPGEF4-AS1	rs56960326	172726684	T	G	0.4746940	-0.0478039	0.0036300	6.3E-44
2	RAPGEF4-AS1	rs767072	172727420	A	G	0.4495610	-0.0468272	0.0036487	1.4E-41
2	RAPGEF4-AS1	rs1349499	172727540	G	A	0.4877370	-0.0477499	0.0036211	1.3E-43
2	RAPGEF4-AS1	rs1349498	172727878	C	T	0.4773100	-0.0482066	0.0036196	1.4E-44
2	RAPGEF4-AS1	rs1349497	172727935	G	C	0.4881200	-0.0478928	0.0036171	7.6E-44
2	RAPGEF4-AS1	rs60951492	172728422	G	C	0.4777330	-0.0482131	0.0036213	1.2E-44
2	RAPGEF4-AS1	rs59172761	172728457	C	T	0.4773690	-0.0480825	0.0036217	2.0E-44
2	RAPGEF4-AS1	rs66743093	172728458	G	GT	0.4773690	-0.0480825	0.0036217	2.0E-44
2	RAPGEF4-AS1	rs67057596	172728650	AT	A	0.4771160	-0.0481901	0.0036205	1.5E-44
2	RAPGEF4-AS1	rs77706112	172728692	T	C	0.4880810	-0.0479090	0.0036203	7.0E-44
2	RAPGEF4-AS1	rs6731917	172728950	T	C	0.4777840	-0.0481352	0.0036247	2.0E-44
2	RAPGEF4-AS1	rs6731931	172728998	T	C	0.4786110	-0.0479807	0.0036294	4.8E-44
2	RAPGEF4-AS1	rs13023591	172730971	C	T	0.4777300	-0.0486167	0.0036218	3.1E-45
2	RAPGEF4-AS1	rs34875551	172731115	G	A	0.4777230	-0.0486071	0.0036217	3.1E-45
2	RAPGEF4-AS1	rs1349496	172731322	C	T	0.4773310	-0.0485047	0.0036219	4.9E-45
2	RAPGEF4-AS1	rs1349495	172731534	G	T	0.4773380	-0.0485157	0.0036220	4.6E-45
2	RAPGEF4-AS1	rs1349494	172731640	A	T	0.4773320	-0.0484972	0.0036222	5.0E-45
2	RAPGEF4-AS1	rs62168084	172731883	C	T	0.4779920	-0.0482963	0.0036254	1.1E-44
2	RAPGEF4-AS1	rs56335137	172732097	C	T	0.4777200	-0.0485949	0.0036221	3.4E-45
2	RAPGEF4-AS1	rs35787281	172732278	G	C	0.4772970	-0.0484376	0.0036224	6.0E-45
2	RAPGEF4-AS1	rs35711056	172733222	C	G	0.4777000	-0.0485858	0.0036222	3.3E-45
2	RAPGEF4-AS1	rs12611769	172733512	G	A	0.4777000	-0.0485849	0.0036222	3.3E-45
2	RAPGEF4-AS1	rs7557133	172733868	A	G	0.4786930	-0.0483390	0.0036269	1.1E-44
2	RAPGEF4-AS1	rs7583805	172733884	G	A	0.4795530	-0.0483980	0.0036282	8.6E-45
2	RAPGEF4-AS1	rs3813816	172734505	G	C	0.4784820	-0.0485339	0.0036209	4.8E-45
2	RAPGEF4-AS1	rs3813815	172734643	A	T	0.4778560	-0.0484549	0.0036199	4.8E-45
2	RAPGEF4-AS1	rs3813814	172735091	A	G	0.4757030	-0.0487890	0.0036182	8.9E-46
2	RAPGEF4-AS1	rs3813813	172735207	G	T	0.4690830	-0.0468184	0.0036256	6.3E-42
2	RAPGEF4	rs4142876	172736339	G	C	0.4498040	-0.0466471	0.0036458	1.4E-41
2	RAPGEF4	rs10657436	172737459	AATAG	A	0.4865640	-0.0462611	0.0036313	1.3E-40
2	RAPGEF4	rs2884281	172739496	T	C	0.4550730	-0.0464764	0.0036739	3.1E-40
2	RAPGEF4	rs6705576	172741998	C	T	0.4830050	-0.0462581	0.0036829	1.7E-39
2	RAPGEF4	rs12616130	172746835	T	C	0.4518660	-0.0344814	0.0036298	2.2E-23
2	RAPGEF4	rs2009432	172767919	T	A	0.4513360	-0.0345235	0.0036360	2.3E-23
2	RAPGEF4	rs55747961	172777365	A	T	0.4603660	-0.0338118	0.0036303	1.3E-22
2	RAPGEF4	rs1863173	1727777509	T	C	0.4566600	-0.0335863	0.0036238	1.4E-22
2	RAPGEF4	rs6713917	172784928	T	C	0.2523030	-0.0251438	0.0042335	1.7E-09
2	RAPGEF4	rs12471745	172786084	G	C	0.2585230	-0.0247620	0.0041924	2.8E-09
2	RAPGEF4	rs12622441	172787234	A	T	0.2542240	-0.0245095	0.0042260	4.9E-09
2	RAPGEF4	rs35928628	172787349	GTCA	G	0.2552010	-0.0247451	0.0042247	3.0E-09
2	RAPGEF4	rs3769320	172799450	G	C	0.3863520	0.0238908	0.0037178	4.6E-11
2	RAPGEF4	rs151005643	172803659	T	G	0.2534220	-0.0242482	0.0041957	5.2E-09
2	RAPGEF4	rs4972862	172807691	T	C	0.3853200	0.0235067	0.0037223	1.1E-10
2	RAPGEF4	rs3769314	172809172	G	A	0.2546030	-0.0246251	0.0041865	2.8E-09
2	RAPGEF4	rs16823271	172811260	A	G	0.2544950	-0.0243901	0.0041806	4.1E-09
2	RAPGEF4	rs2194719	172812009	T	A	0.2555220	-0.0241732	0.0041747	6.2E-09
2	RAPGEF4	rs1863168	172812505	A	G	0.2550650	-0.0244222	0.0041829	4.2E-09
2	RAPGEF4	rs3820852	172815357	A	C	0.2541990	-0.0238291	0.0041824	9.4E-09
2	RAPGEF4	rs16860904	172816625	G	A	0.2560410	-0.0237432	0.0041718	1.2E-08
2	RAPGEF4	rs3769306	172818962	G	A	0.2561580	-0.0237908	0.0041706	1.1E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	RAPGEF4	rs3769304	172820996	C	T	0.3880190	0.0228700	0.0037226	3.2E-10
2	RAPGEF4	rs60249656	172841846	T	C	0.3790590	0.0230197	0.0037535	2.4E-10
2	RAPGEF4	rs4972864	172848374	C	T	0.3944200	0.0220496	0.0037045	8.5E-10
2	EPHA4 *	rs62186153	221169365	G	A	0.2133510	0.0257974	0.0044542	9.4E-09
2	EPHA4 *	rs56237081	221171517	T	C	0.2009930	0.0292671	0.0045385	9.4E-11
2	EPHA4 *	rs7574794	221172851	G	T	0.2019770	0.0300111	0.0045330	2.9E-11
2	EPHA4 *	rs60155163	221183143	A	G	0.2028910	0.0296263	0.0045332	5.7E-11
2	EPHA4 *	rs60380864	221187643	C	A	0.2262580	0.0257607	0.0043370	1.8E-09
2	EPHA4 *	rs59401206	221187831	G	A	0.2260440	0.0257930	0.0043381	1.8E-09
2	EPHA4 *	rs57123201	221188165	A	G	0.2016270	0.0293304	0.0045270	9.9E-11
2	EPHA4 *	chr2:221188169_A_AT	221188169	AT	A	0.2259920	0.0257604	0.0043379	1.9E-09
2	EPHA4 *	rs73993895	221188538	A	G	0.2258390	0.0262191	0.0043369	9.6E-10
2	EPHA4 *	rs62186157	221188582	C	T	0.2258390	0.0262191	0.0043369	9.6E-10
2	EPHA4 *	rs57920471	221188707	T	C	0.2258490	0.0261682	0.0043367	1.0E-09
2	EPHA4 *	rs55853582	221188751	T	A	0.2258560	0.0261798	0.0043366	1.0E-09
2	EPHA4 *	rs58787770	221188771	G	A	0.2258560	0.0261798	0.0043366	1.0E-09
2	EPHA4 *	rs57112177	221188854	T	C	0.2258530	0.0261675	0.0043366	1.0E-09
2	EPHA4 *	rs56241820	221189099	G	A	0.2258570	0.0261891	0.0043366	9.8E-10
2	EPHA4 *	rs55768658	221189187	T	G	0.2258570	0.0261891	0.0043366	9.8E-10
2	EPHA4 *	rs62188463	221189229	G	A	0.2258570	0.0261891	0.0043366	9.8E-10
2	EPHA4 *	rs62188464	221189297	T	A	0.2258570	0.0261891	0.0043366	9.8E-10
2	EPHA4 *	rs62188465	221189341	G	A	0.2258570	0.0261891	0.0043366	9.8E-10
2	EPHA4 *	rs6714776	221189513	A	C	0.2259450	0.0262192	0.0043369	9.2E-10
2	EPHA4 *	rs6715085	221189606	C	G	0.2258610	0.0261894	0.0043364	9.8E-10
2	EPHA4 *	rs6715220	221189852	A	C	0.2253230	0.0259541	0.0043452	1.4E-09
2	EPHA4 *	rs6730490	221189862	C	T	0.2258880	0.0259669	0.0043395	1.3E-09
2	EPHA4 *	chr2:221189896_T_TCA	221189896	TCA	T	0.2257660	0.0260223	0.0043384	1.2E-09
2	EPHA4 *	rs57148208	221190185	C	A	0.2258620	0.0261764	0.0043364	1.0E-09
2	EPHA4 *	rs62188482	221190214	C	T	0.2249200	0.0264618	0.0043479	7.3E-10
2	EPHA4 *	rs62188483	221190274	T	A	0.2258600	0.0261724	0.0043364	1.0E-09
2	EPHA4 *	rs9710851	221190516	A	G	0.2244040	0.0265068	0.0043527	9.0E-10
2	EPHA4 *	rs61625798	221190875	G	A	0.2253420	0.0263186	0.0043556	9.3E-10
2	EPHA4 *	rs55876238	221190919	T	C	0.2190190	0.0260532	0.0044291	2.8E-09
2	EPHA4 *	rs55780955	221190926	G	A	0.1973060	0.0300932	0.0045909	6.2E-11
2	EPHA4 *	rs74742117	221191144	A	G	0.2258480	0.0261983	0.0043366	9.9E-10
2	EPHA4 *	rs76414684	221191253	C	T	0.2258510	0.0262150	0.0043366	9.7E-10
2	EPHA4 *	rs80121272	221191270	G	A	0.2258500	0.0262061	0.0043366	9.8E-10
2	EPHA4 *	rs62188484	221191374	C	T	0.2258520	0.0262037	0.0043366	9.8E-10
2	EPHA4 *	rs62188485	221191608	G	A	0.2258530	0.0262003	0.0043366	9.8E-10
2	EPHA4 *	rs62188486	221192033	T	C	0.2258590	0.0261715	0.0043365	1.0E-09
2	EPHA4 *	rs62188487	221192132	T	G	0.2258610	0.0261742	0.0043365	1.0E-09
2	EPHA4 *	rs76568309	221192208	T	G	0.2258670	0.0261370	0.0043364	1.1E-09
2	EPHA4 *	rs62188488	221192705	A	G	0.2258820	0.0261397	0.0043362	1.1E-09
2	EPHA4 *	rs62188489	221192711	T	C	0.2258820	0.0261397	0.0043362	1.1E-09
2	EPHA4 *	rs35765026	221193452	G	GA	0.2264750	0.0258858	0.0043369	1.4E-09
2	EPHA4 *	rs60162613	221193985	A	G	0.2259090	0.0261176	0.0043358	1.1E-09
2	EPHA4 *	rs60249830	221194026	C	T	0.2259090	0.0261176	0.0043358	1.1E-09
2	EPHA4 *	rs59414472	221194072	G	A	0.2260060	0.0262087	0.0043345	9.6E-10
2	EPHA4 *	rs62188492	221194262	T	C	0.2016410	0.0296965	0.0045240	5.6E-11
2	EPHA4 *	rs62188493	221194522	G	A	0.2258420	0.0260989	0.0043365	1.1E-09
2	EPHA4 *	rs59120802	221194941	G	A	0.2260130	0.0262523	0.0043342	9.2E-10
2	EPHA4 *	rs60780837	221195337	A	C	0.2260160	0.0262387	0.0043341	9.2E-10
2	EPHA4 *	rs143652141	221195564	AT	A	0.2260180	0.0262778	0.0043340	8.6E-10
2	EPHA4 *	rs715023	221196466	T	C	0.2261020	0.0260015	0.0043328	1.2E-09
2	EPHA4 *	rs715021	221196620	G	C	0.2001110	0.0290157	0.0045383	1.8E-10
2	EPHA4 *	rs1368075	221196754	C	T	0.2261090	0.0259982	0.0043324	1.3E-09
2	EPHA4 *	rs1368074	221196755	A	G	0.2261090	0.0259982	0.0043324	1.3E-09
2	EPHA4 *	rs1368073	221197285	A	G	0.2257160	0.0256514	0.0043361	2.1E-09
2	EPHA4 *	rs1368072	221197396	G	A	0.2257630	0.0256859	0.0043354	2.0E-09
2	EPHA4 *	rs12471579	221197761	C	T	0.2262840	0.0259539	0.0043258	1.3E-09
2	EPHA4 *	rs55715942	221197846	A	C	0.2263240	0.0259199	0.0043253	1.3E-09
2	EPHA4 *	rs59024509	221197892	A	G	0.2263160	0.0259016	0.0043253	1.4E-09
2	EPHA4 *	rs12468078	221197919	A	C	0.2263330	0.0259585	0.0043250	1.2E-09
2	EPHA4 *	rs12468244	221198215	A	G	0.2266230	0.0259421	0.0043224	1.2E-09
2	EPHA4 *	rs60539959	221198341	G	A	0.2265300	0.0256629	0.0043215	1.9E-09
2	EPHA4 *	rs1368071	221198532	A	C	0.2263960	0.0259884	0.0043240	1.2E-09
2	EPHA4 *	rs1368070	221198763	A	G	0.2021050	0.0288952	0.0045142	1.7E-10
2	EPHA4 *	rs35441203	221199018	T	TAAAG	0.2005300	0.0286090	0.0045304	2.8E-10
2	EPHA4 *	rs12469320	221199110	T	C	0.2262510	0.0260145	0.0043281	1.2E-09
2	EPHA4 *	rs7597619	221199656	C	T	0.2262140	0.0259617	0.0043289	1.3E-09
2	EPHA4 *	rs62188499	221199895	A	G	0.2262010	0.0259630	0.0043293	1.4E-09
2	EPHA4 *	rs62188500	221200221	T	C	0.2256870	0.0262181	0.0043327	9.3E-10
2	EPHA4 *	rs16862240	221200456	T	A	0.2013080	0.0295140	0.0045245	6.9E-11
2	EPHA4 *	rs16862242	221200528	C	T	0.2228020	0.0258140	0.0043570	1.5E-09
2	EPHA4 *	rs4146100	221200719	A	T	0.2248830	0.0258601	0.0043464	1.1E-09
2	EPHA4 *	rs60681178	221201933	T	TG	0.2141750	0.0263137	0.0044708	2.2E-09
2	EPHA4 *	rs12477147	221202430	G	T	0.2031230	0.0292383	0.0045206	9.0E-11
2	EPHA4 *	rs1835810	221202588	C	T	0.2209210	0.0255793	0.0043880	2.4E-09
2	EPHA4 *	rs12465770	221202991	T	A	0.2189960	0.0247707	0.0044031	1.0E-08
2	EPHA4 *	rs12478119	221203020	C	T	0.2190900	0.0248897	0.0044035	8.4E-09
2	EPHA4 *	rs12473983	221203178	C	G	0.2189850	0.0247401	0.0044036	1.1E-08
2	EPHA4 *	rs7572235	221203882	G	A	0.2191420	0.0250503	0.0044047	7.6E-09
2	EPHA4 *	rs16862260	221205237	A	G	0.2022810	0.0291167	0.0045377	1.4E-10
3	UBE2E2	rs112130825	23579242	G	A	0.1349160	0.0289729	0.0053342	4.0E-08
3	UBE2E2	rs76435632	23590683	G	C	0.1311720	0.0296024	0.0054113	3.2E-08
3	ATXN7	rs2292662	63911539	T	C	0.3979230	-0.0200818	0.0037183	1.9E-08
3	ATXN7	rs6785040	63912239	C	T	0.3995890	-0.0200501	0.0037172	2.0E-08
3	ATXN7	rs6770864	63916953	A	G	0.3804490	-0.0199355	0.0037508	4.5E-08
3	ATXN7	rs59971314	63928942	C	G	0.4059710	-0.0194479	0.0037039	4.0E-08
3	ATXN7	rs7621544	63943005	A	C	0.4070620	-0.0193758	0.0037185	4.8E-08
3	ATXN7	rs9820538	63954833	T	C	0.4019430	-0.0203068	0.0037126	1.2E-08
3	ATXN7	rs28675788	63956512	G	C	0.4033820	-0.0201469	0.0037114	1.3E-08
3	ATXN7	rs3841968	63957270	C	CTG	0.4018800	-0.0203084	0.0037123	1.2E-08
3	ATXN7	rs73117082	63961889	G	A	0.4060930	-0.0200599	0.0037099	1.5E-08
3	ATXN7	rs13433909	63962933	G	C	0.4302570	-0.0195433	0.0036893	1.7E-08
3	ATXN7	rs62252368	63973789	T	C	0.3986050	-0.0208049	0.0037225	4.6E-09
3	ATXN7	rs3774723	63976663	A	G	0.4026100	-0.0205750	0.0037138	7.1E-09
3	ATXN7	rs3774725	63988582	G	T	0.4235300	-0.0188275	0.0036856	3.5E-08
3	ATXN7	rs73119018	63989652	G	A	0.3997560	-0.0196051	0.0037182	2.4E-08
3	MBNL1 *	rs6801043	152615955	A	C	0.4401190	0.0207808	0.0036723	2.2E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	MBNL1 *	rs6440817	152617544	G	A	0.4349150	0.0220053	0.0036774	2.4E-09
3	MBNL1 *	rs6771951	152617848	C	T	0.4407280	0.0208769	0.0036691	1.8E-08
3	MBNL1 *	rs6440819	152619437	C	T	0.4407270	0.0209150	0.0036691	1.7E-08
3	MBNL1 *	rs1878434	152622181	T	C	0.4404860	0.0209354	0.0036701	1.7E-08
3	MBNL1 *	rs1540782	152624256	T	C	0.4404980	0.0209293	0.0036700	1.7E-08
3	MBNL1 *	rs9829634	152624467	G	T	0.4404980	0.0209293	0.0036700	1.7E-08
3	MBNL1 *	rs7646639	152632650	T	A	0.4416260	0.0210707	0.0036679	1.4E-08
3	MBNL1 *	rs4679687	152633950	C	T	0.4416010	0.0211231	0.0036675	1.3E-08
3	MBNL1 *	rs13322285	152634199	G	C	0.4416010	0.0211231	0.0036675	1.3E-08
3	MBNL1 *	rs9289868	152634813	G	T	0.4417340	0.0213472	0.0036678	9.3E-09
3	MBNL1 *	rs6784979	152636111	C	A	0.4415930	0.0211544	0.0036674	1.2E-08
3	MBNL1 *	rs1400609	152639952	T	G	0.4426080	0.0211630	0.0036747	1.2E-08
3	MBNL1 *	rs1356363	152641122	A	C	0.4052100	0.0215190	0.0037422	1.6E-08
3	MBNL1 *	rs9810441	152645996	C	T	0.4095680	0.0217113	0.0037433	1.2E-08
3	MBNL1 *	rs9834087	152646057	T	C	0.4470250	0.0219884	0.0036988	4.4E-09
3	MBNL1 *	rs9852346	152646467	A	G	0.4470840	0.0218947	0.0036993	5.3E-09
3	MBNL1 *	rs4679990	152647232	C	T	0.4462230	0.0216959	0.0037186	8.3E-09
3	MBNL1 *	rs57108866	152647255	CG	C	0.4468410	0.0221047	0.0037232	4.6E-09
3	MBNL1 *	rs1517243	152648565	A	T	0.4227390	0.0235513	0.0037114	1.4E-10
3	P2RY1 *	rs4679993	152650538	A	T	0.2520300	0.0257610	0.0042054	7.2E-11
3	P2RY1 *	rs7616720	152651238	G	A	0.4235710	0.0236827	0.0036991	1.0E-10
3	P2RY1 *	rs7616658	152651331	C	T	0.2528880	0.0264850	0.0042037	2.0E-11
3	P2RY1 *	rs1400610	152651810	T	C	0.2521440	0.0260375	0.0041982	3.8E-11
3	P2RY1 *	rs5853598	152652342	C	CT	0.4243320	0.0239541	0.0036920	5.5E-11
3	P2RY1 *	rs6807032	152653185	G	A	0.2523220	0.0259511	0.0041914	3.9E-11
3	P2RY1 *	rs4679994	152654752	C	T	0.2530040	0.0257756	0.0041851	5.7E-11
3	P2RY1 *	rs4679995	152654874	G	A	0.4237360	0.0240868	0.0036872	4.1E-11
3	P2RY1 *	rs4679996	152655005	G	A	0.2527320	0.0259345	0.0041874	4.2E-11
3	P2RY1 *	rs1517237	152656202	T	C	0.4236260	0.0239386	0.0036903	5.9E-11
3	P2RY1 *	rs1878432	152657161	T	A	0.2528220	0.0260537	0.0041863	3.4E-11
3	P2RY1 *	rs1878433	152657396	C	T	0.4236060	0.0239429	0.0036908	5.3E-11
3	P2RY1 *	rs1983338	152657807	A	C	0.2521000	0.0256721	0.0041910	6.3E-11
3	P2RY1 *	rs1517238	152658181	C	T	0.2528020	0.0258442	0.0041873	4.9E-11
3	P2RY1 *	rs7624935	152659102	C	T	0.2522320	0.0257030	0.0041962	6.2E-11
3	P2RY1 *	rs7636794	152659183	T	C	0.4234850	0.0237522	0.0036936	8.7E-11
3	P2RY1 *	rs1400605	152659540	G	A	0.2526520	0.0259457	0.0041922	4.3E-11
3	P2RY1 *	rs1517239	152659745	C	A	0.2526380	0.0258913	0.0041924	4.7E-11
3	P2RY1 *	rs6806560	152660236	A	G	0.2642180	0.0221061	0.0041327	9.8E-09
3	P2RY1 *	rs35382438	152660298	G	GA	0.2526290	0.0260200	0.0041926	3.9E-11
3	P2RY1 *	rs2102803	152660524	T	C	0.2526230	0.0259454	0.0041927	4.5E-11
3	P2RY1 *	rs2090442	152660710	G	A	0.4236140	0.0237805	0.0036946	8.5E-11
3	P2RY1 *	rs2090443	152660841	T	C	0.2526290	0.0259564	0.0041927	4.4E-11
3	P2RY1 *	rs2090444	152660874	A	G	0.2526290	0.0259564	0.0041927	4.4E-11
3	P2RY1 *	rs11711787	152661497	G	C	0.1956890	0.0250274	0.0045855	9.2E-09
3	P2RY1 *	rs2063947	152661516	T	C	0.2526320	0.0258599	0.0041927	5.0E-11
3	P2RY1 *	rs12493783	152661657	G	T	0.1961020	0.0249960	0.0045830	9.7E-09
3	P2RY1 *	rs6764656	152661897	A	G	0.2537110	0.0263710	0.0041949	2.2E-11
3	P2RY1 *	rs4679688	152662197	A	T	0.4237200	0.0237982	0.0036933	7.8E-11
3	P2RY1 *	rs12629237	152663143	A	G	0.2528420	0.0259457	0.0041946	4.3E-11
3	P2RY1 *	rs1400606	152663503	A	T	0.2528260	0.0259277	0.0041948	4.5E-11
3	P2RY1 *	rs1400607	152663712	G	C	0.2528070	0.0259326	0.0041949	4.4E-11
3	P2RY1 *	rs28663084	152664398	G	A	0.4234520	0.0237700	0.0036973	7.8E-11
3	P2RY1 *	rs1850421	152664563	A	C	0.2528160	0.0256400	0.0041974	7.1E-11
3	P2RY1 *	rs12493136	152664664	A	G	0.1958980	0.0250402	0.0045877	9.2E-09
3	P2RY1 *	rs1517240	152664847	A	G	0.2527860	0.0259554	0.0041952	4.3E-11
3	P2RY1 *	rs76535037	152665208	TC	T	0.2527360	0.0260433	0.0041962	3.8E-11
3	P2RY1 *	rs1400608	152667243	T	C	0.4260170	0.0240839	0.0037099	4.2E-11
3	P2RY1 *	rs35226917	152667349	A	C	0.1955650	0.0250008	0.0045905	1.1E-08
3	P2RY1 *	rs13096682	152667615	T	C	0.1955730	0.0250414	0.0045907	1.0E-08
3	P2RY1 *	rs12234885	152668053	C	T	0.4234850	0.0236714	0.0036975	9.0E-11
3	P2RY1 *	rs9867073	152668322	T	A	0.4234880	0.0236728	0.0036975	8.9E-11
3	P2RY1 *	rs9873341	152669934	T	C	0.2523180	0.0259447	0.0041987	5.0E-11
3	P2RY1 *	rs9857732	152670265	C	T	0.4234650	0.0235935	0.0036974	9.8E-11
3	P2RY1 *	rs73158630	152670601	A	G	0.1955620	0.0250256	0.0045905	1.0E-08
3	P2RY1 *	rs4068585	152670944	AAACT	A	0.4231390	0.0237692	0.0036977	7.2E-11
3	P2RY1 *	rs36117395	152671815	T	A	0.1955600	0.0248826	0.0045904	1.2E-08
3	P2RY1 *	rs12695977	152671968	A	G	0.4245650	0.0237546	0.0036968	9.2E-11
3	P2RY1 *	rs140840929	152674760	G	GT	0.1928090	0.0255693	0.0046269	7.9E-09
3	P2RY1 *	rs9828639	152675088	T	G	0.4185670	0.0235171	0.0037031	1.4E-10
3	P2RY1 *	rs35005495	152675965	G	T	0.1951090	0.0250846	0.0045951	1.1E-08
3	P2RY1 *	rs35557389	152675991	C	T	0.1951090	0.0250846	0.0045951	1.1E-08
3	P2RY1 *	rs4679997	152678677	C	G	0.4185280	0.0234765	0.0037030	1.6E-10
3	P2RY1 *	rs2102804	152679715	G	A	0.4188970	0.0236725	0.0036963	9.2E-11
3	P2RY1 *	rs11293699	152681161	TG	T	0.3804530	0.0257870	0.0037435	3.3E-12
3	P2RY1 *	rs10935897	152681904	A	G	0.3804010	0.0257367	0.0037438	3.7E-12
3	P2RY1 *	rs67232345	152682077	G	T	0.1957610	0.0255163	0.0045806	5.9E-09
3	P2RY1 *	rs66465763	152682796	C	CA	0.3813350	0.0259883	0.0037453	2.3E-12
3	P2RY1 *	rs71623440	152682801	T	C	0.3843200	0.0267772	0.0037644	7.3E-13
3	P2RY1 *	rs1949384	152683166	T	C	0.3812680	0.0259617	0.0037454	2.4E-12
3	P2RY1 *	rs2102805	152683897	C	T	0.1960380	0.0254664	0.0045803	6.4E-09
3	P2RY1 *	rs2090446	152684776	C	T	0.3814060	0.0259152	0.0037449	2.7E-12
3	P2RY1 *	rs1949386	152684948	A	G	0.1962180	0.0256382	0.0045781	5.0E-09
3	P2RY1 *	rs1949385	152685236	C	G	0.1962160	0.0256616	0.0045781	4.9E-09
3	P2RY1 *	rs4679689	152686818	C	T	0.3811410	0.0258357	0.0037454	3.2E-12
3	P2RY1 *	rs9865555	152687313	C	T	0.3815200	0.0259475	0.0037457	2.4E-12
3	P2RY1 *	rs12495095	152687752	T	C	0.1965260	0.0255468	0.0045765	5.1E-09
3	P2RY1 *	rs9871360	152688452	G	A	0.3814060	0.0259152	0.0037449	2.7E-12
3	P2RY1 *	rs1914355	152688574	C	T	0.3812680	0.0259617	0.0037454	2.4E-12
3	P2RY1 *	rs1580255	152689478	G	A	0.3814060	0.0259152	0.0037449	2.7E-12
3	P2RY1 *	rs12491267	152690265	G	A	0.1962160	0.0256616	0.0045781	4.9E-09
3	P2RY1 *	rs35674198	152690534	C	T	0.1962540	0.0256549	0.0045785	4.9E-09
3	P2RY1 *	rs6769082	152691340	G	C	0.3812680	0.0259617	0.0037454	2.4E-12
3	P2RY1 *	rs35623862	152691468	C	CA	0.1965830	0.0259928	0.0045777	3.6E-09
3	P2RY1 *	rs2090445	152692207	A	T	0.3810720	0.0257698	0.0037465	3.7E-12
3	P2RY1 *	rs1841545	152692272	T	C	0.1962160	0.0256616	0.0045781	4.9E-09
3	P2RY1 *	rs9821863	152693137	C	A	0.3814060	0.0259152	0.0037449	2.7E-12
3	P2RY1 *	rs9859756	152693308	A	C	0.3816820	0.0258496	0.0037463	3.3E-12
3	P2RY1 *	rs143777617	152693435	A	C	0.1962160	0.0256616	0.0045781	4.9E-09
3	P2RY1 *	rs138815333	152693877	A	C	0.1963180	0.0256792	0.0045777	4.8E-09
3	P2RY1 *	rs9832904	152695195	G	A	0.3814060	0.0259152	0.0037449	2.7E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	P2RY1 *	rs13086507	152695513	C	G	0.1962140	0.0256454	0.0045781	5.0E-09
3	P2RY1 *	rs73158648	152696295	C	T	0.1962140	0.0256454	0.0045781	5.0E-09
3	P2RY1 *	rs9835403	152697392	T	C	0.3808050	0.0261391	0.0037460	1.7E-12
3	P2RY1 *	rs9816371	152697788	G	T	0.3811130	0.0258959	0.0037454	2.7E-12
3	P2RY1 *	rs1850422	152697840	T	A	0.3811990	0.0259070	0.0037457	2.6E-12
3	P2RY1 *	rs9826861	152699691	G	A	0.3805880	0.0261728	0.0037475	1.6E-12
3	P2RY1 *	rs140691790	152700541	T	C	0.1958370	0.0259407	0.0045828	3.4E-09
3	P2RY1 *	rs6763518	152701705	A	T	0.3804750	0.0260848	0.0037486	1.9E-12
3	P2RY1 *	rs11712631	152702373	T	G	0.3279490	0.0239551	0.0038813	8.7E-10
3	P2RY1 *	rs9848115	152703802	C	T	0.3804870	0.0259162	0.0037480	2.6E-12
3	P2RY1 *	rs34957473	152704217	C	T	0.3279730	0.0238090	0.0038804	1.0E-09
3	P2RY1 *	rs13065792	152704509	C	A	0.3279730	0.0238090	0.0038804	1.0E-09
3	P2RY1 *	rs1517246	152705469	T	C	0.3811650	0.0257516	0.0037476	3.5E-12
3	P2RY1 *	rs1870720	152706028	G	A	0.3804870	0.0259162	0.0037480	2.6E-12
3	P2RY1 *	rs2063948	152706365	A	C	0.3810880	0.0256921	0.0037469	3.9E-12
3	P2RY1 *	rs6762709	152706925	A	G	0.3804870	0.0259162	0.0037480	2.6E-12
3	P2RY1 *	rs17383287	152707769	C	G	0.3279730	0.0238090	0.0038804	1.0E-09
3	P2RY1 *	rs13434372	152708192	A	G	0.3811650	0.0257535	0.0037474	3.5E-12
3	P2RY1 *	rs17442668	152708261	T	C	0.3279730	0.0238090	0.0038804	1.0E-09
3	P2RY1 *	rs554546698	152708483	TTTG	T	0.3278160	0.0239663	0.0038858	8.1E-10
3	P2RY1 *	rs55840739	152709477	A	C	0.3297530	0.0233693	0.0039364	2.6E-09
3	P2RY1 *	rs4680000	152709481	A	C	0.3927120	0.0253769	0.0037888	8.1E-12
3	P2RY1 *	rs34916564	152712107	A	AC	0.3275830	0.0239480	0.0038840	9.3E-10
3	P2RY1 *	rs34928986	152712661	A	T	0.1958890	0.0257916	0.0045821	4.0E-09
3	P2RY1 *	rs34561239	152712817	G	A	0.3279700	0.0238121	0.0038804	1.0E-09
3	P2RY1 *	rs13083426	152712994	C	G	0.3279430	0.0237941	0.0038806	1.1E-09
3	P2RY1 *	rs13088123	152713514	G	A	0.3279700	0.0238121	0.0038804	1.0E-09
3	P2RY1 *	rs1850424	152713579	G	T	0.3810860	0.0256956	0.0037469	3.9E-12
3	P2RY1 *	rs13088939	152713659	A	G	0.3279700	0.0238121	0.0038804	1.0E-09
3	P2RY1 *	rs1850423	152713737	C	A	0.3810860	0.0256956	0.0037469	3.9E-12
3	P2RY1 *	rs9877505	152714253	C	T	0.3805740	0.0258355	0.0037478	3.1E-12
3	P2RY1 *	rs34124563	152714723	C	T	0.3277590	0.0232992	0.0038882	2.4E-09
3	P2RY1 *	rs35497231	152715839	C	T	0.3804350	0.0255498	0.0037580	5.1E-12
3	P2RY1 *	rs12054173	152716925	T	A	0.3276110	0.0229918	0.0038918	3.6E-09
3	P2RY1 *	rs6764808	152719717	C	T	0.3813430	0.0253003	0.0037625	8.6E-12
3	P2RY1 *	rs13061814	152721251	A	G	0.3233570	0.0236045	0.0039155	2.1E-09
3	P2RY1 *	rs17442878	152721487	T	C	0.1882870	0.0247766	0.0046496	2.3E-08
3	P2RY1 *	rs9289869	152723823	C	T	0.3853090	0.0250084	0.0037521	1.6E-11
3	P2RY1 *	rs879284735	152728942	TTCCC	T	0.1875000	0.0284121	0.0047364	5.6E-10
3	P2RY1 *	rs140875340	152730986	A	ATAAAT	0.3286670	0.0225208	0.0039008	8.6E-09
3	P2RY1 *	rs2138712	152732055	G	A	0.1891810	0.0250930	0.0046378	1.3E-08
3	P2RY1 *	rs4680003	152733616	A	G	0.3856950	0.0251069	0.0037507	1.3E-11
3	P2RY1 *	rs12495424	152733943	C	T	0.3304830	0.0228495	0.0038837	4.4E-09
3	P2RY1 *	rs12488256	152736938	G	A	0.3305300	0.0227756	0.0038835	4.8E-09
3	P2RY1 *	rs1461163	152737746	G	A	0.3855730	0.0248857	0.0037496	1.9E-11
3	P2RY1 *	chr3:152737927_GT_G	152737927	GT	G	0.4043290	0.0240612	0.0037636	8.1E-11
3	P2RY1 *	rs34988051	152738565	C	T	0.3305320	0.0228018	0.0038833	4.7E-09
3	P2RY1 *	rs67024100	152739567	A	T	0.3292090	0.0224226	0.0038949	1.1E-08
3	P2RY1 *	rs1599397	152743291	A	T	0.3855680	0.0249013	0.0037496	1.9E-11
3	P2RY1 *	rs66887097	152744778	AG	A	0.3858240	0.0248449	0.0037518	2.1E-11
3	P2RY1 *	rs10433453	152750214	G	T	0.3289770	0.0233300	0.0038990	2.3E-09
3	P2RY1 *	rs10433454	152750217	C	T	0.3299100	0.0229054	0.0038911	4.2E-09
3	P2RY1 *	rs9849407	152751658	A	C	0.2814360	0.0262336	0.0040580	2.0E-11
3	P2RY1 *	rs34319570	152754942	C	T	0.2264110	0.0256189	0.0043604	1.7E-09
3	P2RY1 *	rs7426738	152755029	C	G	0.2817390	0.0261991	0.0040572	2.0E-11
3	P2RY1 *	rs747934920	152758304	C	CTA	0.2790130	0.0262236	0.0040861	2.0E-11
3	P2RY1 *	rs68129846	152758368	A	G	0.2258970	0.0256081	0.0043688	1.8E-09
3	P2RY1 *	rs13095565	152762123	T	C	0.2259450	0.0257212	0.0043703	1.4E-09
3	P2RY1 *	rs12491993	152764056	T	C	0.2255600	0.0256811	0.0043814	1.6E-09
3	P2RY1 *	rs10935899	152767339	G	C	0.2258180	0.0260356	0.0043882	1.1E-09
3	P2RY1 *	rs9289871	152768063	C	T	0.2803220	0.0270595	0.0040881	6.3E-12
3	P2RY1 *	rs9289872	152768161	A	T	0.2803540	0.0270307	0.0040885	6.6E-12
3	P2RY1 *	rs6769849	152769399	A	G	0.2802280	0.0270791	0.0040933	6.7E-12
3	P2RY1 *	rs9875837	152770251	T	C	0.2806120	0.0269295	0.0040974	9.3E-12
3	P2RY1 *	rs12163601	152770328	T	C	0.2245920	0.0264039	0.0044074	7.6E-10
3	P2RY1 *	rs71623443	152771031	C	T	0.2223180	0.0269965	0.0044391	6.3E-10
3	P2RY1 *	rs200002828	152773991	VGACTAT	G	0.2275090	0.0268031	0.0044063	5.2E-10
3	P2RY1 *	rs202227173	152773993	AGAC	A	0.2241800	0.0273364	0.0044371	3.2E-10
3	P2RY1 *	rs759933288	152773994	ATATAGA	T	0.2241800	0.0273364	0.0044371	3.2E-10
3	P2RY1 *	rs370093430	152773996	A	T	0.2241800	0.0273364	0.0044371	3.2E-10
3	P2RY1 *	rs9289874	152774038	A	G	0.2827420	0.0270613	0.0041044	1.1E-11
3	P2RY1 *	rs9289875	152775950	A	T	0.2832980	0.0261464	0.0041128	7.7E-11
3	P2RY1 *	rs34745742	152777479	TTTC	T	0.2791640	0.0253628	0.0041351	3.8E-10
3	P2RY1 *	rs7634426	152783535	A	G	0.2302960	0.0260896	0.0043885	1.8E-09
3	P2RY1 *	rs35907264	152783736	C	T	0.2646310	0.0257039	0.0041970	4.8E-10
3	P2RY1 *	rs4679692	152783937	C	T	0.2646270	0.0257224	0.0041970	4.6E-10
3	P2RY1 *	rs9838641	152786776	G	A	0.2645940	0.0256155	0.0041973	5.4E-10
3	P2RY1 *	rs9825291	152787516	C	T	0.2645690	0.0255499	0.0041975	6.0E-10
3	P2RY1 *	rs1439012	152788352	C	A	0.2645590	0.0254863	0.0041979	6.6E-10
3	P2RY1 *	rs1439011	152788469	T	C	0.2481170	0.0265616	0.0042938	3.5E-10
3	P2RY1 *	rs1978867	152789234	T	C	0.2481740	0.0265545	0.0042941	3.5E-10
3	P2RY1 *	rs67800734	152796749	G	A	0.2345420	0.0236326	0.0043557	2.7E-08
3	P2RY1 *	rs67541322	152797059	A	G	0.2409720	0.0231401	0.0043131	3.4E-08
3	P2RY1 *	rs73158684	152797078	A	C	0.2399750	0.0231967	0.0043227	3.7E-08
3	P2RY1 *	rs56146608	152797960	T	A	0.2369290	0.0238701	0.0043262	2.0E-08
3	P2RY1 *	rs6773552	152798073	A	G	0.2581150	0.0223624	0.0042011	4.8E-08
3	P2RY1 *	rs73158690	152801810	A	C	0.2337270	0.0232668	0.0043015	3.3E-08
3	P2RY1 *	rs113146019	152802277	T	C	0.2335910	0.0231956	0.0043017	3.8E-08
3	P2RY1 *	rs73158696	152805695	C	T	0.2340390	0.0230370	0.0042916	4.1E-08
3	RPL22L1 *	rs13082738	170831189	T	C	0.1730870	-0.0299215	0.0048647	4.5E-10
3	RPL22L1 *	rs34747729	170831309	G	GC	0.1730820	-0.0300518	0.0048626	3.5E-10
3	RPL22L1 *	rs7641088	170832221	A	C	0.1742370	-0.0293044	0.0048373	5.9E-10
3	RPL22L1 *	rs73167704	170838212	C	T	0.1767940	-0.0277533	0.0048241	4.1E-09
3	RPL22L1 *	rs13100528	170839793	T	G	0.1763070	-0.0285912	0.0047936	1.3E-09
3	RPL22L1 *	rs35375820	170841913	C	A	0.1763720	-0.0285625	0.0047926	1.3E-09
3	RPL22L1 *	rs57740581	170842649	G	T	0.1765500	-0.0286828	0.0047909	1.1E-09
3	RPL22L1 *	rs12495896	170844118	T	C	0.1763880	-0.0285404	0.0047920	1.3E-09
3	RPL22L1 *	rs35160042	170845888	A	G	0.1763940	-0.0285499	0.0047919	1.3E-09
3	RPL22L1 *	rs3924867	170846532	T	C	0.1760470	-0.0285369	0.0047976	1.5E-09
3	RPL22L1 *	rs3924868	170846642	A	T	0.1764460	-0.0286199	0.0047910	1.1E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	RPL22L1 *	chr3:170847286_A_AC	170847286	AC	A	0.1747790	-0.0290049	0.0048162	8.4E-10
3	RPL22L1 *	rs6797610	170848219	G	A	0.1764170	-0.0286374	0.0047919	1.2E-09
3	RPL22L1 *	rs6788056	170848843	T	C	0.1764170	-0.0286096	0.0047918	1.2E-09
3	RPL22L1 *	rs12485707	170852790	A	G	0.1772610	-0.0283263	0.0047729	1.7E-09
3	RPL22L1 *	rs13063927	170865099	T	C	0.3839410	-0.0205161	0.0037333	3.3E-08
3	RPL22L1	rs35192046	170866275	C	A	0.3839560	-0.0205674	0.0037320	3.0E-08
3	RPL22L1	rs35683888	170866285	G	A	0.3839620	-0.0205986	0.0037320	2.8E-08
3	RPL22L1	rs3821747	170867828	G	A	0.3840800	-0.0206273	0.0037309	2.8E-08
3	RPL22L1	rs13098713	170869072	G	A	0.1762970	-0.0269168	0.0048050	1.1E-08
3	RPL22L1 *	rs12486780	170871515	C	A	0.1789600	-0.0286948	0.0047407	7.5E-10
3	EIF5A2	rs34539321	170892464	A	G	0.1782760	-0.0284140	0.0047556	1.1E-09
3	EIF5A2	rs35555642	170906108	A	G	0.1778520	-0.0285020	0.0047491	9.6E-10
3	EIF5A2 *	rs13073970	170912731	T	G	0.1989280	-0.0317713	0.0045647	1.2E-12
3	EIF5A2 *	rs61793002	170915454	G	A	0.1988690	-0.0318677	0.0045633	8.8E-13
3	EIF5A2 *	rs68055107	170915630	C	T	0.1984970	-0.0317064	0.0045688	1.2E-12
3	EIF5A2 *	rs189068021	170917444	C	T	0.1896380	-0.0308472	0.0047151	2.4E-11
3	EIF5A2 *	rs35980980	170919440	T	C	0.1985430	-0.0321079	0.0045677	6.0E-13
3	EIF5A2 *	rs6772274	170919875	T	C	0.1990050	-0.0319805	0.0045608	7.4E-13
3	EIF5A2 *	rs35851757	170921919	A	C	0.1990500	-0.0320778	0.0045601	6.3E-13
3	EIF5A2 *	rs34990433	170922222	A	T	0.1988390	-0.0324647	0.0045635	3.4E-13
3	EIF5A2 *	rs13059186	170922480	T	C	0.1990490	-0.0321137	0.0045601	6.0E-13
3	EIF5A2 *	rs9754921	170923555	T	C	0.1975100	-0.0318087	0.0045782	1.3E-12
3	EIF5A2 *	rs75741684	170923731	A	G	0.1943020	-0.0308772	0.0046229	8.5E-12
3	EIF5A2 *	rs75179537	170924995	C	G	0.1991940	-0.0321008	0.0045577	5.6E-13
3	EIF5A2 *	rs78500094	170928234	T	C	0.1992940	-0.0322426	0.0045557	4.7E-13
3	EIF5A2 *	rs35068538	170930719	T	C	0.1994680	-0.0321908	0.0045519	4.7E-13
3	EIF5A2 *	rs2086801	170938969	G	A	0.1994870	-0.0323094	0.0045526	3.9E-13
3	EIF5A2 *	chr3:170943881_C_CAT	170943881	CAT	C	0.1976930	-0.0326412	0.0045814	4.8E-13
3	EIF5A2 *	rs34611289	170945085	G	A	0.1994700	-0.0324152	0.0045513	3.4E-13
3	EIF5A2 *	rs71306686	170948310	T	C	0.1995610	-0.0324289	0.0045492	3.3E-13
3	SLC2A2 *	rs7642480	170953520	G	T	0.1994650	-0.0325640	0.0045524	2.6E-13
3	SLC2A2 *	rs7644261	170958345	G	C	0.2638600	-0.0229528	0.0041285	2.2E-08
3	SLC2A2 *	rs9875793	170968784	G	A	0.2057480	-0.0321802	0.0045004	2.4E-13
3	SLC2A2 *	rs1905505	170977637	A	G	0.2414820	-0.0272054	0.0042516	1.2E-10
3	SLC2A2 *	rs10653660	170978258	TGAA	T	0.2403400	-0.0272950	0.0042557	1.1E-10
3	SLC2A2 *	rs6771575	170981351	G	A	0.2058610	-0.0322486	0.0044992	2.2E-13
3	SLC2A2 *	rs9829457	170982937	C	T	0.2056590	-0.0321047	0.0045015	3.0E-13
3	SLC2A2 *	rs1514895	170987904	G	A	0.2381580	-0.0264525	0.0042742	4.7E-10
3	SLC2A2 *	rs12696316	170989993	C	G	0.2062120	-0.0319067	0.0044905	3.4E-13
3	SLC2A2 *	rs1604038	170991404	T	C	0.2406770	-0.0270887	0.0042487	1.4E-10
3	SLC2A2 *	rs9845527	170992657	T	A	0.2062090	-0.0319108	0.0044905	3.4E-13
3	SLC2A2 *	rs7630490	170993925	T	C	0.2039910	-0.0306256	0.0045342	5.5E-12
3	SLC2A2	rs5398	170998041	A	G	0.2373030	-0.0275821	0.0042734	6.2E-11
3	SLC2A2	rs1499821	171006940	T	C	0.1990310	-0.0312206	0.0045518	2.2E-12
3	SLC2A2	rs8192675	171007094	C	T	0.2324350	-0.0267259	0.0042978	3.3E-10
3	SLC2A2	rs1879442	171009562	A	G	0.2371030	-0.0277524	0.0042720	5.4E-11
3	SLC2A2	rs28720688	171011340	G	A	0.2031210	-0.0321142	0.0045207	3.6E-13
3	SLC2A2	rs7356034	171014810	A	G	0.2061570	-0.0324610	0.0045014	1.7E-13
3	SLC2A2	rs9873618	171015287	A	G	0.2061140	-0.0325842	0.0045015	1.4E-13
3	SLC2A2	rs61791109	171016588	C	T	0.2338720	-0.0266307	0.0043139	3.8E-10
3	SLC2A2	rs73169730	171016649	G	A	0.2349860	-0.0275421	0.0043041	1.0E-10
3	SLC2A2	rs67481408	171016654	TA	T	0.2051990	-0.0324606	0.0045205	2.5E-13
3	SLC2A2	rs6791781	171016845	G	A	0.1995690	-0.0332237	0.0045971	2.0E-13
3	SLC2A2	rs11924032	171017310	A	G	0.2051270	-0.0327527	0.0045200	1.4E-13
3	SLC2A2	rs3774046	171019214	G	A	0.2010370	-0.0321505	0.0045572	5.8E-13
3	SLC2A2	rs2129019	171025262	A	C	0.2336900	-0.0271016	0.0043454	1.7E-10
3	SLC2A2	rs3081362	171025352	ATAT	A	0.2365840	-0.0277104	0.0043170	6.1E-11
3	SLC2A2	rs9828378	171026283	G	C	0.2021290	-0.0317489	0.0045505	8.5E-13
3	SLC2A2 *	rs5396	171027026	C	T	0.2358630	-0.0285509	0.0043156	1.5E-11
3	SLC2A2 *	rs9837316	171033108	T	G	0.2000490	-0.0312680	0.0045682	1.4E-12
3	SLC2A2 *	rs9841632	171039545	A	C	0.1979860	-0.0316637	0.0046039	1.3E-12
3	SEN2	rs111307985	185591035	A	G	0.2322770	0.0249491	0.0043140	3.1E-09
3	SEN2	rs113473966	185591044	G	A	0.2322770	0.0249491	0.0043140	3.1E-09
3	SEN2	rs74705076	185591597	C	T	0.2322770	0.0249491	0.0043140	3.1E-09
3	SEN2	rs78433671	185595239	G	A	0.2322600	0.0249400	0.0043142	3.2E-09
3	SEN2	rs74211200	185595990	A	G	0.2322600	0.0249400	0.0043142	3.2E-09
3	SEN2	rs77975449	185596176	T	C	0.2322600	0.0249400	0.0043142	3.2E-09
3	SEN2	rs6795633	185597957	A	G	0.2322510	0.0249273	0.0043142	3.2E-09
3	SEN2	rs74466592	185598335	A	G	0.2322510	0.0249273	0.0043142	3.2E-09
3	SEN2	rs75457670	185598768	C	T	0.2322490	0.0249053	0.0043143	3.4E-09
3	SEN2	rs12374078	185600011	A	G	0.2314940	0.0249097	0.0043236	3.6E-09
3	SEN2	rs76990827	185601066	C	T	0.2324180	0.0248978	0.0043143	3.3E-09
3	SEN2	rs1464580	185601742	G	A	0.2307290	0.0249767	0.0043306	3.0E-09
3	SEN2	rs59082903	185603158	T	C	0.2313860	0.0252510	0.0043236	2.2E-09
3	SEN2	rs4687523	185607502	C	G	0.2310070	0.0247177	0.0043265	5.2E-09
3	SEN2	rs60397567	185608280	T	TC	0.2322280	0.0248970	0.0043145	3.4E-09
3	SEN2	rs78506856	185611364	G	GTT	0.2322140	0.0249239	0.0043143	3.3E-09
3	SEN2	rs76010631	185611485	G	A	0.2322140	0.0249239	0.0043143	3.3E-09
3	SEN2	rs74430300	185612268	A	G	0.2322080	0.0249735	0.0043144	3.1E-09
3	SEN2	rs80164709	185613991	A	G	0.2321900	0.0248617	0.0043146	3.7E-09
3	SEN2	rs4686688	185614889	C	G	0.2321850	0.0249201	0.0043146	3.4E-09
3	SEN2	rs56856415	185615406	T	C	0.2322980	0.0250094	0.0043157	2.9E-09
3	SEN2	rs79179434	185617267	G	A	0.2318840	0.0252020	0.0043184	2.2E-09
3	SEN2	rs113404329	185617374	G	GT	0.2318840	0.0252020	0.0043184	2.2E-09
3	SEN2	rs4267671	185620209	G	T	0.2318590	0.0251455	0.0043192	2.5E-09
3	SEN2	rs75374456	185622684	T	C	0.2318230	0.0251444	0.0043197	2.5E-09
3	SEN2	rs585069	185624199	C	CT	0.2318080	0.0251517	0.0043201	2.5E-09
3	IGF2BP2 *	rs9857968	185638205	T	C	0.2013760	0.0257294	0.0046068	5.4E-09
3	IGF2BP2 *	rs9878208	185638388	G	T	0.2027840	0.0257996	0.0045948	5.1E-09
3	IGF2BP2 *	rs10575325	185638639	C	CTGAG	0.2020660	0.0255477	0.0045967	6.4E-09
3	IGF2BP2 *	rs9821085	185638828	G	A	0.2029420	0.0258936	0.0046026	3.9E-09
3	IGF2BP2 *	rs9863611	185639367	T	C	0.2007500	0.0261973	0.0046189	3.2E-09
3	IGF2BP2 *	rs9826022	185639472	G	A	0.2019200	0.0264764	0.0046175	2.4E-09
3	IGF2BP2 *	rs9863780	185639512	T	C	0.2022190	0.0263035	0.0046131	2.6E-09
3	IGF2BP2 *	rs111604263	185641791	C	T	0.2125990	0.0252160	0.0045360	8.2E-09
3	IGF2BP2 *	rs75579635	185641894	T	G	0.2111460	0.0253194	0.0045467	8.6E-09
3	IGF2BP2 *	rs13327041	185642309	T	C	0.2012960	0.0274020	0.0046227	7.1E-10
3	IGF2BP2	rs13092876	185777532	A	G	0.2484870	0.0303221	0.0042272	1.4E-13
3	IGF2BP2	rs11706322	185779505	T	C	0.1594940	0.0288463	0.0049712	6.2E-09
3	IGF2BP2	rs5855072	185779764	TA	T	0.2498040	0.0307529	0.0042107	4.6E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
3	IGF2BP2	rs4376068	185779847	C	A	0.2387990	0.0317989	0.0042752	1.9E-14
3	IGF2BP2	rs6801848	185781269	G	C	0.2271080	0.0319589	0.0043496	4.6E-14
3	IGF2BP2	rs6780171	185785668	A	T	0.2240060	0.0302235	0.0043971	1.1E-12
3	IGF2BP2	rs115483294	185786085	A	T	0.1596710	0.0286845	0.0049669	7.3E-09
3	IGF2BP2	chr3:185787732_CA_C	185787732	C	CA	0.2437800	0.0318216	0.0042568	1.1E-14
3	IGF2BP2	rs4481184	185787999	T	C	0.2408010	0.0316901	0.0042519	1.4E-14
3	IGF2BP2	rs9841201	185788196	A	G	0.2517910	0.0307817	0.0041852	2.7E-14
3	IGF2BP2	rs11716491	185788215	C	T	0.1615560	0.0286455	0.0049360	5.7E-09
3	IGF2BP2	rs73061075	185788613	C	A	0.1615560	0.0286455	0.0049360	5.7E-09
3	IGF2BP2	rs4389513	185789069	G	T	0.2517890	0.0307695	0.0041852	2.7E-14
3	IGF2BP2	rs4414887	185789104	T	C	0.2406530	0.0318351	0.0042501	1.0E-14
3	IGF2BP2	rs4490396	185789145	A	T	0.1615560	0.0286455	0.0049360	5.7E-09
3	IGF2BP2	rs11705729	185789511	T	A	0.2517940	0.0307226	0.0041851	3.0E-14
3	IGF2BP2	rs6765808	185790241	T	C	0.2517940	0.0307226	0.0041851	3.0E-14
3	IGF2BP2	rs11927381	185790803	C	T	0.2518320	0.0306860	0.0041851	3.2E-14
3	IGF2BP2	rs7619401	185792218	A	G	0.2406590	0.0317854	0.0042500	1.1E-14
3	IGF2BP2	rs11925294	185792330	T	C	0.1615570	0.0286251	0.0049360	5.8E-09
3	IGF2BP2	rs11929397	185792402	C	T	0.2406590	0.0317854	0.0042500	1.1E-14
3	IGF2BP2	rs11925455	185792624	A	G	0.1615570	0.0286251	0.0049360	5.8E-09
3	IGF2BP2	rs7633675	185792825	G	T	0.2518010	0.0306681	0.0041849	3.2E-14
3	IGF2BP2	rs16860334	185793096	C	A	0.1724360	0.0282666	0.0048094	2.5E-09
3	IGF2BP2	rs4402960	185793899	T	G	0.2407070	0.0318924	0.0042501	9.2E-15
3	IGF2BP2	rs16860235	185794573	A	G	0.1609970	0.0282899	0.0049992	7.8E-09
3	IGF2BP2	rs35909974	185795291	T	C	0.1724030	0.0282078	0.0048106	2.8E-09
3	IGF2BP2	rs7640539	185795508	A	T	0.2406930	0.0317987	0.0042496	1.2E-14
3	IGF2BP2	rs7651090	185795604	G	A	0.2407070	0.0318671	0.0042494	1.0E-14
3	IGF2BP2	rs7631557	185795858	C	G	0.2406930	0.0317987	0.0042496	1.2E-14
3	IGF2BP2	rs9808924	185796401	A	G	0.2512450	0.0305296	0.0041907	4.3E-14
3	IGF2BP2	rs6786649	185796435	A	C	0.2406930	0.0317987	0.0042496	1.2E-14
3	IGF2BP2	rs6444081	185796605	C	T	0.2407780	0.0316017	0.0042502	1.6E-14
3	IGF2BP2	rs7646518	185797143	C	T	0.2409970	0.0318564	0.0042500	1.1E-14
3	IGF2BP2	rs11716713	185797822	C	G	0.2398050	0.0318606	0.0042579	1.2E-14
3	IGF2BP2	rs7637773	185797847	A	G	0.2401420	0.0316309	0.0042550	1.7E-14
3	IGF2BP2	rs4686696	185798732	A	G	0.2406960	0.0317692	0.0042495	1.2E-14
3	IGF2BP2	rs4686697	185798795	T	C	0.2434510	0.0316679	0.0042614	2.1E-14
3	IGF2BP2	rs73061095	185799019	G	T	0.2516720	0.0305253	0.0041864	4.3E-14
3	IGF2BP2	rs11928319	185800453	C	G	0.2398520	0.0317607	0.0042597	1.6E-14
3	IGF2BP2	rs372943686	185800711	CCA	C	0.1618040	0.0287785	0.0049372	4.9E-09
3	IGF2BP2	rs34122893	185800713	AC	A	0.1591980	0.0276800	0.0049765	2.9E-08
3	IGF2BP2	rs73061097	185800743	A	T	0.1791020	0.0272000	0.0047620	8.0E-09
3	IGF2BP2	rs35510946	185801122	A	G	0.2384780	0.0318024	0.0042636	1.4E-14
3	IGF2BP2	rs76922886	185801133	A	G	0.2384780	0.0318024	0.0042636	1.4E-14
3	IGF2BP2	rs71320321	185801319	A	G	0.2385280	0.0317753	0.0042638	1.5E-14
3	IGF2BP2	rs7633811	185802060	G	C	0.2384830	0.0317910	0.0042636	1.5E-14
3	IGF2BP2	rs10544430	185802234	T	TAG	0.2384830	0.0317910	0.0042636	1.5E-14
3	IGF2BP2	rs11269661	185802297	GACTAAT	G	0.2369370	0.0321686	0.0042773	9.5E-15
3	IGF2BP2	rs10428126	185802554	C	T	0.2384830	0.0317910	0.0042636	1.5E-14
3	IGF2BP2	rs6767484	185802790	G	A	0.2385080	0.0317214	0.0042634	1.7E-14
3	IGF2BP2	rs6767577	185802944	C	A	0.1594480	0.0286860	0.0049619	6.8E-09
3	IGF2BP2	rs9854769	185803160	G	A	0.2498750	0.0308439	0.0041996	3.4E-14
3	IGF2BP2	rs34782298	185803208	A	G	0.2387300	0.0318923	0.0042656	1.4E-14
3	IGF2BP2	rs7615045	185803338	G	A	0.2498770	0.0308505	0.0041996	3.3E-14
3	IGF2BP2	rs71164544	185804436	CA	C	0.2309360	0.0310795	0.0043405	1.5E-13
3	IGF2BP2	rs7640744	185804659	A	G	0.1704020	0.0283967	0.0048329	2.6E-09
3	IGF2BP2	rs66513933	185805582	C	T	0.1703090	0.0282081	0.0048335	3.3E-09
3	IGF2BP2	rs7646519	185806065	A	G	0.2496110	0.0306810	0.0041974	4.1E-14
3	IGF2BP2	rs4686392	185806293	G	A	0.2383860	0.0305158	0.0042638	1.9E-13
3	IGF2BP2	rs13060777	185807411	G	A	0.1594890	0.0287663	0.0049618	6.2E-09
3	IGF2BP2	rs7630554	185808274	G	A	0.2496220	0.0306432	0.0041976	4.4E-14
3	IGF2BP2	chr3:185808320_CA_C	185808320	C	CA	0.2488130	0.0304798	0.0042067	6.5E-14
3	IGF2BP2	rs73063004	185808557	T	C	0.2496220	0.0306432	0.0041976	4.4E-14
3	IGF2BP2	rs11711477	185808902	A	T	0.2496240	0.0306487	0.0041976	4.4E-14
3	IGF2BP2	rs4453875	185809107	C	T	0.1705950	0.0269985	0.0048264	1.8E-08
3	IGF2BP2	rs1470579	185811292	C	A	0.2496990	0.0306035	0.0041967	4.6E-14
3	IGF2BP2	rs1470580	185811386	A	T	0.2496740	0.0305675	0.0041968	4.8E-14
3	IGF2BP2	rs1470581	185811539	G	A	0.1707120	0.0268889	0.0048257	2.0E-08
3	IGF2BP2	rs9852647	185811841	G	T	0.1663050	0.0267821	0.0048985	2.8E-08
3	IGF2BP2	rs71164546	185811865	T	TCTCTCT	0.1530660	0.0283271	0.0050747	1.6E-08
3	IGF2BP2	rs6769511	185812502	C	T	0.2496880	0.0307134	0.0041967	3.9E-14
3	IGF2BP2	rs9837654	185812534	A	G	0.1706310	0.0269218	0.0048254	2.0E-08
3	IGF2BP2	rs9859406	185816694	A	G	0.2495470	0.0304524	0.0041998	5.8E-14
3	IGF2BP2	rs6444082	185818435	T	G	0.2373750	0.0305471	0.0042705	1.8E-13
3	IGF2BP2	chr3:185819848_G_GT	185819848	GT	G	0.2503900	0.0302396	0.0041979	8.7E-14
3	IGF2BP2	rs73063010	185820218	G	A	0.1707140	0.0268451	0.0048281	2.4E-08
3	IGF2BP2	rs11717959	185823425	T	G	0.1591260	0.0278463	0.0049703	2.1E-08
3	IGF2BP2 *	rs11705701	185826521	A	G	0.2199480	0.0294642	0.0044333	3.5E-12
3	IGF2BP2 *	rs6444083	185827902	G	C	0.1844830	0.0259008	0.0046968	3.2E-08
3	IGF2BP2 *	rs6808882	185828792	A	T	0.2527430	0.0299517	0.0042456	5.9E-13
3	IGF2BP2 *	rs6444084	185829531	G	A	0.1845320	0.0261506	0.0046980	2.3E-08
3	IGF2BP2 *	rs764129	185830129	T	C	0.2582760	0.0297650	0.0041887	2.1E-13
3	IGF2BP2 *	rs720389	185830874	C	T	0.1847650	0.0261146	0.0046938	2.1E-08
3	IGF2BP2 *	rs720390	185830895	A	G	0.1687190	0.0279111	0.0048536	9.2E-09
3	IGF2BP2 *	rs62289131	185835858	G	A	0.2143020	0.0254429	0.0045361	6.1E-09
3	IGF2BP2 *	rs9866563	185835971	A	C	0.2132380	0.0251160	0.0045035	1.1E-08
3	IGF2BP2 *	rs9832166	185841644	C	T	0.2142890	0.0246213	0.0044838	2.2E-08
4	RNF212 *	rs12506595	1125616	A	G	0.1463150	-0.0352198	0.0052384	2.6E-11
4	RNF212 *	rs75307101	1136415	A	T	0.1462010	-0.0352771	0.0052400	2.4E-11
4	SPON2	rs872894	1195420	T	C	0.1661930	-0.0361988	0.0049489	2.1E-13
4	LOC100130872, SPON2	rs4974570	1202805	T	C	0.1647170	-0.0358784	0.0049658	4.3E-13
4	SPON2 *	rs1680068	1209371	T	C	0.2173380	-0.0286246	0.0044467	2.2E-10
4	SPON2 *	rs1732127	1209372	G	A	0.2181020	-0.0283908	0.0044435	2.7E-10
4	SPON2 *	rs900024	1209760	C	T	0.2180880	-0.0287613	0.0044384	1.3E-10
4	CTBP1, CTBP1-AS	rs11247979	1213729	T	C	0.2178930	-0.0279736	0.0044275	3.9E-10
4	CTBP1, CTBP1-AS	rs2306475	1214093	C	T	0.4550280	0.0233828	0.0036712	1.4E-10
4	CTBP1, CTBP1-AS	rs1265923	1215386	C	T	0.2179560	-0.0281924	0.0044197	2.7E-10
4	CTBP1	rs1250090	1219909	T	C	0.2195590	-0.0285082	0.0044111	1.7E-10
4	CTBP1	rs1250089	1220699	C	T	0.4548000	0.0234652	0.0036693	1.1E-10
4	CTBP1	rs1268975	1221312	G	A	0.2182390	-0.0280978	0.0044165	2.9E-10
4	CTBP1	rs56277097	1223078	GC	G	0.2182960	-0.0284979	0.0044183	1.8E-10
4	CTBP1	rs2020137	1223163	A	C	0.2180480	-0.0283297	0.0044173	2.2E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
4	CTBP1	rs2004531	1223268	G	A	0.2197730	-0.0288320	0.0044176	8.9E-11
4	CTBP1	rs1732117	1224118	A	G	0.2118120	-0.0265332	0.0044789	2.3E-09
4	CTBP1	rs900021	1225008	A	G	0.2180730	-0.0283199	0.0044171	2.2E-10
4	CTBP1	rs1680058	1226255	G	C	0.2182770	-0.0281114	0.0044162	2.8E-10
4	CTBP1	rs1680057	1226456	T	C	0.2183320	-0.0280926	0.0044156	2.8E-10
4	CTBP1	rs1680054	1227348	T	C	0.2181260	-0.0282881	0.0044164	2.3E-10
4	CTBP1	rs2046152	1227543	T	C	0.2223250	-0.0282078	0.0044205	3.0E-10
4	CTBP1	rs2046151	1227653	T	C	0.2201220	-0.0279324	0.0044129	3.7E-10
4	CTBP1	rs3836584	1228720	AG	A	0.2182870	-0.0280541	0.0044159	3.1E-10
4	CTBP1	rs1732110	1228775	T	C	0.2182840	-0.0280521	0.0044158	3.1E-10
4	CTBP1	rs900019	1229048	A	C	0.2182870	-0.0280789	0.0044158	2.9E-10
4	CTBP1	rs1250116	1230799	T	C	0.2181530	-0.0282740	0.0044158	2.3E-10
4	CTBP1	rs1250115	1230843	C	T	0.2183550	-0.0280913	0.0044149	2.8E-10
4	CTBP1	rs3836583	1231213	C	CTCG	0.2181650	-0.0282531	0.0044156	2.3E-10
4	CTBP1	rs1250112	1231935	A	G	0.2182200	-0.0282489	0.0044145	2.3E-10
4	CTBP1	rs884421	1233681	C	T	0.2184740	-0.0283045	0.0044124	2.2E-10
4	CTBP1	rs1250108	1235306	G	A	0.4556970	0.0235308	0.0036742	1.1E-10
4	CTBP1	rs1250107	1236150	A	C	0.2181350	-0.0282576	0.0044150	2.3E-10
4	CTBP1	rs3755934	1242295	T	C	0.3413280	-0.0323218	0.0038345	2.9E-17
4	CTBP1	rs73069940	1242714	G	C	0.3418510	-0.0319209	0.0038341	6.2E-17
4	CTBP1	rs730831	1246511	G	T	0.3388550	-0.0320919	0.0038488	7.3E-17
4	CTBP1-AS2	rs79407053	1250430	A	G	0.3388130	-0.0323540	0.0038461	3.8E-17
4	CTBP1-AS2	rs72501962	1252250	T	A	0.3388110	-0.0322951	0.0038454	4.4E-17
4	CTBP1 *	rs2199956	1255131	T	C	0.4879180	0.0259744	0.0036469	7.4E-13
4	CTBP1 *	rs75331561	1259225	A	G	0.2126850	0.0239163	0.0044720	2.3E-08
4	CTBP1 *	rs7656416	1260747	T	C	0.3381330	-0.0322209	0.0038399	4.2E-17
4	CTBP1 *	rs4974576	1266178	T	A	0.4419040	-0.0300942	0.0036844	2.6E-16
4	CTBP1 *	rs34911726	1268369	A	AT	0.4672320	-0.0292772	0.0036655	1.5E-15
4	CTBP1 *	rs11933653	1268420	T	C	0.4394980	-0.0310215	0.0036838	2.9E-17
4	MAEA *	rs74327005	1270012	TA	T	0.4394630	-0.0311264	0.0036856	2.4E-17
4	MAEA *	rs1250123	1271076	A	G	0.4651340	-0.0295378	0.0036754	9.7E-16
4	MAEA *	rs1680025	1271689	T	C	0.4671510	-0.0294427	0.0036698	1.1E-15
4	MAEA *	rs56903463	1276463	T	C	0.4541720	0.0250686	0.0036783	9.7E-12
4	MAEA *	rs4974579	1276492	A	G	0.4396510	-0.0316085	0.0037022	7.4E-18
4	MAEA *	rs35317148	1280212	A	G	0.4456740	-0.0302967	0.0036787	9.7E-17
4	MAEA *	rs11247980	1280946	G	A	0.4462190	-0.0302510	0.0036750	8.7E-17
4	MAEA *	rs76691263	1281345	A	G	0.2803360	-0.0261276	0.0040855	1.5E-10
4	MAEA *	rs62293658	1282628	C	T	0.4906690	0.0221674	0.0036572	1.0E-09
4	MAEA *	rs1732102	1284136	C	T	0.4908740	0.0225548	0.0036527	4.6E-10
4	MAEA *	rs1680081	1284349	T	C	0.4323250	-0.0277365	0.0036887	3.3E-14
4	MAEA *	rs35945848	1284817	GCA	G	0.4903470	0.0225327	0.0036551	5.1E-10
4	MAEA *	rs1620928	1285336	T	C	0.4908750	0.0225970	0.0036525	4.2E-10
4	MAEA *	rs1680074	1285833	A	G	0.4906270	0.0223899	0.0036519	5.8E-10
4	MAEA *	rs1680073	1286549	A	G	0.4906200	0.0224160	0.0036519	5.5E-10
4	MAEA *	rs4974583	1286693	T	C	0.4323370	-0.0276145	0.0036877	4.2E-14
4	MAEA *	rs9992932	1286829	C	T	0.4881900	0.0222992	0.0036648	8.9E-10
4	MAEA *	rs4974584	1286834	G	A	0.4881900	0.0222992	0.0036648	8.9E-10
4	MAEA *	rs9992934	1286838	C	T	0.4881900	0.0222992	0.0036648	8.9E-10
4	MAEA *	rs10023922	1286889	T	C	0.4911280	0.0224621	0.0036569	6.6E-10
4	MAEA *	rs10000874	1286922	A	G	0.4908310	0.0225742	0.0036527	4.5E-10
4	MAEA *	rs10024013	1287004	T	C	0.4866810	0.0226248	0.0036714	6.3E-10
4	MAEA *	rs34026785	1287726	GAGT	G	0.4324920	-0.0278463	0.0036973	3.4E-14
4	MAEA *	rs1680072	1287907	G	T	0.4909170	0.0225441	0.0036520	4.9E-10
4	MAEA *	rs1732100	1287973	T	C	0.4906690	0.0224060	0.0036515	5.9E-10
4	MAEA *	rs34808560	1288679	A	ATC	0.4909530	0.0226038	0.0036521	4.5E-10
4	MAEA *	rs1732099	1288908	C	T	0.4906730	0.0224339	0.0036515	5.7E-10
4	MAEA *	rs922698	1288934	T	C	0.4909250	0.0225732	0.0036518	4.7E-10
4	MAEA *	rs9631804	1289244	T	A	0.4902100	0.0225469	0.0036566	5.7E-10
4	MAEA *	rs9631805	1289247	C	T	0.4902100	0.0225469	0.0036566	5.7E-10
4	MAEA *	rs17131840	1289276	TGCCCCG	G	0.4894480	0.0224004	0.0036601	7.1E-10
4	MAEA *	rs17164589	1289820	T	G	0.4323670	-0.0276461	0.0036864	4.3E-14
4	MAEA	rs73069965	1290448	T	C	0.4324030	-0.0276980	0.0036860	3.9E-14
4	MAEA	rs55875205	1290727	C	T	0.4315610	-0.0276677	0.0036856	4.8E-14
4	MAEA	rs4974585	1290907	C	T	0.4315620	-0.0276670	0.0036856	4.8E-14
4	MAEA	rs4974586	1290944	C	G	0.4315620	-0.0276670	0.0036856	4.8E-14
4	MAEA	rs2178442	1290953	T	C	0.4315620	-0.0276670	0.0036856	4.8E-14
4	MAEA	rs2178441	1291033	G	A	0.4315620	-0.0276670	0.0036856	4.8E-14
4	MAEA	rs2141653	1291176	A	T	0.4313980	-0.0275530	0.0036864	6.2E-14
4	MAEA	rs4974587	1291641	G	C	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs4974588	1292022	T	C	0.4315890	-0.0275247	0.0036858	6.5E-14
4	MAEA	rs73069970	1292439	T	A	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs36051935	1292532	T	C	0.4319490	-0.0276672	0.0036868	5.1E-14
4	MAEA	rs35385487	1292551	G	A	0.4319490	-0.0276672	0.0036868	5.1E-14
4	MAEA	rs73795288	1292590	T	C	0.4313710	-0.0275355	0.0036866	6.5E-14
4	MAEA	rs73069973	1292597	T	C	0.4313710	-0.0275355	0.0036866	6.5E-14
4	MAEA	rs73796044	1292643	C	T	0.4309600	-0.0276933	0.0036896	4.6E-14
4	MAEA	rs73069974	1292689	A	C	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs73069976	1292716	C	T	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs4399931	1292925	G	A	0.4297810	-0.0268998	0.0037115	3.6E-13
4	MAEA	chr4:1293210_GT_G	1293210	G	GT	0.4294270	-0.0274913	0.0037114	9.5E-14
4	MAEA	rs78147894	1293348	G	A	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs147893865	1293383	T	C	0.4301580	-0.0272684	0.0036954	1.2E-13
4	MAEA	rs4974589	1293564	C	T	0.4320430	-0.0275201	0.0036885	7.3E-14
4	MAEA	rs4974590	1293689	G	A	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs1344300	1294002	T	C	0.4316630	-0.0274904	0.0036860	6.5E-14
4	MAEA	rs73069979	1294190	G	A	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs113254479	1294213	G	A	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs1344301	1294243	C	T	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs73796048	1294281	G	C	0.4317750	-0.0277432	0.0036863	4.3E-14
4	MAEA	rs73069980	1294338	T	C	0.4317830	-0.0275792	0.0036851	5.6E-14
4	MAEA	rs73069981	1294345	G	A	0.4317830	-0.0275792	0.0036851	5.6E-14
4	MAEA	rs73069982	1294440	G	T	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs76731644	1294497	A	G	0.4315310	-0.0276217	0.0036854	5.2E-14
4	MAEA	rs140392870	1294551	AG	A	0.4318790	-0.0277726	0.0036946	4.0E-14
4	MAEA	rs73796053	1294588	T	C	0.4317300	-0.0277953	0.0036866	3.8E-14
4	MAEA	rs79680136	1294693	G	T	0.4303370	-0.0279318	0.0036966	3.2E-14
4	MAEA	rs114327728	1294703	C	T	0.4303370	-0.0279318	0.0036966	3.2E-14
4	MAEA	rs73796055	1294757	A	G	0.4303900	-0.0279952	0.0037021	4.0E-14
4	MAEA	rs140782463	1294774	GA	G	0.4308250	-0.0285648	0.0037062	1.3E-14
4	MAEA	rs76002147	1294795	C	A	0.4305680	-0.0280477	0.0036986	3.6E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
4	MAEA	rs73069983	1295639	C	T	0.4241370	-0.0269559	0.0037345	4.1E-13
4	MAEA	rs73069985	1295674	T	C	0.4290230	-0.0282616	0.0036980	1.8E-14
4	MAEA	rs114981738	1295885	C	T	0.4243020	-0.0270432	0.0037303	2.7E-13
4	MAEA	rs66879211	1296392	C	G	0.4227600	-0.0273835	0.0037428	1.6E-13
4	MAEA	rs72501965	1296403	T	C	0.4227600	-0.0273835	0.0037428	1.6E-13
4	MAEA	rs73069986	1296453	T	C	0.4238810	-0.0272006	0.0037355	2.0E-13
4	MAEA	rs75214475	1296490	C	T	0.4306320	-0.0278975	0.0036973	3.6E-14
4	MAEA	rs78054639	1296494	A	G	0.4306320	-0.0278975	0.0036973	3.6E-14
4	MAEA	rs34298138	1296525	T	GCCTTGT	0.42272350	-0.0272280	0.0037475	2.8E-13
4	MAEA	chr4:1296551_T_TTC	1296551	TTC	T	0.4192170	-0.0276763	0.0037647	1.7E-13
4	MAEA	rs73069988	1296605	A	G	0.4299710	-0.0276207	0.0036969	5.9E-14
4	MAEA	rs142360848	1296629	AACT	A	0.4287050	-0.0278780	0.0037008	3.7E-14
4	MAEA	rs55932747	1296643	G	GC	0.4942090	0.0223248	0.0036633	9.0E-10
4	MAEA	rs73796057	1296992	G	C	0.4251470	-0.0267725	0.0037060	4.2E-13
4	MAEA	rs73796058	1297000	T	C	0.4251470	-0.0267725	0.0037060	4.2E-13
4	MAEA	rs73796059	1297045	T	C	0.4251080	-0.0268221	0.0037060	3.8E-13
4	MAEA	rs78122234	1297085	T	C	0.4302290	-0.0277980	0.0036945	4.2E-14
4	MAEA	rs6823741	1297458	T	C	0.4582720	-0.0272456	0.0036904	1.9E-13
4	MAEA	rs6848799	1297461	G	A	0.4578020	-0.0258826	0.0036668	1.7E-12
4	MAEA	rs73069998	1297614	A	G	0.4300350	-0.0272974	0.0036894	1.3E-13
4	MAEA	rs73069999	1297675	G	C	0.4284520	-0.0272073	0.0036969	1.8E-13
4	MAEA	rs2293632	1297690	T	C	0.4285120	-0.0272230	0.0037033	1.8E-13
4	MAEA	rs2293633	1297852	T	C	0.4913300	0.0223064	0.0036488	7.7E-10
4	MAEA	rs11723894	1298181	T	C	0.4303270	-0.0271881	0.0036928	1.4E-13
4	MAEA	rs11723920	1298182	T	C	0.4303270	-0.0271881	0.0036928	1.4E-13
4	MAEA	rs11729031	1298226	C	T	0.4315370	-0.0275576	0.0036854	6.0E-14
4	MAEA	rs11729033	1298235	G	T	0.4315370	-0.0275576	0.0036854	6.0E-14
4	MAEA	rs35996294	1298868	A	AATT	0.4306560	-0.0272864	0.0036910	1.2E-13
4	MAEA	rs11939426	1298984	C	T	0.4315370	-0.0275576	0.0036854	6.0E-14
4	MAEA	rs1316487	1299417	T	C	0.4315370	-0.0275576	0.0036854	6.0E-14
4	MAEA	rs6819243	1299457	C	T	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs6837701	1299514	T	C	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs6814328	1299540	T	A	0.4315420	-0.0275284	0.0036854	6.4E-14
4	MAEA	rs59579894	1299604	G	GC	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs11247985	1300098	G	C	0.4306860	-0.0274242	0.0036909	7.9E-14
4	MAEA	rs35317516	1300103	T	C	0.4301110	-0.0270280	0.0036949	2.0E-13
4	MAEA	rs12508297	1300440	G	T	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs12503555	1300580	T	C	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs56887292	1300676	A	T	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs61367508	1300765	G	A	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs60555464	1300792	T	C	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs11936387	1301058	T	C	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs6599296	1301690	G	C	0.4315310	-0.0275486	0.0036853	6.1E-14
4	MAEA	rs143016100	1301726	GTAAA	G	0.4313150	-0.0276308	0.0036870	5.4E-14
4	MAEA	rs75023965	1301733	C	T	0.4313150	-0.0276308	0.0036870	5.4E-14
4	MAEA	rs6599297	1301783	C	G	0.4313150	-0.0276308	0.0036870	5.4E-14
4	MAEA	rs138442398	1301966	T	TAAAG	0.4315310	-0.0275518	0.0036853	6.1E-14
4	MAEA	rs6829118	1302105	G	A	0.4315310	-0.0275518	0.0036853	6.1E-14
4	MAEA	rs6852991	1302200	G	C	0.4315280	-0.0275390	0.0036853	6.2E-14
4	MAEA	rs6853002	1302203	C	T	0.4921140	0.0226042	0.0036523	4.5E-10
4	MAEA	rs79358245	1302240	G	T	0.4315250	-0.0275513	0.0036853	6.1E-14
4	MAEA	rs58847530	1302375	C	T	0.4315290	-0.0275451	0.0036852	6.2E-14
4	MAEA	rs12509700	1302533	A	G	0.4924960	0.0226007	0.0036539	4.2E-10
4	MAEA	rs148865237	1302548	T	C	0.4297220	-0.0275246	0.0036936	7.0E-14
4	MAEA	rs57415102	1302590	C	T	0.4315290	-0.0275451	0.0036852	6.2E-14
4	MAEA	rs73071923	1302701	T	C	0.4312690	-0.0275410	0.0036872	6.1E-14
4	MAEA	rs113332232	1302755	C	T	0.4312770	-0.0275301	0.0036872	6.3E-14
4	MAEA	rs79143022	1302769	T	C	0.4315290	-0.0275451	0.0036852	6.2E-14
4	MAEA	rs73071929	1302880	T	C	0.4315290	-0.0275451	0.0036852	6.2E-14
4	MAEA	rs73071932	1302894	A	G	0.4315290	-0.0275451	0.0036852	6.2E-14
4	MAEA	rs73071934	1303050	T	C	0.4315290	-0.0275451	0.0036852	6.2E-14
4	MAEA	rs73071935	1303076	G	C	0.4308610	-0.0274992	0.0036918	6.6E-14
4	MAEA	rs76136921	1303110	G	C	0.4323510	-0.0274750	0.0036893	8.2E-14
4	MAEA	rs61359788	1303441	G	A	0.4292800	-0.0274933	0.0036952	8.6E-14
4	MAEA	rs55955526	1303452	C	G	0.4292790	-0.0274946	0.0036952	8.6E-14
4	MAEA	rs58572555	1303472	C	T	0.4310390	-0.0275667	0.0036873	6.1E-14
4	MAEA	rs56758128	1303592	T	C	0.4311190	-0.0275504	0.0036876	6.2E-14
4	MAEA	rs60897436	1303600	A	G	0.4311190	-0.0275504	0.0036876	6.2E-14
4	MAEA	rs75548562	1303635	T	G	0.4293720	-0.0275224	0.0037002	9.3E-14
4	MAEA	rs60133030	1303665	T	G	0.4315380	-0.0276280	0.0036851	5.2E-14
4	MAEA	rs56085572	1303756	A	G	0.4315290	-0.0276050	0.0036851	5.4E-14
4	MAEA	rs73072001	1304109	C	G	0.4312400	-0.0275171	0.0036862	6.8E-14
4	MAEA	rs73073703	1304142	T	G	0.4314500	-0.0277396	0.0036856	4.2E-14
4	MAEA	rs56404604	1304228	G	A	0.4315230	-0.0276082	0.0036850	5.2E-14
4	MAEA	rs4974547	1304400	T	C	0.4315230	-0.0276082	0.0036850	5.2E-14
4	MAEA	rs4974592	1304607	C	A	0.4315240	-0.0275995	0.0036850	5.3E-14
4	MAEA	rs4974593	1304835	G	A	0.4315280	-0.0276223	0.0036850	5.1E-14
4	MAEA	rs7666876	1305381	C	G	0.4315290	-0.0276229	0.0036850	5.1E-14
4	MAEA	rs7671585	1305418	A	G	0.4315290	-0.0276229	0.0036850	5.1E-14
4	MAEA	rs7696746	1305433	G	A	0.4315290	-0.0276229	0.0036850	5.1E-14
4	MAEA	rs74478546	1305682	A	G	0.4315250	-0.0276245	0.0036850	5.1E-14
4	MAEA	rs59944614	1305729	G	A	0.4315250	-0.0276245	0.0036850	5.1E-14
4	MAEA	rs7673398	1306289	G	A	0.4917980	0.0226555	0.0036518	3.9E-10
4	MAEA	rs7668661	1306384	A	G	0.4917980	0.0226540	0.0036519	3.9E-10
4	MAEA	rs7668719	1306470	G	A	0.4318430	-0.0275176	0.0036846	5.9E-14
4	MAEA	rs4974594	1306692	A	G	0.4917980	0.0226558	0.0036519	3.8E-10
4	MAEA	rs4974595	1307213	T	C	0.4314380	-0.0276904	0.0036844	4.4E-14
4	MAEA	rs71168825	1307406	A	AT	0.4917990	0.0226949	0.0036517	3.7E-10
4	MAEA	rs4974597	1307731	G	A	0.4315450	-0.0275901	0.0036849	5.7E-14
4	MAEA	rs58058346	1307815	C	A	0.4316690	-0.0274437	0.0036848	7.6E-14
4	MAEA	rs56240712	1307854	G	A	0.4307730	-0.0271862	0.0036870	1.2E-13
4	MAEA	rs17164620	1310373	G	A	0.4316820	-0.0275507	0.0036838	6.2E-14
4	MAEA	rs7672093	1310955	A	C	0.4316110	-0.0274832	0.0036826	6.6E-14
4	MAEA	rs6599229	1311230	C	T	0.4323180	-0.0271440	0.0036819	1.3E-13
4	MAEA	rs6599300	1311481	A	G	0.4316320	-0.0274958	0.0036820	6.3E-14
4	MAEA	rs17164638	1312807	G	C	0.4315720	-0.0277665	0.0036807	3.7E-14
4	MAEA	rs6826029	1313901	A	G	0.4913710	0.0223289	0.0036420	6.2E-10
4	MAEA	rs11247988	1314541	G	C	0.4309100	-0.0276163	0.0036794	4.5E-14
4	MAEA	rs11247989	1314549	G	A	0.4309100	-0.0276163	0.0036794	4.5E-14
4	MAEA	rs11247990	1314748	C	G	0.4313760	-0.0275224	0.0036755	5.0E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAf	BETA	SE	P
4	MAEA	rs11247991	1314776	G	A	0.4313910	-0.0276285	0.0036755	4.2E-14
4	MAEA	rs2272481	1315628	T	C	0.4303770	-0.0270848	0.0036893	1.3E-13
4	MAEA	rs6815464	1316113	G	C	0.4313720	-0.0277087	0.0036718	3.5E-14
4	MAEA	rs35420448	1316310	G	ACTGCT	0.4259630	-0.0274144	0.0037076	1.1E-13
4	MAEA	rs11727376	1316327	C	T	0.2808520	0.0220620	0.0040722	1.4E-08
4	MAEA	rs60640478	1316394	C	A	0.4306000	-0.0278228	0.0036787	3.3E-14
4	MAEA	rs11946375	1319700	C	T	0.2754170	0.0218114	0.0041045	2.6E-08
4	MAEA	rs11946384	1319778	C	T	0.4647740	-0.0247594	0.0036717	1.6E-11
4	MAEA	rs57556979	1319783	CCCAAC	A	0.4645550	-0.0247680	0.0036732	1.6E-11
4	MAEA	rs57385687	1319785	TC	T	0.4648290	-0.0247810	0.0036753	1.6E-11
4	MAEA	rs59544360	1319787	T	G	0.4638740	-0.0248190	0.0036779	1.6E-11
4	MAEA	rs5013707	1319989	A	C	0.4663940	-0.0251022	0.0036598	7.3E-12
4	MAEA	rs577025785	1320187	AAAAG	A	0.4484820	-0.0263557	0.0037077	4.3E-13
4	MAEA	rs6148273	1320414	A	G	0.4672130	-0.0246223	0.0036583	2.0E-11
4	MAEA	rs11933854	1321384	A	G	0.4670840	-0.0245756	0.0036535	1.8E-11
4	MAEA	rs11933855	1321395	A	G	0.4671500	-0.0246213	0.0036531	1.6E-11
4	MAEA	rs2293631	1322129	A	C	0.4661270	-0.0250396	0.0036621	9.6E-12
4	MAEA	rs28712208	1322907	T	A	0.4663400	-0.0243177	0.0036599	4.1E-11
4	MAEA	rs2141656	1323404	C	T	0.4560480	0.0203322	0.0036594	3.1E-08
4	MAEA	rs11725015	1327364	A	G	0.4217080	-0.0268811	0.0037300	7.4E-13
4	MAEA	rs11726178	1328184	T	G	0.4392880	-0.0272174	0.0036858	1.3E-13
4	MAEA	rs11726179	1328190	A	G	0.4395520	-0.0272577	0.0036840	1.2E-13
4	MAEA	rs6850727	1329485	C	G	0.4702490	-0.0251896	0.0036551	6.8E-12
4	MAEA	rs4333131	1330001	G	A	0.4688010	-0.0251315	0.0036602	7.0E-12
4	MAEA	rs9990527	1330572	T	C	0.4769450	-0.0241976	0.0036734	6.1E-11
4	MAEA	rs10012582	1330693	G	A	0.4906970	0.0218253	0.0036759	4.5E-09
4	MAEA	rs5019560	1331005	A	G	0.4683800	-0.0249874	0.0036552	9.8E-12
4	MAEA	rs80097454	1331205	T	C	0.4403860	-0.0269840	0.0036797	2.1E-13
4	MAEA	rs61073965	1331777	A	G	0.4420310	-0.0270166	0.0036830	2.1E-13
4	MAEA	rs4974600	1332955	C	G	0.4135170	-0.0262838	0.0037512	1.8E-12
4	MAEA	rs59764624	1334381	G	GCTTT	0.4548860	0.0218191	0.0036911	5.0E-09
4	MAEA	rs3856982	1335075	C	T	0.4724430	-0.0246862	0.0036732	2.2E-11
4	MAEA	rs10006789	1336545	C	T	0.4476780	-0.0248366	0.0037172	2.5E-11
4	MAEA	rs1128427	1336971	T	C	0.4774970	0.0203568	0.0037059	3.8E-08
4	MAEA	rs28418481	1337187	G	C	0.4721090	-0.0250736	0.0036731	1.0E-11
4	MAEA	rs28493051	1337242	C	A	0.4721000	-0.0250726	0.0036732	1.0E-11
4	MAEA	rs59742652	1337334	GACTGA	T	0.4710250	-0.0246696	0.0036800	2.3E-11
4	MAEA *	rs73075548	1340472	C	G	0.4458560	-0.0269721	0.0037065	3.1E-13
4	MAEA *	rs6843025	1340630	C	G	0.4521980	0.0206361	0.0036977	2.5E-08
4	MAEA *	rs13117476	1340933	T	C	0.4513390	0.0203091	0.0036993	4.4E-08
4	MAEA *	rs34947293	1341246	T	C	0.4450710	0.0221533	0.0037251	3.8E-09
4	MAEA *	rs73075553	1342236	G	C	0.4464300	-0.0259358	0.0037167	2.7E-12
4	UVSSA *	rs58552306	1345295	C	G	0.4440430	-0.0262413	0.0037295	1.4E-12
4	WFS1 *	rs28529265	6262067	G	C	0.0104823	-0.1089440	0.0178838	5.1E-09
4	WFS1 *	rs560127499	6262076	T	C	0.0104822	-0.1089390	0.0178838	5.1E-09
4	WFS1 *	rs557562585	6266657	GACTC	G	0.0110304	-0.1078170	0.0174142	3.1E-09
4	WFS1 *	rs1478858814	6266659	C	T	0.0110304	-0.1078170	0.0174142	3.1E-09
4	WFS1 *	rs565283909	6266660	C	T	0.0110304	-0.1078170	0.0174142	3.1E-09
4	WFS1 *	rs148537544	6266784	G	C	0.0110304	-0.1078170	0.0174142	3.1E-09
4	WFS1 *	rs140127258	6267344	C	T	0.0110337	-0.1075310	0.0174114	3.5E-09
4	WFS1 *	chr4:6267597_A_AT	6267597	AT	A	0.0114640	-0.1037090	0.0171109	6.7E-09
4	WFS1 *	rs115535967	6267637	C	A	0.0110438	-0.1073630	0.0174033	3.7E-09
4	WFS1 *	rs181843156	6269620	T	C	0.0110888	-0.1070380	0.0173624	3.4E-09
4	WFS1	rs571212929	6270363	G	C	0.0111024	-0.1068790	0.0173516	3.5E-09
4	WFS1	rs186415193	6270489	A	C	0.0111024	-0.1068790	0.0173516	3.5E-09
4	WFS1	rs551239114	6270749	T	A	0.0111022	-0.1068920	0.0173516	3.4E-09
4	WFS1	rs112030398	6270879	A	C	0.0111022	-0.1068920	0.0173516	3.4E-09
4	WFS1	rs556546980	6274036	C	T	0.0100642	-0.1068970	0.0182219	1.2E-08
4	WFS1	rs766486951	6274221	G	TATTTT	0.0111457	-0.1070530	0.0173165	2.7E-09
4	WFS1	rs111823345	6276412	T	C	0.0111627	-0.1076340	0.0173005	2.1E-09
4	WFS1	rs4558932	6276524	C	T	0.0664993	-0.0395314	0.0073254	4.8E-08
4	WFS1	rs79271440	6277196	C	G	0.0111702	-0.1078870	0.0172923	1.9E-09
4	WFS1	rs112770295	6277246	C	G	0.0111702	-0.1078870	0.0172923	1.9E-09
4	WFS1	rs561390520	6277963	C	T	0.0111768	-0.1075620	0.0172870	2.1E-09
4	WFS1	rs6833032	6280200	T	C	0.0111764	-0.1075630	0.0172870	2.1E-09
4	WFS1	rs77135664	6282257	C	T	0.0111986	-0.1064510	0.0172682	2.9E-09
4	WFS1	rs183938823	6283267	T	C	0.0112313	-0.1045590	0.0172415	4.7E-09
4	WFS1	rs1418950298	6285150	TTGGCTC	A	0.0112381	-0.1042970	0.0172362	5.0E-09
4	WFS1	rs189549489	6286579	G	A	0.0112416	-0.1043390	0.0172336	5.0E-09
4	WFS1	rs181271017	6286964	G	A	0.0112415	-0.1043370	0.0172336	5.0E-09
4	WFS1	rs544404823	6287753	A	G	0.0112450	-0.1043030	0.0172309	5.1E-09
4	WFS1	rs111852841	6288823	G	A	0.0112485	-0.1044570	0.0172283	4.6E-09
4	WFS1	rs75990806	6290580	G	A	0.0112500	-0.1045090	0.0172255	4.7E-09
4	WFS1	rs201476662	6292044	T	C	0.0112524	-0.1041710	0.0172228	5.1E-09
4	WFS1	rs7655482	6292075	C	T	0.0675242	-0.0392512	0.0072529	4.7E-08
4	WFS1	rs184179861	6293663	C	T	0.0112524	-0.1041710	0.0172228	5.1E-09
4	WFS1	rs141974389	6294004	ATC	A	0.0674948	-0.0393952	0.0072539	4.1E-08
4	WFS1	rs28729642	6294048	T	C	0.0115600	-0.1033830	0.0169976	4.8E-09
4	WFS1	rs7691824	6295290	A	G	0.0112455	-0.1039280	0.0172281	5.4E-09
4	WFS1	rs188514031	6295877	A	G	0.0112455	-0.1039280	0.0172281	5.4E-09
4	WFS1	rs538927343	6295949	A	G	0.0112455	-0.1039280	0.0172281	5.4E-09
4	WFS1	rs554724470	6296051	C	T	0.0112455	-0.1039280	0.0172281	5.4E-09
4	WFS1	rs113703919	6296978	A	C	0.0112455	-0.1039280	0.0172281	5.4E-09
4	WFS1	rs79408528	6297287	T	C	0.0112420	-0.1039840	0.0172307	5.4E-09
4	WFS1	rs546680947	6298844	C	T	0.0112316	-0.1040790	0.0172387	5.1E-09
4	WFS1	rs540568674	6299425	C	T	0.0112281	-0.1035800	0.0172414	6.1E-09
4	WFS1	rs562612530	6299445	A	G	0.0112281	-0.1035800	0.0172414	6.1E-09
4	WFS1	rs185610144	6299801	G	T	0.0124570	-0.0929419	0.0163935	3.5E-08
4	WFS1	rs147974629	6301104	A	G	0.0112248	-0.1039000	0.0172440	5.6E-09
4	WFS1 *	rs557896700	6303419	T	C	0.0111272	-0.1054950	0.0173214	4.6E-09
4	WFS1 *	rs575655491	6304120	T	C	0.0110406	-0.1037390	0.0173890	1.1E-08
4	WFS1 *	rs576579579	6304536	G	A	0.0109302	-0.1011030	0.0174769	3.3E-08
4	WFS1 *	rs531204618	6304677	A	G	0.0114222	-0.1018900	0.0171159	1.5E-08
5	ANKRD55 *	rs157504	56498248	C	T	0.2932000	-0.0227235	0.0040849	1.6E-08
5	ANKRD55 *	rs3074482	56498680	T	TGG	0.2941220	-0.0234698	0.0040676	4.7E-09
5	ANKRD55 *	rs151837	56498732	T	C	0.2941830	-0.0235325	0.0040668	4.2E-09
5	ANKRD55 *	rs151838	56498738	T	C	0.2942020	-0.0235714	0.0040664	4.0E-09
5	ANKRD55 *	rs157505	56498801	T	C	0.2940960	-0.0238182	0.0040656	2.6E-09
5	ANKRD55 *	rs588898	56501555	A	G	0.2975720	-0.0233823	0.0039817	3.4E-09
5	ANKRD55 *	rs245109	56501758	C	T	0.2975890	-0.0233723	0.0039813	3.4E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	ANKRD55 *	rs173443	56501772	C	T	0.2975280	-0.0234084	0.0039818	3.3E-09
5	ANKRD55 *	rs42392	56508102	G	A	0.2983910	-0.0234838	0.0039734	2.9E-09
5	ANKRD55 *	rs25757	56508377	G	C	0.2983740	-0.0234699	0.0039734	2.9E-09
5	ANKRD55 *	rs459193	56510924	A	G	0.4700180	-0.0310515	0.0036361	2.6E-18
5	LOC101928448	rs464605	56511543	C	T	0.4702950	-0.0310376	0.0036381	2.8E-18
5	LOC101928448	rs245143	56512322	G	A	0.2961440	-0.0227328	0.0039992	1.3E-08
5	LOC101928448	rs157507	56512451	T	C	0.3304930	-0.0270971	0.0038626	1.2E-12
5	LOC101928448	rs392794	56512515	C	T	0.4701780	-0.0311047	0.0036390	2.4E-18
5	LOC101928448	rs465002	56512648	C	T	0.4701770	-0.0311465	0.0036390	2.1E-18
5	LOC101928448	rs157510	56513139	C	A	0.3304320	-0.0270246	0.0038620	1.4E-12
5	LOC101928448	rs157512	56513300	C	T	0.4354610	-0.0298038	0.0036679	3.4E-17
5	LOC101928448	rs256903	56513311	C	A	0.4694660	-0.0311509	0.0036425	2.0E-18
5	LOC101928448	rs173964	56513638	A	G	0.4692120	-0.0313095	0.0036432	1.4E-18
5	LOC101928448	rs256904	56514478	A	T	0.4697450	-0.0308833	0.0036435	3.9E-18
5	LOC101928448	rs245142	56514622	A	G	0.3301340	-0.0270244	0.0038621	1.4E-12
5	LOC101928448	rs456867	56515265	T	C	0.3302330	-0.0269491	0.0038601	1.5E-12
5	LOC101928448	rs459447	56515514	A	G	0.3289820	-0.0271337	0.0038666	1.2E-12
5	LOC101928448	rs465983	56516303	G	A	0.4385560	-0.0282928	0.0036704	1.5E-15
5	LOC101928448	rs2448427	56516855	T	C	0.2953980	-0.0223526	0.0040125	2.3E-08
5	LOC101928448	rs405176	56517885	G	A	0.3691610	-0.0262537	0.0037755	4.2E-12
5	LOC101928448	rs455660	56521061	T	C	0.3810340	-0.0266948	0.0037397	1.1E-12
5	MIR583 *	rs17085428	96052311	A	G	0.3267410	-0.0199787	0.0039044	4.6E-08
5	MIR583 *	rs4365863	96101907	A	G	0.4399390	-0.0188607	0.0036600	1.8E-08
5	MIR583 *	rs10073810	96105935	T	G	0.4074070	-0.0198514	0.0037025	8.3E-09
5	MIR583 *	rs6865400	96106449	G	C	0.4065060	-0.0200047	0.0037085	6.9E-09
5	MIR583 *	rs4330486	96109615	C	G	0.4398630	-0.0189133	0.0036601	1.7E-08
5	MIR583 *	rs58666663	96131448	T	C	0.4079220	-0.0202817	0.0037030	4.4E-09
5	MIR583 *	rs72656690	96134191	T	A	0.3278370	-0.0241305	0.0038890	5.8E-11
5	MIR583 *	rs6875999	96135285	G	A	0.4068060	-0.0203485	0.0037106	3.6E-09
5	MIR583 *	rs58926517	96137317	G	A	0.4090890	-0.0211226	0.0037013	1.2E-09
5	MIR583 *	rs66853776	96152168	G	A	0.4105130	-0.0212049	0.0036966	1.1E-09
5	MIR583 *	rs72656691	96162091	A	G	0.4084630	-0.0211849	0.0037039	1.2E-09
5	MIR583 *	rs72656692	96164577	G	A	0.4102220	-0.0210277	0.0036979	1.4E-09
5	MIR583 *	rs10062096	96167690	C	T	0.4421340	-0.0206617	0.0037490	1.2E-08
5	MIR583 *	rs13163809	96168431	T	C	0.4981250	-0.0213347	0.0037262	4.1E-09
5	MIR583 *	rs13183436	96168516	G	A	0.4957160	-0.0236607	0.0037120	7.7E-11
5	MIR583 *	rs13187598	96168590	T	C	0.4918750	0.0222946	0.0037041	7.3E-10
5	MIR583 *	rs11956194	96168778	A	G	0.3451600	-0.0324853	0.0038915	2.0E-18
5	MIR583 *	rs4357059	96173022	G	A	0.4931590	0.0224774	0.0036951	4.5E-10
5	MIR583 *	rs28757605	96179252	A	G	0.4975220	-0.0218632	0.0037050	1.3E-09
5	MIR583 *	rs13177227	96181754	T	C	0.3201980	-0.0315598	0.0039650	1.7E-16
5	MIR583 *	rs4869270	96188291	T	C	0.4893700	0.0223750	0.0036728	4.7E-10
5	MIR583 *	rs56198733	96191353	C	G	0.3350410	-0.0335292	0.0038667	8.8E-20
5	MIR583 *	rs7714279	96191679	C	T	0.4932210	0.0232645	0.0036494	6.4E-11
5	MIR583 *	rs4869272	96203744	C	T	0.3424100	-0.0344288	0.0038301	6.1E-21
5	MIR583 *	rs4869273	96203832	C	T	0.3426590	-0.0348100	0.0038308	2.4E-21
5	MIR583 *	rs10476663	96204485	C	A	0.4926130	0.0235239	0.0036487	3.9E-11
5	MIR583 *	rs13179048	96207022	A	C	0.3413270	-0.0346153	0.0038330	3.8E-21
5	MIR583 *	rs36101807	96213582	T	G	0.3394790	-0.0340506	0.0038437	2.5E-20
5	PCSK1 *	rs7716096	96239212	T	C	0.4945970	0.0227020	0.0036395	1.6E-10
5	PCSK1 *	rs10052354	96248385	C	T	0.4966580	0.0225113	0.0036387	2.0E-10
5	PCSK1 *	rs10074626	96248690	T	C	0.4965280	0.0225782	0.0036398	1.8E-10
5	PCSK1 *	rs5869709	96255565	C	CT	0.4940410	0.0228538	0.0036378	1.1E-10
5	PCSK1 *	rs7443470	96255748	C	A	0.4944020	0.0227611	0.0036402	1.4E-10
5	PCSK1 *	rs12054709	96255876	A	G	0.4940300	0.0228250	0.0036378	1.2E-10
5	PCSK1 *	rs6882897	96256022	A	G	0.4940300	0.0228252	0.0036378	1.2E-10
5	PCSK1 *	chr5:96256370_AAT_A	96256370	A	AAT	0.4919350	0.0233514	0.0036464	5.3E-11
5	PCSK1 *	rs72018276	96258808	A	ATG	0.4942040	0.0226347	0.0036417	1.9E-10
5	PCSK1 *	rs7706771	96259661	T	C	0.4943380	0.0226045	0.0036423	2.0E-10
5	PCSK1 *	rs4355545	96260990	T	A	0.4967630	0.0221819	0.0036422	4.0E-10
5	PCSK1 *	rs6868247	96261819	G	A	0.4946970	0.0222918	0.0036420	3.4E-10
5	PCSK1 *	rs10065122	96274816	C	T	0.4952380	0.0216954	0.0036379	5.7E-10
5	PCSK1 *	rs4336380	96279156	T	C	0.4632030	0.0200593	0.0036487	1.0E-08
5	PCSK1 *	rs4288139	96281143	C	T	0.4652650	0.0197844	0.0036456	1.5E-08
5	PCSK1 *	rs6556913	96282519	A	G	0.4652560	0.0198279	0.0036459	1.4E-08
5	PCSK1 *	rs6868724	96286021	C	T	0.4651230	0.0201195	0.0036518	7.9E-09
5	PCSK1 *	rs6864629	96286085	G	A	0.4651020	0.0201647	0.0036520	7.3E-09
5	PCSK1 *	rs7733672	96287540	T	C	0.4654690	0.0201126	0.0036525	8.1E-09
5	PCSK1 *	rs6556914	96289194	T	C	0.4649290	0.0202474	0.0036520	6.3E-09
5	PCSK1 *	rs12522310	96289844	T	C	0.4658020	0.0201361	0.0036541	7.9E-09
5	PCSK1 *	rs5869713	96289941	T	A	0.3492880	-0.0360169	0.0038694	2.4E-22
5	PCSK1 *	rs60590576	96290481	A	AG	0.4654830	0.0199445	0.0036521	9.9E-09
5	PCSK1 *	rs10476666	96290539	G	A	0.4654040	0.0199918	0.0036516	9.5E-09
5	PCSK1 *	rs7714951	96293365	A	G	0.4651230	0.0202337	0.0036523	6.5E-09
5	PCSK1 *	rs7737206	96293434	C	A	0.4654790	0.0201746	0.0036546	7.6E-09
5	PCSK1 *	rs12186664	96294521	T	A	0.3473200	-0.0351853	0.0038316	7.4E-22
5	PCSK1 *	rs17085593	96295001	G	C	0.3373070	-0.0374444	0.0038593	4.3E-24
5	PCSK1 *	rs11950062	96295438	A	G	0.4650830	0.0201713	0.0036532	7.2E-09
5	PCSK1 *	rs79419016	96297048	T	TGGGGA	0.4674930	0.0203115	0.0036604	5.9E-09
5	PCSK1 *	rs62367172	96297049	T	A	0.4674930	0.0203115	0.0036604	5.9E-09
5	PCSK1 *	rs2350002	96302738	G	A	0.3372480	-0.0375573	0.0038604	3.1E-24
5	PCSK1 *	rs12517140	96303368	T	C	0.3982130	0.0207897	0.0037234	6.0E-09
5	PCSK1 *	rs13162665	96306815	G	T	0.3365950	-0.0375510	0.0038656	3.3E-24
5	PCSK1 *	rs6899303	96315271	A	C	0.4659790	0.0201247	0.0036582	8.1E-09
5	PCSK1 *	rs1477368	96333746	A	G	0.4780060	0.0206532	0.0036728	4.3E-09
5	PCSK1 *	rs4869282	96334461	T	C	0.4833830	0.0248498	0.0036666	2.9E-12
5	PCSK1 *	rs10040098	96338562	T	C	0.3275790	-0.0380655	0.0039014	5.1E-24
5	PCSK1 *	rs35247507	96352838	G	A	0.3183200	-0.0393269	0.0039258	2.2E-25
5	PCSK1 *	rs36115340	96353360	G	A	0.3183290	-0.0391920	0.0039256	3.1E-25
5	PCSK1 *	rs12109272	96357306	G	A	0.3181180	-0.0384883	0.0039192	1.2E-24
5	PCSK1 *	rs144489757	96358905	G	C	0.3191320	-0.0390653	0.0039143	2.2E-25
5	PCSK1 *	rs6863434	96359969	T	C	0.3279790	-0.0372537	0.0038921	1.8E-23
5	PCSK1 *	rs1820177	96360725	T	C	0.3281320	-0.0372551	0.0038914	1.7E-23
5	PCSK1 *	rs1820176	96360881	C	T	0.3297990	-0.0370025	0.0038862	2.4E-23
5	PCSK1 *	rs34874677	96366078	C	T	0.3182200	-0.0385570	0.0039399	2.7E-24
5	PCSK1 *	rs6876986	96367625	C	G	0.3292130	-0.0366414	0.0038729	4.3E-23
5	PCSK1 *	rs10476552	96373428	C	T	0.3291550	-0.0368096	0.0038714	2.8E-23
5	PCSK1 *	rs10036439	96374664	C	G	0.3291740	-0.0367054	0.0038711	3.7E-23
5	PCSK1 *	rs6869253	96375200	C	A	0.3285390	-0.0365642	0.0038767	6.7E-23
5	PCSK1 *	rs6890994	96378400	C	T	0.3182430	-0.0395081	0.0039043	5.9E-26

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	PCSK1 *	rs59139497	96379021	G	A	0.3199060	-0.0391522	0.0038984	1.1E-25
5	PCSK1 *	rs7713317	96381018	G	A	0.3199780	-0.0390461	0.0038957	1.4E-25
5	PCSK1 *	rs7722200	96381736	C	T	0.3293620	-0.0364784	0.0038660	5.9E-23
5	PCSK1 *	rs12332295	96382499	C	G	0.3276920	-0.0367040	0.0038713	4.5E-23
5	PCSK1 *	rs10476553	96383142	C	G	0.3293510	-0.0363565	0.0038672	8.3E-23
5	PCSK1 *	rs9285019	96383590	T	C	0.3292260	-0.0365753	0.0038715	6.2E-23
5	PCSK1 *	rs10213965	96383963	C	G	0.3286110	-0.0365832	0.0038737	6.6E-23
5	PCSK1 *	rs10213823	96383972	C	T	0.3291120	-0.0365777	0.0038691	5.1E-23
5	PCSK1 *	rs17085655	96384100	G	A	0.3293410	-0.0363812	0.0038674	8.0E-23
5	PCSK1 *	rs17085658	96384219	G	A	0.3293410	-0.0363755	0.0038675	8.0E-23
5	PCSK1 *	rs7700417	96384655	C	T	0.3292970	-0.0364474	0.0038678	6.8E-23
5	PCSK1 *	rs17085665	96387677	A	G	0.3216940	-0.0395897	0.0038933	3.2E-26
5	PCSK1 *	rs35648612	96388635	G	A	0.3215640	-0.0396903	0.0038960	3.1E-26
5	PCSK1	rs2882298	96391471	G	A	0.3221770	-0.0398137	0.0038905	1.6E-26
5	PCSK1	rs17085675	96391960	T	A	0.3222910	-0.0397201	0.0038883	2.0E-26
5	PCSK1	chr5:96392174_GT_G	96392174	G	GT	0.3202270	-0.0392916	0.0039060	1.5E-25
5	PCSK1	rs5869716	96392261	CAGA	C	0.3223010	-0.0397456	0.0038879	1.9E-26
5	PCSK1	rs199528625	96392267	A	G	0.2995060	-0.0382804	0.0040519	9.4E-23
5	PCSK1	rs6235	96393194	G	C	0.3218690	-0.0396059	0.0038896	2.8E-26
5	PCSK1	rs6234	96393270	C	G	0.3202610	-0.0400235	0.0038951	1.3E-26
5	PCSK1	rs13169290	96393702	A	G	0.3218750	-0.0396357	0.0038900	2.5E-26
5	PCSK1	rs10628666	96395843	T	TAA	0.4065710	0.0200630	0.0037087	1.5E-08
5	PCSK1	rs13168460	96396865	T	A	0.3203120	-0.0402155	0.0039002	7.0E-27
5	PCSK1	rs11395420	96400856	GA	G	0.3166850	-0.0371466	0.0039755	1.4E-22
5	PCSK1	rs35364611	96412259	T	TCTC	0.2706160	-0.0312636	0.0041061	3.2E-15
5	PCSK1	chr5:96415805_A_AT	96415805	A	AT	0.4882060	0.0227292	0.0036699	7.7E-11
5	PCSK1	rs10515237	96415845	G	A	0.2718900	-0.0306164	0.0041009	1.0E-14
5	PCSK1	rs13154597	96419328	T	A	0.2717900	-0.0306505	0.0040999	9.3E-15
5	PCSK1	rs3811951	96426773	G	A	0.2688290	-0.0309787	0.0041456	1.1E-14
5	FBLN1 *	rs7446039	168529258	G	A	0.4797260	-0.0204559	0.0036585	3.8E-08
6	RREB1	rs7743323	7195451	T	C	0.0432347	-0.0495410	0.0089530	6.2E-09
6	RREB1	rs77630070	7196090	T	G	0.0424169	-0.0500464	0.0090391	9.6E-09
6	RREB1	rs74409395	7196091	T	C	0.0424169	-0.0500464	0.0090391	9.6E-09
6	RREB1	rs75431224	7199299	T	A	0.0434585	-0.0488583	0.0089302	9.4E-09
6	RREB1	rs145693428	7201991	TA	T	0.0434811	-0.0488703	0.0089272	9.1E-09
6	RREB1	rs76207590	7203762	C	A	0.0434837	-0.0488451	0.0089268	9.3E-09
6	RREB1	rs17603945	7212783	A	G	0.0434542	-0.0479864	0.0089208	1.8E-08
6	RREB1	rs76052955	7213674	C	A	0.0434542	-0.0479864	0.0089208	1.8E-08
6	RREB1	rs17672692	7214266	T	C	0.0434686	-0.0478955	0.0089191	1.8E-08
6	RREB1	rs78588343	7249227	A	G	0.0386995	-0.0494206	0.0094823	3.4E-08
6	RREB1	rs3778321	7250037	A	G	0.0386882	-0.0486979	0.0094854	4.6E-08
6	RREB1	rs55792466	7250241	T	C	0.0384726	-0.0496166	0.0095083	2.8E-08
6	RREB1	rs41302869	7250406	G	A	0.0386876	-0.0486197	0.0094854	4.8E-08
6	RREB1 *	rs9505097	7255417	T	C	0.0510769	-0.0460438	0.0083377	7.9E-09
6	CDKAL1 *	rs9368197	20533152	G	T	0.4837960	-0.0244855	0.0036752	1.9E-11
6	CDKAL1 *	rs10806920	20534218	T	A	0.4818790	-0.0249271	0.0036720	9.2E-12
6	CDKAL1	rs965054	20536708	T	A	0.4831790	-0.0245216	0.0036666	1.7E-11
6	CDKAL1	rs2328525	20537221	A	G	0.4828860	-0.0250428	0.0036537	5.0E-12
6	CDKAL1	rs58761454	20540935	C	T	0.4846340	-0.0242466	0.0036407	1.8E-11
6	CDKAL1	rs9348432	20540949	C	T	0.4820400	-0.0242225	0.0036419	2.1E-11
6	CDKAL1	rs9368200	20543881	C	T	0.4835320	-0.0246274	0.0036385	9.2E-12
6	CDKAL1	rs11759517	20544512	C	T	0.4841540	-0.0245974	0.0036421	1.0E-11
6	CDKAL1	rs9366354	20545237	A	G	0.4811080	-0.0246466	0.0036399	9.4E-12
6	CDKAL1	rs9358342	20545680	C	T	0.4845290	-0.0245380	0.0036399	1.1E-11
6	CDKAL1	rs9368201	20545881	A	G	0.4817170	-0.0246290	0.0036414	9.9E-12
6	CDKAL1	rs34206163	20546170	AAT	A	0.4849300	-0.0244439	0.0036414	1.5E-11
6	CDKAL1	rs45559831	20546595	C	T	0.4839330	-0.0246105	0.0036383	9.6E-12
6	CDKAL1	rs9348433	20549570	C	G	0.4812470	-0.0245119	0.0036399	1.2E-11
6	CDKAL1	rs9350257	20554720	A	C	0.4819130	-0.0243805	0.0036381	1.7E-11
6	CDKAL1	rs9350258	20556674	G	A	0.4823350	-0.0246409	0.0036381	1.1E-11
6	CDKAL1	rs9368202	20562788	C	T	0.4832170	-0.0248236	0.0036395	7.3E-12
6	CDKAL1	rs58102569	20563411	AG	A	0.4831930	-0.0248139	0.0036394	7.3E-12
6	CDKAL1	rs4712506	20565205	A	G	0.4819310	-0.0246449	0.0036400	1.0E-11
6	CDKAL1	rs2064321	20569757	T	C	0.4847220	-0.0255064	0.0036451	1.7E-12
6	CDKAL1	rs4291090	20569808	C	T	0.4827160	-0.0253772	0.0036457	2.3E-12
6	CDKAL1	rs9358344	20570213	C	T	0.4826940	-0.0253868	0.0036458	2.3E-12
6	CDKAL1	rs962576	20574358	A	G	0.4843400	-0.0252119	0.0036435	3.3E-12
6	CDKAL1	rs9350260	20576059	T	A	0.4840350	-0.0253755	0.0036510	2.2E-12
6	CDKAL1	rs9358345	20576435	G	A	0.4818910	-0.0253041	0.0036518	2.6E-12
6	CDKAL1	rs1012627	20576652	G	A	0.4816500	-0.0256199	0.0036526	1.5E-12
6	CDKAL1	rs1012626	20577330	G	T	0.4814970	-0.0256028	0.0036560	1.6E-12
6	CDKAL1	rs9350261	20579716	C	T	0.4818960	-0.0257274	0.0036562	1.3E-12
6	CDKAL1	rs9368204	20580662	G	T	0.4711000	-0.0264704	0.0036640	2.9E-13
6	CDKAL1	rs9358346	20580811	T	C	0.4715750	-0.0264466	0.0036744	4.4E-13
6	CDKAL1	rs9460523	20581912	A	C	0.4710460	-0.0269891	0.0036682	1.2E-13
6	CDKAL1	rs9465816	20581913	G	T	0.4707930	-0.0267543	0.0036647	1.7E-13
6	CDKAL1	rs9350262	20584192	G	A	0.4766750	-0.0263249	0.0036637	5.4E-13
6	CDKAL1	rs4712507	20584909	G	A	0.4757420	-0.0260495	0.0036670	1.1E-12
6	CDKAL1	rs9348436	20585150	G	A	0.4748680	-0.0257699	0.0036713	2.5E-12
6	CDKAL1	rs9368206	20585206	A	G	0.4748510	-0.0255860	0.0036728	3.2E-12
6	CDKAL1	rs9368207	20585242	T	C	0.4759240	-0.0259137	0.0036744	1.7E-12
6	CDKAL1	rs9368209	20590056	G	C	0.4762980	-0.0263852	0.0036656	6.3E-13
6	CDKAL1	rs9358349	20593421	A	G	0.4741960	-0.0260813	0.0036660	1.3E-12
6	CDKAL1	rs4710934	20594436	T	G	0.4741960	-0.0260712	0.0036661	1.4E-12
6	CDKAL1	rs113016089	20594520	C	T	0.4716110	-0.0259254	0.0036785	1.7E-12
6	CDKAL1	rs67121595	20594861	G	C	0.4743260	-0.0261699	0.0036664	1.1E-12
6	CDKAL1	rs73386591	20595035	A	G	0.4741920	-0.0260795	0.0036661	1.3E-12
6	CDKAL1	rs9358350	20595961	G	A	0.4764560	-0.0264034	0.0036654	6.2E-13
6	CDKAL1	rs11758281	20597087	G	A	0.4778140	-0.0264052	0.0036640	5.0E-13
6	CDKAL1	rs9366357	20599397	C	T	0.4812320	-0.0256143	0.0036598	2.3E-12
6	CDKAL1	rs2294809	20599657	C	T	0.4831800	-0.0256519	0.0036595	1.9E-12
6	CDKAL1	rs4712516	20600812	T	G	0.4892740	-0.0253515	0.0036898	5.4E-12
6	CDKAL1	rs10946393	20601462	A	G	0.4812210	-0.0254766	0.0036599	3.2E-12
6	CDKAL1	rs10946394	20601684	A	C	0.4830650	-0.0257230	0.0036589	1.8E-12
6	CDKAL1	rs11964057	20602566	A	G	0.4810920	-0.0255393	0.0036598	2.9E-12
6	CDKAL1	rs4710936	20603594	G	A	0.4811320	-0.0256794	0.0036614	2.4E-12
6	CDKAL1	rs72830645	20603921	C	T	0.4829050	-0.0255790	0.0036713	3.5E-12
6	CDKAL1	rs6925097	20605590	T	C	0.4811100	-0.0257397	0.0036623	2.2E-12
6	CDKAL1	rs2328527	20610486	A	C	0.4872420	-0.0283264	0.0036687	1.1E-14
6	CDKAL1	rs2876574	20610710	T	C	0.4865410	-0.0283587	0.0036676	9.7E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	CDKAL1	rs34877824	20611821	G	A	0.4888300	-0.0283033	0.0036637	1.0E-14
6	CDKAL1	rs9358353	20612493	C	T	0.4888520	-0.0283080	0.0036636	1.1E-14
6	CDKAL1	rs9350265	20612679	C	G	0.4867110	-0.0286183	0.0036631	5.2E-15
6	CDKAL1	rs11752592	20613297	C	T	0.4888220	-0.0283026	0.0036638	1.1E-14
6	CDKAL1	rs9350267	20613305	C	T	0.4888220	-0.0283026	0.0036638	1.1E-14
6	CDKAL1	rs978988	20613544	A	G	0.4888640	-0.0282916	0.0036635	1.1E-14
6	CDKAL1	rs978986	20613696	T	C	0.4889430	-0.0281924	0.0036634	1.3E-14
6	CDKAL1	chr6:20613985_GT_G	20613985	GT	G	0.4885560	-0.0283152	0.0036658	1.1E-14
6	CDKAL1	rs9348439	20614449	T	A	0.4889080	-0.0282933	0.0036633	1.0E-14
6	CDKAL1	rs9356739	20614451	C	G	0.4889080	-0.0282933	0.0036633	1.0E-14
6	CDKAL1	rs9356740	20614483	C	T	0.4913940	-0.0270786	0.0036570	1.1E-13
6	CDKAL1	rs148105915	20616262	G	A	0.4885940	-0.0281732	0.0036654	1.5E-14
6	CDKAL1	rs12528468	20616678	T	G	0.4884150	-0.0280834	0.0036627	1.5E-14
6	CDKAL1	rs12530107	20616949	A	T	0.4895150	-0.0282264	0.0036655	1.3E-14
6	CDKAL1	rs9368212	20616966	C	T	0.4895110	-0.0282328	0.0036655	1.2E-14
6	CDKAL1	rs79501071	20617284	TA	T	0.4864850	-0.0282135	0.0036513	9.3E-15
6	CDKAL1	rs9368213	20617428	T	A	0.4898410	-0.0277856	0.0036524	2.3E-14
6	CDKAL1	rs11966749	20618958	G	T	0.4863200	-0.0280584	0.0036524	1.2E-14
6	CDKAL1	rs59621846	20618973	C	G	0.4862200	-0.0281198	0.0036521	1.1E-14
6	CDKAL1	rs9350268	20619772	A	G	0.4864530	-0.0280643	0.0036512	1.3E-14
6	CDKAL1	rs2069015	20620080	T	G	0.4861940	-0.0281701	0.0036596	1.2E-14
6	CDKAL1	rs10214549	20620886	A	G	0.3708680	-0.0212571	0.0038405	1.1E-08
6	CDKAL1	rs59800273	20620906	G	A	0.3301430	0.0440706	0.0039263	2.2E-30
6	CDKAL1	rs61663643	20620924	G	A	0.3302740	0.0437682	0.0039347	5.3E-30
6	CDKAL1	rs72657614	20621174	G	T	0.3623050	-0.0262794	0.0038123	2.0E-12
6	CDKAL1	rs9295472	20622121	G	C	0.3562270	0.0469349	0.0038325	1.9E-36
6	CDKAL1	rs5874775	20622732	GCTAT	G	0.3619060	-0.0272054	0.0037964	2.3E-13
6	CDKAL1	rs1569658	20622773	C	A	0.3621550	-0.0272358	0.0037946	2.1E-13
6	CDKAL1	rs5028948	20622974	T	C	0.3642350	-0.0264242	0.0037852	8.3E-13
6	CDKAL1	rs6456360	20623161	T	C	0.3646160	-0.0269819	0.0037846	2.8E-13
6	CDKAL1	rs6456361	20623163	G	A	0.3646160	-0.0269819	0.0037846	2.8E-13
6	CDKAL1	rs6456362	20623170	T	G	0.3646160	-0.0269819	0.0037846	2.8E-13
6	CDKAL1	rs6922571	20623374	T	C	0.3641140	-0.0270098	0.0037878	3.0E-13
6	CDKAL1	rs9465836	20623740	G	A	0.3639330	-0.0265339	0.0037836	6.8E-13
6	CDKAL1	rs9465837	20623948	G	C	0.3582250	0.0461215	0.0038118	1.3E-35
6	CDKAL1	rs714831	20624127	T	C	0.3639850	-0.0265508	0.0037831	6.5E-13
6	CDKAL1	chr6:20624373_GT_G	20624373	GT	G	0.3639860	-0.0265518	0.0037831	6.5E-13
6	CDKAL1	rs9356741	20624869	T	C	0.3673220	-0.0269918	0.0037759	2.2E-13
6	CDKAL1	rs9366358	20624870	G	A	0.3674050	-0.0271549	0.0037754	1.6E-13
6	CDKAL1	rs9356742	20625036	T	C	0.3673720	-0.0269381	0.0037761	2.5E-13
6	CDKAL1	rs2206579	20625403	G	A	0.2747670	-0.0224834	0.0040926	1.4E-08
6	CDKAL1	rs76235859	20626102	C	T	0.2747290	-0.0224413	0.0040929	1.5E-08
6	CDKAL1	rs6917583	20626151	A	G	0.3672580	-0.0271693	0.0037769	1.6E-13
6	CDKAL1	rs6917599	20626178	A	G	0.3640120	-0.0265381	0.0037832	6.6E-13
6	CDKAL1	rs13437429	20626420	T	C	0.3553160	0.0467753	0.0038179	1.7E-36
6	CDKAL1	rs4515379	20627210	G	C	0.3561380	0.0460705	0.0038209	1.7E-35
6	CDKAL1	rs2223620	20627546	T	C	0.2745890	-0.0224940	0.0040949	1.5E-08
6	CDKAL1	rs9465839	20627660	G	A	0.2746810	-0.0224411	0.0040933	1.5E-08
6	CDKAL1	rs9465841	20629477	T	C	0.3584350	0.0459881	0.0038109	1.9E-35
6	CDKAL1	rs9465842	20629557	C	G	0.2746530	-0.0224591	0.0040936	1.5E-08
6	CDKAL1	rs9460535	20629627	G	C	0.3642280	-0.0264401	0.0037843	8.2E-13
6	CDKAL1	rs9465843	20629850	A	G	0.3654420	-0.0265853	0.0037863	7.0E-13
6	CDKAL1	rs9465844	20630241	G	A	0.3644580	-0.0264618	0.0037858	8.1E-13
6	CDKAL1	rs2328528	20631314	T	A	0.3522410	0.0468049	0.0038297	4.5E-36
6	CDKAL1	rs2328529	20631722	A	C	0.3233190	0.0437065	0.0039235	3.1E-30
6	CDKAL1	rs9460537	20631879	T	C	0.3527440	0.0468561	0.0038330	4.6E-36
6	CDKAL1	rs17224527	20632535	A	T	0.2647570	-0.0222305	0.0041470	4.1E-08
6	CDKAL1	rs9465845	20633066	T	G	0.4638750	-0.0316669	0.0036690	5.2E-19
6	CDKAL1	rs7768642	20633676	A	G	0.3521960	0.0469722	0.0038322	2.9E-36
6	CDKAL1	rs56241903	20633896	C	T	0.3522560	0.0468901	0.0038316	3.6E-36
6	CDKAL1	rs9465846	20634110	T	C	0.3522650	0.0468757	0.0038319	3.9E-36
6	CDKAL1	rs9465847	20634197	T	G	0.3522730	0.0469012	0.0038326	3.3E-36
6	CDKAL1	rs7755830	20634655	C	T	0.4493970	-0.0320030	0.0036761	3.1E-19
6	CDKAL1	rs7756031	20634795	C	T	0.4613680	-0.0317233	0.0036678	4.8E-19
6	CDKAL1	rs6940200	20635031	T	C	0.3518400	0.0466803	0.0038364	1.0E-35
6	CDKAL1	chr6:20635488_AT_A	20635488	A	AT	0.3581280	0.0462076	0.0038278	2.0E-35
6	CDKAL1	rs7751957	20637778	G	C	0.3546920	0.0470823	0.0038306	1.8E-36
6	CDKAL1	rs7341291	20638647	T	C	0.4477350	-0.0316777	0.0036897	7.0E-19
6	CDKAL1	rs6921014	20638747	A	G	0.4639590	-0.0313295	0.0036827	2.0E-18
6	CDKAL1	rs9465850	20639178	T	C	0.3458740	0.0480407	0.0038568	1.8E-37
6	CDKAL1	rs7758612	20639373	A	G	0.4707610	-0.0328444	0.0036800	3.0E-20
6	CDKAL1	rs9465851	20640085	T	C	0.4669550	-0.0322556	0.0036634	1.2E-19
6	CDKAL1	rs9460538	20640306	A	G	0.4672730	-0.0322395	0.0036578	1.3E-19
6	CDKAL1	rs4710938	20640673	G	A	0.4650110	-0.0323911	0.0036393	6.6E-20
6	CDKAL1	rs9348440	20641105	T	C	0.3439180	0.0446430	0.0038180	1.4E-32
6	CDKAL1	rs9465852	20641669	A	G	0.4671460	-0.0325366	0.0036417	4.4E-20
6	CDKAL1	rs72334115	20641830	G	GGGTGTC	0.4589360	-0.0324539	0.0036771	1.1E-19
6	CDKAL1	rs6925328	20642554	G	A	0.4669080	-0.0326203	0.0036376	3.5E-20
6	CDKAL1	rs4235999	20642991	G	C	0.4637550	-0.0327099	0.0036314	2.0E-20
6	CDKAL1	rs2328531	20643521	G	A	0.4663740	-0.0326565	0.0036320	2.4E-20
6	CDKAL1	rs4710939	20644713	G	A	0.4630910	-0.0327331	0.0036340	2.4E-20
6	CDKAL1	rs72830669	20644895	G	A	0.3583460	0.0474358	0.0037902	1.6E-37
6	CDKAL1	rs143684160	20645768	A	AATTTT	0.4633450	-0.0326591	0.0036333	2.7E-20
6	CDKAL1	rs11965062	20647731	A	T	0.4636070	-0.0325559	0.0036324	3.0E-20
6	CDKAL1	rs9460540	20648531	G	A	0.4516760	-0.0326510	0.0036403	3.1E-20
6	CDKAL1	rs6456364	20649023	T	A	0.3590730	0.0475230	0.0037860	7.9E-38
6	CDKAL1	rs2876576	20650177	G	A	0.4633630	-0.0324695	0.0036350	4.2E-20
6	CDKAL1	rs7766844	20650590	A	G	0.3583800	0.0473767	0.0037847	1.4E-37
6	CDKAL1	rs2050225	20651890	C	G	0.4636860	-0.0324827	0.0036336	4.1E-20
6	CDKAL1	rs9295474	20652486	G	C	0.3736150	0.0465836	0.0037533	5.6E-37
6	CDKAL1	rs9295475	20652534	G	A	0.3591320	0.0477499	0.0037839	3.5E-38
6	CDKAL1	rs2328545	20653319	C	G	0.3574170	0.0480479	0.0037866	1.3E-38
6	CDKAL1	rs2876582	20653569	G	A	0.3569160	0.0481145	0.0037913	1.3E-38
6	CDKAL1	rs6456366	20654069	C	G	0.3561050	0.0486271	0.0037982	2.4E-39
6	CDKAL1	rs9358355	20654666	C	T	0.3575500	0.0481142	0.0037878	1.2E-38
6	CDKAL1	rs9368216	20654879	G	A	0.3574440	0.0480393	0.0037877	1.4E-38
6	CDKAL1	rs4712522	20656569	G	C	0.3595050	0.0478158	0.0037819	2.8E-38
6	CDKAL1	rs4712523	20657333	G	A	0.3721140	0.0471824	0.0037567	9.4E-38
6	CDKAL1	rs4712524	20657634	G	A	0.3599470	0.0479388	0.0037802	1.8E-38
6	CDKAL1	rs4710940	20657781	C	A	0.3605520	0.0477386	0.0037809	3.4E-38

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	CDKAL1	rs142204888	20658566	GTTTGT	G	0.3590180	0.0475494	0.0037863	5.8E-38
6	CDKAL1	rs149618394	20658649	T	TGTAATA	0.3597320	0.0477861	0.0037813	3.0E-38
6	CDKAL1	rs67077402	20658747	C	A	0.3598070	0.0478599	0.0037808	2.4E-38
6	CDKAL1	rs6906327	20659228	A	G	0.3598990	0.0479270	0.0037810	1.9E-38
6	CDKAL1	rs6456367	20659356	A	T	0.3597990	0.0476208	0.0037808	6.4E-38
6	CDKAL1	rs6456368	20659575	C	T	0.3598210	0.0478624	0.0037807	2.3E-38
6	CDKAL1	rs6456369	20660134	C	T	0.3600600	0.0478221	0.0037800	2.9E-38
6	CDKAL1	rs10946396	20660459	A	G	0.3600320	0.0478712	0.0037802	2.6E-38
6	CDKAL1	rs10946397	20660462	T	A	0.3600600	0.0478221	0.0037800	2.9E-38
6	CDKAL1	rs11759505	20660500	C	T	0.3597850	0.0478577	0.0037803	2.6E-38
6	CDKAL1	rs10946398	20660803	C	A	0.3597940	0.0478513	0.0037802	2.7E-38
6	CDKAL1	rs7774594	20660912	A	T	0.3597840	0.0478457	0.0037803	2.9E-38
6	CDKAL1	rs7754840	20661019	C	G	0.3596050	0.0477403	0.0037797	4.4E-38
6	CDKAL1	rs9460544	20661298	T	G	0.3599570	0.0478464	0.0037814	2.7E-38
6	CDKAL1	rs9460545	20661319	C	T	0.3597820	0.0478424	0.0037805	2.8E-38
6	CDKAL1	rs56676529	20661606	A	C	0.3535020	0.0471019	0.0038199	2.3E-36
6	CDKAL1	rs58723416	20661611	C	T	0.3571750	0.0472768	0.0037945	2.8E-37
6	CDKAL1	rs6456370	20661882	G	A	0.3598200	0.0478480	0.0037809	2.8E-38
6	CDKAL1	rs979614	20661892	G	A	0.4518540	-0.0326278	0.0036504	3.6E-20
6	CDKAL1	rs35456723	20661986	C	T	0.3594330	0.0476510	0.0037826	6.4E-38
6	CDKAL1	rs9368218	20662361	A	G	0.3596200	0.0476825	0.0037813	4.9E-38
6	CDKAL1	rs4712525	20662735	T	C	0.3597660	0.0477495	0.0037796	3.9E-38
6	CDKAL1	rs4712526	20662804	A	T	0.3596230	0.0476944	0.0037812	4.7E-38
6	CDKAL1	chr6:20663232_G_GTT	20663232	GTT	G	0.3549200	0.0473379	0.0038083	3.3E-37
6	CDKAL1	rs9460546	20663401	G	T	0.3596130	0.0476548	0.0037813	5.3E-38
6	CDKAL1	rs9465860	20663869	T	C	0.3575720	0.0478260	0.0037948	5.4E-38
6	CDKAL1	rs742642	20664850	A	G	0.3571570	0.0476890	0.0037868	5.5E-38
6	CDKAL1	rs7748382	20665318	A	G	0.3596400	0.0476885	0.0037817	4.3E-38
6	CDKAL1	chr6:20665330_GA_G	20665330	G	GA	0.3571470	0.0476820	0.0037868	5.4E-38
6	CDKAL1	rs28665000	20665360	A	G	0.3571470	0.0476820	0.0037868	5.4E-38
6	CDKAL1	rs58048170	20665499	C	T	0.3571470	0.0476820	0.0037868	5.4E-38
6	CDKAL1	rs59036478	20665676	ATAACTT	A	0.3593660	0.0474483	0.0037843	1.4E-37
6	CDKAL1	rs7772603	20665715	C	T	0.3602330	0.0473029	0.0037867	2.7E-37
6	CDKAL1	rs7752780	20665791	A	G	0.3587580	0.0473730	0.0037850	2.0E-37
6	CDKAL1	rs7752906	20665824	A	G	0.3595900	0.0476536	0.0037812	5.3E-38
6	CDKAL1	rs2206739	20666013	G	A	0.3595720	0.0476610	0.0037814	5.2E-38
6	CDKAL1	rs2206738	20666015	G	A	0.3593700	0.0476033	0.0037828	6.4E-38
6	CDKAL1	rs35540121	20667007	T	TG	0.3553010	0.0484132	0.0038073	1.2E-38
6	CDKAL1	rs9358356	20667151	C	T	0.3566480	0.0488692	0.0038035	2.0E-39
6	CDKAL1	rs9356743	20667457	T	C	0.4245700	0.0341136	0.0036793	9.3E-21
6	CDKAL1	chr6:20667482_A_AC	20667482	AC	A	0.4483920	0.0398737	0.0036759	8.7E-28
6	CDKAL1	rs9350270	20667568	G	A	0.4649620	0.0389822	0.0036602	2.6E-27
6	CDKAL1	rs72657615	20670853	C	A	0.1397680	-0.0282845	0.0052912	4.2E-08
6	CDKAL1	rs111629317	20672892	G	T	0.2006130	-0.0272790	0.0045975	3.2E-10
6	CDKAL1	rs7451008	20673649	C	T	0.4549580	0.0437569	0.0036604	4.6E-35
6	CDKAL1	rs9368219	20674460	T	C	0.3431780	0.0551004	0.0038323	1.7E-50
6	CDKAL1	rs1012635	20675064	G	A	0.4647710	-0.0382786	0.0036496	3.2E-28
6	CDKAL1	rs35261542	20675561	A	C	0.3450630	0.0553379	0.0038231	3.9E-51
6	CDKAL1	rs34499031	20676183	TAA	T	0.3447450	0.0555282	0.0038268	3.0E-51
6	CDKAL1	rs12660618	20677079	T	G	0.4478400	0.0442978	0.0036816	2.4E-35
6	CDKAL1	rs1569699	20679079	G	T	0.4589460	0.0427243	0.0036439	1.2E-33
6	CDKAL1	rs7756992	20679478	G	A	0.4589860	0.0426785	0.0036434	1.6E-33
6	CDKAL1	rs9348441	20680447	A	T	0.3477960	0.0543771	0.0038140	2.1E-49
6	CDKAL1	rs35612982	20682391	C	T	0.3460250	0.0544928	0.0038194	1.4E-49
6	CDKAL1	rs60229538	20682552	A	TCGTGA	0.3419260	0.0548640	0.0038444	2.1E-49
6	CDKAL1	rs9350271	20682933	A	G	0.3470790	0.0547094	0.0038205	1.0E-49
6	CDKAL1	rs9356744	20685255	C	T	0.3485050	0.0547108	0.0038120	4.9E-50
6	CDKAL1	rs7766070	20686342	A	C	0.3480170	0.0549875	0.0038156	1.9E-50
6	CDKAL1	rs67131976	20686647	T	C	0.3455900	0.0552451	0.0038199	8.1E-51
6	CDKAL1	rs9368222	20686765	A	C	0.3477740	0.0547183	0.0038155	6.5E-50
6	CDKAL1	rs61243430	20691297	G	GAGC	0.3453990	0.0550539	0.0038229	2.3E-50
6	CDKAL1	rs138420022	20693466	A	AT	0.3455120	0.0550264	0.0038212	2.3E-50
6	CDKAL1	rs4710941	20693997	T	C	0.3432020	0.0551971	0.0038322	1.7E-50
6	CDKAL1	rs2206734	20694653	T	C	0.3454660	0.0549110	0.0038200	3.0E-50
6	CDKAL1	rs181914052	20700365	T	A	0.1950520	-0.0260852	0.0046711	5.2E-09
6	CDKAL1	rs6931514	20703721	G	A	0.4586600	0.0427704	0.0036533	1.6E-33
6	CDKAL1	rs72830699	20704193	A	G	0.4552690	0.0430991	0.0036523	5.4E-34
6	CDKAL1	rs11753081	20705359	G	T	0.4552470	0.0421359	0.0036515	1.0E-32
6	CDKAL1	rs6901559	20705999	A	G	0.4608040	0.0422385	0.0036525	1.0E-32
6	CDKAL1	rs77402376	20706749	A	T	0.1913260	-0.0268193	0.0046751	1.4E-09
6	CDKAL1	rs10536170	20707989	G	GTATAT	0.3429620	0.0544236	0.0038337	1.0E-48
6	CDKAL1	rs3749925	20712230	G	C	0.2011610	-0.0258702	0.0045910	1.6E-09
6	CDKAL1	rs1040558	20713475	G	A	0.4623280	0.0421464	0.0036501	1.4E-32
6	CDKAL1	chr6:20714111_C_CT	20714111	CT	C	0.4596040	0.0420297	0.0036597	2.2E-32
6	CDKAL1	rs6456371	20714235	C	T	0.4613020	0.0422103	0.0036498	9.8E-33
6	CDKAL1	rs10946402	20715595	G	T	0.4646700	0.0411979	0.0036491	2.1E-31
6	CDKAL1	rs9295478	20716022	A	G	0.4569750	0.0428482	0.0036483	9.6E-34
6	CDKAL1	rs2328547	20716339	G	A	0.4613730	0.0417887	0.0036462	3.8E-32
6	CDKAL1	rs3060781	20716553	CAG	C	0.4614150	0.0417243	0.0036459	4.4E-32
6	CDKAL1	rs2328548	20716727	A	G	0.4614910	0.0416798	0.0036465	4.9E-32
6	CDKAL1	rs11427712	20716815	TC	T	0.4615350	0.0417392	0.0036472	4.5E-32
6	CDKAL1	rs6935599	20716864	G	A	0.4614040	0.0417072	0.0036458	4.8E-32
6	CDKAL1	rs9465871	20717024	C	T	0.4683590	0.0406145	0.0036408	3.3E-30
6	CDKAL1	rs10946403	20717173	G	A	0.4616570	0.0414228	0.0036459	9.8E-32
6	CDKAL1	rs2328549	20718009	T	A	0.4906700	0.0386683	0.0036855	6.8E-27
6	CDKAL1	rs9358357	20718914	G	A	0.4562230	0.0418387	0.0036566	4.5E-32
6	CDKAL1	rs9368224	20719001	A	T	0.4562550	0.0417971	0.0036563	5.2E-32
6	CDKAL1	rs9358358	20719162	C	A	0.4559510	0.0415180	0.0036568	1.4E-31
6	CDKAL1	rs9460550	20719330	A	G	0.4561620	0.0418667	0.0036566	4.3E-32
6	CDKAL1	rs9356746	20720048	C	T	0.4558500	0.0415434	0.0036576	1.3E-31
6	CDKAL1	rs9350272	20720587	G	A	0.4430350	0.0436870	0.0036672	5.3E-34
6	CDKAL1	rs61128991	20720948	T	G	0.4426690	0.0441987	0.0036707	1.3E-34
6	CDKAL1	rs9368225	20721490	A	G	0.4432290	0.0440893	0.0036685	1.6E-34
6	CDKAL1	rs9368226	20722826	C	T	0.4440650	0.0418212	0.0036686	4.5E-31
6	CDKAL1	rs6903175	20724003	G	A	0.4445980	0.0421350	0.0036655	1.4E-31
6	CDKAL1	rs6903744	20724019	A	G	0.4432030	0.0420887	0.0036664	1.3E-31
6	CDKAL1	rs12111351	20724327	G	T	0.4448470	0.0423789	0.0036632	5.5E-32
6	CDKAL1	rs4712536	20724544	T	C	0.3545160	-0.0305748	0.0038021	3.6E-17
6	CDKAL1	rs9356747	20724776	A	T	0.4452640	0.0421471	0.0036535	7.2E-32
6	CDKAL1	rs9356748	20724866	A	T	0.4446250	0.0418795	0.0036546	1.7E-31

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	CDKAL1	rs7767391	20725009	C	T	0.4449010	0.0420887	0.0036534	8.4E-32
6	CDKAL1	rs7747752	20725192	C	G	0.4452110	0.0421023	0.0036526	7.5E-32
6	CDKAL1	rs6915155	20725709	T	G	0.3534700	-0.0307211	0.0038094	2.8E-17
6	CDKAL1	rs4712537	20727339	A	C	0.4431900	0.0419200	0.0036673	3.2E-31
6	CDKAL1	rs6928012	20728282	T	C	0.3562740	-0.0307787	0.0037860	1.2E-17
6	CDKAL1	rs56017320	20735955	T	C	0.3340770	0.0300869	0.0039090	1.0E-14
6	CDKAL1	rs58789330	20736161	G	TAGCAA	0.3321280	0.0298907	0.0039246	1.5E-14
6	CDKAL1	rs9688471	20736586	T	C	0.3342260	0.0302815	0.0039066	7.4E-15
6	CDKAL1	rs72832313	20741449	C	T	0.3367420	0.0281518	0.0038891	4.3E-13
6	CDKAL1	rs72832315	20743270	A	C	0.3337130	0.0287074	0.0038975	1.3E-13
6	CDKAL1	rs56251119	20749670	T	C	0.3343020	0.0284096	0.0038799	1.4E-13
6	CDKAL1	rs118099849	20749953	A	G	0.3353660	0.0279392	0.0038711	3.5E-13
6	CDKAL1	rs113622454	20753160	C	CA	0.3356990	0.0279249	0.0038697	3.1E-13
6	CDKAL1	rs143631482	20753261	T	TG	0.3356980	0.0278946	0.0038697	3.3E-13
6	CDKAL1	rs74185130	20753262	T	G	0.3284070	0.0274228	0.0039133	1.6E-12
6	CDKAL1	rs2819994	20753705	T	C	0.3356980	0.0278946	0.0038697	3.3E-13
6	CDKAL1	rs2493995	20753888	A	G	0.3351870	0.0277420	0.0038732	4.2E-13
6	CDKAL1	rs111711269	20754290	CT	C	0.3346570	0.0277473	0.0038753	5.5E-13
6	CDKAL1	rs2745931	20754395	A	T	0.3346580	0.0277420	0.0038753	5.5E-13
6	CDKAL1	rs2745930	20754506	C	T	0.3346580	0.0277420	0.0038753	5.5E-13
6	CDKAL1	rs2819996	20755701	A	G	0.3347050	0.0277639	0.0038758	5.6E-13
6	CDKAL1	rs2473651	20756546	C	T	0.3362270	0.0276735	0.0038630	5.2E-13
6	CDKAL1	rs72832323	20757269	A	G	0.3353320	0.0279471	0.0038679	3.2E-13
6	CDKAL1	rs2819998	20758295	C	G	0.3361140	0.0275458	0.0038636	6.3E-13
6	CDKAL1	rs2820001	20758712	G	T	0.3362230	0.0275515	0.0038635	5.9E-13
6	CDKAL1	rs72832325	20758979	T	G	0.3354780	0.0279516	0.0038676	3.3E-13
6	CDKAL1	rs55987458	20759358	C	A	0.3358060	0.0276325	0.0038655	5.8E-13
6	CDKAL1	rs6909558	20759946	T	C	0.3349790	0.0274855	0.0038713	9.2E-13
6	CDKAL1	rs12664021	20760849	T	C	0.3350040	0.0273802	0.0038704	1.1E-12
6	CDKAL1	rs72832326	20761066	G	A	0.3348180	0.0274851	0.0038707	9.2E-13
6	CDKAL1	rs57087943	20764241	T	C	0.3350440	0.0276292	0.0038713	6.3E-13
6	CDKAL1	rs59840719	20764282	C	T	0.3352530	0.0276453	0.0038699	6.2E-13
6	CDKAL1	rs60893008	20764773	T	C	0.3350280	0.0276367	0.0038712	6.3E-13
6	CDKAL1	rs7452218	20767240	T	C	0.3356800	0.0275252	0.0038661	6.9E-13
6	CDKAL1	rs72832333	20770162	T	C	0.3357730	0.0273931	0.0038653	8.6E-13
6	CDKAL1	rs72832335	20771132	G	A	0.3363330	0.0273809	0.0038654	9.2E-13
6	CDKAL1	rs72832338	20775181	A	G	0.3354530	0.0279970	0.0038715	3.8E-13
6	CDKAL1	rs4493738	20775429	G	A	0.3377820	0.0279898	0.0038585	3.0E-13
6	CDKAL1	rs72832344	20786267	T	C	0.3371900	0.0283451	0.0038603	1.5E-13
6	CDKAL1	rs72832348	20790586	T	C	0.3357750	0.0283902	0.0038678	1.6E-13
6	CDKAL1	rs72832359	20815661	G	A	0.3351450	0.0275443	0.0038548	6.6E-13
6	CDKAL1	rs12665734	20818162	G	A	0.3300760	0.0261003	0.0038727	1.5E-11
6	CDKAL1	chr6:20819569_AC_A	20819569	A	AC	0.3296020	0.0261658	0.0038771	1.4E-11
6	CDKAL1	rs115309952	20819571	G	C	0.3296020	0.0261658	0.0038771	1.4E-11
6	CDKAL1	rs9368244	20831934	C	T	0.4187680	0.0219293	0.0036922	1.7E-09
6	CDKAL1	rs9350288	20832597	A	T	0.4187480	0.0219671	0.0036921	1.5E-09
6	CDKAL1	rs72832371	20833205	T	C	0.3351420	0.0273380	0.0038527	8.8E-13
6	CDKAL1	rs72832373	20833328	A	G	0.3351530	0.0273372	0.0038526	8.9E-13
6	CDKAL1	rs9465914	20835982	G	A	0.3365080	0.0268075	0.0038495	2.3E-12
6	CDKAL1	rs9465915	20836118	A	G	0.4181040	0.0219860	0.0036935	1.6E-09
6	CDKAL1	rs60568948	20836736	C	T	0.3355920	0.0271363	0.0038503	1.3E-12
6	CDKAL1	chr6:20839106_C_CT	20839106	CT	C	0.3292400	0.0267977	0.0038913	3.8E-12
6	CDKAL1	rs7765060	20841061	C	G	0.3359300	0.0271723	0.0038505	1.1E-12
6	CDKAL1	rs11967047	20841249	C	T	0.3339870	0.0262720	0.0038539	4.2E-12
6	CDKAL1	rs11967068	20841362	C	T	0.3358330	0.0270914	0.0038513	1.3E-12
6	CDKAL1	rs72832379	20844005	A	G	0.3357620	0.0270625	0.0038429	1.4E-12
6	CDKAL1	rs72832380	20844462	A	G	0.3367070	0.0268337	0.0038416	2.0E-12
6	CDKAL1	rs142784970	20844707	AAAC	A	0.4217420	0.0221198	0.0037009	1.2E-09
6	CDKAL1	rs72832381	20844712	G	A	0.3371160	0.0274750	0.0038453	7.0E-13
6	CDKAL1	rs7751431	20844843	A	T	0.3369890	0.0267879	0.0038400	2.0E-12
6	CDKAL1	rs6920045	20845795	C	T	0.3367880	0.0269144	0.0038416	1.7E-12
6	CDKAL1	rs6941508	20846372	C	A	0.3376120	0.0266090	0.0038405	3.3E-12
6	CDKAL1	rs7742468	20847157	T	C	0.3363650	0.0271899	0.0038424	1.1E-12
6	CDKAL1	rs11417705	20848156	C	CG	0.4180990	0.0224343	0.0036896	6.8E-10
6	CDKAL1	rs7753271	20849181	T	C	0.3366470	0.0269354	0.0038416	1.5E-12
6	CDKAL1	rs12663147	20850149	A	T	0.3371500	0.0269262	0.0038412	1.6E-12
6	CDKAL1	chr6:20851020_GT_G	20851020	GT	G	0.3375140	0.0270388	0.0038476	1.3E-12
6	CDKAL1	rs4712556	20856472	A	G	0.4163110	0.0226900	0.0036898	3.9E-10
6	CDKAL1	rs16884229	20857694	C	T	0.3363980	0.0269301	0.0038422	1.8E-12
6	CDKAL1	rs56091419	20857899	A	G	0.3345360	0.0274707	0.0038491	6.8E-13
6	CDKAL1	rs4712558	20858029	G	C	0.4184870	0.0222802	0.0036843	8.4E-10
6	CDKAL1	rs9366363	20858621	T	G	0.3355360	0.0272418	0.0038427	7.7E-13
6	CDKAL1	rs9350291	20860611	A	G	0.3372800	0.0267803	0.0038406	2.1E-12
6	CDKAL1	rs9350292	20860717	A	G	0.3374230	0.0266228	0.0038414	2.9E-12
6	CDKAL1	rs16901585	20860921	A	G	0.3314770	0.0271675	0.0038967	3.5E-12
6	CDKAL1	rs5007237	20860995	A	T	0.3355110	0.0272268	0.0038695	1.8E-12
6	CDKAL1	rs9356757	20862380	A	G	0.3372620	0.0269419	0.0038384	1.3E-12
6	CDKAL1	rs9368246	20866626	C	T	0.4211690	0.0223985	0.0036873	6.9E-10
6	CDKAL1	rs10554344	20867583	G	GAC	0.3354930	0.0270587	0.0038467	1.3E-12
6	CDKAL1	rs55738226	20871435	C	T	0.3361470	0.0271057	0.0038455	1.3E-12
6	CDKAL1	rs72832387	20872572	G	A	0.3361750	0.0270958	0.0038452	1.4E-12
6	CDKAL1	rs62398106	20874920	T	A	0.3359570	0.0271328	0.0038451	1.2E-12
6	CDKAL1	rs62398107	20875581	T	C	0.3359270	0.0270661	0.0038447	1.4E-12
6	CDKAL1	rs4077403	20876279	T	G	0.3363960	0.0270763	0.0038431	1.2E-12
6	CDKAL1	rs62398108	20878895	G	A	0.3360860	0.0271774	0.0038463	1.2E-12
6	CDKAL1	rs56027426	20892569	A	G	0.3315430	0.0262246	0.0038886	1.0E-11
6	CDKAL1	rs5874792	20894204	A	AT	0.4151380	0.0216110	0.0037228	4.1E-09
6	CDKAL1	rs62398111	20897431	A	G	0.3321420	0.0256525	0.0039127	3.4E-11
6	CDKAL1	rs7759877	20897909	C	T	0.4175200	0.0214253	0.0037556	5.9E-09
6	CDKAL1	rs9358376	20898018	T	G	0.4165380	0.0210938	0.0037598	9.5E-09
6	GLP1R	rs10305435	39056165	T	C	0.1684890	-0.0360071	0.0049654	1.2E-14
6	GLP1R	rs3765468	39065817	A	G	0.2095830	0.0269096	0.0044694	4.3E-11
6	GLP1R	rs3765467	39065819	A	G	0.2413110	-0.0452237	0.0042577	1.8E-28
6	GLP1R	rs57248948	39068402	GC	G	0.2093030	0.0267492	0.0044720	5.4E-11
6	GLP1R	rs80228310	39068969	T	C	0.1191020	0.0312285	0.0056633	2.1E-08
6	GLP1R	rs144285292	39069399	T	C	0.2095670	0.0269059	0.0044694	4.4E-11
6	GLP1R	rs113120569	39069526	A	G	0.2127760	0.0283044	0.0044450	4.3E-12
6	GLP1R	rs9380826	39069886	C	G	0.2413110	-0.0451971	0.0042575	1.9E-28
6	GLP1R	rs4711574	39070179	G	A	0.2119290	0.0284970	0.0044528	3.8E-12
6	GLP1R	rs9296285	39072693	G	A	0.2384770	-0.0446941	0.0042759	7.7E-28

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	GLP1R	rs10305479	39073934	T	C	0.2087230	0.0272184	0.0044785	3.3E-11
6	GLP1R	rs932443	39074558	C	T	0.3418300	0.0232546	0.0039068	1.7E-09
6	GLP1R	rs2268647	39075402	T	C	0.2284490	0.0280394	0.0043426	2.5E-12
6	GLP1R	rs2268646	39075740	T	C	0.2128640	0.0290276	0.0044474	1.8E-12
6	GLP1R	rs2268645	39076216	A	G	0.2099730	0.0276779	0.0044683	1.8E-11
6	GLP1R	rs1077680	39077806	T	C	0.2104210	0.0276443	0.0044620	1.9E-11
6	GLP1R	rs761387	39078425	G	A	0.2103410	0.0276745	0.0044639	1.9E-11
6	GLP1R	rs742762	39078868	C	A	0.3181840	-0.0404275	0.0039755	5.4E-26
6	GLP1R	rs742761	39078879	T	C	0.2339140	-0.0463014	0.0043366	3.4E-29
6	GLP1R	rs761386	39079095	T	C	0.2097640	0.0276185	0.0044696	2.7E-11
6	GLP1R	chr6:39079259_CAG_C	39079259	C	CAG	0.2099170	0.0276762	0.0044695	2.5E-11
6	SAYS1	rs3823212	39110849	T	G	0.0805637	-0.0370430	0.0067164	8.3E-09
6	SAYS1	rs78992609	39113912	A	G	0.0750717	-0.0395256	0.0069231	2.9E-09
6	KCNK5	rs3892126	39222183	G	C	0.0814959	-0.0380174	0.0067657	5.1E-09
6	RFX6	rs339343	116896219	T	C	0.3526890	-0.0200983	0.0037854	4.1E-08
6	RFX6	rs339347	116898361	C	A	0.3523720	-0.0201496	0.0037858	3.7E-08
6	RFX6	rs339299	116900999	G	T	0.3523660	-0.0201023	0.0037860	4.0E-08
6	RFX6	rs339300	116901066	C	T	0.3523640	-0.0200974	0.0037859	4.0E-08
6	RFX6	rs10706356	116901818	A	AT	0.3523580	-0.0200997	0.0037859	4.0E-08
6	RFX6	rs1321371	116914493	C	G	0.3752780	-0.0207421	0.0037349	1.9E-08
6	RFX6	rs1406982	116915690	A	T	0.3752720	-0.0206567	0.0037344	2.3E-08
6	RFX6	rs1321372	116916361	A	G	0.3752730	-0.0206593	0.0037344	2.2E-08
6	RFX6	rs6936629	116917978	C	T	0.3755840	-0.0204150	0.0037354	3.3E-08
6	RFX6	rs9489066	116918336	C	T	0.3754090	-0.0203969	0.0037336	3.3E-08
6	RFX6	rs1321366	116919430	A	G	0.3753770	-0.0204395	0.0037335	3.1E-08
6	RFX6	rs12202378	116920858	C	T	0.3775660	-0.0219165	0.0037575	4.0E-09
6	RFX6	rs7764347	116922097	C	T	0.3728760	-0.0254751	0.0037416	4.7E-12
6	RFX6	rs7770158	116923211	C	T	0.3739170	-0.0254903	0.0037381	4.2E-12
6	RFX6	rs7774506	116923513	C	T	0.3739750	-0.0254424	0.0037384	4.8E-12
6	RFX6	rs9320585	116923693	G	A	0.3739350	-0.0255977	0.0037383	3.5E-12
6	RFX6	rs9320586	116923734	C	G	0.3739320	-0.0254547	0.0037388	4.6E-12
6	RFX6	rs4946204	116923838	C	T	0.3737530	-0.0251876	0.0037393	7.7E-12
6	RFX6	rs4946205	116924226	C	T	0.3741850	-0.0252923	0.0037400	5.4E-12
6	RFX6	rs9489067	116925266	C	A	0.3737860	-0.0254733	0.0037383	4.4E-12
6	RFX6	rs67292089	116925413	G	GA	0.4536060	-0.0194461	0.0036408	4.1E-08
6	RFX6	rs4946206	116925556	T	C	0.3739280	-0.0255834	0.0037383	3.5E-12
6	RFX6	rs66592749	116925897	A	ATTAG	0.3739020	-0.0255094	0.0037381	4.0E-12
6	RFX6	rs673065	116926095	T	G	0.3739020	-0.0255094	0.0037381	4.0E-12
6	RFX6	rs673906	116926251	G	A	0.3739020	-0.0255094	0.0037381	4.0E-12
6	RFX6	rs675233	116926529	G	A	0.3738440	-0.0255375	0.0037390	3.7E-12
6	RFX6	rs675266	116926552	T	C	0.3738950	-0.0255445	0.0037378	3.8E-12
6	RFX6	rs676152	116926744	C	A	0.3738600	-0.0255359	0.0037379	3.8E-12
6	RFX6	rs611349	116927055	C	T	0.3739210	-0.0254993	0.0037381	4.1E-12
6	RFX6	rs10872150	116927796	G	C	0.4510940	-0.0201755	0.0036587	1.3E-08
6	RFX6	rs594785	116928038	C	A	0.3696840	-0.0260485	0.0037607	1.7E-12
6	RFX6	rs595698	116928221	C	A	0.3739600	-0.0254408	0.0037385	4.8E-12
6	RFX6	rs675811	116928395	T	C	0.3738850	-0.0255416	0.0037381	3.8E-12
6	RFX6	rs675784	116928411	T	C	0.3733280	-0.0258096	0.0037421	2.7E-12
6	RFX6	rs596732	116928462	C	T	0.3739210	-0.0255942	0.0037382	3.4E-12
6	RFX6	rs597688	116928684	G	A	0.3741890	-0.0256863	0.0037393	3.1E-12
6	RFX6	rs673055	116929019	T	C	0.3738320	-0.0256125	0.0037394	3.4E-12
6	RFX6	rs661894	116929224	A	G	0.3739030	-0.0255913	0.0037380	3.5E-12
6	RFX6	rs610979	116929352	C	G	0.3740140	-0.0256705	0.0037390	3.3E-12
6	RFX6	rs657963	116930088	T	C	0.3739000	-0.0256261	0.0037385	3.3E-12
6	RFX6	rs3073158	116930280	T	TAGAC	0.3736200	-0.0254292	0.0037403	4.8E-12
6	RFX6	rs625821	116930332	G	A	0.3739000	-0.0255823	0.0037381	3.5E-12
6	RFX6	rs11361585	116930363	A	AT	0.37113050	-0.0258458	0.0037429	2.6E-12
6	RFX6	rs645745	116930500	T	C	0.3738960	-0.0255759	0.0037381	3.6E-12
6	RFX6	rs627551	116930724	G	A	0.3738800	-0.0255806	0.0037382	3.5E-12
6	RFX6	rs643943	116930928	C	T	0.3739250	-0.0255725	0.0037383	3.5E-12
6	RFX6	rs643550	116930973	A	G	0.3738750	-0.0255697	0.0037381	3.5E-12
6	RFX6	rs643474	116931034	T	C	0.3737370	-0.0255813	0.0037389	3.5E-12
6	RFX6	rs639170	116931084	T	C	0.3739320	-0.0255810	0.0037379	3.4E-12
6	RFX6	rs639646	116931178	G	A	0.3739600	-0.0254183	0.0037373	4.7E-12
6	RFX6	rs631089	116931509	A	C	0.3740000	-0.0254519	0.0037383	4.7E-12
6	RFX6	rs630695	116931596	G	T	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs617426	116932271	T	G	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs616347	116932474	G	A	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs619307	116932702	C	A	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs630434	116932876	C	T	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs630458	116932893	G	A	0.3734280	-0.0253881	0.0037409	5.4E-12
6	RFX6 *	rs35960019	116932961	A	AG	0.3738180	-0.0256067	0.0037385	3.3E-12
6	RFX6 *	rs631642	116933119	A	G	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs632159	116933273	A	T	0.3738680	-0.0255655	0.0037381	3.6E-12
6	RFX6 *	rs5879395	116933300	AG	A	0.4529790	-0.0195603	0.0036417	3.2E-08
6	RFX6 *	rs633898	116933664	G	A	0.3739140	-0.0257212	0.0037387	2.6E-12
6	RFX6 *	rs587174	116934397	G	A	0.3738920	-0.0257664	0.0037394	2.6E-12
6	RFX6 *	rs584917	116934932	G	T	0.3738920	-0.0257664	0.0037394	2.6E-12
6	RFX6 *	rs11320531	116935540	T	TG	0.3738870	-0.0257722	0.0037394	2.5E-12
6	RFX6 *	rs10655223	116935566	TGA	T	0.3738870	-0.0257722	0.0037394	2.5E-12
6	RFX6 *	rs2210715	116935765	G	T	0.4533250	-0.0194197	0.0036411	4.3E-08
6	RFX6 *	rs678375	116935843	C	A	0.3745080	-0.0257130	0.0037389	2.8E-12
6	RFX6 *	rs674621	116935855	C	T	0.3745080	-0.0257130	0.0037389	2.8E-12
6	RFX6 *	rs675495	116936036	T	C	0.3744510	-0.0258218	0.0037403	2.2E-12
6	RFX6 *	rs665401	116936380	C	T	0.3747830	-0.0255585	0.0037443	4.2E-12
6	RFX6 *	rs56234303	116936408	C	CA	0.3718690	-0.0257045	0.0037517	4.0E-12
6	RFX6 *	rs55915982	116936419	C	T	0.3721320	-0.0261205	0.0037533	1.7E-12
6	RFX6 *	rs677383	116936482	A	C	0.3702740	-0.0266768	0.0037701	8.7E-13
6	RFX6 *	rs678230	116936632	T	C	0.3746000	-0.0257118	0.0037412	2.6E-12
6	RFX6 *	rs71012345	116937001	CTTGAG	C	0.3747320	-0.0257803	0.0037417	2.5E-12
6	RFX6 *	rs662657	116937037	G	A	0.3747330	-0.0257698	0.0037417	2.6E-12
6	RFX6 *	rs1761881	116937181	A	G	0.3742230	-0.0257570	0.0037437	2.8E-12
6	RFX6 *	rs6907088	116937511	C	T	0.3741970	-0.0258463	0.0037423	2.3E-12
6	RFX6 *	rs9400975	116937785	C	T	0.3745570	-0.0258003	0.0037411	2.5E-12
6	RFX6 *	rs9374627	116937894	T	C	0.3746390	-0.0256153	0.0037417	3.5E-12
6	RFX6 *	rs2782298	116937939	G	A	0.3745430	-0.0257754	0.0037412	2.6E-12
6	RFX6 *	rs2750418	116938012	A	G	0.3741560	-0.0257893	0.0037444	2.6E-12
6	RFX6 *	rs2750417	116938028	C	T	0.3745620	-0.0257945	0.0037411	2.5E-12
6	RFX6 *	rs2782299	116938098	C	A	0.3719690	-0.0260345	0.0037458	1.9E-12
6	RFX6 *	rs2750416	116938386	A	G	0.3745580	-0.0257810	0.0037411	2.6E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	RFX6 *	rs1632019	116938417	C	T	0.3745580	-0.0257810	0.0037411	2.6E-12
6	RFX6 *	rs1631199	116938510	G	C	0.3745520	-0.0257911	0.0037411	2.5E-12
6	RFX6 *	rs1631116	116938539	T	C	0.3744440	-0.0258660	0.0037418	2.2E-12
6	RFX6 *	rs1761879	116938614	C	A	0.3745600	-0.0257854	0.0037412	2.5E-12
6	RFX6 *	rs9387439	116939067	A	G	0.3745630	-0.0257663	0.0037411	2.6E-12
6	RFX6 *	rs9320588	116939076	G	A	0.4535490	-0.0194030	0.0036455	4.8E-08
6	RFX6 *	rs1741663	116939272	T	C	0.4531470	-0.0196748	0.0036416	3.0E-08
6	RFX6 *	rs1741662	116939616	G	A	0.3745350	-0.0256455	0.0037407	3.2E-12
6	RFX6 *	rs1741661	116939793	T	C	0.3732340	-0.0260959	0.0037490	1.7E-12
6	RFX6 *	rs1741660	116939846	C	T	0.3743800	-0.0258228	0.0037404	2.3E-12
6	RFX6 *	rs1741659	116939906	T	C	0.3743800	-0.0258228	0.0037404	2.3E-12
6	RFX6 *	rs1761878	116940174	G	A	0.3743040	-0.0257672	0.0037416	2.6E-12
6	RFX6 *	rs1761877	116940180	T	C	0.3742900	-0.0257181	0.0037414	2.8E-12
6	RFX6 *	rs1741658	116940202	T	C	0.3742830	-0.0257285	0.0037415	2.8E-12
6	RFX6 *	rs1741657	116941059	A	C	0.3760500	-0.0255724	0.0037457	4.0E-12
6	RFX6 *	rs1761876	116941287	A	G	0.3717900	-0.0260549	0.0037451	1.8E-12
6	RFX6 *	rs1761875	116942095	A	C	0.3743800	-0.0258228	0.0037404	2.3E-12
6	RFX6 *	rs1761874	116942126	C	T	0.3743790	-0.0258156	0.0037404	2.4E-12
6	RFX6 *	rs1334669	116942146	T	G	0.3743790	-0.0258156	0.0037404	2.4E-12
6	RFX6 *	rs1334668	116942195	G	A	0.3743790	-0.0258156	0.0037404	2.4E-12
6	RFX6 *	rs1334667	116942442	A	G	0.3743800	-0.0258228	0.0037404	2.3E-12
6	RFX6 *	rs10670873	116942560	T	C	0.3717900	-0.0260549	0.0037451	1.8E-12
6	RFX6 *	rs11414223	116942670	G	A	0.3743800	-0.0258228	0.0037404	2.3E-12
6	RFX6 *	rs11282512	116943022	G	GCACAA	0.3758840	-0.0257498	0.0037484	3.3E-12
6	RFX6 *	rs1334667	116943078	T	TA	0.3743800	-0.0258228	0.0037404	2.3E-12
6	RFX6 *	rs1761870	116943389	A	GCATTA	0.3759500	-0.0256206	0.0037462	4.3E-12
6	RFX6 *	rs1741652	116943550	C	A	0.3747260	-0.0255211	0.0037407	4.5E-12
6	RFX6 *	rs1334666	116943822	G	A	0.3722620	-0.0257649	0.0037453	3.6E-12
6	RFX6 *	rs1334665	116943827	G	A	0.3748530	-0.0255165	0.0037405	4.7E-12
6	RFX6 *	rs1334665	116943962	T	C	0.3748470	-0.0257762	0.0037399	2.8E-12
6	RFX6 *	rs1761867	116944186	T	C	0.3749720	-0.0259427	0.0037415	2.2E-12
6	RFX6 *	rs1334664	116944395	T	C	0.3753380	-0.0257890	0.0037450	2.9E-12
6	RFX6 *	rs376060962	116944658	G	C	0.3720750	-0.0257883	0.0037442	3.2E-12
6	RFX6 *	rs1761865	116944891	TTA	T	0.3759340	-0.0260299	0.0037427	1.8E-12
6	RFX6 *	rs1761864	116944997	T	G	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1761863	116945069	T	A	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1761862	116945086	T	C	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1761861	116945332	T	C	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1761860	116945625	A	G	0.3711980	-0.0252602	0.0037498	9.4E-12
6	RFX6 *	rs1618533	116945637	A	G	0.3737860	-0.0250299	0.0037449	1.2E-11
6	RFX6 *	rs1618412	116945826	A	G	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1334663	116946347	G	T	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs5879398	116946395	A	T	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1334662	116946687	T	C	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1413742	116946739	TG	T	0.3746230	-0.0255715	0.0037398	3.9E-12
6	RFX6 *	rs1413741	116946805	C	T	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1413740	116946907	T	C	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs984258	116946920	T	C	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs1334661	116947014	C	T	0.3746660	-0.0255741	0.0037394	3.9E-12
6	RFX6 *	rs5024233	116947074	T	C	0.4532920	-0.0195493	0.0036416	3.8E-08
6	RFX6 *	rs373174746	116947275	A	C	0.3747160	-0.0256060	0.0037401	3.7E-12
6	RFX6 *	rs5024232	116947315	G	A	0.3748690	-0.0256067	0.0037466	3.5E-12
6	RFX6 *	rs5024230	116947316	T	TAC	0.3750100	-0.0255801	0.0037453	3.8E-12
6	RFX6 *	rs1761859	116947317	G	A	0.3745410	-0.0255742	0.0037448	3.8E-12
6	RFX6 *	rs1406985	116947320	T	C	0.3745410	-0.0255742	0.0037448	3.8E-12
6	RFX6 *	rs1406984	116947663	C	T	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1406983	116948095	T	G	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1406982	116948105	T	C	0.3749490	-0.0257076	0.0037401	3.2E-12
6	RFX6 *	rs1406981	116948196	C	A	0.3746900	-0.0256486	0.0037399	3.4E-12
6	RFX6 *	rs1413739	116948478	C	T	0.3773600	-0.0263198	0.0037355	6.8E-13
6	RFX6 *	chr6:116948541_AT_A	116948497	T	A	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1334660	116948541	AT	A	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1334659	116948726	G	A	0.3720420	-0.0258632	0.0037445	2.8E-12
6	RFX6 *	rs1334658	116948887	T	C	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1334657	116948931	T	G	0.3746330	-0.0256485	0.0037397	3.5E-12
6	RFX6 *	rs1741671	116949044	C	T	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1413738	116949115	C	G	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1413737	116949170	A	G	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs966900	116949248	T	C	0.3720570	-0.0258884	0.0037444	2.7E-12
6	RFX6 *	rs1413736	116949525	A	G	0.4532390	-0.0194645	0.0036412	4.4E-08
6	RFX6 *	rs1413735	116949652	T	G	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs16849	116949963	T	G	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs17175	116950071	G	A	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1334654	116950146	G	T	0.3744610	-0.0255233	0.0037407	4.4E-12
6	RFX6 *	rs2210714	116950293	CT	C	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1970175	116950522	C	G	0.3751560	-0.0255320	0.0037406	4.3E-12
6	RFX6 *	rs1761847	116951026	C	T	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs2353358	116951184	G	C	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1741688	116951453	C	A	0.3720570	-0.0258884	0.0037444	2.7E-12
6	RFX6 *	rs3073178	116952136	T	C	0.3749750	-0.0254545	0.0037418	4.8E-12
6	RFX6 *	rs1741687	116952282	C	T	0.3783940	-0.0261837	0.0037377	9.0E-13
6	RFX6 *	rs1741686	116952760	A	ATGACT	0.3722630	-0.0257071	0.0037456	3.6E-12
6	RFX6 *	rs1413735	116952850	G	T	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1618384	116952933	A	G	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1360755	116953048	C	A	0.3723950	-0.0255795	0.0037463	4.6E-12
6	RFX6 *	rs1761845	116953067	G	T	0.3749890	-0.0253623	0.0037416	5.6E-12
6	RFX6 *	rs1761844	116953582	C	T	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1761843	116953681	G	T	0.3748410	-0.0254314	0.0037409	5.0E-12
6	RFX6 *	rs1761842	116953836	A	T	0.3746480	-0.0256734	0.0037396	3.2E-12
6	RFX6 *	rs1761841	116954048	T	G	0.3744390	-0.0253224	0.0037429	6.4E-12
6	RFX6 *	rs7755339	116954239	C	G	0.3738230	-0.0256324	0.0037459	3.2E-12
6	RFX6 *	rs7755337	116954253	G	A	0.3738230	-0.0256324	0.0037459	3.2E-12
6	RFX6 *	rs1761840	116954273	C	G	0.3739410	-0.0256559	0.0037450	3.2E-12
6	RFX6 *	rs1761839	116954331	C	T	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1761838	116954366	C	T	0.3775710	-0.0261362	0.0037367	9.5E-13
6	RFX6 *	rs1761837	116954482	G	A	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1761836	116954609	T	TG	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1761835	116954626	G	A	0.3748560	-0.0254907	0.0037409	4.4E-12
6	RFX6 *	rs1761834	116955236	T	C	0.3747290	-0.0255175	0.0037416	4.3E-12
6	RFX6 *	rs1761833	116955477	T	C	0.3749910	-0.0254554	0.0037418	5.0E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	RFX6 *	rs1413734	116955671	G	A	0.3748400	-0.0255146	0.0037407	4.3E-12
6	RFX6 *	rs1413732	116955779	A	G	0.3746320	-0.0256971	0.0037395	3.1E-12
6	RFX6 *	rs1741677	116955909	T	C	0.3748230	-0.0255649	0.0037408	3.9E-12
6	RFX6 *	rs1413731	116956057	G	A	0.3746610	-0.0255803	0.0037413	4.0E-12
6	RFX6 *	rs1741676	116956468	A	T	0.3748230	-0.0255649	0.0037408	3.9E-12
6	RFX6 *	rs1334653	116956590	C	T	0.3748130	-0.0255443	0.0037409	4.0E-12
6	RFX6 *	rs768581	116956809	T	C	0.3748130	-0.0255443	0.0037409	4.0E-12
6	RFX6 *	rs768582	116957055	C	T	0.3748130	-0.0255459	0.0037409	4.0E-12
6	RFX6 *	rs1741675	116957398	A	C	0.3742900	-0.0253417	0.0037462	5.9E-12
6	RFX6 *	rs1741674	116957444	T	A	0.3744440	-0.0251160	0.0037512	8.9E-12
6	RFX6 *	rs1321374	116958491	T	A	0.3823830	-0.0245707	0.0037627	2.4E-11
6	RFX6 *	rs9489073	116958741	G	T	0.3807390	-0.0246294	0.0037770	2.8E-11
6	RFX6 *	rs1761834	116958822	T	G	0.3764090	-0.0244626	0.0037964	5.1E-11
6	RFX6 *	rs1741672	116959149	A	T	0.3995340	-0.0232347	0.0037458	5.8E-10
6	RFX6 *	rs1761832	116959271	C	T	0.4027650	-0.0231860	0.0037515	6.9E-10
6	RFX6 *	rs2353359	116960239	C	T	0.4025520	-0.0225220	0.0037520	2.5E-09
6	RFX6 *	rs6149769	116960517	C	GAAACCC	0.4027430	-0.0224442	0.0037664	4.1E-09
6	RFX6 *	rs783652	116961157	G	C	0.4026240	-0.0224774	0.0037522	2.6E-09
6	RFX6 *	rs783651	116961798	G	A	0.4042130	-0.0224458	0.0037580	2.9E-09
6	RFX6 *	rs783650	116962129	A	G	0.3998430	-0.0224466	0.0037576	3.4E-09
6	RFX6 *	rs783649	116962219	T	C	0.3999020	-0.0225045	0.0037566	3.1E-09
6	RFX6 *	rs783648	116962292	A	T	0.3999020	-0.0225045	0.0037566	3.1E-09
6	RFX6 *	rs706939	116963854	T	A	0.4020330	-0.0220007	0.0037565	5.5E-09
6	RFX6 *	rs783647	116964479	T	A	0.4016270	-0.0225200	0.0037620	3.1E-09
6	RFX6 *	rs35643068	116964553	GA	G	0.4069430	-0.0233509	0.0037568	5.2E-10
6	RFX6 *	rs783646	116965057	G	C	0.4035970	-0.0222044	0.0037661	5.4E-09
6	RGS17	chr6:153079082_AT_A	153079082	A	AT	0.2964520	-0.0211917	0.0040085	4.2E-08
6	RGS17	rs11155892	153083026	C	T	0.2930650	-0.0211484	0.0039903	4.7E-08
6	RGS17	rs6932473	153117438	A	T	0.3240550	-0.0213569	0.0038742	1.7E-08
6	RGS17	rs6557273	153122024	A	G	0.3226120	-0.0212388	0.0038820	2.2E-08
6	RGS17	chr6:153122930_T_TTACTCCAATGTACATTGGAGTAAATGGAGTATTAA	153122930	T	TGGAGT	0.3224150	-0.0212682	0.0038782	2.0E-08
6	RGS17	rs9371676	153124830	C	A	0.3222340	-0.0212284	0.0038783	2.2E-08
6	RGS17	rs13215045	153126381	C	T	0.3223010	-0.0209566	0.0038769	2.9E-08
6	RGS17	rs6932847	153127172	G	A	0.3220780	-0.0206946	0.0038771	4.4E-08
6	RGS17	rs71017584	153130998	GTCGCGC	G	0.3289850	-0.0209209	0.0038800	3.1E-08
7	DGKB	rs11414474	147321197	A	AT	0.3514120	-0.0305161	0.0038894	2.1E-15
7	DGKB	rs4721364	14732254	G	A	0.3514510	-0.0305837	0.0038886	1.8E-15
7	DGKB	rs7809161	14732886	T	A	0.3519630	-0.0302567	0.0038836	2.8E-15
7	DGKB	rs6957593	14733284	A	G	0.3493930	-0.0303805	0.0038837	2.3E-15
7	DGKB	rs2091258	14734335	G	A	0.4309590	-0.0247000	0.0036827	2.2E-11
7	DGKB	rs2884369	14734574	G	A	0.4310610	-0.0245635	0.0036782	2.9E-11
7	DGKB	rs1880550	14734867	A	C	0.4309590	-0.0246317	0.0036768	2.5E-11
7	DGKB	rs957032	14735402	T	G	0.4314250	-0.0244537	0.0036702	3.0E-11
7	DGKB	rs10253369	14735816	C	T	0.2326530	-0.0268613	0.0042976	3.6E-10
7	DGKB	rs10237911	14735923	G	C	0.4320050	-0.0247621	0.0036681	1.9E-11
7	DGKB	rs66786499	14736196	TG	T	0.4362970	-0.0245715	0.0036807	2.6E-11
7	DGKB	rs80024169	14736199	A	C	0.4362970	-0.0245715	0.0036807	2.6E-11
7	DGKB	rs11455738	14736474	A	AC	0.4314030	-0.0244719	0.0036698	3.0E-11
7	DGKB	rs7783453	14736812	A	C	0.4305990	-0.0245484	0.0036708	2.5E-11
7	DGKB	rs12699660	14737863	C	T	0.4326560	-0.0246510	0.0036756	2.4E-11
7	DGKB	rs1525094	14738283	T	G	0.3552170	-0.0310073	0.0037913	1.9E-16
7	DGKB	rs10807775	14738325	G	A	0.4319060	-0.0249598	0.0036706	1.1E-11
7	DGKB	rs1525095	14738390	G	A	0.3580180	-0.0308685	0.0037880	2.6E-16
7	DGKB	rs12699661	14739515	C	A	0.4321560	-0.0249153	0.0036661	1.3E-11
7	DGKB	rs1464821	14739652	C	T	0.4313250	-0.0243884	0.0036686	3.4E-11
7	DGKB	rs7799347	14740210	A	T	0.4334080	-0.0242828	0.0036707	4.2E-11
7	DGKB	rs12699662	14741679	C	G	0.4318540	-0.0243235	0.0036676	3.7E-11
7	DGKB	rs6977546	14742388	A	G	0.4317650	-0.0246401	0.0036660	2.1E-11
7	DGKB	rs1852071	14742812	G	C	0.4328950	-0.0250731	0.0036650	9.3E-12
7	DGKB	rs10267536	14743216	A	G	0.2332060	-0.0271895	0.0042890	2.2E-10
7	DGKB	rs1917552	14743925	C	G	0.4325300	-0.0248956	0.0036653	1.3E-11
7	DGKB	rs1917551	14743931	C	T	0.4326800	-0.0249409	0.0036662	1.3E-11
7	DGKB	rs60863241	14744143	G	A	0.3575820	-0.0307273	0.0037851	3.3E-16
7	DGKB	rs12699664	14744349	A	G	0.4320610	-0.0247572	0.0036642	1.7E-11
7	DGKB	rs1639237	14744979	A	T	0.4330590	-0.0250956	0.0036638	8.5E-12
7	DGKB	rs2098145	14745627	A	G	0.3576230	-0.0308302	0.0037837	2.7E-16
7	DGKB	rs1723256	14746496	G	T	0.4266340	-0.0252213	0.0036730	7.9E-12
7	DGKB	rs1723255	14746623	T	C	0.4267430	-0.0248684	0.0036737	1.5E-11
7	DGKB	rs1525098	14746882	C	T	0.4264800	-0.0250573	0.0036720	1.2E-11
7	DGKB	rs1525097	14747039	G	A	0.4266700	-0.0249936	0.0036721	1.3E-11
7	DGKB	rs1525096	14747089	C	G	0.4266700	-0.0249936	0.0036721	1.3E-11
7	DGKB	rs1723252	14747259	T	C	0.4265400	-0.0250034	0.0036716	1.2E-11
7	DGKB	chr7:14747362_G_GT	14747362	GT	G	0.4216040	-0.0240885	0.0037039	1.1E-10
7	DGKB	rs1723251	14747546	G	A	0.4265620	-0.0250161	0.0036715	1.2E-11
7	DGKB	rs1639233	14747560	G	T	0.4265620	-0.0250161	0.0036715	1.2E-11
7	DGKB	rs1723250	14747705	A	C	0.4265740	-0.0250030	0.0036716	1.2E-11
7	DGKB	rs149679900	14747773	GCA	G	0.2324290	-0.0271839	0.0042960	2.3E-10
7	DGKB	rs1723248	14747829	T	C	0.4266270	-0.0251410	0.0036727	9.2E-12
7	DGKB	rs1723247	14748299	G	A	0.4284260	-0.0254170	0.0036705	4.5E-12
7	DGKB	rs1639234	14748496	G	T	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1723246	14748551	C	T	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1723245	14748614	G	A	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1723244	14748781	G	A	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1639236	14749212	G	T	0.4267380	-0.0251131	0.0036763	8.9E-12
7	DGKB	rs1880553	14749432	C	T	0.3586830	-0.0312869	0.0037828	8.2E-17
7	DGKB	rs1880552	14749469	G	T	0.3580440	-0.0312784	0.0037881	9.3E-17
7	DGKB	rs1880551	14749582	G	T	0.3583150	-0.0312376	0.0037863	1.0E-16
7	DGKB	rs12673261	14750018	G	C	0.2347450	-0.0274086	0.0042764	1.2E-10
7	DGKB	rs1723239	14750219	C	A	0.4281690	-0.0254094	0.0036693	4.1E-12
7	DGKB	rs1723238	14750321	A	G	0.4281580	-0.0253702	0.0036695	4.7E-12
7	DGKB	rs1723237	14750404	T	C	0.4282800	-0.0254806	0.0036695	3.8E-12
7	DGKB	rs10278278	14750817	T	C	0.4375930	-0.0237151	0.0037074	1.7E-10
7	DGKB	rs10234845	14750834	G	T	0.3588100	-0.0311458	0.0037849	1.1E-16
7	DGKB	rs4719419	14750948	T	C	0.4278460	-0.0254924	0.0036715	4.0E-12
7	DGKB	rs4721368	14751053	T	C	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1639238	14751178	T	C	0.4277460	-0.0256679	0.0036731	2.9E-12
7	DGKB	rs1723236	14751654	G	A	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1639239	14751743	T	C	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1639240	14751822	C	T	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1639241	14751947	C	G	0.4279890	-0.0255132	0.0036710	3.9E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	DGKB	rs1723235	14751956	G	T	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1723234	14752153	G	C	0.4283710	-0.0254121	0.0036701	4.6E-12
7	DGKB	rs1723233	14752205	G	T	0.4283710	-0.0254121	0.0036701	4.6E-12
7	DGKB	rs34978381	14752337	AG	A	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1723232	14752381	G	A	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1723231	14752403	G	A	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1525092	14752583	T	C	0.4282160	-0.0254306	0.0036695	4.5E-12
7	DGKB	rs1525091	14753038	C	T	0.4279330	-0.0254995	0.0036725	4.2E-12
7	DGKB	rs1723230	14753235	C	T	0.4282650	-0.0253603	0.0036699	5.1E-12
7	DGKB	rs1723229	14753483	G	T	0.4278990	-0.0254143	0.0036715	4.6E-12
7	DGKB	rs1723228	14753511	G	A	0.4282140	-0.0254280	0.0036695	4.5E-12
7	DGKB	rs1723227	14753717	G	A	0.4213460	-0.0256724	0.0036888	2.1E-12
7	DGKB	rs1723226	14753746	C	T	0.4213060	-0.0256789	0.0036892	2.0E-12
7	DGKB	rs1723225	14753774	C	T	0.4213400	-0.0256926	0.0036890	2.1E-12
7	DGKB	rs1723224	14753853	C	T	0.4280760	-0.0255781	0.0036723	3.2E-12
7	DGKB	rs17168389	14754071	G	A	0.2349570	-0.0276871	0.0042818	9.1E-11
7	DGKB	rs4632953	14754099	C	G	0.4283010	-0.0256818	0.0036758	2.8E-12
7	DGKB	rs1880549	14754222	A	G	0.4278240	-0.0258667	0.0036791	2.0E-12
7	DGKB	rs1723223	14754371	G	C	0.4272130	-0.0249846	0.0036824	1.2E-11
7	DGKB	rs1525090	14754455	A	G	0.4276210	-0.0251303	0.0036824	9.2E-12
7	DGKB	rs17168390	14754467	A	T	0.2348440	-0.0274581	0.0042830	1.3E-10
7	DGKB	rs1639230	14754498	G	A	0.4280030	-0.0256653	0.0036796	3.1E-12
7	DGKB	rs1723222	14754501	T	C	0.4280030	-0.0256653	0.0036796	3.1E-12
7	DGKB	rs1723221	14754519	T	C	0.4283680	-0.0254409	0.0036771	4.7E-12
7	DGKB	rs112379401	14754578	G	GA	0.4286430	-0.0256513	0.0036907	3.1E-12
7	DGKB	rs55846217	14754587	C	A	0.4282890	-0.0255112	0.0036792	4.5E-12
7	DGKB	rs56127930	14754589	C	T	0.4282890	-0.0255112	0.0036792	4.5E-12
7	DGKB	rs7786354	14754581	G	C	0.4302800	-0.0256308	0.0036740	2.7E-12
7	DGKB	rs10277424	14756156	A	C	0.2348440	-0.0269333	0.0042826	2.8E-10
7	DGKB	chr7:14757555_T_TAC	14757555	TAC	T	0.3595820	-0.0318088	0.0037923	2.3E-17
7	DGKB	rs10226709	14758009	A	C	0.4299510	-0.0257315	0.0036782	2.3E-12
7	DGKB	rs61338771	14759328	C	T	0.4363370	-0.0249080	0.0036710	1.5E-11
7	DGKB	rs79396525	14759371	T	C	0.2398110	-0.0252539	0.0042524	3.9E-09
7	DGKB	rs979498	14759915	C	A	0.4367440	-0.0250139	0.0036711	1.2E-11
7	DGKB	rs979499	14760067	C	G	0.3665510	-0.0303245	0.0037753	7.2E-16
7	DGKB	rs979501	14760114	C	T	0.3664870	-0.0304402	0.0037751	5.7E-16
7	DGKB	rs10081218	14760345	A	C	0.4363370	-0.0250834	0.0036711	1.1E-11
7	DGKB	rs6952066	14762007	A	G	0.4357580	-0.0250002	0.0036724	1.2E-11
7	DGKB	rs4518556	14762734	T	C	0.4356290	-0.0245199	0.0036802	3.9E-11
7	DGKB	rs9886266	14763365	G	T	0.2406690	-0.0259600	0.0042487	1.2E-09
7	DGKB	rs17168405	14764589	C	G	0.4368830	-0.0252435	0.0036749	8.4E-12
7	DGKB	rs2358067	14766933	T	G	0.3632830	-0.0302114	0.0037830	1.2E-15
7	DGKB	rs2191477	14767069	T	A	0.4351460	-0.0243568	0.0036761	4.8E-11
7	DGKB	rs982707	14771441	T	C	0.4336140	-0.0246423	0.0036752	3.7E-11
7	DGKB	rs2012289	14771733	T	A	0.4336230	-0.0246451	0.0036751	3.7E-11
7	DGKB	rs7789633	14773455	G	A	0.4397690	-0.0244437	0.0036708	4.6E-11
7	DGKB	rs7808899	14773549	G	T	0.4398760	-0.0242554	0.0036703	6.6E-11
7	DGKB	rs7776924	14773790	A	T	0.4397120	-0.0243498	0.0036710	5.2E-11
7	DGKB	rs17168419	14774407	A	G	0.2402910	-0.0255311	0.0042475	3.2E-09
7	DGKB	rs7456390	14777929	G	C	0.4338020	-0.0246671	0.0036792	3.7E-11
7	DGKB	rs6980373	14779363	C	T	0.4369160	-0.0244326	0.0036792	4.6E-11
7	DGKB	chr7:14780631_A_AT	14780631	AT	A	0.3634060	-0.0303610	0.0037901	1.1E-15
7	DGKB	rs10258190	14781481	G	C	0.4355650	-0.0248293	0.0036811	2.3E-11
7	DGKB	rs12673704	14782192	C	T	0.3645700	-0.0301217	0.0037831	1.7E-15
7	DGKB	rs714980	14782671	G	A	0.4396260	-0.0238962	0.0036774	1.4E-10
7	DGKB	rs10236189	14782796	G	A	0.4396190	-0.0239452	0.0036774	1.3E-10
7	DGKB	rs10270104	14783779	C	G	0.3657080	-0.0304618	0.0037892	8.8E-16
7	DGKB	rs10270111	14783792	C	G	0.3652960	-0.0305897	0.0037923	8.0E-16
7	DGKB	rs17168428	14784106	C	T	0.3616630	-0.0301308	0.0037995	2.2E-15
7	DGKB	rs995871	14784883	A	T	0.4335880	-0.0248229	0.0036869	2.7E-11
7	DGKB	rs10215697	14785818	A	C	0.4367500	-0.0233921	0.0036856	3.1E-10
7	DGKB	rs10215015	14785984	G	A	0.3618620	-0.0299091	0.0037856	2.5E-15
7	DGKB	rs67562594	14787939	A	TTACAG	0.2262540	-0.0252663	0.0043577	1.1E-08
7	DGKB	rs6946750	14789007	G	A	0.3623130	-0.0299185	0.0037750	1.6E-15
7	DGKB	rs6967001	14789020	C	T	0.3620330	-0.0299392	0.0037736	1.4E-15
7	DGKB	rs10226574	14789676	C	T	0.3571410	-0.0303063	0.0037772	4.9E-16
7	DGKB	rs34811388	14789724	T	TA	0.3571410	-0.0303063	0.0037772	4.9E-16
7	DGKB	rs10243441	14789885	G	A	0.3571410	-0.0303063	0.0037772	4.9E-16
7	DGKB	rs10230027	14790184	C	T	0.3570560	-0.0301763	0.0037770	6.5E-16
7	DGKB	rs10273475	14790216	G	C	0.3570560	-0.0301648	0.0037770	6.7E-16
7	DGKB	rs10273485	14790233	T	C	0.3570580	-0.0301427	0.0037769	6.9E-16
7	DGKB	rs10244060	14790353	G	A	0.3570950	-0.0300514	0.0037769	8.4E-16
7	DGKB	rs57172001	14790448	A	ACATC	0.3570800	-0.0300263	0.0037785	9.3E-16
7	DGKB	rs61430679	14790498	T	TTTG	0.3569610	-0.0300012	0.0037776	9.4E-16
7	DGKB	rs10273894	14790567	T	C	0.3570660	-0.0301134	0.0037769	7.3E-16
7	DGKB	rs10277225	14790735	C	G	0.3597440	-0.0298903	0.0037736	1.1E-15
7	DGKB	rs9690434	14790792	C	T	0.3598560	-0.0297952	0.0037741	1.4E-15
7	DGKB	rs9692356	14790902	T	C	0.4310680	-0.0241763	0.0036735	3.8E-11
7	DGKB	rs6977839	14791060	C	T	0.3609840	-0.0302710	0.0037735	4.2E-16
7	DGKB	rs2215431	14791461	A	G	0.3609370	-0.0302615	0.0037736	4.1E-16
7	DGKB	rs2215432	14791504	G	C	0.3609370	-0.0302615	0.0037736	4.1E-16
7	DGKB	rs35646663	14791537	T	TA	0.4307760	-0.0241084	0.0036763	4.1E-11
7	DGKB	rs6978851	14791678	C	T	0.3609500	-0.0301966	0.0037740	4.7E-16
7	DGKB	rs75602715	14792034	C	T	0.2365690	-0.0259714	0.0042658	9.5E-10
7	DGKB	rs10281913	14792317	G	C	0.3610900	-0.0302432	0.0037743	4.5E-16
7	DGKB	rs7796559	14792443	A	C	0.3607320	-0.0302356	0.0037763	4.7E-16
7	DGKB	rs7796443	14792466	C	A	0.3610900	-0.0302432	0.0037743	4.5E-16
7	DGKB	rs61564030	14792730	ACATAAT	G	0.3585390	-0.0303609	0.0037902	4.1E-16
7	DGKB	rs17168437	14793281	A	G	0.2364890	-0.0261335	0.0042663	7.3E-10
7	DGKB	rs1079947	14794350	A	G	0.4326890	-0.0241161	0.0036790	3.4E-11
7	DGKB	rs1079946	14794373	A	T	0.4327520	-0.0241513	0.0036791	3.3E-11
7	DGKB	rs2191480	14794931	A	T	0.4330230	-0.0237922	0.0036788	6.9E-11
7	DGKB	rs2109497	14795392	G	T	0.4334630	-0.0239434	0.0036816	5.3E-11
7	DGKB	rs1120408	14795543	G	A	0.4304840	-0.0248828	0.0036891	1.1E-11
7	DGKB	rs1120409	14795932	C	T	0.4296150	-0.0249883	0.0036893	9.0E-12
7	DGKB	rs6461129	14796326	C	T	0.4299780	-0.0249492	0.0036901	1.0E-11
7	DGKB	rs7790164	14796535	T	C	0.4299140	-0.0247816	0.0036895	1.4E-11
7	DGKB	rs10280027	14796819	A	C	0.4330630	-0.0236670	0.0036837	9.6E-11
7	DGKB	rs2215433	14797112	A	C	0.4272180	-0.0248517	0.0036928	1.6E-11
7	DGKB	rs975432	14797475	A	G	0.4318300	-0.0239455	0.0036871	6.7E-11

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7	DGKB	rs6461130	14797692	C	A	0.4306310	-0.0243225	0.0036913	3.9E-11
7	DGKB	rs6461131	14797837	G	A	0.4319750	-0.0239090	0.0036872	7.4E-11
7	DGKB	rs6461132	14797852	C	A	0.4316440	-0.0240990	0.0036892	5.5E-11
7	DGKB	rs7799842	14798086	A	G	0.4315870	-0.0239129	0.0036892	7.2E-11
7	DGKB	rs7782835	14798183	C	T	0.4316550	-0.0238759	0.0036895	8.0E-11
7	DGKB	rs113869808	14798453	TTTTA	T	0.4313980	-0.0241757	0.0036916	4.9E-11
7	DGKB	rs10230585	14799558	A	G	0.2325970	-0.0263817	0.0043049	7.5E-10
7	DGKB	rs10233958	14800158	T	C	0.2338680	-0.0258158	0.0043015	1.7E-09
7	DGKB	rs56141933	14800779	C	T	0.2338540	-0.0264063	0.0043017	7.1E-10
7	DGKB	rs6461133	14801429	C	G	0.4261480	-0.0252242	0.0037146	9.9E-12
7	DGKB	rs7798664	14801552	C	T	0.4287140	-0.0249447	0.0037086	1.4E-11
7	DGKB	rs7789696	14803317	A	G	0.4284390	-0.0254480	0.0037160	5.2E-12
7	DGKB	rs10658306	14803675	CATGT	C	0.4294940	-0.0252828	0.0037140	7.6E-12
7	DGKB	rs6942721	14803703	C	T	0.4297320	-0.0251861	0.0037124	8.6E-12
7	DGKB	rs57037859	14804386	A	T	0.4317790	-0.0245993	0.0037113	2.2E-11
7	DGKB	rs60449488	14804439	A	G	0.2316490	-0.0258506	0.0043197	2.2E-09
7	DGKB	rs10487779	14804711	G	A	0.4318850	-0.0246322	0.0037120	2.2E-11
7	DGKB	rs6976200	14805259	T	A	0.4308020	-0.0248751	0.0037172	1.4E-11
7	DGKB	rs17168451	14805647	C	A	0.2315870	-0.0272809	0.0043278	2.3E-10
7	DGKB	rs4719421	14805998	T	G	0.4287130	-0.0242375	0.0037231	5.1E-11
7	DGKB	rs4719422	14806073	T	C	0.4285500	-0.0250429	0.0037238	1.4E-11
7	DGKB	rs34450119	14806508	A	AATT	0.2307470	-0.0275107	0.0043323	2.0E-10
7	DGKB	rs10253171	14806666	C	T	0.4311350	-0.0248724	0.0037199	1.6E-11
7	DGKB	rs6948538	14807021	A	G	0.4423530	0.0281976	0.0037176	1.7E-14
7	DGKB	rs10241439	14807238	T	G	0.2284900	-0.0263007	0.0043463	1.3E-09
7	DGKB	rs4719425	14808364	A	G	0.4429750	0.0279097	0.0037131	3.0E-14
7	DGKB	rs4721376	14808756	C	G	0.4290680	-0.0240369	0.0037236	7.2E-11
7	DGKB	rs10249582	14809025	T	G	0.2297470	-0.0259521	0.0043385	2.2E-09
7	DGKB	rs28610468	14809708	A	T	0.4293790	-0.0242916	0.0037269	4.4E-11
7	DGKB	rs6461134	14810057	C	T	0.4294130	-0.0243078	0.0037294	4.8E-11
7	DGKB	rs6461135	14810058	G	T	0.4294130	-0.0243078	0.0037294	4.8E-11
7	DGKB	rs35098567	14810377	T	TACA	0.2286630	-0.0265285	0.0043518	1.1E-09
7	DGKB	rs1981680	14810428	T	A	0.4258050	-0.0255179	0.0037352	5.5E-12
7	DGKB	rs10257298	14810828	T	C	0.2285510	-0.0265926	0.0043526	9.9E-10
7	DGKB	rs2358069	14810875	C	G	0.4256660	-0.0255834	0.0037352	4.4E-12
7	DGKB	rs7458312	14811419	G	A	0.4306240	-0.0243100	0.0037248	4.2E-11
7	DGKB	rs5014691	14811536	A	G	0.4304920	-0.0243407	0.0037252	3.8E-11
7	DGKB	rs11972669	14811707	T	A	0.4304090	-0.0246436	0.0037273	2.2E-11
7	DGKB	rs11274836	14811813	TTGTATT	C	0.4297380	-0.0243783	0.0037323	3.9E-11
7	DGKB	rs67104645	14811845	C	T	0.4310080	-0.0245470	0.0037273	2.7E-11
7	DGKB	rs11459015	14811895	CT	C	0.4307020	-0.0244273	0.0037286	3.4E-11
7	DGKB	rs10277367	14811992	C	T	0.4312470	-0.0247033	0.0037293	2.0E-11
7	DGKB	rs10232210	14812098	C	A	0.4317800	-0.0241451	0.0037272	6.1E-11
7	DGKB	rs766366	14812669	A	G	0.4377990	0.0276122	0.0037189	4.6E-14
7	DGKB	rs7782994	14814643	G	C	0.4236580	-0.0254321	0.0037470	9.4E-12
7	DGKB	rs7779072	14814918	G	T	0.4229810	-0.0252937	0.0037531	1.2E-11
7	DGKB	rs10276530	14817300	C	T	0.4334280	-0.0326670	0.0036894	7.6E-20
7	DGKB	rs112538930	14819512	T	C	0.3988270	0.0489675	0.0037575	5.0E-41
7	DGKB	rs2191481	14819626	A	G	0.3779930	-0.0347279	0.0037600	2.0E-21
7	DGKB	rs41379551	14820698	G	A	0.1615070	-0.0278621	0.0049866	1.1E-08
7	DGKB	rs2215434	14822477	C	T	0.4080800	0.0501683	0.0037221	7.2E-44
7	DGKB	rs2191482	14823397	G	A	0.4327770	-0.0314992	0.0036600	1.0E-18
7	DGKB	rs79297350	14823613	A	G	0.1342010	-0.0289080	0.0053688	3.4E-08
7	DGKB	rs6461137	14824305	A	C	0.3789170	-0.0354134	0.0037250	1.6E-22
7	DGKB	rs7806534	14824568	G	A	0.3784140	-0.0355698	0.0037296	9.9E-23
7	DGKB	rs7789829	14824580	A	T	0.2838550	-0.0355495	0.0040177	5.6E-20
7	DGKB	rs7806933	14824584	C	G	0.3776800	-0.0361763	0.0037271	2.4E-23
7	DGKB	rs62448750	14824705	C	T	0.1584920	-0.0304572	0.0050177	5.4E-10
7	DGKB	rs10242291	14825018	G	A	0.1558070	-0.0307317	0.0051021	6.1E-10
7	DGKB	rs60739407	14825261	G	A	0.4545640	0.0490934	0.0036925	5.7E-43
7	DGKB	rs2109499	14825574	A	G	0.3785450	-0.0353466	0.0037263	2.0E-22
7	DGKB	rs60557254	14826083	C	T	0.3789350	-0.0361285	0.0037268	2.9E-23
7	DGKB	rs2109500	14826258	A	G	0.3778200	-0.0358105	0.0037239	6.6E-23
7	DGKB	rs35197364	14827919	TC	T	0.4352140	-0.0322971	0.0036560	1.6E-19
7	DGKB	rs10241696	14828599	C	T	0.4349150	-0.0325177	0.0036475	6.3E-20
7	DGKB	rs10085416	14829188	A	G	0.3788710	-0.0351203	0.0037267	4.1E-22
7	DGKB	rs10085417	14829329	T	C	0.2857700	-0.0356415	0.0040029	3.4E-20
7	DGKB	rs10487781	14829580	G	A	0.4347500	-0.0327190	0.0036430	3.2E-20
7	DGKB	rs10085569	14829616	C	T	0.4348820	-0.0328026	0.0036427	2.5E-20
7	DGKB	rs2358071	14829731	C	T	0.4349150	-0.0329297	0.0036435	1.8E-20
7	DGKB	rs148963012	14830861	TAACTT/	G	0.4371520	-0.0319650	0.0036500	3.0E-19
7	DGKB	rs929522	14830968	G	C	0.4342610	-0.0323341	0.0036485	1.1E-19
7	DGKB	rs929523	14831044	G	A	0.4356230	-0.0317679	0.0036470	4.2E-19
7	DGKB	rs6461140	14832231	A	G	0.3787000	-0.0351598	0.0037302	3.5E-22
7	DGKB	rs7803362	14832481	A	T	0.1603370	-0.0290031	0.0049944	2.2E-09
7	DGKB	rs7784739	14832552	G	A	0.4329780	-0.0320649	0.0036490	2.2E-19
7	DGKB	rs35429786	14833400	T	TTA	0.2852340	-0.0354619	0.0040252	8.1E-20
7	DGKB	rs7790062	14833695	G	T	0.3812350	-0.0352083	0.0037369	3.2E-22
7	DGKB	rs7793794	14833766	G	C	0.3818120	-0.0358040	0.0037354	6.5E-23
7	DGKB	rs10479935	14834606	A	T	0.2851940	-0.0354390	0.0040264	1.1E-19
7	DGKB	rs2041409	14834756	C	T	0.4350970	-0.0327123	0.0036637	5.2E-20
7	DGKB	rs2041410	14834816	C	T	0.1746710	-0.0261241	0.0048357	1.4E-08
7	DGKB	rs17168465	14835174	G	A	0.4418420	0.0496489	0.0037112	4.8E-44
7	DGKB	rs7777002	14835716	A	G	0.2807830	-0.0361123	0.0040524	4.9E-20
7	DGKB	rs62448753	14835742	C	A	0.1756940	-0.0255759	0.0048297	2.9E-08
7	DGKB	rs10241170	14837292	A	C	0.2821070	-0.0371060	0.0040571	4.2E-21
7	DGKB	rs72595977	14837778	A	G	0.3338480	0.0455251	0.0039183	4.2E-33
7	DGKB	rs10260713	14838182	C	T	0.2823770	-0.0373358	0.0040589	2.7E-21
7	DGKB	rs10245925	14838564	C	G	0.2865570	-0.0369578	0.0040371	3.3E-21
7	DGKB	rs10245728	14838579	A	C	0.2841440	-0.0373995	0.0040452	1.5E-21
7	DGKB	rs4719427	14839530	T	C	0.2826850	-0.0366190	0.0040608	1.4E-20
7	DGKB	rs7797480	14840047	T	C	0.2815280	-0.0365890	0.0040576	1.4E-20
7	DGKB	rs10487783	14840246	G	T	0.2669550	-0.0332465	0.0041594	7.9E-17
7	DGKB	rs2286767	14840857	C	T	0.1771660	-0.0256143	0.0048163	2.3E-08
7	DGKB *	rs10261580	14841866	C	G	0.2830280	-0.0358706	0.0040596	5.4E-20
7	DGKB *	rs11979624	14842192	A	C	0.1747670	-0.0267961	0.0048406	5.1E-09
7	DGKB *	rs34561304	14846042	A	C	0.3741740	-0.0386784	0.0038007	7.2E-26
7	DGKB *	rs10256424	14846067	A	G	0.2867070	-0.0385246	0.0040507	4.8E-23
7	DGKB *	rs10257070	14846580	C	G	0.2861280	-0.0379611	0.0040541	1.8E-22
7	DGKB *	rs9691738	14847825	A	G	0.2863010	-0.0383759	0.0040466	5.7E-23

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	DGKB *	rs1117749	14848772	A	T	0.2874220	-0.0383808	0.0040342	4.2E-23
7	DGKB *	rs1117750	14848793	T	C	0.2873810	-0.0383056	0.0040341	4.7E-23
7	DGKB *	rs10225316	14848837	T	A	0.3744730	-0.0387430	0.0037870	3.7E-26
7	DGKB *	rs961634	14850334	A	G	0.2808690	-0.0431211	0.0040218	8.3E-29
7	DGKB *	rs7791432	14851548	T	C	0.2810860	-0.0430932	0.0040173	9.3E-29
7	DGKB *	rs4721382	14853631	C	T	0.3575840	-0.0450798	0.0038063	1.9E-34
7	DGKB *	rs1988291	14853715	A	C	0.3534540	-0.0443742	0.0038079	2.7E-33
7	DGKB *	rs12669279	14854255	C	T	0.2835760	-0.0440861	0.0040132	3.8E-30
7	DGKB *	rs1016649	14856002	C	T	0.1514180	-0.0353323	0.0051488	1.0E-12
7	DGKB *	chr7:14856655_T_TTG	14856655	TTG	T	0.2826860	-0.0431926	0.0040222	8.3E-29
7	DGKB *	rs7794154	14856854	G	T	0.2833650	-0.0434108	0.0040199	4.3E-29
7	DGKB *	rs10950538	14857299	G	A	0.2818230	-0.0433893	0.0040265	4.6E-29
7	DGKB *	rs58021112	14857453	C	T	0.3535710	-0.0448297	0.0037972	4.2E-34
7	DGKB *	rs1990380	14857700	T	A	0.2818780	-0.0431136	0.0040253	9.2E-29
7	DGKB *	rs1990381	14857705	A	G	0.2818780	-0.0431136	0.0040253	9.2E-29
7	DGKB *	rs17168484	14858227	A	G	0.2812800	-0.0434337	0.0040265	3.9E-29
7	DGKB *	rs994369	14858527	T	C	0.3526960	-0.0452972	0.0037980	8.1E-35
7	DGKB *	rs17168486	14858657	T	C	0.4803910	0.0607310	0.0036275	6.8E-67
7	DGKB *	rs6972201	14859112	C	G	0.1637160	-0.0335794	0.0049158	2.1E-12
7	DGKB *	rs17310345	14859642	C	T	0.1762480	-0.0292979	0.0047841	1.9E-10
7	DGKB *	rs10950539	14859809	G	C	0.2823000	-0.0437044	0.0040273	1.5E-29
7	DGKB *	rs10249790	14860431	C	T	0.2815600	-0.0434775	0.0040284	3.9E-29
7	DGKB *	rs10950540	14860473	A	G	0.3519840	-0.0448624	0.0038079	4.5E-34
7	DGKB *	rs10237527	14860821	A	C	0.2810790	-0.0434044	0.0040301	5.0E-29
7	DGKB *	rs7797226	14860857	T	G	0.3529150	-0.0452387	0.0038049	1.4E-34
7	DGKB *	rs10237698	14860995	T	C	0.2810810	-0.0434576	0.0040304	4.3E-29
7	DGKB *	rs36058960	14861327	ATT	A	0.2810570	-0.0440561	0.0040350	9.4E-30
7	DGKB *	rs10241980	14862069	T	C	0.2832860	-0.0442479	0.0040247	3.6E-30
7	DGKB *	rs217549	14862290	C	T	0.2836430	-0.0444304	0.0040222	1.8E-30
7	DGKB *	rs10653568	14863120	G	G	0.2834400	-0.0445007	0.0040216	1.5E-30
7	DGKB *	rs7788886	14863128	C	A	0.3569980	-0.0462035	0.0037998	4.2E-36
7	DGKB *	rs10262324	14863554	C	T	0.2823910	-0.0442778	0.0040281	3.6E-30
7	DGKB *	rs217550	14865165	G	C	0.2829270	-0.0442978	0.0040155	1.9E-30
7	DGKB *	rs7802040	14865171	A	T	0.2829290	-0.0442961	0.0040155	1.9E-30
7	DGKB *	rs7783245	14865175	T	G	0.2830860	-0.0445467	0.0040148	8.7E-31
7	DGKB *	rs7788248	14866213	T	C	0.2834420	-0.0440916	0.0040356	4.0E-30
7	DGKB *	rs217554	14866308	A	G	0.2145740	-0.0374361	0.0045034	4.5E-17
7	DGKB *	rs77163900	14867433	G	GT	0.2582710	-0.0391481	0.0041672	6.7E-23
7	DGKB *	rs6966249	14868615	C	T	0.3598300	-0.0457020	0.0038075	1.4E-35
7	DGKB *	rs7802899	14868784	C	G	0.2857310	-0.0430233	0.0040361	7.3E-29
7	DGKB *	rs2041372	14869502	C	T	0.2835180	-0.0435949	0.0040463	1.6E-29
7	DGKB *	rs79885579	14869708	G	C	0.1400950	-0.0313995	0.0052949	1.8E-09
7	DGKB *	rs217557	14869922	A	C	0.2831460	-0.0435875	0.0040541	2.7E-29
7	DGKB *	rs4721385	14869938	G	A	0.2839860	-0.0434504	0.0040483	3.2E-29
7	DGKB *	rs2358072	14870624	C	T	0.3586470	-0.0451119	0.0038261	1.6E-34
7	DGKB *	rs11766729	14870748	T	A	0.3563730	-0.0454685	0.0038260	5.5E-35
7	DGKB *	rs7777788	14871190	G	A	0.2816680	-0.0435384	0.0040597	2.8E-29
7	DGKB *	rs77777701	14871287	C	T	0.3561560	-0.0456854	0.0038288	3.1E-35
7	DGKB *	rs217558	14871485	T	C	0.2803440	-0.0433164	0.0040686	6.7E-29
7	DGKB *	rs217559	14871494	A	T	0.2799660	-0.0430750	0.0040725	1.3E-28
7	DGKB *	rs58737612	14871499	A	G	0.2570650	-0.0401846	0.0041840	3.8E-24
7	DGKB *	rs7782555	14871969	G	A	0.3843570	-0.0397820	0.0037787	5.0E-28
7	DGKB *	rs217560	14871977	G	A	0.2798130	-0.0428476	0.0040716	2.4E-28
7	DGKB *	rs2191345	14872510	A	G	0.2798030	-0.0433628	0.0040769	4.6E-29
7	DGKB *	rs10270993	14872549	C	A	0.2819430	-0.0430409	0.0040771	1.4E-28
7	DGKB *	rs217562	14872690	C	T	0.2816000	-0.0424083	0.0040799	8.0E-28
7	DGKB *	rs217564	14873677	A	G	0.2771980	-0.0414369	0.0041060	2.2E-26
7	DGKB *	rs12669743	14874234	A	G	0.2903410	-0.0387846	0.0040598	1.8E-23
7	DGKB *	rs2358073	14874838	T	G	0.0997660	-0.0351567	0.0060871	1.1E-08
7	DGKB *	rs77808739	14891062	T	C	0.0673575	0.0462544	0.0073449	2.8E-11
7	DGKB *	rs78095403	15003839	A	T	0.0378395	-0.0622688	0.0096951	8.4E-11
7	DGKB *	rs4719430	15007655	C	G	0.2617210	-0.0563291	0.0041595	4.2E-42
7	DGKB *	rs7784091	15008012	A	G	0.2621710	-0.0569719	0.0041486	2.8E-43
7	DGKB *	rs6976086	15008986	G	T	0.2625660	-0.0570565	0.0041426	1.2E-43
7	DGKB *	rs17168594	15009151	C	T	0.4508840	0.0354620	0.0036631	5.7E-22
7	DGKB *	rs6976381	15009189	C	T	0.4517340	0.0354510	0.0036695	7.4E-22
7	DGKB *	rs12699673	15009979	C	T	0.2627490	-0.0573282	0.0041410	4.7E-44
7	DGKB *	rs6962498	15010680	G	C	0.4494350	0.0357736	0.0036682	2.8E-22
7	DGKB *	rs12666046	15010756	G	A	0.4507900	0.0357179	0.0036688	3.6E-22
7	DGKB *	rs10950546	15010766	T	C	0.2582830	-0.0575507	0.0041690	1.3E-43
7	DGKB *	rs6972333	15012018	A	G	0.4488240	0.0351047	0.0036571	1.5E-21
7	DGKB *	rs6972516	15012164	T	G	0.4518630	0.0355422	0.0036530	4.1E-22
7	DGKB *	rs12113083	15012318	C	G	0.4518100	0.0352153	0.0036518	9.0E-22
7	DGKB *	rs75042408	15012554	A	GGACAA	0.4519780	0.0354900	0.0036525	5.1E-22
7	DGKB *	rs62448618	15012586	A	T	0.4522050	0.0354428	0.0036513	5.5E-22
7	DGKB *	rs6960043	15013235	C	T	0.4478060	0.0344847	0.0036557	7.1E-21
7	DGKB *	rs10264063	15013568	C	G	0.2650260	-0.0568254	0.0041177	1.3E-43
7	DGKB *	rs6978885	15013682	A	G	0.4339740	0.0335664	0.0036822	7.6E-20
7	DGKB *	rs62448644	15013860	T	C	0.4343040	0.0340003	0.0036816	2.7E-20
7	DGKB *	rs10267273	15013964	T	C	0.2651630	-0.0567557	0.0041177	1.6E-43
7	DGKB *	rs10238161	15014202	T	A	0.2650750	-0.0567273	0.0041165	1.3E-43
7	DGKB *	rs2191346	15014253	C	G	0.2624450	-0.0574638	0.0041291	2.2E-44
7	DGKB *	rs2358158	15014438	C	T	0.2651000	-0.0569173	0.0041166	8.1E-44
7	DGKB *	rs10807778	15014565	G	C	0.2649940	-0.0568439	0.0041162	1.0E-43
7	DGKB *	rs10238625	15014607	G	A	0.2649570	-0.0567961	0.0041158	1.2E-43
7	DGKB *	rs10264723	15014745	C	T	0.3766310	-0.0368402	0.0037916	1.4E-22
7	DGKB *	rs10643202	15015203	GATATA	G	0.3766930	-0.0369355	0.0037945	1.1E-22
7	DGKB *	chr7:15015236_T_TTA	15015236	TTA	T	0.4495050	0.0345395	0.0036633	7.4E-21
7	DGKB *	rs2358159	15015283	C	T	0.3762990	-0.0366507	0.0037933	2.3E-22
7	DGKB *	rs6980437	15015291	G	T	0.4491410	0.0345367	0.0036598	6.3E-21
7	DGKB *	rs2215381	15015310	A	C	0.3761110	-0.0366728	0.0037935	2.2E-22
7	DGKB *	rs2215382	15015385	G	C	0.3768650	-0.0368248	0.0037916	1.4E-22
7	DGKB *	rs7798124	15015991	A	G	0.2648610	-0.0567574	0.0041133	9.6E-44
7	DGKB *	rs7798360	15016347	G	A	0.2613500	-0.0573727	0.0041334	2.4E-44
7	DGKB *	rs7781710	15016420	A	T	0.3754230	-0.0376505	0.0037966	1.7E-23
7	DGKB *	rs10950548	15018103	A	G	0.2597310	-0.0573325	0.0041463	5.2E-44
7	DGKB *	rs10950549	15018204	A	G	0.2634100	-0.0566453	0.0041246	1.7E-43
7	DGKB *	rs10266209	15019066	C	T	0.2639340	-0.0569809	0.0041248	6.6E-44
7	DGKB *	rs12538003	15019067	A	G	0.2603890	-0.0572920	0.0041417	5.1E-44
7	DGKB *	rs12538043	15019373	G	C	0.2610190	-0.0573877	0.0041381	2.8E-44

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	DGKB *	rs11514706	15019647	C	A	0.4509560	0.0353467	0.0036634	9.8E-22
7	DGKB *	rs12540947	15019701	C	T	0.1984580	-0.0608602	0.0045976	1.7E-40
7	DGKB *	rs6461153	15020171	G	C	0.2640830	-0.0560799	0.0041243	1.1E-42
7	DGKB *	rs4721400	15020281	A	G	0.2622790	-0.0559685	0.0041363	2.5E-42
7	DGKB *	rs7786873	15020785	G	A	0.4478150	0.0345739	0.0036669	8.1E-21
7	AGMO *	rs13220985	15023069	G	A	0.3103070	-0.0622846	0.0039285	9.7E-58
7	AGMO *	rs2215383	15023358	T	C	0.3099710	-0.0623311	0.0039292	1.2E-57
7	AGMO *	rs10487796	15023805	A	T	0.3073390	-0.0622968	0.0039417	1.7E-57
7	AGMO *	rs10228066	15023944	C	T	0.3104630	-0.0623567	0.0039232	5.2E-58
7	AGMO *	rs10950550	15024298	G	T	0.3105020	-0.0624049	0.0039229	4.6E-58
7	AGMO *	rs10228456	15024301	C	T	0.3103240	-0.0624369	0.0039245	4.4E-58
7	AGMO *	rs10228561	15024336	C	T	0.3105080	-0.0624545	0.0039228	3.7E-58
7	AGMO *	rs10228796	15024565	C	G	0.3105250	-0.0623759	0.0039230	5.0E-58
7	AGMO *	rs10258074	15024591	A	T	0.3105960	-0.0622192	0.0039234	9.8E-58
7	AGMO *	rs2191348	15024630	G	T	0.3106780	-0.0623763	0.0039225	5.6E-58
7	AGMO *	rs2191349	15024684	G	T	0.3105900	-0.0624394	0.0039221	3.8E-58
7	AGMO *	rs11760782	15025163	A	T	0.2020870	-0.0632994	0.0045753	1.7E-44
7	AGMO *	rs66825728	15025258	A	GAAAGA	0.2018550	-0.0633624	0.0045788	1.4E-44
7	AGMO *	rs4721401	15025271	T	G	0.3102430	-0.0627135	0.0039249	1.3E-58
7	AGMO *	rs6947830	15025359	G	A	0.3108010	-0.0628506	0.0039218	5.2E-59
7	AGMO *	rs4719433	15025378	T	C	0.3096810	-0.0627636	0.0039266	1.1E-58
7	AGMO *	rs6967891	15025449	T	C	0.3099130	-0.0627473	0.0039263	1.1E-58
7	AGMO *	rs1974619	15025675	C	T	0.3091400	-0.0628013	0.0039318	1.3E-58
7	AGMO *	rs1974620	15025842	C	T	0.3100880	-0.0624962	0.0039222	3.0E-58
7	AGMO *	rs1558317	15025939	T	A	0.3095070	-0.0621038	0.0039263	2.2E-57
7	AGMO *	rs1558318	15025987	A	T	0.3094820	-0.0620732	0.0039265	2.4E-57
7	AGMO *	rs62448650	15027008	C	G	0.3363970	0.0236528	0.0038335	1.9E-09
7	AGMO *	rs62448651	15027016	A	C	0.3319830	0.0231476	0.0038696	7.4E-09
7	AGMO *	rs9986706	15105665	T	C	0.2759680	-0.0269293	0.0041447	2.3E-11
7	AGMO *	rs7808380	15106056	T	C	0.2956280	-0.0247759	0.0040545	2.3E-10
7	AGMO *	rs763868	15106488	G	A	0.2917250	-0.0244665	0.0040650	4.2E-10
7	AGMO *	rs10237757	15107623	A	C	0.2925930	-0.0245595	0.0040492	2.9E-10
7	AGMO *	rs10241045	15107736	A	G	0.2922980	-0.0241071	0.0040492	5.5E-10
7	AGMO *	rs10256464	15107896	C	T	0.2963600	-0.0239564	0.0040380	5.7E-10
7	AGMO *	rs4719438	15108114	C	T	0.2947800	-0.0240030	0.0040376	5.7E-10
7	AGMO *	rs2215654	15109065	A	G	0.2953560	-0.0232902	0.0040272	1.8E-09
7	AGMO *	rs7792638	15109981	C	A	0.2811950	-0.0257423	0.0040616	7.3E-11
7	AGMO *	rs7357086	15110498	C	T	0.3004780	-0.0233124	0.0039974	1.5E-09
7	AGMO *	rs6964655	15110806	G	A	0.2992580	-0.0237765	0.0040007	7.3E-10
7	AGMO *	rs10647859	15112138	CCTT	C	0.3026150	-0.0243469	0.0039781	2.6E-10
7	AGMO *	rs34747351	15112567	T	C	0.2947180	-0.0245384	0.0040016	3.3E-10
7	AGMO *	rs10274264	15112663	C	T	0.3025390	-0.0244211	0.0039765	2.3E-10
7	AGMO *	rs10274265	15112667	C	T	0.3019670	-0.0242511	0.0039787	2.9E-10
7	AGMO *	rs6958082	15113003	C	T	0.3026420	-0.0245962	0.0039751	1.7E-10
7	AGMO *	rs12540109	15113469	C	T	0.3018570	-0.0244511	0.0039818	2.2E-10
7	AGMO *	rs4593427	15113890	G	C	0.3007000	-0.0240735	0.0039750	4.2E-10
7	AGMO *	rs4721408	15114555	G	A	0.2775250	-0.0263320	0.0040549	3.6E-11
7	AGMO *	rs4719439	15114594	C	T	0.2775250	-0.0263320	0.0040549	3.6E-11
7	AGMO *	rs6461155	15115285	G	A	0.2800210	-0.0254447	0.0040478	1.0E-10
7	AGMO *	rs60771996	15115564	C	CAA	0.2799500	-0.0259375	0.0040495	4.5E-11
7	AGMO *	rs60653190	15115679	G	C	0.2830470	-0.0250672	0.0040419	1.6E-10
7	AGMO *	rs12538991	15116747	C	T	0.2757930	-0.0270966	0.0040576	1.0E-11
7	AGMO *	rs12531053	15116790	C	A	0.2770850	-0.0270949	0.0040546	8.7E-12
7	AGMO *	rs12670759	15117345	C	T	0.2829420	-0.0268579	0.0040289	7.4E-12
7	AGMO *	rs2191995	15117516	C	A	0.2866640	-0.0262963	0.0040191	1.7E-11
7	AGMO *	rs2191996	15117604	G	C	0.2849930	-0.0260511	0.0040258	3.3E-11
7	AGMO *	rs2041556	15118063	G	T	0.2824900	-0.0264067	0.0040334	1.9E-11
7	AGMO *	rs6956836	15118211	C	T	0.2701150	-0.0264632	0.0041140	5.0E-11
7	AGMO *	rs57764041	15118415	G	A	0.2851950	-0.0260695	0.0040301	2.9E-11
7	AGMO *	rs55899240	15118764	C	T	0.2781550	-0.0265316	0.0040718	1.6E-11
7	AGMO *	rs12532628	15119204	C	A	0.2753500	-0.0263433	0.0040914	3.7E-11
7	AGMO *	rs1547962	15119434	A	C	0.2748040	-0.0256574	0.0040896	1.1E-10
7	AGMO *	rs1547963	15119858	C	T	0.2726370	-0.0259492	0.0040979	6.4E-11
7	AGMO *	chr7:15119931_CTT_C	15119931	C	CTT	0.2742760	-0.0258055	0.0041011	1.0E-10
7	AGMO *	rs2109948	15120216	T	C	0.2805320	-0.0257258	0.0040656	4.8E-11
7	AGMO *	chr7:15120751_ATTTC_A	15120751	ATTTC	A	0.2871500	-0.0258507	0.0040470	4.0E-11
7	AGMO *	rs6963945	15123385	G	C	0.2817280	-0.0254497	0.0040614	7.4E-11
7	AGMO *	rs17387298	15123985	C	T	0.3002220	-0.0250953	0.0040199	4.9E-11
7	AGMO *	rs12164053	15125737	T	A	0.2835490	-0.0261179	0.0040572	2.7E-11
7	AGMO *	rs2080042	15129726	T	C	0.2869970	-0.0254089	0.0040411	5.3E-11
7	AGMO *	rs6977242	15130887	G	A	0.2791750	-0.0258217	0.0040766	5.5E-11
7	AGMO *	rs764702	15132838	G	A	0.2876330	-0.0260927	0.0040378	1.9E-11
7	AGMO *	rs2358162	15133426	G	C	0.2801520	-0.0263577	0.0040716	2.1E-11
7	AGMO *	rs57949413	15133498	AGCT	A	0.2803910	-0.0264918	0.0040699	1.7E-11
7	AGMO *	rs2961245	15134483	C	T	0.2798040	-0.0262618	0.0040759	2.6E-11
7	AGMO *	rs12671631	15134555	T	C	0.2885180	-0.0263205	0.0040382	1.4E-11
7	AGMO *	rs11370724	15134817	AT	A	0.2803160	-0.0265520	0.0040709	1.5E-11
7	AGMO *	rs2961249	15155541	C	T	0.2806980	-0.0266728	0.0040703	1.3E-11
7	AGMO *	rs2961250	15135656	C	G	0.2791660	-0.0264568	0.0040802	2.0E-11
7	AGMO *	rs34015655	15135750	CTTAA	C	0.2809290	-0.0266458	0.0040691	1.3E-11
7	AGMO *	rs2961252	15135776	G	T	0.2809310	-0.0266596	0.0040691	1.3E-11
7	AGMO *	rs2961253	15135802	C	T	0.2809310	-0.0266596	0.0040691	1.3E-11
7	AGMO *	rs2961254	15136243	C	T	0.2801060	-0.0266098	0.0040713	1.2E-11
7	AGMO *	rs36105917	15136321	TA	T	0.2806550	-0.0265978	0.0040694	1.3E-11
7	AGMO *	rs12699684	15136353	T	C	0.2884930	-0.0263110	0.0040355	1.2E-11
7	AGMO *	rs5882485	15136494	A	AT	0.2808540	-0.0266894	0.0040712	1.1E-11
7	AGMO *	rs10950553	15137077	G	A	0.2974070	-0.0256740	0.0039954	2.9E-11
7	AGMO *	rs10950554	15137511	G	A	0.2974290	-0.0259551	0.0039910	1.6E-11
7	AGMO *	rs13233744	15137584	G	A	0.2925500	-0.0251606	0.0040088	4.7E-11
7	AGMO *	rs13233550	15137676	A	T	0.3092380	-0.0231885	0.0039338	4.6E-10
7	AGMO *	rs9639222	15137745	C	T	0.3029510	-0.0234383	0.0039584	4.7E-10
7	AGMO *	rs9639223	15137759	G	T	0.3031150	-0.0233038	0.0039579	6.3E-10
7	AGMO *	rs9639224	15137871	C	G	0.3018870	-0.0226525	0.0039634	1.7E-09
7	AGMO *	rs9639225	15138542	C	T	0.3025230	-0.0231197	0.0039577	9.6E-10
7	AGMO *	rs71004362	15138613	T	TA	0.3032910	-0.0234030	0.0039530	6.3E-10
7	AGMO *	rs12668555	15138665	C	T	0.3033230	-0.0234521	0.0039527	5.8E-10
7	AGMO *	rs17387801	15138714	C	T	0.3044340	-0.0233217	0.0039420	6.3E-10
7	AGMO *	chr7:15138837_CA_C	15138837	CA	C	0.3044260	-0.0236094	0.0039490	4.1E-10
7	AGMO *	rs12699685	15138865	C	T	0.3112890	-0.0232114	0.0039217	4.7E-10
7	AGMO *	rs12669092	15138892	G	A	0.3057240	-0.0239110	0.0039541	2.5E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	AGMO *	rs9639226	15139258	G	A	0.3042960	-0.0232421	0.0039487	7.1E-10
7	AGMO *	rs9639227	15139281	T	C	0.3112240	-0.0230749	0.0039227	6.1E-10
7	AGMO *	rs9639228	15139351	G	A	0.3066780	-0.0227480	0.0039442	1.7E-09
7	AGMO *	rs9639229	15139411	C	T	0.3121540	-0.0231002	0.0039221	6.0E-10
7	AGMO *	rs9886159	15139898	C	T	0.3137770	-0.0223440	0.0039406	2.5E-09
7	AGMO *	rs35452785	15139965	C	T	0.3092760	-0.0228049	0.0039454	1.6E-09
7	HECW1	rs17172209	43447285	G	A	0.0318280	0.0608160	0.0103288	1.8E-09
7	URGCP, URGCP-MRPS24	rs189741536	43892283	C	G	0.0169390	0.0799317	0.0140742	1.2E-08
7	URGCP, URGCP-MRPS24	rs539481994	43897613	A	T	0.0144398	-0.0853003	0.0152695	4.8E-08
7	UBE2D4	rs534249582	43927344	T	G	0.0121584	0.0965150	0.0165368	5.0E-09
7	UBE2D4	rs60037258	43933023	T	C	0.4971870	0.0211031	0.0036509	2.3E-09
7	UBE2D4	rs41279600	43938680	A	C	0.4923000	0.0197773	0.0036464	2.5E-08
7	POLR2J4, UBE2D4	rs929380	43942540	C	T	0.4928100	0.0200721	0.0036525	1.8E-08
7	POLR2J4, UBE2D4	rs2074727	43942883	A	C	0.4928590	0.0201405	0.0036529	1.6E-08
7	POLR2J4, UBE2D4	rs7785378	43946004	G	A	0.4933620	0.0201810	0.0036617	1.4E-08
7	DBNL	rs75690519	44051665	A	G	0.0134011	0.0942617	0.0157782	2.9E-09
7	AEBP1 *	rs145000405	44096312	A	C	0.0282203	0.1082580	0.0110228	6.0E-24
7	AEBP1 *	rs74976016	44103603	G	T	0.0112136	0.1332590	0.0173961	3.4E-15
7	AEBP1 *	rs73693651	44110650	A	G	0.0316726	0.1100020	0.0103636	1.2E-27
7	POLD2	rs2075070	44115653	G	A	0.2615090	-0.0621451	0.0042231	1.8E-50
7	POLD2	rs148680081	44116129	A	G	0.0133770	0.0963426	0.0158358	1.6E-09
7	POLD2	rs3087367	44116547	A	G	0.2612860	-0.0618654	0.0042225	3.6E-50
7	POLD2	rs3217964	44118226	C	T	0.2386650	-0.0660917	0.0043270	2.0E-54
7	POLD2	rs3217962	44118379	G	A	0.2621910	-0.0621567	0.0042076	7.4E-51
7	POLD2	rs3087370	44122210	G	A	0.2344250	-0.0679338	0.0043335	2.5E-57
7	POLD2 *	rs3217944	44124463	A	C	0.2345800	-0.0680566	0.0043261	9.5E-58
7	POLD2 *	rs3217943	44124492	C	T	0.2350240	-0.0680409	0.0043234	9.1E-58
7	POLD2 *	chr7:44125897_CT_C	44125897	C	CT	0.4659060	-0.0388811	0.0038665	5.5E-27
7	POLD2 *	rs113784062	44126070	T	C	0.2349690	-0.0683855	0.0043222	1.6E-58
7	POLD2 *	rs4724288	44127150	A	C	0.4568180	-0.0392602	0.0036807	2.1E-27
7	POLD2 *	rs4724289	44127151	A	C	0.4568140	-0.0392610	0.0036807	2.1E-27
7	POLD2 *	rs12538223	44127298	G	A	0.2351960	-0.0685462	0.0043150	5.2E-59
7	POLD2 *	chr7:44127645_A_AT	44127645	AT	A	0.2419360	-0.0637442	0.0042942	6.9E-52
7	POLD2 *	rs7794794	44129176	A	G	0.4577210	-0.0395889	0.0036740	4.6E-28
7	POLD2 *	rs10629899	44129193	CAT	C	0.4580260	-0.0398774	0.0036720	2.0E-28
7	POLD2 *	rs12535289	44129630	G	A	0.2356830	-0.0685060	0.0043032	2.9E-59
7	POLD2 *	rs55907525	44129790	C	G	0.2322610	-0.0690775	0.0043301	7.7E-60
7	POLD2 *	rs17769566	44129973	C	A	0.2357520	-0.0684663	0.0043014	2.4E-59
7	POLD2 *	rs56902462	44130156	A	G	0.2351350	-0.0682154	0.0043054	7.1E-59
7	POLD2 *	rs12531534	44130798	T	C	0.2358950	-0.0684542	0.0042986	2.0E-59
7	POLD2 *	rs10951757	44130986	A	G	0.4580780	-0.0400971	0.0036741	9.7E-29
7	MYL7 *	rs2922666	44131606	T	G	0.1907950	0.0509771	0.0046998	1.1E-28
7	MYL7 *	rs189718107	44133410	G	T	0.0129255	0.0890023	0.0161280	3.1E-08
7	MYL7 *	rs17831589	44133526	A	G	0.2358690	-0.0686354	0.0042952	5.1E-60
7	MYL7 *	rs2971682	44134216	A	C	0.1909340	0.0512069	0.0046952	5.0E-29
7	MYL7 *	rs11979448	44134359	G	T	0.4610750	-0.0384778	0.0036836	1.3E-26
7	MYL7 *	rs11975874	44134360	A	C	0.4610750	-0.0384778	0.0036836	1.3E-26
7	MYL7 *	rs62460071	44134541	T	C	0.2362030	-0.0686399	0.0042884	4.5E-60
7	MYL7 *	rs17135975	44134572	T	C	0.4610480	-0.0384139	0.0036825	1.6E-26
7	MYL7 *	rs4397301	44135828	G	C	0.2377400	-0.0695737	0.0042744	5.4E-62
7	MYL7 *	rs9791709	44136188	T	C	0.2380640	-0.0695032	0.0042700	5.5E-62
7	MYL7 *	rs17136076	44137592	G	A	0.2398420	-0.0701972	0.0042622	2.8E-63
7	MYL7 *	rs17769733	44137813	T	C	0.2395780	-0.0701153	0.0042640	3.4E-63
7	MYL7 *	rs882021	44138273	C	T	0.2419120	-0.0710948	0.0042529	5.9E-65
7	MYL7	rs1008384	44139027	G	A	0.2568730	-0.0645495	0.0042142	7.1E-56
7	MYL7	rs882020	44139144	T	C	0.1879580	0.0533573	0.0047298	5.5E-31
7	MYL7	rs741033	44140166	G	C	0.2546860	-0.0675905	0.0042724	3.9E-58
7	GCK *	rs2908277	44143834	A	G	0.1728880	0.0707168	0.0048516	6.8E-50
7	GCK	rs76374134	44144289	T	C	0.0283062	-0.1349590	0.0110981	4.6E-36
7	GCK	rs76323047	44146356	G	A	0.1755160	0.0711283	0.0048281	2.3E-50
7	GCK	rs2268577	44149411	T	C	0.1794650	0.0685767	0.0047321	1.5E-48
7	GCK	rs2268575	44149675	C	T	0.1794080	0.0684560	0.0047325	1.8E-48
7	GCK	rs35786405	44149940	A	C	0.0121996	0.2007230	0.0166567	4.2E-35
7	GCK	rs200698872	44154235	T	C	0.0131368	0.0911321	0.0159927	1.8E-08
7	GCK	rs62460075	44161550	T	C	0.2116030	-0.0741661	0.0045450	1.1E-61
7	GCK	rs2908294	44164827	T	C	0.1654680	0.0860736	0.0048960	1.3E-69
7	GCK	rs12540369	44165915	T	A	0.2333180	-0.0732576	0.0042949	8.3E-68
7	GCK	rs12535229	44166006	A	G	0.2333220	-0.0732793	0.0042949	7.7E-68
7	GCK	rs77460615	44166296	T	C	0.0360747	0.0529170	0.0098582	3.9E-08
7	GCK	rs2971672	44166307	C	A	0.4590920	0.0532860	0.0036399	7.2E-50
7	GCK	rs77851840	44166756	G	GAT	0.2333290	-0.0732969	0.0042949	7.0E-68
7	GCK	rs62460076	44166795	A	T	0.2332030	-0.0733245	0.0042971	7.3E-68
7	GCK	rs62460077	44167083	T	C	0.2333230	-0.0733788	0.0042950	4.9E-68
7	GCK	rs73112269	44168408	A	G	0.2334910	-0.0733641	0.0042927	4.2E-68
7	GCK	rs2908293	44169723	A	G	0.1662670	0.0863658	0.0048763	7.8E-71
7	GCK	rs2908292	44171111	T	C	0.1722850	0.0827725	0.0048024	2.2E-67
7	GCK	rs2971671	44171738	C	T	0.1722610	0.0829128	0.0048025	1.4E-67
7	GCK	rs16881016	44171808	C	T	0.2348790	-0.0726771	0.0042813	2.9E-67
7	GCK	rs112745774	44172019	T	C	0.2345130	-0.0723906	0.0042849	1.3E-66
7	GCK	rs60275913	44172686	T	G	0.2347110	-0.0724783	0.0042832	8.6E-67
7	GCK	rs74778451	44173346	T	C	0.0149655	-0.0952039	0.0149261	6.2E-11
7	GCK	rs59419319	44174275	T	C	0.2356500	-0.0726158	0.0042788	3.0E-67
7	GCK	rs201501016	44174676	C	CT	0.0654462	-0.0792100	0.0074824	1.4E-27
7	GCK	rs3779606	44175415	C	T	0.2357840	-0.0725170	0.0042770	4.1E-67
7	GCK	rs62460080	44176272	A	G	0.2357890	-0.0725235	0.0042767	4.0E-67
7	GCK	rs17172566	44176513	A	G	0.2357910	-0.0725161	0.0042767	4.1E-67
7	GCK	rs2908290	44176538	A	G	0.4584680	0.0535355	0.0036377	1.2E-50
7	GCK	rs62459064	44176698	T	C	0.2357790	-0.0725274	0.0042767	3.8E-67
7	GCK	rs2284777	44176999	C	T	0.2354980	-0.0721842	0.0042800	1.8E-66
7	GCK	rs2284775	44177762	G	A	0.2359130	-0.0726819	0.0042768	2.1E-67
7	GCK	rs2284774	44178742	A	C	0.2358920	-0.0726484	0.0042771	2.4E-67
7	GCK	rs2300587	44179195	C	T	0.2358970	-0.0726675	0.0042771	2.3E-67
7	GCK	rs2300584	44179739	G	A	0.1518030	0.0917605	0.0050533	1.7E-74
7	GCK	rs10259649	44180106	C	T	0.1491640	0.0939154	0.0051147	3.5E-76
7	GCK	rs12534104	44180143	A	C	0.2262990	-0.0730133	0.0044055	3.5E-64
7	GCK	rs1990458	44183203	T	C	0.3202720	-0.0543666	0.0039581	2.6E-43
7	GCK	rs34380942	44183693	TA	T	0.0941074	-0.0768100	0.0062172	4.8E-36
7	GCK	rs34780996	44183696	A	G	0.0940822	-0.0765990	0.0062182	7.3E-36
7	GCK	rs741038	44183880	G	A	0.2738100	-0.0372525	0.0040586	7.5E-21
7	GCK	rs59727929	44183959	T	C	0.0940089	-0.0767238	0.0062210	5.5E-36

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	GCK	rs730497	44184122	A	G	0.1967540	0.1222090	0.0045657	7.0E-161
7	GCK	rs2908289	44184343	A	G	0.1967390	0.1224130	0.0045672	2.9E-161
7	GCK	rs67253402	44184933	G	GAT	0.0898310	-0.0751020	0.0063766	3.3E-33
7	GCK	rs201139382	44185031	C	CAG	0.0887078	-0.0751786	0.0064168	8.2E-33
7	GCK	rs3808319	44185252	A	G	0.3588710	-0.0571183	0.0037912	1.0E-51
7	GCK	rs34859037	44185887	C	G	0.0941490	-0.0763834	0.0062182	1.1E-35
7	GCK	rs34807880	44186230	G	A	0.0941519	-0.0763752	0.0062181	1.2E-35
7	GCK	rs2268570	44186491	G	C	0.3702820	-0.0555849	0.0037636	1.1E-49
7	GCK	rs2971670	44186502	T	C	0.1943450	0.1232580	0.0045981	3.4E-161
7	GCK	rs13239289	44187089	G	C	0.0941513	-0.0763742	0.0062177	1.2E-35
7	GCK	rs41314139	44187345	A	G	0.0941513	-0.0763742	0.0062177	1.2E-35
7	GCK	rs35276355	44187357	G	T	0.0941513	-0.0763742	0.0062177	1.2E-35
7	GCK	rs34976798	44187686	C	A	0.0940907	-0.0764966	0.0062197	9.8E-36
7	GCK	rs35079658	44188298	T	C	0.0941507	-0.0763912	0.0062177	1.2E-35
7	GCK	rs34672149	44188548	G	GC	0.0941507	-0.0763912	0.0062177	1.2E-35
7	GCK	rs13306391	44189037	C	G	0.0941839	-0.0763238	0.0062163	1.3E-35
7	GCK	rs13306390	44189168	C	T	0.0179252	-0.0752455	0.0136607	1.4E-08
7	GCK *	rs1799884	44189469	T	C	0.1947920	0.1232160	0.0045864	1.1E-161
7	GCK *	rs12702070	44189633	C	T	0.0941790	-0.0763353	0.0062163	1.3E-35
7	GCK *	rs35670475	44189721	A	G	0.0941790	-0.0763353	0.0062163	1.3E-35
7	GCK *	rs1476891	44190369	G	A	0.2756020	-0.0360621	0.0040566	1.1E-19
7	GCK *	rs36205690	44191222	T	G	0.0125015	-0.1243280	0.0163577	2.0E-14
7	GCK *	rs3757840	44191617	G	T	0.4654810	-0.0784909	0.0036408	3.1E-104
7	GCK *	rs3757839	44191638	G	T	0.0931960	-0.0749215	0.0062446	4.7E-34
7	GCK *	rs3757838	44191711	T	A	0.0932047	-0.0749814	0.0062440	4.1E-34
7	GCK *	rs62459076	44191993	G	T	0.0933405	-0.0748712	0.0062395	4.3E-34
7	GCK *	rs2971669	44192179	T	C	0.3539410	0.0886240	0.0037938	4.1E-123
7	GCK *	rs6975024	44192287	C	T	0.2046620	0.1191000	0.0044989	4.9E-157
7	GCK *	rs34443021	44192533	T	C	0.0928489	-0.0742417	0.0062597	2.7E-33
7	GCK *	rs62459077	44192990	T	C	0.0934180	-0.0746854	0.0062355	5.6E-34
7	GCK *	rs7789273	44193006	T	C	0.3707180	-0.0563928	0.0037643	4.3E-51
7	GCK *	rs58053084	44193014	G	T	0.0934528	-0.0745165	0.0062345	7.3E-34
7	GCK *	rs741037	44193234	A	G	0.1980080	0.1218570	0.0045640	7.8E-160
7	GCK *	rs62459079	44193279	T	C	0.0934180	-0.0746854	0.0062355	5.6E-34
7	GCK *	rs62459080	44193319	A	G	0.0934180	-0.0746854	0.0062355	5.6E-34
7	GCK *	rs3065186	44193493	CTCTTT	C	0.2747940	-0.0349996	0.0040648	1.2E-18
7	GCK *	rs735670	44193746	T	A	0.0934180	-0.0746854	0.0062355	5.6E-34
7	GCK *	rs35902302	44194829	A	C	0.0932949	-0.0749064	0.0062408	3.7E-34
7	GCK *	rs741036	44195114	A	G	0.0932920	-0.0749196	0.0062409	3.7E-34
7	GCK *	rs2908286	44195138	T	C	0.1976750	0.1217880	0.0045627	6.8E-160
7	YKT6 *	rs741034	44195261	C	T	0.0932920	-0.0749196	0.0062409	3.7E-34
7	YKT6 *	rs71533226	44195594	T	A	0.0923655	-0.0745295	0.0062742	1.9E-33
7	YKT6 *	rs4607517	44196069	A	G	0.1977840	0.1211650	0.0045561	9.7E-159
7	YKT6 *	rs55794846	44196764	G	C	0.0932775	-0.0749319	0.0062416	3.8E-34
7	YKT6 *	rs150486663	44200116	A	G	0.0932613	-0.0749122	0.0062430	4.3E-34
7	YKT6 *	rs71563938	44200289	T	TTC	0.0932613	-0.0749122	0.0062430	4.3E-34
7	YKT6 *	rs1985469	44200725	T	A	0.1915440	0.1208220	0.0046569	1.8E-150
7	YKT6 *	rs1004558	44200808	T	C	0.1975560	0.1213620	0.0045650	1.1E-158
7	YKT6 *	rs35832856	44200964	T	C	0.0930948	-0.0748432	0.0062480	4.7E-34
7	YKT6	rs11540050	44201065	T	G	0.0923744	-0.0738346	0.0062746	8.9E-33
7	YKT6	rs61324019	44201373	A	G	0.0932640	-0.0749046	0.0062430	4.4E-34
7	YKT6	rs34110131	44202297	C	T	0.0932729	-0.0748337	0.0062427	5.0E-34
7	YKT6	rs2971668	44203839	C	G	0.2066390	0.1185000	0.0044863	1.7E-156
7	YKT6	rs2072440	44204895	C	G	0.0932508	-0.0748332	0.0062435	5.1E-34
7	YKT6	rs2971667	44205461	C	T	0.1978460	0.1212520	0.0045591	8.1E-159
7	YKT6	rs10278336	44205764	G	A	0.3690530	-0.0563157	0.0037636	7.0E-51
7	YKT6	rs145999791	44206195	T	C	0.0348301	0.1150430	0.0099331	9.3E-32
7	YKT6	rs917793	44206254	T	A	0.1978720	0.1212470	0.0045585	8.1E-159
7	YKT6	rs2075068	44206935	G	A	0.0933420	-0.0748820	0.0062397	4.0E-34
7	YKT6	rs41279621	44207134	C	A	0.0933420	-0.0748820	0.0062397	4.0E-34
7	YKT6	rs3824065	44207659	T	C	0.3695360	-0.0565195	0.0037549	1.9E-51
7	YKT6	rs34256495	44209029	T	C	0.0933219	-0.0747963	0.0062406	5.2E-34
7	YKT6	rs57597270	44209121	C	T	0.0933225	-0.0747936	0.0062406	5.2E-34
7	YKT6	rs2908282	44209229	A	G	0.1977210	0.1209120	0.0045621	8.6E-158
7	YKT6	chr7:44210714_A_ATG	44210714	ATG	A	0.0769959	-0.0678049	0.0068932	9.0E-24
7	YKT6	chr7:44210722_G_GTA	44210722	GTA	G	0.0929695	-0.0750830	0.0062559	4.6E-34
7	YKT6	rs12670584	44212419	G	C	0.0932311	-0.0743201	0.0062475	1.5E-33
7	YKT6	rs3840674	44212591	C	CTG	0.1983410	0.1192860	0.0045741	3.2E-153
7	YKT6	rs3840673	44212709	T	TG	0.0932284	-0.0745683	0.0062460	8.7E-34
7	YKT6	rs11540051	44213422	T	G	0.0931929	-0.0745748	0.0062470	8.4E-34
7	YKT6	rs1045776	44213786	C	T	0.0931900	-0.0745986	0.0062471	8.1E-34
7	YKT6 *	rs62459085	44215304	G	C	0.0932806	-0.0746900	0.0062458	6.2E-34
7	YKT6 *	rs62459086	44215515	C	T	0.0932774	-0.0747253	0.0062463	5.8E-34
7	YKT6 *	rs62459087	44215516	T	G	0.0932774	-0.0747253	0.0062463	5.8E-34
7	CAMK2B *	rs35197372	44215937	G	A	0.0932428	-0.0744730	0.0062481	9.4E-34
7	CAMK2B *	rs787521	44216044	A	G	0.3548180	0.0876521	0.0037907	1.6E-120
7	CAMK2B	chr7:44217409_G_GA	44217409	GA	G	0.0131806	0.1301140	0.0160756	9.2E-17
7	CAMK2B	rs78359497	44217896	A	G	0.1719120	0.1193200	0.0048719	2.7E-135
7	CAMK2B	rs758982	44218344	T	C	0.1730390	0.1183750	0.0048630	1.1E-133
7	CAMK2B	rs35148004	44219975	T	C	0.0928607	-0.0742417	0.0062667	2.3E-33
7	CAMK2B	rs1065359	44220107	A	G	0.3559440	-0.0579031	0.0038043	2.5E-52
7	CAMK2B	rs1127065	44220272	T	C	0.3705110	-0.0587881	0.0037652	3.5E-55
7	CAMK2B	rs34775092	44221182	A	G	0.0977305	-0.0724666	0.0061280	3.4E-33
7	CAMK2B	rs58958064	44221545	GCAGCA	C	0.0965062	-0.0728481	0.0061650	3.8E-33
7	CAMK2B	rs59877240	44221670	A	G	0.0980022	-0.0725370	0.0061214	1.9E-33
7	CAMK2B	rs56958012	44221683	T	C	0.0976241	-0.0725168	0.0061312	3.2E-33
7	CAMK2B	rs57522294	44221720	GC	G	0.0976168	-0.0724257	0.0061315	3.7E-33
7	CAMK2B	rs62459090	44222066	A	G	0.0976382	-0.0723249	0.0061342	4.8E-33
7	CAMK2B	rs62459091	44222249	A	G	0.0975522	-0.0724906	0.0061343	3.5E-33
7	CAMK2B	rs732360	44222379	A	G	0.1974650	0.1154090	0.0046175	3.6E-140
7	CAMK2B	rs2003563	44222454	G	T	0.0956656	-0.0732376	0.0061989	4.3E-33
7	CAMK2B	rs75929284	44222646	G	A	0.0970806	-0.0728105	0.0061537	3.2E-33
7	CAMK2B	rs62459092	44223167	G	A	0.2620510	-0.0287158	0.0042105	2.9E-12
7	CAMK2B	rs62459093	44224074	A	G	0.0946173	-0.0731347	0.0062588	1.1E-32
7	CAMK2B	rs149144486	44224253	A	.GCTCAA	0.0939274	-0.0732067	0.0062847	2.0E-32
7	CAMK2B	rs2877285	44226036	A	G	0.0947978	-0.0717767	0.0062823	1.9E-31
7	CAMK2B	rs917792	44226380	T	C	0.0965970	-0.0697872	0.0062423	2.9E-30
7	CAMK2B	rs117998298	44229771	T	C	0.0819612	-0.0674973	0.0067291	8.6E-25
7	CAMK2B	rs79282401	44231427	T	C	0.0884502	-0.0666807	0.0064727	4.0E-26
7	CAMK2B	rs2075075	44235097	T	C	0.0808524	-0.0599368	0.0067286	4.1E-20

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	CAMK2B	rs79495881	44235964	T	C	0.0880747	-0.0644688	0.0064453	6.7E-25
7	CAMK2B	rs78185111	44236885	T	C	0.0881889	-0.0641899	0.0064405	9.6E-25
7	CAMK2B	rs75831906	44237177	G	T	0.0881848	-0.0644341	0.0064400	6.8E-25
7	CAMK2B	rs76624683	44237572	G	C	0.0881778	-0.0640950	0.0064389	1.0E-24
7	CAMK2B	rs79349916	44237881	A	G	0.0881991	-0.0643033	0.0064384	7.3E-25
7	CAMK2B	rs149636252	44238698	T	C	0.0149307	0.0980838	0.0151097	1.9E-10
7	CAMK2B	rs75079129	44239085	A	G	0.0879005	-0.0644103	0.0064514	6.9E-25
7	CAMK2B	rs76144629	44240596	T	G	0.0840948	-0.0643190	0.0065750	5.1E-24
7	CAMK2B	rs116841749	44241434	A	G	0.0839963	-0.0641389	0.0065825	7.2E-24
7	CAMK2B	rs74790674	44243161	T	C	0.0835197	-0.0640836	0.0066051	8.8E-24
7	CAMK2B	rs11542227	44243278	G	A	0.1353810	-0.0345301	0.0054089	2.7E-11
7	CAMK2B	rs17172630	44243329	A	G	0.0840704	-0.0653684	0.0065866	1.3E-24
7	CAMK2B	rs35661323	44245184	T	C	0.1284310	-0.0380786	0.0055247	7.3E-13
7	CAMK2B	rs141234985	44247783	A	T	0.0829553	-0.0633150	0.0066273	3.8E-23
7	CAMK2B	rs10441113	44249066	A	G	0.1129000	-0.0444686	0.0058045	1.2E-15
7	CAMK2B	rs77715675	44249899	C	G	0.0839987	-0.0628712	0.0065888	4.2E-23
7	CAMK2B	rs74907537	44250264	A	G	0.0617726	-0.0586436	0.0075719	4.1E-16
7	CAMK2B	rs60463592	44252272	T	C	0.0611178	-0.0570185	0.0076102	3.4E-15
7	CAMK2B	rs56898552	44252592	A	G	0.0618309	-0.0570981	0.0075505	2.0E-15
7	CAMK2B	rs565987131	44253144	T	TA	0.0120266	0.1172580	0.0168055	6.6E-13
7	CAMK2B	rs147143275	44262602	T	C	0.0155629	0.0901841	0.0148153	2.7E-09
7	CAMK2B	rs201424627	44323005	C	A	0.0142779	0.0941669	0.0154013	8.3E-10
7	CAMK2B *	rs62459126	44339249	A	G	0.2346680	-0.0272412	0.0042639	7.7E-11
7	CAMK2B *	rs62459127	44347415	A	G	0.2379580	-0.0269353	0.0042589	1.1E-10
7	NUDCD3 *	rs116940590	44376772	A	C	0.0160150	-0.0836211	0.0145823	3.7E-09
7	NUDCD3	rs2331071	44390652	T	G	0.2467160	-0.0229082	0.0042397	3.2E-08
7	NUDCD3	rs138672084	44425129	A	C	0.0159865	-0.0859583	0.0145982	1.4E-09
7	NUDCD3 *	rs191577159	44492247	T	A	0.0133843	0.0908308	0.0158698	1.8E-08
7	C7orf72 *	rs4598207	50218883	T	A	0.2474190	0.0273624	0.0042649	1.4E-10
7	C7orf72 *	rs34767118	50231468	G	A	0.2605210	0.0281330	0.0041308	5.7E-12
7	IKZF1 *	rs144164538	50231748	T	A	0.2070610	0.0255227	0.0045014	3.1E-09
7	IKZF1 *	rs11773763	50231903	T	C	0.2605210	0.0281330	0.0041308	5.7E-12
7	IKZF1 *	rs62445350	50238591	T	A	0.2606040	0.0282478	0.0041300	4.6E-12
7	IKZF1 *	rs62445352	50249908	A	G	0.2037950	0.0259371	0.0045316	2.3E-09
7	IKZF1 *	rs55935382	50250073	A	C	0.2596640	0.0282666	0.0041361	5.0E-12
7	IKZF1 *	rs60969753	50255709	C	CT	0.2603370	0.0283936	0.0041323	3.4E-12
7	IKZF1 *	rs11185602	50259481	G	A	0.2617710	0.0282991	0.0041338	4.4E-12
7	IKZF1 *	rs4917014	50266267	G	T	0.3147530	0.0278396	0.0039032	4.8E-13
7	IKZF1 *	rs4385425	50267738	G	A	0.3605240	0.0225160	0.0037822	2.4E-09
7	IKZF1 *	rs876036	50268114	C	T	0.3062140	0.0224034	0.0039387	1.4E-08
7	IKZF1 *	rs876038	50268931	T	C	0.2603240	0.0286839	0.0041301	1.8E-12
7	IKZF1 *	rs876037	50269096	A	T	0.2611210	0.0286010	0.0041285	2.1E-12
7	IKZF1 *	rs876039	50269215	C	G	0.2604560	0.0287348	0.0041296	1.7E-12
7	IKZF1 *	rs62447171	50270294	A	G	0.2601680	0.0288382	0.0041318	1.4E-12
7	IKZF1 *	rs10276356	50273756	A	G	0.3871400	0.0211393	0.0037212	7.8E-09
7	IKZF1 *	rs2219345	50274703	G	T	0.2882190	0.0261966	0.0040039	1.5E-11
7	IKZF1 *	rs17552904	50278712	T	G	0.2602390	0.0288587	0.0041324	1.4E-12
7	IKZF1 *	rs7385730	50279342	T	G	0.2065700	0.0259543	0.0045065	1.8E-09
7	IKZF1 *	rs4917015	50279753	T	C	0.2643400	0.0289822	0.0041109	6.8E-13
7	IKZF1 *	rs1026423	50280022	A	T	0.2883210	0.0261509	0.0040056	1.5E-11
7	IKZF1 *	rs1026422	50280211	A	G	0.2645660	0.0289613	0.0041096	6.6E-13
7	IKZF1 *	rs3034469	50280835	TTTTG	T	0.2883100	0.0263914	0.0040103	9.7E-12
7	IKZF1 *	rs17634369	50281878	A	G	0.2647960	0.0289589	0.0041089	6.7E-13
7	IKZF1 *	rs4917129	50283578	C	T	0.2636130	0.0286674	0.0041326	1.3E-12
7	IKZF1 *	rs6964608	50284441	T	G	0.2635330	0.0285244	0.0041487	2.0E-12
7	GRB10	rs17544225	50620357	C	T	0.0688880	0.0435357	0.0071944	1.8E-09
7	GRB10	rs2237439	50621539	C	T	0.0689740	0.0434268	0.0071871	1.7E-09
7	GRB10	rs2299151	50623090	A	G	0.0670267	0.0422674	0.0072881	6.9E-09
7	GRB10	rs2299152	50623183	C	G	0.0687271	0.0436375	0.0072005	1.5E-09
7	GRB10	rs2715140	50625014	T	A	0.0665437	0.0441363	0.0073178	1.6E-09
7	GRB10	rs10486757	50626161	A	G	0.0658090	0.0429231	0.0073620	5.7E-09
7	GRB10	rs2529394	50628551	C	T	0.0600853	0.0426374	0.0077315	2.3E-08
7	GRB10	rs6976501	50692523	G	A	0.0714745	0.0395202	0.0070434	4.9E-08
7	GRB10	rs7791286	50789095	G	A	0.0692997	0.0402027	0.0071475	2.8E-08
7	POR	rs2286819	75981445	G	A	0.1564840	0.0343163	0.0050265	2.6E-11
7	POR	chr7:75983340_CAT_C	75983340	CA	C	0.1600360	0.0350937	0.0050168	8.1E-12
7	POR	rs13223707	75983452	C	G	0.1566500	0.0343777	0.0050246	2.5E-11
7	POR	rs13240147	75983465	G	A	0.1566500	0.0343777	0.0050246	2.5E-11
7	POR	rs4732515	75984711	T	C	0.1443940	0.0357821	0.0051744	1.2E-11
7	POR	rs4732516	75984764	C	G	0.1440860	0.0355603	0.0051829	1.9E-11
7	POR	rs6961174	75985406	G	A	0.1566930	0.0345577	0.0050193	1.8E-11
7	POR	rs2302431	75985545	T	C	0.1450540	0.0359705	0.0051624	7.5E-12
7	POR	rs2302432	75985546	G	T	0.1547770	0.0356669	0.0050425	4.2E-12
7	POR	rs2228104	75985635	T	C	0.1428540	0.0361893	0.0052022	1.0E-11
7	STYXL1 *	rs11376502	75995809	CA	C	0.1581390	0.0329260	0.0049951	1.2E-10
7	STYXL1	rs59972190	76001403	A	G	0.1630440	0.0336581	0.0049139	1.9E-11
7	STYXL1	rs34823136	76005951	A	T	0.1611770	0.0323774	0.0049507	1.4E-10
7	STYXL1	rs57086307	76007537	T	C	0.1629120	0.0335986	0.0049153	2.1E-11
7	STYXL1	rs55662429	76007612	T	C	0.1627920	0.0335556	0.0049173	2.3E-11
7	STYXL1	rs3839764	76010442	A	AG	0.1611640	0.0339954	0.0049331	1.6E-11
7	STYXL1	rs2903769	76013199	A	G	0.1611670	0.0339963	0.0049332	1.6E-11
7	STYXL1	rs9642168	76014581	A	G	0.1608590	0.0334910	0.0049371	3.3E-11
7	STYXL1	chr7:76014803_CAT_C	76014803	C	CAT	0.1611800	0.0338642	0.0049327	1.9E-11
7	STYXL1	rs6958829	76017743	T	C	0.1612020	0.0339471	0.0049361	1.6E-11
7	STYXL1	rs6467975	76021767	C	T	0.1632220	0.0338336	0.0049054	1.2E-11
7	STYXL1	rs58925536	76025256	T	C	0.1618300	0.0343425	0.0049194	7.7E-12
7	STYXL1	rs35017320	76029698	T	TG	0.1615300	0.0338098	0.0049221	1.5E-11
7	STYXL1	rs34052883	76029702	T	G	0.1615300	0.0338098	0.0049221	1.5E-11
7	STYXL1	rs6964643	76029999	C	A	0.1589320	0.0330048	0.0049653	6.8E-11
7	STYXL1	rs67925951	76032355	T	C	0.1582830	0.0340718	0.0049821	2.6E-11
7	STYXL1	rs55948004	76032697	T	C	0.1619470	0.0343734	0.0049167	7.1E-12
7	STYXL1	rs34170456	76033972	T	C	0.1618850	0.0344505	0.0049153	6.1E-12
7	STYXL1	rs56320636	76042468	A	G	0.1609030	0.0335575	0.0049258	2.2E-11
7	MDH2	rs3815457	76066590	G	A	0.1607190	0.0342019	0.0049240	7.9E-12
7	MDH2 *	rs148894041	76068199	TG	T	0.1712720	0.0321973	0.0048132	8.7E-11
7	MDH2 *	rs60500915	76069162	G	A	0.1614010	0.0340352	0.0049268	1.1E-11
7	MDH2 *	rs11761014	76071463	T	C	0.1599780	0.0342044	0.0049334	7.5E-12
7	MDH2 *	rs11761015	76071472	T	C	0.1602550	0.0344190	0.0049294	5.7E-12
7	MDH2 *	rs11762977	76073753	T	C	0.1595040	0.0341461	0.0049430	8.3E-12
7	MDH2 *	rs6467994	76090137	G	C	0.1706590	0.0322089	0.0048229	8.6E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	MDH2 *	rs6467995	76090293	A	G	0.1599420	0.0344970	0.0049365	5.8E-12
7	MDH2 *	rs34100047	76090726	T	C	0.1601360	0.0342909	0.0049338	6.8E-12
7	MDH2 *	rs10954759	76095368	T	G	0.1602340	0.0342321	0.0049347	7.4E-12
7	MDH2 *	rs9691269	76097053	C	G	0.1600380	0.0342166	0.0049354	7.5E-12
7	MDH2 *	rs7809786	76101486	C	T	0.1708780	0.0323224	0.0048191	7.1E-11
7	MDH2 *	rs3973174	76103682	C	A	0.1705290	0.0325757	0.0048253	5.6E-11
7	MDH2 *	rs7807590	76109003	T	C	0.1799340	0.0313465	0.0047526	5.8E-11
7	MDH2 *	rs56087308	76115328	G	A	0.1547110	0.0338650	0.0050373	3.3E-11
7	MDH2 *	rs58542692	76116474	A	G	0.1601040	0.0344820	0.0049339	5.1E-12
7	MDH2 *	rs9649679	76133301	G	T	0.1657420	0.0325914	0.0048647	2.1E-11
7	SRRM3 *	rs59579580	76135839	C	G	0.1600570	0.0340224	0.0049346	9.7E-12
7	SRRM3 *	rs11769774	76136897	C	G	0.1580680	0.0341345	0.0049728	1.0E-11
7	SRRM3 *	rs11489549	76141191	T	C	0.1657420	0.0325914	0.0048647	2.1E-11
7	SRRM3 *	rs34243499	76148530	C	CAT	0.1599600	0.0340951	0.0049360	8.6E-12
7	SRRM3 *	rs11981163	76149872	G	C	0.1599600	0.0340951	0.0049360	8.6E-12
7	SRRM3 *	rs6945686	76150448	T	C	0.1656380	0.0326495	0.0048661	1.9E-11
7	SRRM3 *	rs1806884	76156302	A	G	0.1599840	0.0341089	0.0049362	8.5E-12
7	SRRM3 *	rs58762064	76161079	A	G	0.1636740	0.0329494	0.0049148	1.8E-11
7	SRRM3 *	chr7:76161874_AT_A	76161874	A	AT	0.1593460	0.0332427	0.0049799	4.2E-11
7	SRRM3 *	rs11768535	76162683	C	T	0.1585060	0.0345720	0.0049765	6.5E-12
7	SRRM3 *	rs11773047	76165024	C	G	0.1579980	0.0345011	0.0049834	9.0E-12
7	SRRM3 *	rs6944211	76170628	G	T	0.1621270	0.0332565	0.0049385	2.1E-11
7	SRRM3 *	rs73369682	76172037	A	G	0.1638260	0.0323237	0.0049151	5.3E-11
7	SRRM3 *	rs11761920	76172984	A	G	0.1579870	0.0344157	0.0049835	1.0E-11
7	SRRM3 *	rs61556289	76176116	A	G	0.1631450	0.0328154	0.0049216	2.6E-11
7	SRRM3 *	rs55638089	76176527	A	G	0.1581610	0.0348016	0.0049814	6.1E-12
7	SRRM3 *	rs66848883	76176620	G	A	0.1632750	0.0328666	0.0049223	2.4E-11
7	SRRM3 *	rs111516304	76180955	T	C	0.1623340	0.0321284	0.0049376	7.8E-11
7	SRRM3 *	rs76619441	76181044	G	A	0.1570240	0.0341374	0.0049986	1.6E-11
7	SRRM3 *	rs66846055	76181519	A	G	0.1571500	0.0341919	0.0049960	1.5E-11
7	SRRM3 *	rs57916702	76183868	T	C	0.1566570	0.0332062	0.0050052	5.4E-11
7	SRRM3 *	rs10952854	76187973	C	A	0.1575740	0.0342580	0.0049999	1.4E-11
7	SRRM3 *	rs11523700	76190114	T	C	0.1571270	0.0340846	0.0049972	1.7E-11
7	SRRM3 *	rs7802358	76190521	A	G	0.1571520	0.0341025	0.0049968	1.7E-11
7	SRRM3 *	rs7803382	76191254	A	G	0.1572070	0.0339229	0.0049955	2.1E-11
7	SRRM3 *	rs11767284	76196146	T	C	0.1571600	0.0340331	0.0049963	1.7E-11
7	SRRM3 *	rs4437574	76198674	A	G	0.1571580	0.0340466	0.0049962	1.7E-11
7	SRRM3	rs117974597	76201932	A	G	0.1572870	0.0339082	0.0049951	2.1E-11
7	SRRM3	rs11773549	76204273	G	A	0.1570810	0.0341646	0.0049979	1.5E-11
7	SRRM3	rs67070387	76206705	T	C	0.1567970	0.0343817	0.0050016	1.1E-11
7	SRRM3	rs6946174	76210940	T	C	0.1567530	0.0344489	0.0050035	1.1E-11
7	SRRM3	rs11979016	76215120	A	G	0.1362370	0.0378570	0.0053233	2.9E-12
7	SRRM3	rs55804588	76223268	G	C	0.1361030	0.0386544	0.0053318	9.4E-13
7	SRRM3	rs11767259	76226201	T	C	0.1120450	0.0477764	0.0058394	3.1E-15
7	SRRM3	rs7779012	76238692	A	G	0.2471070	0.0231663	0.0042640	3.6E-08
7	STEAP2-AS1	rs4512312	90098938	G	A	0.3152820	0.0218538	0.0039018	7.5E-09
7	STEAP2-AS1	rs4397318	90098955	G	A	0.1826670	0.0301443	0.0046933	3.3E-11
7	STEAP2-AS1	rs4481514	90099863	A	G	0.2401820	0.0231120	0.0042330	2.9E-08
7	STEAP2-AS1	rs2888738	90102666	T	C	0.2401820	0.0231120	0.0042330	2.9E-08
7	STEAP2-AS1	rs259133	90102967	A	G	0.1825530	0.0300022	0.0046928	4.2E-11
7	STEAP2-AS1	rs5885709	90103354	GATCAT	A	0.2413460	0.0230950	0.0042365	3.1E-08
7	STEAP2-AS1	rs34401934	90103790	CT	C	0.2403990	0.0232752	0.0042313	2.1E-08
7	STEAP2-AS1	rs39198	90104504	C	T	0.1825510	0.0299236	0.0046924	4.7E-11
7	STEAP2-AS1	rs39200	90104743	T	C	0.2403950	0.0232100	0.0042309	2.3E-08
7	STEAP2-AS1	rs39201	90104790	A	G	0.1826490	0.0297935	0.0046925	5.7E-11
7	STEAP2-AS1	rs39202	90104869	G	A	0.2403800	0.0232369	0.0042313	2.3E-08
7	STEAP2-AS1	rs39203	90104968	A	G	0.2404280	0.0231650	0.0042310	2.6E-08
7	STEAP2-AS1	rs39204	90105004	A	C	0.1825560	0.0299213	0.0046923	4.7E-11
7	STEAP2-AS1	rs39205	90105539	A	T	0.3120370	0.0222232	0.0039063	4.6E-09
7	STEAP2-AS1	rs39206	90106001	G	A	0.3121340	0.0220528	0.0039076	6.4E-09
7	STEAP2-AS1	rs39207	90106185	A	G	0.2403800	0.0232369	0.0042313	2.3E-08
7	STEAP2-AS1	rs34505862	90106910	G	A	0.3136210	0.0218767	0.0039015	7.7E-09
7	STEAP2-AS1	rs39208	90108096	T	C	0.2403660	0.0232831	0.0042315	2.1E-08
7	STEAP2-AS1	rs59702587	90108503	TGTAA	T	0.3137160	0.0220621	0.0039025	5.7E-09
7	STEAP2-AS1	rs39212	90108526	G	C	0.2401710	0.0231690	0.0042332	2.7E-08
7	STEAP2-AS1	rs39213	90108533	G	T	0.2406520	0.0233211	0.0042338	2.0E-08
7	STEAP2-AS1	rs39214	90108972	T	C	0.2403560	0.0233633	0.0042319	1.9E-08
7	STEAP2-AS1	rs39215	90109235	A	G	0.2403560	0.0233633	0.0042319	1.9E-08
7	STEAP2-AS1	rs39216	90109422	A	G	0.2403560	0.0233633	0.0042319	1.9E-08
7	STEAP2-AS1	rs39217	90109655	C	G	0.2373930	0.0231731	0.0042599	3.5E-08
7	STEAP2-AS1	rs39218	90110704	C	T	0.1825400	0.0301116	0.0046927	3.7E-11
7	STEAP2-AS1	rs12668992	90111547	G	A	0.3136940	0.0217190	0.0039023	1.0E-08
7	STEAP2-AS1	rs2190231	90112096	A	C	0.1825330	0.0300957	0.0046928	3.8E-11
7	STEAP2-AS1	rs39219	90112188	A	G	0.3118150	0.0221446	0.0039087	5.9E-09
7	STEAP2-AS1	rs39220	90113883	G	A	0.3123500	0.0219600	0.0039065	7.5E-09
7	STEAP2-AS1	rs71557076	90115176	A	G	0.3133470	0.0224098	0.0039068	3.5E-09
7	STEAP2-AS1	rs39225	90118066	G	A	0.2400840	0.0232306	0.0042380	2.7E-08
7	STEAP2-AS1	rs6962676	90118740	G	C	0.3135770	0.0221125	0.0039052	5.4E-09
7	STEAP2-AS1	rs117400415	90119386	G	C	0.1645200	0.0311552	0.0049163	7.2E-11
7	STEAP2-AS1	rs28469174	90119390	C	G	0.3131640	0.0224197	0.0039086	3.3E-09
7	DPY19L2P4, STEAP2-AS1	rs11552168	90119574	G	A	0.3130900	0.0221178	0.0039085	5.9E-09
7	DPY19L2P4, STEAP2-AS1	rs58370593	90119613	T	TC	0.1820630	0.0301540	0.0047001	3.8E-11
7	DPY19L2P4, STEAP2-AS1	rs39230	90121803	G	C	0.1823640	0.0299653	0.0046957	5.0E-11
7	DPY19L2P4, STEAP2-AS1	rs39233	90122924	C	G	0.1823830	0.0300041	0.0046955	4.7E-11
7	DPY19L2P4, STEAP2-AS1	rs35427539	90122971	G	T	0.3128680	0.0221049	0.0039102	6.2E-09
7	DPY19L2P4, STEAP2-AS1	rs10952994	90124545	G	C	0.1823870	0.0299776	0.0046954	4.9E-11
7	DPY19L2P4, STEAP2-AS1	rs39239	90125513	C	A	0.1820090	0.0299211	0.0047009	5.6E-11
7	STEAP2-AS1	rs12155481	90125907	G	A	0.3133560	0.0221389	0.0039082	5.5E-09
7	STEAP2-AS1	rs7808893	90126475	G	T	0.3131970	0.0220236	0.0039088	7.1E-09
7	STEAP2-AS1	rs10271746	90129031	G	A	0.3131700	0.0219664	0.0039090	7.7E-09
7	STEAP2-AS1	rs11282146	90131501	G	GCCTCAC	0.1838540	0.0301578	0.0046977	3.2E-11
7	STEAP2-AS1	rs7809315	90133994	G	A	0.2409170	0.0228622	0.0042352	4.1E-08
7	STEAP2-AS1	rs39249	90134006	A	G	0.1822830	0.0296896	0.0046969	7.1E-11
7	STEAP2-AS1	rs12667902	90134671	T	G	0.1646750	0.0310930	0.0049131	7.5E-11
7	STEAP2-AS1	rs57791048	90134847	G	C	0.3129320	0.0222197	0.0039096	4.9E-09
7	STEAP2-AS1	rs55955519	90135032	T	C	0.3126550	0.0219052	0.0039136	1.0E-08
7	STEAP2-AS1	chr7:90135619_GA_G	90135619	G	GA	0.1825570	0.0299525	0.0046921	5.0E-11
7	STEAP2-AS1	rs3953556	90135755	C	G	0.2411310	0.0230796	0.0042327	3.1E-08
7	STEAP2-AS1	rs39252	90135901	C	T	0.1825570	0.0299323	0.0046921	5.2E-11
7	STEAP2-AS1	rs39254	90136394	T	G	0.1825600	0.0299169	0.0046921	5.3E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	STEAP2-AS1	rs39256	90136660	A	G	0.1825600	0.0299169	0.0046921	5.3E-11
7	STEAP2-AS1	rs39257	90136894	A	G	0.1825600	0.0299169	0.0046921	5.3E-11
7	STEAP2-AS1	rs2214119	90137291	A	G	0.1824890	0.0300098	0.0046932	4.8E-11
7	STEAP2-AS1	rs59809020	90138220	A	G	0.3131470	0.0221641	0.0039114	5.0E-09
7	STEAP2-AS1	rs39263	90141030	A	T	0.1813100	0.0309372	0.0047124	1.3E-11
7	STEAP2-AS1	rs39266	90141654	A	G	0.1810330	0.0298377	0.0047164	7.5E-11
7	STEAP2-AS1	rs39267	90142195	G	A	0.1826160	0.0299419	0.0046911	5.2E-11
7	STEAP2-AS1	rs39268	90142673	G	A	0.1823410	0.0298412	0.0046955	6.7E-11
7	STEAP2-AS1	rs4728871	90143170	C	A	0.1836800	0.0303665	0.0046864	2.7E-11
7	STEAP2-AS1	rs39270	90143312	T	A	0.1826260	0.0298847	0.0046909	5.6E-11
7	STEAP2-AS1	rs72615116	90143507	A	C	0.3147710	0.0221623	0.0039074	5.3E-09
7	STEAP2-AS1	rs39272	90144082	C	T	0.1826320	0.0298468	0.0046907	5.9E-11
7	STEAP2-AS1	rs74404813	90144658	G	A	0.3132070	0.0223520	0.0039083	3.6E-09
7	STEAP2-AS1	rs6979720	90144966	C	T	0.3129460	0.0222475	0.0039097	4.7E-09
7	STEAP2-AS1	rs34102421	90145028	T	TACA	0.1723970	0.0301072	0.0048381	1.5E-10
7	STEAP2-AS1	rs182366501	90145625	C	T	0.1647590	0.0309858	0.0049114	8.8E-11
7	STEAP2-AS1	rs39274	90145746	C	A	0.1826500	0.0297029	0.0046904	7.1E-11
7	STEAP2-AS1	rs39275	90145856	G	A	0.1826520	0.0297049	0.0046904	7.1E-11
7	STEAP2-AS1	rs39276	90145891	A	G	0.1826520	0.0297049	0.0046904	7.1E-11
7	STEAP2-AS1	rs3924493	90147103	A	G	0.2413420	0.0230358	0.0042312	3.2E-08
7	STEAP2-AS1	rs39281	90149175	G	A	0.1829910	0.0297258	0.0046858	6.6E-11
7	STEAP2-AS1	rs6150223	90149578	T	CTGGGG	0.1774950	0.0302183	0.0047736	7.8E-11
7	STEAP2-AS1	rs57909887	90150444	A	G	0.2413340	0.0230377	0.0042313	3.2E-08
7	STEAP2-AS1	rs12531385	90151825	T	C	0.2413360	0.0230533	0.0042313	3.2E-08
7	STEAP2-AS1	rs3857792	90152636	C	G	0.3135110	0.0225195	0.0039077	2.7E-09
7	STEAP1, STEAP2-AS1	rs7799132	90154581	C	T	0.2413820	0.0231614	0.0042307	2.6E-08
7	STEAP1, STEAP2-AS1	rs9791638	90158086	A	G	0.2413470	0.0231022	0.0042309	2.9E-08
7	STEAP1, STEAP2-AS1	rs39283	90159492	A	C	0.1830610	0.0298882	0.0046845	5.3E-11
7	STEAP1, STEAP2-AS1	rs6965789	90160289	A	G	0.2413560	0.0230456	0.0042308	3.1E-08
7	STEAP1, STEAP2-AS1	rs39284	90162667	C	T	0.1832570	0.0300246	0.0046796	3.6E-11
7	STEAP1, STEAP2-AS1	rs2374250	90162845	T	G	0.2415740	0.0231828	0.0042271	2.2E-08
7	STEAP1, STEAP2-AS1	rs2051959	90164079	G	T	0.3135830	0.0221279	0.0039026	4.8E-09
7	STEAP1, STEAP2-AS1	rs2286253	90164128	T	A	0.3135630	0.0221726	0.0039026	4.5E-09
7	STEAP1, STEAP2-AS1	rs2286254	90164327	T	C	0.3139070	0.0223706	0.0039019	3.0E-09
7	STEAP2-AS1	rs17863943	90165817	C	T	0.3139790	0.0225392	0.0039014	2.3E-09
7	STEAP2-AS1	rs259134	90166538	A	G	0.1842890	0.0301140	0.0046750	3.1E-11
7	STEAP2-AS1	rs10540742	90166596	CTGT	C	0.1838280	0.0304386	0.0046757	2.1E-11
7	STEAP2-AS1	rs7780937	90168975	A	G	0.3139020	0.0219025	0.0039017	7.4E-09
7	STEAP2-AS1	rs2158747	90169107	A	C	0.1832710	0.0301085	0.0046793	3.2E-11
7	STEAP2-AS1	rs17862111	90169812	G	A	0.3127710	0.0221193	0.0039056	5.8E-09
7	STEAP2-AS1	rs67367956	90170059	CT	C	0.3137450	0.0218823	0.0039028	7.5E-09
7	STEAP2-AS1	rs13242882	90170739	T	A	0.1832710	0.0301085	0.0046793	3.2E-11
7	STEAP2-AS1	rs6978118	90170927	A	T	0.1832710	0.0301085	0.0046793	3.2E-11
7	STEAP2-AS1	rs7783739	90172473	C	T	0.1840440	0.0295795	0.0046749	6.8E-11
7	STEAP2-AS1	rs13224065	90173049	A	G	0.1832750	0.0301046	0.0046793	3.3E-11
7	STEAP2-AS1	rs10257064	90173282	A	G	0.1832750	0.0301046	0.0046793	3.3E-11
7	STEAP2-AS1	rs17862114	90173970	G	A	0.3139060	0.0219081	0.0039017	7.3E-09
7	STEAP2-AS1	chr7:90174098_C_CA	90174098	CA	C	0.1745630	0.0293264	0.0048124	2.3E-10
7	STEAP2-AS1	rs6956980	90174320	C	T	0.1832750	0.0301046	0.0046793	3.3E-11
7	STEAP2-AS1	rs17869687	90174974	T	C	0.3142120	0.0220593	0.0039008	5.4E-09
7	STEAP2-AS1	rs10281047	90175410	T	C	0.3135640	0.0222425	0.0039024	4.1E-09
7	STEAP2-AS1	rs11770630	90175927	T	C	0.1981490	0.0261766	0.0045659	3.2E-09
7	STEAP2-AS1	rs17863031	90176499	G	A	0.1839170	0.0305370	0.0046818	1.8E-11
7	STEAP2-AS1	rs10251313	90177140	C	A	0.3139030	0.0219187	0.0039017	7.2E-09
7	STEAP2-AS1	rs10251952	90177437	G	A	0.3139030	0.0219187	0.0039017	7.2E-09
7	STEAP2-AS1	rs10225358	90177586	A	T	0.3139030	0.0219187	0.0039017	7.2E-09
7	STEAP2-AS1	rs10270950	90177982	A	T	0.1832700	0.0301308	0.0046793	3.1E-11
7	STEAP2-AS1	rs11563947	90179450	C	T	0.1832700	0.0301311	0.0046793	3.1E-11
7	STEAP2-AS1	rs11563340	90180265	G	A	0.1832700	0.0301311	0.0046793	3.1E-11
7	STEAP2-AS1	rs10224488	90180947	C	T	0.1834990	0.0297730	0.0046787	5.7E-11
7	STEAP2-AS1	rs2374254	90183965	C	T	0.3242960	0.0226365	0.0039457	3.3E-09
7	STEAP2-AS1	rs4310132	90183999	G	T	0.3152780	0.0226831	0.0038988	2.0E-09
7	STEAP2-AS1	rs12535357	90184416	A	G	0.3151760	0.0228386	0.0038981	1.6E-09
7	STEAP2-AS1	rs17874779	90184981	T	C	0.3152720	0.0228851	0.0038981	1.5E-09
7	STEAP2-AS1	rs12154246	90185355	C	A	0.3151770	0.0228629	0.0038981	1.5E-09
7	STEAP2-AS1	rs6972160	90186059	G	C	0.1832700	0.0301311	0.0046793	3.1E-11
7	STEAP2-AS1	rs11563944	90187020	A	G	0.3151760	0.0228386	0.0038981	1.6E-09
7	STEAP2-AS1	rs67339037	90187129	T	TA	0.1835800	0.0296757	0.0046796	6.2E-11
7	STEAP2-AS1	rs11563943	90187197	G	A	0.3157490	0.0226094	0.0038988	2.5E-09
7	STEAP2-AS1	rs11563564	90187387	G	A	0.1832700	0.0301311	0.0046793	3.1E-11
7	STEAP2-AS1	rs10715230	90188895	T	TA	0.1831930	0.0301363	0.0046807	3.2E-11
7	STEAP2-AS1	rs66891868	90189233	GCTATCT	G	0.3146420	0.0226087	0.0039045	2.6E-09
7	STEAP2-AS1	rs11763820	90189631	G	T	0.2529390	0.0269247	0.0041753	1.7E-11
7	STEAP2-AS1	rs17867585	90189860	T	C	0.1791970	0.0302377	0.0047224	3.5E-11
7	STEAP2-AS1	rs12667090	90191547	C	T	0.3116580	0.0219631	0.0039125	7.1E-09
7	STEAP2-AS1	rs6465244	90191568	C	A	0.2530730	0.0262961	0.0041716	4.9E-11
7	STEAP2-AS1	rs17862120	90192286	G	A	0.3115990	0.0219050	0.0039131	7.6E-09
7	STEAP2-AS1	rs7777170	90192968	T	A	0.2529960	0.0263768	0.0041728	4.1E-11
7	STEAP2-AS1	rs7777282	90192991	G	A	0.2529960	0.0263768	0.0041728	4.1E-11
7	STEAP2-AS1	rs7777651	90193030	A	G	0.1791140	0.0302203	0.0047243	3.5E-11
7	STEAP2-AS1	rs17866355	90194011	G	T	0.3113200	0.0223603	0.0039280	3.8E-09
7	STEAP2-AS1	rs17867586	90195413	C	T	0.3115750	0.0220397	0.0039173	5.7E-09
7	STEAP2-AS1	rs6465248	90195426	T	C	0.1793030	0.0298821	0.0047277	5.7E-11
7	STEAP2-AS1	rs6465249	90195439	T	A	0.2529700	0.0265101	0.0041774	3.1E-11
7	STEAP2-AS1	rs757844	90195862	G	A	0.3113080	0.0222979	0.0039141	3.8E-09
7	STEAP2-AS1	rs67648521	90195964	G	GT	0.2526560	0.0267460	0.0041744	2.1E-11
7	STEAP2-AS1	rs17867587	90196688	C	T	0.3100340	0.0222903	0.0039177	4.6E-09
7	STEAP2-AS1	rs2079409	90196856	A	G	0.3101350	0.0225021	0.0039182	3.4E-09
7	STEAP2-AS1	rs2079410	90196863	A	G	0.3100340	0.0222903	0.0039177	4.6E-09
7	STEAP2-AS1	rs6975005	90197414	G	A	0.2506910	0.0266777	0.0041996	3.6E-11
7	STEAP2-AS1	rs201392143	90197453	TTTG	T	0.1790990	0.0302163	0.0047246	3.5E-11
7	STEAP2-AS1	rs17863951	90197485	G	A	0.3120800	0.0210910	0.0039309	3.0E-08
7	STEAP2-AS1	rs17863952	90197896	C	G	0.3100340	0.0222903	0.0039177	4.6E-09
7	STEAP2-AS1	rs12155202	90198810	C	A	0.2514610	0.0269256	0.0041813	2.0E-11
7	STEAP2-AS1	rs12154563	90198912	T	G	0.1790970	0.0302045	0.0047246	3.6E-11
7	STEAP2-AS1	rs722245	90200180	C	A	0.3104110	0.0225762	0.0039174	2.7E-09
7	STEAP2-AS1	rs10247900	90200637	G	T	0.3111680	0.0222034	0.0039219	5.3E-09
7	STEAP2-AS1	rs10248155	90200811	G	A	0.3160720	0.0210581	0.0039222	2.4E-08
7	STEAP2-AS1	rs111412743	90201021	C	T	0.1724890	0.0296782	0.0047961	1.6E-10
7	STEAP2-AS1	rs12535435	90201503	A	G	0.1692810	0.0294472	0.0048465	2.8E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	STEAP2-AS1	rs12670095	90201824	C	T	0.3114640	0.0227465	0.0039245	2.4E-09
7	STEAP2-AS1	rs151032522	90202514	A	G	0.3100150	0.0222269	0.0039177	5.0E-09
7	STEAP2-AS1	rs140643854	90203130	A	C	0.3100120	0.0222415	0.0039176	4.9E-09
7	STEAP2-AS1	rs150666279	90204503	C	T	0.3100120	0.0222415	0.0039176	4.9E-09
7	STEAP2-AS1	rs62470760	90204671	C	G	0.2513960	0.0268311	0.0041813	2.2E-11
7	STEAP2-AS1	rs6980439	90205399	G	T	0.3100120	0.0222415	0.0039176	4.9E-09
7	STEAP2-AS1	rs17862121	90206196	C	T	0.3100120	0.0222415	0.0039176	4.9E-09
7	STEAP2-AS1	rs17862122	90206950	T	G	0.3100130	0.0222395	0.0039176	4.9E-09
7	STEAP2-AS1	rs1541428	90206965	G	A	0.2513960	0.0268311	0.0041813	2.2E-11
7	STEAP2-AS1	rs2190228	90207428	A	G	0.3100130	0.0222719	0.0039176	4.6E-09
7	STEAP2-AS1	rs10691186	90208934	T	TATG	0.1724310	0.0297016	0.0047968	1.5E-10
7	STEAP2-AS1	rs6972868	90209379	A	G	0.3101460	0.0225498	0.0039139	2.9E-09
7	STEAP2-AS1	rs17862123	90210140	A	C	0.3102160	0.0223833	0.0039124	3.7E-09
7	STEAP2-AS1	rs194501	90210659	G	A	0.3103050	0.0222224	0.0039108	4.5E-09
7	STEAP2-AS1	rs35203010	90210688	A	AG	0.2513740	0.0266522	0.0041774	2.9E-11
7	STEAP2-AS1	rs194502	90211561	G	A	0.3099160	0.0218083	0.0039141	7.9E-09
7	STEAP2	rs194503	90211770	A	G	0.3095070	0.0217131	0.0039158	9.0E-09
7	STEAP2	rs194504	90211904	A	G	0.3097300	0.0219601	0.0039159	7.1E-09
7	STEAP2	rs194505	90211993	A	G	0.1724370	0.0292643	0.0047976	2.6E-10
7	STEAP2	rs17874783	90213007	C	G	0.3093420	0.0215579	0.0039239	1.9E-08
7	STEAP2	rs194507	90214246	T	G	0.2526160	0.0257298	0.0041783	1.6E-10
7	STEAP2	rs34485307	90214690	AG	A	0.3116420	0.0215338	0.0039138	1.4E-08
7	STEAP2	rs17867591	90216235	G	A	0.3114180	0.0217482	0.0039157	1.0E-08
7	STEAP2	rs11563440	90216589	G	A	0.3116490	0.0215751	0.0039138	1.3E-08
7	STEAP2	rs194511	90217413	G	A	0.1738850	0.0284486	0.0047876	8.3E-10
7	STEAP2	rs17867181	90217702	C	T	0.3116490	0.0215751	0.0039138	1.3E-08
7	STEAP2	rs17863956	90218472	T	C	0.3116460	0.0215761	0.0039137	1.3E-08
7	STEAP2	rs6465250	90218565	G	A	0.3108930	0.0211326	0.0039159	2.6E-08
7	STEAP2	rs6465251	90218567	G	C	0.2523130	0.0253436	0.0041788	2.7E-10
7	STEAP2	rs79497929	90219451	T	TA	0.3116480	0.0215740	0.0039137	1.3E-08
7	STEAP2	rs10282668	90219617	C	G	0.3116480	0.0215740	0.0039137	1.3E-08
7	STEAP2	rs147707733	90220563	TC	T	0.3123140	0.0219855	0.0039200	7.5E-09
7	STEAP2	rs17864927	90220755	G	C	0.3116480	0.0215740	0.0039137	1.3E-08
7	STEAP2	rs194513	90220856	T	G	0.2527510	0.0255742	0.0041766	1.9E-10
7	STEAP2	rs76472156	90220873	AT	A	0.3116480	0.0215740	0.0039137	1.3E-08
7	STEAP2	rs17863958	90221721	C	T	0.3125940	0.0216225	0.0039200	1.3E-08
7	STEAP2	rs194518	90223835	A	G	0.1734760	0.0282115	0.0047892	1.2E-09
7	STEAP2	rs194519	90224111	G	A	0.3113320	0.0213859	0.0039146	1.8E-08
7	STEAP2	rs17863045	90224207	G	C	0.3116480	0.0215740	0.0039137	1.3E-08
7	STEAP2	rs194520	90225132	G	T	0.1738820	0.0282726	0.0047874	1.1E-09
7	STEAP2	rs110360	90227294	T	C	0.2497240	0.0268048	0.0041990	2.4E-11
7	STEAP2	rs3810889	90227770	T	A	0.3112180	0.0219435	0.0039199	7.2E-09
7	STEAP2	rs10487105	90228436	G	T	0.3112400	0.0219540	0.0039201	7.2E-09
7	STEAP2	rs17862126	90228611	A	G	0.3112530	0.0219820	0.0039202	6.9E-09
7	STEAP2	rs10487106	90229436	C	T	0.3112720	0.0219869	0.0039206	6.9E-09
7	STEAP2	rs194523	90231260	T	A	0.2531020	0.0259269	0.0041809	1.2E-10
7	STEAP2	rs10281548	90232019	A	C	0.3120470	0.0221818	0.0039268	5.3E-09
7	STEAP2	rs194524	90232518	A	G	0.1733450	0.0282712	0.0047936	1.2E-09
7	STEAP2	rs194529	90234999	A	T	0.3033720	0.0216807	0.0039694	1.6E-08
7	STEAP2 *	rs2013992	90238055	C	G	0.2201180	0.0292738	0.0044175	2.2E-11
7	STEAP2 *	chr7:90238132_T_TCTG	90238132	TCTG	T	0.2192480	0.0291849	0.0044229	2.8E-11
7	C7orf63 *	rs194533	90241463	G	A	0.1930200	0.0278222	0.0046294	1.5E-09
7	C7orf63 *	chr7:90242085_GA_G	90242085	GA	G	0.3509550	0.0213341	0.0038529	1.6E-08
7	C7orf63	rs10237082	90251027	A	T	0.3535930	0.0207897	0.0038208	1.9E-08
7	C7orf63	rs2157793	90251040	G	C	0.1909490	0.0280903	0.0046351	9.3E-10
7	C7orf63	rs2106274	90251234	T	C	0.1909500	0.0280799	0.0046351	9.4E-10
7	C7orf63	rs10240790	90251635	G	A	0.2479980	0.0230581	0.0042202	3.9E-08
7	C7orf63	rs916646	90251919	A	T	0.2507880	0.0227995	0.0042073	4.3E-08
7	C7orf63	rs916647	90251925	G	C	0.2506360	0.0228405	0.0042039	4.0E-08
7	C7orf63	rs7787503	90252832	A	G	0.3534510	0.0208140	0.0038226	1.9E-08
7	C7orf63	rs6959675	90253815	C	T	0.3536260	0.0206916	0.0038203	2.3E-08
7	C7orf63	rs10228672	90256135	C	T	0.3536760	0.0208358	0.0038198	1.8E-08
7	C7orf63	rs11771963	90258273	T	G	0.1910910	0.0279687	0.0046321	1.2E-09
7	C7orf63	rs4380867	90258563	C	T	0.3537010	0.0209137	0.0038187	1.6E-08
7	C7orf63	rs13247629	90260271	G	A	0.1924850	0.0272629	0.0046174	2.7E-09
7	C7orf63	rs10227385	90261054	A	C	0.1912530	0.0278848	0.0046292	1.3E-09
7	C7orf63	chr7:90261082_A_ATT	90261082	ATT	A	0.3397330	0.0204977	0.0039198	4.5E-08
7	C7orf63	rs10952996	90261233	G	A	0.3538400	0.0210103	0.0038171	1.3E-08
7	C7orf63	rs17866763	90261308	C	T	0.3538430	0.0209976	0.0038171	1.4E-08
7	C7orf63	rs66730094	90261384	TA	T	0.3537200	0.0211336	0.0038177	1.1E-08
7	C7orf63	rs12669304	90261726	C	T	0.1912600	0.0278419	0.0046291	1.4E-09
7	C7orf63	rs12668268	90263948	G	A	0.3557830	0.0208165	0.0038279	2.0E-08
7	C7orf63	rs6972119	90264694	C	T	0.1913890	0.0278188	0.0046270	1.4E-09
7	C7orf63	rs6952405	90264874	A	G	0.3539700	0.0208626	0.0038158	1.7E-08
7	C7orf63	rs17867605	90268515	T	C	0.2970450	0.0229303	0.0039951	2.9E-09
7	C7orf63	rs3747800	90270174	T	G	0.1913000	0.0279834	0.0046268	1.1E-09
7	C7orf63	rs11563435	90270893	C	A	0.1913360	0.0280225	0.0046260	1.0E-09
7	C7orf63	rs10262472	90271069	C	T	0.2955110	0.0234547	0.0039991	1.4E-09
7	C7orf63	rs17867607	90272940	G	A	0.2966600	0.0230937	0.0039921	2.5E-09
7	C7orf63	rs10226014	90273219	G	A	0.1914180	0.0279086	0.0046245	1.2E-09
7	C7orf63	rs3761805	90277295	C	T	0.3008260	0.0234540	0.0040064	1.6E-09
7	C7orf63	rs3810890	90279519	T	G	0.1876840	0.0280373	0.0046747	1.3E-09
7	C7orf63	rs3810891	90279537	G	A	0.1778820	0.0289924	0.0048294	1.8E-09
7	C7orf63	rs10262603	90280128	A	G	0.1922970	0.0274332	0.0046144	2.0E-09
7	C7orf63	rs111690384	90280201	C	CTTTG	0.1088190	0.0315995	0.0058267	2.8E-08
7	C7orf63	rs10266179	90280668	A	G	0.1923050	0.0274798	0.0046142	1.9E-09
7	C7orf63	rs2027965	90283199	T	C	0.1925020	0.0272709	0.0046108	2.4E-09
7	C7orf63	rs1015402	90283955	T	C	0.1925220	0.0273157	0.0046104	2.3E-09
7	C7orf63	rs1015403	90284388	G	A	0.1925170	0.0273037	0.0046101	2.3E-09
7	C7orf63	rs1015404	90284632	C	G	0.1925160	0.0273112	0.0046101	2.3E-09
7	C7orf63	rs12704518	90285074	T	G	0.1925210	0.0272125	0.0046100	2.6E-09
7	C7orf63	rs3761804	90286024	A	G	0.1925300	0.0272692	0.0046101	2.4E-09
7	C7orf63	chr7:90288883_A_AT	90288883	A	AT	0.3027040	0.0222855	0.0040093	9.4E-09
7	C7orf63	rs10234301	90288964	C	T	0.2956360	0.0234108	0.0039915	1.4E-09
7	C7orf63	rs6973816	90291758	T	C	0.2954170	0.0234134	0.0039937	1.3E-09
7	C7orf63	rs10260905	90292197	G	A	0.1922720	0.0273049	0.0046139	2.2E-09
7	C7orf63	rs4728877	90293144	T	C	0.2976760	0.0232122	0.0039861	1.7E-09
7	C7orf63	rs17863978	90294705	G	C	0.2972790	0.0233646	0.0039862	1.4E-09
7	C7orf63	rs4728878	90294918	G	T	0.1922890	0.0272951	0.0046137	2.3E-09
7	C7orf63	rs4728879	90294923	G	T	0.2954380	0.0234205	0.0039934	1.3E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	C7orf63	rs13239439	90295086	A	C	0.1922870	0.0272984	0.0046137	2.3E-09
7	C7orf63	rs7786771	90295453	A	G	0.1948190	0.0272856	0.0046008	1.8E-09
7	C7orf63	rs2040514	90296247	G	A	0.2959720	0.0235946	0.0039902	1.0E-09
7	C7orf63	rs2040515	90298302	T	C	0.2971870	0.0232505	0.0039851	1.7E-09
7	C7orf63	chr7:90299796_C_CT	90299796	CT	C	0.2907500	0.0232605	0.0040315	2.4E-09
7	C7orf63	rs143152578	90300636	A	TTTTCCT	0.1905560	0.0296343	0.0046726	1.8E-10
7	C7orf63	rs2040517	90300866	T	G	0.1925570	0.0272795	0.0046094	2.5E-09
7	C7orf63	rs111756383	90301982	G	T	0.2978310	0.0232186	0.0039911	1.9E-09
7	C7orf63	rs6465257	90302201	G	A	0.1925770	0.0273046	0.0046092	2.4E-09
7	C7orf63	rs9655741	90304560	G	C	0.1916510	0.0277797	0.0046171	1.5E-09
7	C7orf63	chr7:90305384_C_CAA	90305384	CAA	C	0.1925150	0.0273160	0.0046084	2.3E-09
7	C7orf63	rs34335301	90305732	C	CTT	0.1925150	0.0273160	0.0046084	2.3E-09
7	C7orf63	rs11563909	90306390	G	A	0.1918960	0.0277396	0.0046153	1.4E-09
7	C7orf63	rs10487111	90306574	C	A	0.2959960	0.0236096	0.0039899	1.0E-09
7	C7orf63	chr7:90307713_CA_C	90307713	C	CA	0.3039070	0.0225360	0.0040015	6.4E-09
7	C7orf63	rs4728881	90307896	A	G	0.2971100	0.0233498	0.0039841	1.4E-09
7	C7orf63	rs6948139	90308467	A	T	0.1925210	0.0273605	0.0046082	2.2E-09
7	C7orf63	rs6970376	90308772	T	C	0.1915090	0.0276832	0.0046226	1.6E-09
7	C7orf63	rs6970750	90308877	A	G	0.1924990	0.0274447	0.0046086	1.9E-09
7	C7orf63	rs1134956	90309366	T	C	0.1925110	0.0272085	0.0046089	2.7E-09
7	C7orf63	rs12375075	90311017	A	G	0.2955470	0.0236111	0.0039901	1.0E-09
7	C7orf63 *	rs2157790	90312450	G	T	0.2971770	0.0233084	0.0039849	1.5E-09
7	C7orf63 *	rs12374728	90312570	C	T	0.1925720	0.0273477	0.0046090	2.2E-09
7	C7orf63 *	rs11367400	90313707	A	AG	0.2955540	0.0235635	0.0039900	1.1E-09
7	C7orf63 *	rs12673914	90314075	T	C	0.1917990	0.0277660	0.0046146	1.3E-09
7	C7orf63 *	rs2157791	90314869	C	G	0.2970770	0.0233190	0.0039843	1.5E-09
7	C7orf63 *	rs71987368	90314959	C	CTT	0.1087640	0.0317734	0.0058274	2.4E-08
7	C7orf63 *	rs174059	90316089	T	C	0.1910050	0.0271549	0.0046182	3.5E-09
7	C7orf63 *	rs10225744	90316689	C	T	0.2935450	0.0234997	0.0039950	1.6E-09
7	C7orf63 *	rs6953331	90318440	A	G	0.2971630	0.0226066	0.0039979	5.5E-09
7	C7orf63 *	rs17867618	90319502	A	G	0.1074800	0.0315567	0.0058515	3.9E-08
7	C7orf63 *	rs42609	90320541	T	A	0.1910360	0.0269953	0.0046178	4.3E-09
7	C7orf63 *	rs42611	90320746	A	C	0.1910360	0.0269953	0.0046178	4.3E-09
7	C7orf63 *	rs42613	90320989	T	C	0.1908440	0.0269940	0.0046198	4.3E-09
7	C7orf63 *	rs42614	90321049	G	C	0.2945030	0.0233259	0.0039933	2.1E-09
7	C7orf63 *	rs42615	90321187	T	G	0.1912610	0.0273242	0.0046214	2.7E-09
7	C7orf63 *	rs36079451	90322057	GT	G	0.1910380	0.0269846	0.0046178	4.3E-09
7	C7orf63 *	rs42617	90322732	A	T	0.1910360	0.0269815	0.0046178	4.3E-09
7	C7orf63 *	rs1468105	90322803	G	A	0.2954210	0.0228720	0.0039899	3.8E-09
7	C7orf63 *	rs7790552	90325631	G	A	0.2956040	0.0230244	0.0039908	3.0E-09
7	C7orf63 *	rs6957839	90326167	A	G	0.2957410	0.0231747	0.0039913	2.3E-09
7	C7orf63 *	rs42620	90326253	T	G	0.1912170	0.0270880	0.0046187	3.9E-09
7	C7orf63 *	rs12673695	90326303	A	T	0.2934260	0.0232218	0.0040053	2.7E-09
7	C7orf63 *	rs42621	90327170	G	A	0.1912120	0.0270542	0.0046186	4.0E-09
7	C7orf63 *	rs42622	90327510	G	A	0.2033350	0.0268166	0.0045105	2.2E-09
7	C7orf63 *	chr7:90327672_CA_C	90327672	C	CA	0.1936760	0.0266397	0.0046102	6.5E-09
7	C7orf63 *	rs42624	90328227	G	C	0.2032950	0.0267564	0.0045100	2.3E-09
7	GTPBP10 *	rs2188232	90329000	C	A	0.1906250	0.0270280	0.0046247	4.4E-09
7	GTPBP10 *	rs2188233	90329001	A	G	0.1906250	0.0270280	0.0046247	4.4E-09
7	GTPBP10 *	rs42625	90331135	G	T	0.3031220	0.0231135	0.0039685	1.9E-09
7	GTPBP10 *	rs10952997	90332372	A	G	0.2953460	0.0230420	0.0039901	2.9E-09
7	GTPBP10 *	rs42627	90332562	A	G	0.1910720	0.0269736	0.0046174	4.5E-09
7	GTPBP10 *	rs42629	90334010	T	G	0.1914050	0.0270167	0.0046171	4.2E-09
7	GTPBP10 *	rs4236517	90334151	T	A	0.1914870	0.0274416	0.0046220	2.6E-09
7	GTPBP10 *	rs3948749	90334315	C	G	0.2957660	0.0228436	0.0039913	3.7E-09
7	GTPBP10 *	rs42630	90334498	C	G	0.1914400	0.0270684	0.0046161	4.0E-09
7	GTPBP10 *	rs2374259	90334836	G	A	0.2957600	0.0229063	0.0039911	3.4E-09
7	LOC101927446	rs42635	90336884	A	T	0.1915480	0.0268129	0.0046128	5.3E-09
7	LOC101927446	rs6977224	90338315	C	G	0.2973820	0.0231394	0.0039804	2.4E-09
7	LOC101927446	rs42636	90338663	A	G	0.1835630	0.0276286	0.0047461	3.4E-09
7	LOC101927446	rs42637	90340517	G	A	0.2058610	0.0252099	0.0044850	1.6E-08
7	LOC101927446	rs2285399	90340564	G	A	0.2039230	0.0258989	0.0045016	7.4E-09
7	LOC101927446	rs1557650	90342242	C	A	0.2039000	0.0259015	0.0045007	7.3E-09
7	LOC101927446	rs42641	90343450	C	T	0.2039330	0.0262134	0.0045008	4.5E-09
7	LOC101927446	rs2106272	90344041	T	C	0.3101500	0.0233617	0.0039396	1.2E-09
7	GTPBP10 *	rs2027968	90344208	A	G	0.3089760	0.0221639	0.0039335	6.2E-09
7	GTPBP10 *	rs42644	90345550	A	G	0.1912900	0.0265142	0.0046092	6.8E-09
7	GTPBP10	rs68057103	90346823	GTTC	G	0.3090390	0.0225387	0.0039341	3.6E-09
7	GTPBP10	rs17867622	90348418	T	C	0.3085310	0.0222239	0.0039333	5.6E-09
7	GTPBP10	rs42648	90348446	G	A	0.2060410	0.0258081	0.0044869	6.5E-09
7	GTPBP10	rs42649	90348475	T	A	0.2045980	0.0256014	0.0044931	9.2E-09
7	GTPBP10	chr7:90348736_TC_T	90348736	TC	T	0.3085230	0.0222236	0.0039333	5.6E-09
7	GTPBP10	rs42651	90349276	G	A	0.2045610	0.0253635	0.0044938	1.2E-08
7	GTPBP10	rs17862152	90351350	C	A	0.3082720	0.0216105	0.0039377	1.4E-08
7	GTPBP10	rs17867279	90351563	A	G	0.2961100	0.0214516	0.0039867	2.7E-08
7	GTPBP10	rs56116343	90351752	A	G	0.1903620	0.0263586	0.0046209	9.1E-09
7	GTPBP10	rs42656	90352322	G	A	0.1921190	0.0255581	0.0046041	2.1E-08
7	ACTL6B *	chr7:100664500_AT_A	100664500	AT	A	0.0657275	-0.0442350	0.0075071	1.1E-09
7	GNB2 *	rs221786	100668458	T	C	0.0609352	-0.0478467	0.0076338	1.0E-10
7	GNB2	chr7:100673815_GCGC_G	100673815	GCGC	G	0.0746947	-0.0422691	0.0069843	9.6E-10
7	GNB2	rs221789	100673898	T	C	0.0607134	-0.0503738	0.0076412	1.1E-11
7	GIGYF1	rs221792	100681034	A	G	0.0613063	-0.0506334	0.0075724	6.1E-12
7	GIGYF1	rs221794	100684145	T	C	0.0612833	-0.0524410	0.0075881	1.1E-12
7	GIGYF1	rs35436931	100686887	TG	T	0.0606474	-0.0526809	0.0076224	1.6E-12
7	GIGYF1	rs221796	100687290	C	G	0.0641694	-0.0489878	0.0074479	1.0E-11
7	GIGYF1	rs221797	100688351	A	C	0.0608695	-0.0524706	0.0076031	1.5E-12
7	GIGYF1 *	rs221798	100689872	C	G	0.0607834	-0.0518579	0.0076013	2.6E-12
7	GIGYF1 *	rs221800	100690929	T	C	0.0607834	-0.0518579	0.0076013	2.6E-12
7	GIGYF1 *	rs373899398	100691506	A	TTTTTTT	0.0607834	-0.0518579	0.0076013	2.6E-12
7	GIGYF1 *	rs221803	100693577	C	T	0.0607861	-0.0518447	0.0076011	2.6E-12
7	GIGYF1 *	rs748455947	100694170	GGACGGG	G	0.0605457	-0.0515695	0.0076238	3.9E-12
7	GIGYF1 *	rs221784	100695207	A	G	0.0610649	-0.0513137	0.0075847	3.5E-12
7	GIGYF1 *	rs221783	100695291	T	C	0.0610333	-0.0514519	0.0075871	3.2E-12
7	GIGYF1 *	rs55719620	100697387	A	AGGTTTG	0.0618773	-0.0493516	0.0075484	1.6E-11
7	POP7 *	rs221781	100698285	A	G	0.0607639	-0.0507006	0.0076034	7.8E-12
7	POP7 *	rs221780	100699412	G	C	0.0611086	-0.0510507	0.0075815	4.7E-12
7	POP7 *	rs221779	100700275	T	C	0.0610358	-0.0514404	0.0075863	3.2E-12
7	POP7 *	rs35722278	100700309	C	CG	0.0610358	-0.0514404	0.0075863	3.2E-12
7	POP7 *	rs221778	100700401	A	G	0.0610495	-0.0515088	0.0075855	3.0E-12
7	POP7 *	rs221774	100701361	A	G	0.0610389	-0.0515333	0.0075861	3.0E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	POP7 *	rs2432929	100701405	C	T	0.0610389	-0.0515333	0.0075861	3.0E-12
7	POP7 *	rs221770	100704471	A	T	0.0610456	-0.0515805	0.0075852	2.8E-12
7	POP7 *	rs1734911	100711188	C	G	0.0617707	-0.0503876	0.0075610	7.9E-12
7	EPO *	rs534043	100715101	A	G	0.0611971	-0.0514129	0.0075754	3.6E-12
7	EPO *	rs492430	100715476	T	G	0.0612258	-0.0514120	0.0075736	3.5E-12
7	EPO *	rs506597	100715797	A	G	0.0612258	-0.0514120	0.0075736	3.5E-12
7	EPO *	rs1734907	100717894	A	G	0.0612845	-0.0513095	0.0075698	3.6E-12
7	EPO	chr7:100722508_TTCAC_T	100722508	TTCAC	T	0.0751802	-0.0424040	0.0069504	1.4E-10
7	EPO	rs564449	100723515	T	G	0.0555999	-0.0527791	0.0079522	1.1E-11
7	ZAN *	rs4727462	100729466	G	C	0.0594144	-0.0520710	0.0076808	4.2E-12
7	ZAN *	rs7807429	100731167	C	T	0.0649938	-0.0514753	0.0074360	2.3E-12
7	ZAN *	rs6465775	100731455	A	C	0.0649894	-0.0515150	0.0074368	2.2E-12
7	ZAN *	rs6975957	100731566	C	T	0.0651057	-0.0513949	0.0074356	2.3E-12
7	ZAN *	rs2406257	100731944	G	A	0.0647386	-0.0516297	0.0074580	2.4E-12
7	ZAN *	rs58927259	100731991	T	ACAGAGC	0.0647399	-0.0515887	0.0074586	2.6E-12
7	ZAN *	chr7:100732353_CA_C	100732353	CA	C	0.0661232	-0.0502277	0.0074121	1.1E-11
7	ZAN *	rs2406256	100732468	T	C	0.0646194	-0.0518809	0.0074660	2.1E-12
7	ZAN	rs12673246	100732414	T	C	0.0608169	-0.0511982	0.0077294	2.2E-11
7	ZAN	rs3895793	100735374	C	G	0.0605614	-0.0498384	0.0077565	1.2E-10
7	ZAN	rs75834296	100736933	C	G	0.0596731	-0.0505809	0.0078185	8.3E-11
7	ZAN	rs113727587	100737791	A	G	0.0589205	-0.0504314	0.0078642	1.1E-10
7	ZAN	rs111977689	100738042	C	T	0.0588137	-0.0507912	0.0078721	8.3E-11
7	ZAN	rs75348008	100738249	C	T	0.0587584	-0.0505802	0.0078761	1.0E-10
7	ZAN	rs140939785	100738870	C	T	0.0604607	-0.0476647	0.0077952	7.5E-10
7	ZNF800 *	rs77874204	127423553	T	C	0.1600280	-0.0270965	0.0050394	4.3E-08
7	ZNF800 *	rs62468924	127425322	T	C	0.1604500	-0.0273563	0.0050451	3.3E-08
7	ZNF800 *	rs7455212	127425512	C	T	0.1600280	-0.0270965	0.0050394	4.3E-08
7	ZNF800 *	rs12672879	127427085	C	T	0.1600490	-0.0270487	0.0050391	4.5E-08
7	ZNF800 *	rs9640842	127431409	C	T	0.1600570	-0.0271538	0.0050391	3.9E-08
7	ZNF800 *	rs2106177	127432641	T	G	0.1600120	-0.0270580	0.0050394	4.5E-08
7	ZNF800 *	rs10487482	127433905	T	C	0.1600450	-0.0270879	0.0050393	4.3E-08
7	PAX4 *	rs61160304	127609605	T	C	0.1221860	0.0524772	0.0056358	1.8E-21
7	PAX4	rs2233580	127613496	T	C	0.1063810	0.0619276	0.0058933	1.4E-26
7	PAX4 *	rs3757787	127618330	T	C	0.1184650	0.0549179	0.0056826	6.6E-23
7	SND1	rs201976370	127969728	A	AAAAAAC	0.0990032	0.0615088	0.0061797	5.3E-24
7	MIR129-1 *	rs7778167	128211575	A	G	0.1261460	0.0300805	0.0055255	1.5E-08
7	MIR129-1 *	rs34494123	128212855	T	C	0.1298910	0.0284824	0.0054441	4.8E-08
7	MIR129-1 *	rs4728093	128219357	C	G	0.1299280	0.0279206	0.0054081	4.8E-08
7	LEP *	rs72607746	128259665	T	C	0.0795714	0.0419719	0.0068350	6.7E-10
7	LEP *	rs72607747	128263219	T	C	0.0748405	0.0442301	0.0070492	2.4E-10
7	LMBR1	rs10273333	156798874	T	C	0.3238230	-0.0235142	0.0039511	1.2E-09
7	LMBR1	rs6459709	156827897	A	C	0.3276050	-0.0219365	0.0039348	1.1E-08
7	LMBR1	rs17837699	156833983	C	G	0.2338510	-0.0284750	0.0043523	2.6E-11
7	LMBR1	rs2192510	156839543	T	C	0.2343880	-0.0290506	0.0043477	1.1E-11
7	LMBR1	rs10258503	156853154	G	A	0.2395980	-0.0274808	0.0043266	1.2E-10
7	NOM1 *	rs10549574	156949138	GCGT	G	0.2761200	-0.0272276	0.0040909	2.2E-11
7	NOM1	rs56180474	156953387	G	C	0.2778180	-0.0281106	0.0040722	3.7E-12
7	NOM1	rs12698000	156954756	T	C	0.2785150	-0.0281524	0.0040672	3.3E-12
7	NOM1	rs7810790	156955002	A	G	0.2779330	-0.0282521	0.0040696	2.7E-12
7	NOM1	rs12668289	156955201	C	G	0.2780410	-0.0282405	0.0040683	2.8E-12
7	NOM1	rs12670963	156955225	T	C	0.2780410	-0.0282405	0.0040683	2.8E-12
7	NOM1	rs12670999	156955347	T	G	0.2780470	-0.0282584	0.0040682	2.7E-12
7	NOM1	rs35042241	156955482	T	TAC	0.2781570	-0.0283774	0.0040688	2.2E-12
7	NOM1	rs4716446	156955580	A	C	0.2780980	-0.0283625	0.0040673	2.3E-12
7	NOM1	rs4716663	156955668	T	C	0.2780540	-0.0282837	0.0040681	2.6E-12
7	NOM1	rs10949615	156955865	A	G	0.2780530	-0.0282735	0.0040681	2.6E-12
7	NOM1	rs11768381	156955929	T	G	0.2780520	-0.0282761	0.0040680	2.6E-12
7	NOM1	rs1419933	156956314	A	C	0.2780620	-0.0283984	0.0040678	2.0E-12
7	NOM1	rs10949616	156957047	A	T	0.2781580	-0.0283495	0.0040672	2.2E-12
7	NOM1	rs6459718	156957647	T	C	0.2784080	-0.0283152	0.0040680	2.3E-12
7	NOM1	chr7:156959106_CT_C	156959106	CT	C	0.4523810	-0.0204360	0.0036886	3.4E-08
7	NOM1	rs10249994	156959349	A	G	0.2782050	-0.0286426	0.0040798	1.0E-12
7	NOM1	rs10263635	156959637	G	A	0.2776760	-0.0287369	0.0040748	9.0E-13
7	NOM1	rs2079986	156960652	A	G	0.2775670	-0.0289783	0.0040740	5.8E-13
7	NOM1	rs2079985	156960687	T	C	0.2775670	-0.0289877	0.0040740	5.7E-13
7	NOM1	rs10272070	156961655	G	A	0.2623620	-0.0291046	0.0041860	2.0E-12
7	NOM1	rs12672076	156962656	T	C	0.2773180	-0.0301812	0.0040522	5.2E-14
7	NOM1	rs10274639	156964759	T	C	0.2796100	-0.0299030	0.0040496	8.6E-14
7	NOM1	rs10256184	156964819	C	A	0.2818040	-0.0292224	0.0040415	2.3E-13
7	NOM1	rs2024265	156964925	T	C	0.2811080	-0.0293586	0.0040413	2.0E-13
7	NOM1	rs10949618	156965431	T	G	0.2813000	-0.0294729	0.0040403	1.5E-13
7	NOM1	rs35458218	156965796	T	TC	0.2815170	-0.0295532	0.0040433	1.3E-13
7	NOM1	rs10527083	156965916	AAAAAAC	A	0.2820420	-0.0291905	0.0040430	2.4E-13
7	NOM1	rs6951811	156965942	C	T	0.2813970	-0.0294653	0.0040441	1.5E-13
7	NOM1	rs1990436	156967654	G	A	0.2825990	-0.0290050	0.0040509	4.1E-13
7	NOM1	rs11767045	156970645	A	C	0.2781860	-0.0301054	0.0040544	5.6E-14
7	NOM1 *	rs4716668	156973332	T	C	0.2799950	-0.0299369	0.0040474	6.7E-14
7	NOM1 *	rs34875867	156974974	G	GT	0.2800210	-0.0296869	0.0040537	1.5E-13
7	NOM1 *	rs4716671	156975524	A	T	0.2779300	-0.0300833	0.0040553	5.8E-14
7	NOM1 *	rs59984064	156976622	TGTTTT	C	0.2836870	-0.0313537	0.0040758	7.3E-15
7	NOM1 *	rs10267664	156977804	C	G	0.2776250	-0.0302297	0.0040608	5.1E-14
7	NOM1 *	rs6459719	156978803	G	A	0.2797060	-0.0302856	0.0040676	6.5E-14
7	NOM1 *	rs6952665	156979108	T	C	0.2773440	-0.0301917	0.0040974	1.2E-13
7	NOM1 *	rs72621116	156979949	C	T	0.2578300	-0.0311534	0.0041923	4.4E-14
7	NOM1 *	rs10688639	156982140	C	CAT	0.2771650	-0.0290094	0.0041062	1.3E-12
7	NOM1 *	rs6459721	156986746	C	A	0.2758490	-0.0291299	0.0041143	1.3E-12
7	NOM1 *	rs1974632	156988068	G	C	0.2759380	-0.0291513	0.0041138	1.2E-12
7	NOM1 *	rs1558428	156988491	G	T	0.2740340	-0.0289691	0.0041308	1.6E-12
7	MNX1 *	rs6459723	156989897	T	G	0.2748820	-0.0291189	0.0041269	1.7E-12
7	MNX1 *	rs10949619	156990802	T	G	0.2750840	-0.0291880	0.0041222	1.3E-12
7	MNX1 *	rs6959718	156990829	T	G	0.2750440	-0.0292415	0.0041226	1.2E-12
8	PPP1R3B *	rs7002551	9320625	C	T	0.0100913	0.1246210	0.0181555	7.4E-12
8	PPP1R3B *	rs6984305	9320758	A	T	0.0100012	0.1215470	0.0182336	2.1E-11
8	LOC157273	rs9987289	9325848	A	G	0.0100048	0.1197380	0.0182304	4.3E-11
8	LOC157273	rs4841132	9326086	A	G	0.0100618	0.1216160	0.0181869	2.2E-11
8	LOC157273	rs10106829	9327118	A	G	0.0101226	0.1204680	0.0181277	3.0E-11
8	LOC157273	rs6601299	9327181	T	C	0.0102152	0.1110020	0.0180478	6.6E-10
8	LOC157273	rs2126260	9327571	T	C	0.0101262	0.1205100	0.0181246	3.0E-11
8	LOC157273	rs28529330	9328573	T	C	0.0101264	0.1204930	0.0181246	3.0E-11
8	LOC157273	rs9772631	9328576	T	C	0.0101264	0.1204930	0.0181246	3.0E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LOC157273	rs35323122	9329938	G	GC	0.0101263	0.1205070	0.0181246	3.0E-11
8	LOC157273	rs7004769	9330085	A	G	0.0101367	0.1197780	0.0181154	3.8E-11
8	LOC157273	rs6985493	9330344	C	T	0.0101298	0.1203220	0.0181216	3.2E-11
8	TRPS1	rs147733984	115543619	TTTC	T	0.1317460	0.0293189	0.0053809	3.9E-08
8	TRPS1	rs12056626	115545728	C	G	0.1318300	0.0290297	0.0053760	4.8E-08
8	TRPS1	rs3808434	115547208	A	G	0.1318720	0.0292901	0.0053715	4.2E-08
8	TRPS1	rs3808435	115547667	G	A	0.1318610	0.0292964	0.0053717	4.1E-08
8	TRPS1	rs7825679	115548392	T	C	0.1318270	0.0294854	0.0053733	3.3E-08
8	TRPS1	rs3808436	115548740	A	G	0.1318230	0.0294742	0.0053733	3.3E-08
8	TRPS1	rs3808437	115549516	T	C	0.1319660	0.0295389	0.0053703	3.1E-08
8	TRPS1	rs10097784	115549597	C	A	0.1318310	0.0294193	0.0053741	3.8E-08
8	TRPS1	rs10955753	115549942	C	A	0.1319440	0.0294542	0.0053699	3.4E-08
8	TRPS1	rs3808438	115551346	T	C	0.1319190	0.0294358	0.0053705	3.5E-08
8	TRPS1	rs3808439	115551448	A	G	0.1319190	0.0294358	0.0053705	3.5E-08
8	TRPS1	rs3808440	115551469	G	A	0.1313340	0.0295442	0.0053843	3.3E-08
8	TRPS1	rs1351744	115551652	A	C	0.1321660	0.0296140	0.0053648	2.7E-08
8	TRPS1	rs1483589	115552569	A	G	0.1372840	0.0293285	0.0052773	2.0E-08
8	TRPS1	rs3802219	115553138	T	C	0.1354890	0.0297690	0.0053131	1.6E-08
8	TRPS1	rs3802220	115553225	G	A	0.1372010	0.0292072	0.0052766	2.3E-08
8	TRPS1	rs2884366	115553612	C	A	0.1374820	0.0292606	0.0052753	2.2E-08
8	TRPS1	rs2358019	115553741	C	G	0.1373170	0.0292317	0.0052780	2.2E-08
8	TRPS1	rs6998448	115554088	T	C	0.1375280	0.0288386	0.0052759	3.3E-08
8	TRPS1	rs5894275	115555375	TC	T	0.1372030	0.0291887	0.0052766	2.3E-08
8	TRPS1	chr8:115555868_CA_C	115555868	CA	C	0.1368470	0.0295030	0.0052926	2.0E-08
8	TRPS1	rs6469597	115558403	G	A	0.1372090	0.0291923	0.0052763	2.3E-08
8	TRPS1	rs3808444	115558750	C	T	0.1339100	0.0294202	0.0053322	2.5E-08
8	TRPS1	rs2178948	115559711	G	A	0.1330430	0.0297360	0.0053469	1.7E-08
8	TRPS1	rs3802221	115560699	T	C	0.1330430	0.0297360	0.0053469	1.7E-08
8	TRPS1	rs3779879	115560796	C	T	0.1330430	0.0297360	0.0053469	1.7E-08
8	TRPS1	rs3808446	115562182	G	A	0.1363400	0.0295123	0.0052906	1.5E-08
8	TRPS1	rs6469600	115562634	C	T	0.1365980	0.0291941	0.0052866	2.0E-08
8	TRPS1	rs3808447	115563232	G	A	0.1363390	0.0295433	0.0052905	1.5E-08
8	TRPS1	rs3808448	115564600	C	T	0.1363560	0.0294326	0.0052911	1.7E-08
8	TRPS1	rs3808449	115564751	G	A	0.1363450	0.0294626	0.0052904	1.6E-08
8	TRPS1	rs60439418	115565492	TTTTTTG	T	0.1392000	0.0282909	0.0052790	4.2E-08
8	TRPS1	rs3808450	115566821	G	A	0.1363450	0.0294626	0.0052904	1.6E-08
8	TRPS1	rs2223103	115567092	A	T	0.1363450	0.0294626	0.0052904	1.6E-08
8	TRPS1	rs3832573	115567147	AC	A	0.1363450	0.0294626	0.0052904	1.6E-08
8	TRPS1	rs6986967	115567840	G	A	0.1363450	0.0294626	0.0052904	1.6E-08
8	TRPS1	rs1160333	115568497	T	G	0.1366390	0.0297047	0.0052969	1.3E-08
8	TRPS1	rs1028274	115571324	T	G	0.1369480	0.0290565	0.0052820	2.1E-08
8	TRPS1	rs1963677	115571642	G	A	0.1366440	0.0292718	0.0052881	1.9E-08
8	TRPS1	rs3808454	115571882	T	C	0.1367230	0.0291959	0.0052915	2.2E-08
8	TRPS1	rs1963678	115571890	C	T	0.1368370	0.0292399	0.0052902	2.0E-08
8	TRPS1	rs33922136	115572450	ATT	A	0.1367400	0.0293173	0.0052864	1.8E-08
8	TRPS1	rs2103481	115572930	C	T	0.1363860	0.0293268	0.0052893	1.8E-08
8	TRPS1	rs3779881	115574233	C	T	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs2358021	115575231	G	A	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs2049864	115576099	C	A	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs2049865	115576319	C	A	0.1388070	0.0294388	0.0052697	1.4E-08
8	TRPS1	rs2049867	115576343	T	C	0.1371100	0.0288530	0.0052842	2.8E-08
8	TRPS1	rs3808456	115576991	A	G	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs3808457	115577270	T	A	0.1361650	0.0299086	0.0053028	8.5E-09
8	TRPS1	rs719422	115578033	A	T	0.1360560	0.0288746	0.0052985	2.7E-08
8	TRPS1	rs11989423	115578806	G	A	0.1367850	0.0292587	0.0052835	1.7E-08
8	TRPS1	rs11785504	115579061	A	G	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs3808459	115579679	T	C	0.1367660	0.0291118	0.0052835	2.0E-08
8	TRPS1	chr8:115579918_GA_G	115579918	GA	G	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs6993253	115580880	T	C	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs7011494	115581092	C	T	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs4326410	115581355	C	T	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs4599845	115581371	T	C	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	rs2178949	115581911	T	G	0.1367340	0.0292391	0.0052838	1.7E-08
8	TRPS1	chr8:115583270_TA_T	115583270	TA	T	0.1352530	0.0306442	0.0053277	3.9E-09
8	TRPS1	rs71566093	115583377	ATTACT	A	0.1374770	0.0296074	0.0052865	1.4E-08
8	TRPS1	rs9297541	115583486	A	G	0.1368160	0.0289435	0.0052848	2.4E-08
8	TRPS1	rs6469603	115583961	C	T	0.1367860	0.0292673	0.0052828	1.6E-08
8	TRPS1	rs1057517	115584890	G	A	0.1366900	0.0294117	0.0052845	1.5E-08
8	TRPS1	rs13271228	115585182	T	G	0.1367460	0.0292027	0.0052836	1.8E-08
8	TRPS1	rs3808460	115585408	T	C	0.1357370	0.0297029	0.0053027	1.1E-08
8	TRPS1	rs3808461	115585489	C	T	0.1357370	0.0297029	0.0053027	1.1E-08
8	TRPS1	rs7012216	115588558	G	A	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs6998144	115588795	T	C	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs10808475	115588844	C	T	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs7357472	115589175	T	A	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs6469605	115589667	C	T	0.1380090	0.0283097	0.0052743	3.8E-08
8	TRPS1	rs6469606	115589675	C	T	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs12679749	115590232	T	C	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs13267535	115590449	G	A	0.1373650	0.0288243	0.0052817	2.5E-08
8	TRPS1	rs13269499	115590568	T	C	0.1374670	0.0286152	0.0052831	3.3E-08
8	TRPS1	rs10505258	115590628	T	C	0.1374320	0.0286934	0.0052840	3.1E-08
8	TRPS1	rs13275142	115590647	G	A	0.1374320	0.0286934	0.0052840	3.1E-08
8	TRPS1	rs2737203	115590776	T	C	0.1373810	0.0287013	0.0052816	2.8E-08
8	TRPS1	rs2721954	115590876	C	T	0.1374530	0.0284562	0.0052828	3.7E-08
8	TRPS1	rs2721926	115596001	T	G	0.1385890	0.0305523	0.0052641	2.3E-09
8	TRPS1	rs2737205	115597953	T	C	0.1385890	0.0305523	0.0052641	2.3E-09
8	TRPS1	rs7834300	115599405	G	C	0.1390710	0.0300885	0.0052616	3.5E-09
8	TRPS1	rs2737206	115599675	T	C	0.1385830	0.0305711	0.0052643	2.2E-09
8	TRPS1	rs2721929	115601031	G	A	0.1386450	0.0305749	0.0052631	2.1E-09
8	TRPS1	rs2737207	115602316	C	A	0.1386560	0.0305607	0.0052631	2.2E-09
8	TRPS1	rs997806	115607129	C	T	0.1386740	0.0304193	0.0052625	2.5E-09
8	TRPS1	rs2721932	115608077	G	A	0.1380560	0.0304810	0.0052788	2.6E-09
8	TRPS1	rs2737212	115608987	C	T	0.1379320	0.0310547	0.0052876	1.6E-09
8	TRPS1	rs2245019	115610679	C	A	0.1381100	0.0310909	0.0052898	1.7E-09
8	TRPS1	rs2737214	115612760	C	G	0.1219630	0.0307941	0.0055677	1.4E-08
8	SLC30A8	rs17812443	116995056	A	C	0.1872700	-0.0258192	0.0046686	4.7E-08
8	SLC30A8	rs62510505	117068208	T	C	0.1208460	0.0313274	0.0055660	3.5E-08
8	SLC30A8	rs58516434	117105538	T	A	0.2371710	-0.0247685	0.0042760	4.7E-09
8	SLC30A8	rs924921	117106100	G	A	0.2371890	-0.0247469	0.0042758	4.9E-09
8	SLC30A8	rs79361938	117106772	T	C	0.0869452	0.0449695	0.0065062	1.6E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	SLC30A8	rs10505314	117106933	G	A	0.2357650	-0.0256052	0.0042890	1.4E-09
8	SLC30A8	rs4876702	117109495	G	A	0.2371830	-0.0247579	0.0042756	4.8E-09
8	SLC30A8	rs10531300	117109591	C	CGT	0.2371820	-0.0246974	0.0042757	5.2E-09
8	SLC30A8	rs62510518	117113283	A	T	0.1185380	0.0314873	0.0056256	4.0E-08
8	SLC30A8	rs11776475	117150576	C	T	0.2370620	-0.0245666	0.0042772	5.7E-09
8	SLC30A8	rs2466300	117170685	A	C	0.1864460	0.0525556	0.0047178	1.5E-28
8	SLC30A8	rs115080302	117170894	C	T	0.0780661	0.0603053	0.0067959	3.6E-19
8	SLC30A8	rs114074793	117171015	T	A	0.0780970	0.0600844	0.0067944	4.8E-19
8	SLC30A8	rs2464592	117171312	G	A	0.1825100	0.0579982	0.0046970	1.2E-34
8	SLC30A8	rs2466299	117171348	A	G	0.1809820	0.0584296	0.0047196	7.3E-35
8	SLC30A8	rs2466298	117171419	C	A	0.1868940	0.0572096	0.0047252	1.8E-33
8	SLC30A8	rs2464591	117171586	A	G	0.1807490	0.0583964	0.0047237	9.9E-35
8	SLC30A8	rs2466297	117171653	T	C	0.1806890	0.0584729	0.0047246	7.8E-35
8	SLC30A8	rs2466296	117171888	A	G	0.1809600	0.0586110	0.0047211	4.7E-35
8	SLC30A8	rs13266634	117172544	T	C	0.4600100	-0.0748002	0.0036452	4.3E-95
8	SLC30A8	rs16889462	117172545	A	G	0.0782285	0.0600816	0.0067893	4.6E-19
8	SLC30A8	rs3802178	117172719	G	A	0.0782329	0.0601510	0.0067890	4.2E-19
8	SLC30A8	rs3802177	117172786	A	G	0.4604050	-0.0745098	0.0036415	2.2E-94
8	SLC30A8	rs2466295	117172802	C	T	0.1825920	0.0579810	0.0047042	1.7E-34
8	SLC30A8	rs2466294	117172824	C	G	0.1824900	0.0581536	0.0047034	1.1E-34
8	SLC30A8	rs11558471	117173494	G	A	0.4666010	-0.0734421	0.0036358	4.1E-92
8	SLC30A8	rs2466293	117173699	G	A	0.3559060	0.0428676	0.0038026	1.1E-30
8	SLC30A8	rs114765737	117174506	T	C	0.0747694	0.0563617	0.0069215	1.5E-16
8	SLC30A8	rs114831870	117174993	G	C	0.0779611	0.0598241	0.0067986	7.3E-19
8	SLC30A8	rs114031443	117175502	A	G	0.0746540	0.0565458	0.0069257	1.7E-16
8	SLC30A8 *	rs2466292	117177292	C	T	0.1824040	0.0580832	0.0047088	1.5E-34
8	SLC30A8 *	rs2466291	117178154	A	G	0.1818390	0.0582818	0.0047208	1.3E-34
8	SLC30A8 *	rs16889471	117178381	A	G	0.0863750	0.0567477	0.0064607	1.8E-18
8	SLC30A8 *	rs35859536	117179236	T	C	0.4614460	-0.0744242	0.0036483	6.3E-94
8	SLC30A8 *	rs2466290	117180961	G	T	0.0906530	0.0448874	0.0063389	2.3E-12
8	SLC30A8 *	chr8:117181998_TATA_T	117181998	T	TATA	0.0816993	0.0591216	0.0066508	5.3E-19
8	SLC30A8 *	rs10584444	117182245	TTAAAA	T	0.1816020	0.0577377	0.0047286	6.9E-34
8	SLC30A8 *	rs2466289	117183331	G	A	0.1814080	0.0575846	0.0047301	1.3E-33
8	SLC30A8 *	rs2464597	117183333	G	A	0.0902704	0.0451188	0.0063527	2.3E-12
8	SLC30A8 *	rs1578978	117184564	G	A	0.3544360	0.0424816	0.0038167	5.0E-30
8	SLC30A8 *	rs2464598	117185832	C	T	0.0906599	0.0450299	0.0063388	2.0E-12
8	SLC30A8 *	rs2466288	117187949	G	C	0.1815090	0.0579637	0.0047252	4.0E-34
8	SLC30A8 *	rs79319503	117188664	C	A	0.0850710	0.0560099	0.0065417	1.2E-17
8	SLC30A8 *	rs2464587	117190133	C	T	0.0906942	0.0449394	0.0063381	2.4E-12
8	SLC30A8 *	chr8:117190552_CT_C	117190552	C	CT	0.0798852	0.0582900	0.0067132	2.3E-18
8	SLC30A8 *	rs6469681	117191195	G	A	0.0893316	0.0582675	0.0063707	7.2E-20
8	SLC30A8 *	rs2464586	117191457	T	C	0.0906563	0.0450779	0.0063392	1.9E-12
8	SLC30A8 *	rs9650069	117191781	T	C	0.4652140	-0.0719249	0.0036264	8.3E-89
8	SLC30A8 *	rs4265213	117193432	C	A	0.0890402	0.0583772	0.0063807	6.1E-20
8	SLC30A8 *	rs4573311	117193438	A	G	0.0890402	0.0583772	0.0063807	6.1E-20
8	SLC30A8 *	rs4573312	117193480	A	G	0.0890402	0.0583772	0.0063807	6.1E-20
8	SLC30A8 *	rs150298768	117194123	T	C	0.0906213	0.0448512	0.0063413	2.6E-12
8	SLC30A8 *	rs141866157	117194176	T	C	0.0906213	0.0448512	0.0063413	2.6E-12
8	SLC30A8 *	rs2954237	117195345	A	C	0.0906183	0.0448327	0.0063414	2.7E-12
8	SLC30A8 *	rs7820405	117196066	G	A	0.0907251	0.0444412	0.0063422	3.9E-12
8	SLC30A8 *	rs75562530	117197912	T	C	0.0798562	0.0584362	0.0067144	1.8E-18
8	SLC30A8 *	rs2464583	117200223	A	G	0.0906232	0.0448065	0.0063419	2.8E-12
8	SLC30A8 *	rs2466324	117200773	A	G	0.0906013	0.0447697	0.0063419	2.8E-12
8	SLC30A8 *	rs73319559	117201100	A	G	0.0798562	0.0584362	0.0067144	1.8E-18
8	SLC30A8 *	rs73319561	117201333	T	C	0.0798562	0.0584362	0.0067144	1.8E-18
8	SLC30A8 *	rs2466323	117201537	C	T	0.0906013	0.0447697	0.0063419	2.8E-12
8	SLC30A8 *	rs2464582	117202281	C	A	0.0905911	0.0446980	0.0063429	3.1E-12
8	SLC30A8 *	rs6998120	117203062	G	A	0.0801046	0.0582031	0.0067045	2.5E-18
8	SLC30A8 *	rs2466321	117203498	C	G	0.0905444	0.0448401	0.0063443	2.7E-12
8	SLC30A8 *	rs145142295	117203572	A	ACT	0.0797580	0.0582305	0.0067179	2.9E-18
8	SLC30A8 *	rs10101645	117204156	G	T	0.0891751	0.0582294	0.0063753	9.6E-20
8	SLC30A8 *	rs2464579	117204399	C	T	0.0904776	0.0449992	0.0063475	2.2E-12
8	SLC30A8 *	rs2466320	117204434	G	T	0.1819090	0.0568603	0.0047370	8.8E-33
8	SLC30A8 *	rs2464578	117204973	C	T	0.0922220	0.0460350	0.0062956	3.9E-13
8	SLC30A8 *	rs10105491	117205032	C	T	0.0889266	0.0582963	0.0063841	8.8E-20
8	SLC30A8 *	rs2466318	117205068	T	C	0.1809740	0.0575136	0.0047300	1.4E-33
8	SLC30A8 *	rs4300038	117205676	A	G	0.4644630	-0.0720974	0.0036369	8.8E-89
8	SLC30A8 *	rs2464577	117206282	A	G	0.0903206	0.0452786	0.0063540	1.6E-12
8	SLC30A8 *	rs34658639	117206390	A	3AGGAG/	0.0797328	0.0585579	0.0067226	2.1E-18
8	SLC30A8 *	rs4442172	117206783	A	C	0.0888451	0.0587396	0.0063894	5.5E-20
8	SLC30A8 *	rs2466315	117207144	G	A	0.0902717	0.0452441	0.0063558	1.8E-12
8	SLC30A8 *	rs2466314	117207368	A	G	0.0902458	0.0452402	0.0063569	1.8E-12
8	SLC30A8 *	rs4573313	117207413	G	A	0.0889107	0.0585893	0.0063877	7.0E-20
8	SLC30A8 *	rs4392934	117207534	G	A	0.0888989	0.0585943	0.0063881	6.9E-20
8	SLC30A8 *	rs2466313	117207774	C	G	0.0901956	0.0451937	0.0063591	2.0E-12
8	SLC30A8 *	rs2464576	117207950	C	T	0.0906138	0.0454634	0.0063531	1.3E-12
8	SLC30A8 *	rs11774700	117208031	C	T	0.4702780	-0.0719833	0.0036434	1.3E-88
8	SLC30A8 *	rs2466312	117208084	G	T	0.0901812	0.0451292	0.0063597	2.1E-12
8	SLC30A8 *	rs2466311	117208857	G	C	0.1772510	0.0575562	0.0047839	6.5E-33
8	SLC30A8 *	rs2464574	117209760	C	G	0.0895080	0.0452534	0.0063919	2.1E-12
8	SLC30A8 *	rs2464573	117210159	G	A	0.1751470	0.0574199	0.0048286	3.0E-32
8	SLC30A8 *	rs2466310	117210464	T	C	0.0807044	0.0471158	0.0067199	3.9E-12
8	SLC30A8 *	rs13267156	117211276	C	T	0.1740370	0.0567171	0.0048705	5.3E-31
8	SLC30A8 *	rs11987251	117211716	G	A	0.0820287	0.0593962	0.0066857	9.3E-19
8	SLC30A8 *	rs112129735	117212243	T	C	0.1707400	0.0564905	0.0049320	3.4E-30
8	SLC30A8 *	rs1995222	117217523	T	C	0.4392260	-0.0339437	0.0036578	1.2E-20
8	SLC30A8 *	rs951337	117217997	T	C	0.4390970	-0.0334854	0.0036560	4.1E-20
8	SLC30A8 *	rs1024069	117219041	G	A	0.4412340	-0.0333275	0.0036675	7.4E-20
8	SLC30A8 *	rs1024068	117219403	C	G	0.4397210	-0.0339152	0.0036620	1.6E-20
8	SLC30A8 *	rs28529793	117219712	T	C	0.4428240	-0.0345372	0.0036646	2.5E-21
8	SLC30A8 *	rs28552442	117219731	T	C	0.4395570	-0.0340143	0.0036611	1.3E-20
8	SLC30A8 *	rs12549811	117219872	T	G	0.4397170	-0.0338909	0.0036627	1.7E-20
8	SLC30A8 *	rs12544930	117220003	G	A	0.4416480	-0.0331680	0.0036665	1.1E-19
8	SLC30A8 *	rs4876711	117220098	A	C	0.4410820	-0.0332009	0.0036644	9.4E-20
8	SLC30A8 *	rs78014057	117220108	G	A	0.1508550	-0.0377199	0.0050852	5.9E-14
8	SLC30A8 *	rs12545006	117220390	G	A	0.4419080	-0.0333590	0.0036697	7.4E-20
8	SLC30A8 *	rs7004660	117221602	C	A	0.4407340	-0.0339671	0.0036677	1.6E-20
8	SLC30A8 *	rs7005140	117221908	G	A	0.4406850	-0.0339582	0.0036692	1.7E-20
8	SLC30A8 *	rs7005548	117221948	C	G	0.4400120	-0.0338578	0.0036719	2.5E-20
8	SLC30A8 *	rs10955806	117222679	C	T	0.4782060	-0.0268103	0.0036593	6.0E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	SLC30A8 *	rs1392042	11722870	C	G	0.4838550	-0.0258396	0.0036735	5.4E-13
8	SLC30A8 *	rs1392041	11722911	C	T	0.4780170	-0.0269809	0.0036625	5.5E-14
8	SLC30A8 *	rs1392040	11722964	C	G	0.4784540	-0.0268670	0.0036589	5.6E-14
8	SLC30A8 *	rs2649098	117223033	C	T	0.4855120	-0.0262562	0.0036798	2.8E-13
8	SLC30A8 *	rs75303356	117223633	A	G	0.1506070	-0.0382683	0.0050739	2.8E-14
8	SLC30A8 *	rs961630	117223771	C	T	0.4787790	-0.0273782	0.0036581	2.7E-14
8	SLC30A8 *	rs12545397	117223952	C	T	0.4383710	-0.0337251	0.0036795	3.0E-20
8	SLC30A8 *	rs10955807	117224332	A	G	0.4342040	-0.0355415	0.0037249	6.3E-22
9	KANK1	rs2021846	537031	A	G	0.3100690	-0.0282793	0.0039519	3.5E-13
9	KANK1	rs10120392	537358	C	T	0.3241070	-0.0284816	0.0038811	8.6E-14
9	KANK1	rs10975042	538401	C	T	0.3173100	-0.0296276	0.0038965	8.6E-15
9	KANK1	rs10975046	540219	T	C	0.4442720	0.0335207	0.0037112	3.4E-20
9	KANK1	rs10815178	540267	G	T	0.3210480	-0.0285851	0.0038980	9.7E-14
9	KANK1	rs9299011	541031	A	C	0.3210540	-0.0284653	0.0039097	1.4E-13
9	KANK1	chr9:541123_G_GAA	541123	GAA	G	0.3249170	-0.0279189	0.0038983	4.8E-13
9	KANK1	rs78032619	542067	T	C	0.3109820	-0.0287446	0.0039610	1.7E-13
9	KANK1	rs10975058	543284	A	G	0.2743790	-0.0319182	0.0040944	1.6E-15
9	KANK1	rs12342270	545893	A	G	0.4873110	0.0364973	0.0036946	1.2E-24
9	KANK1	rs10758683	546198	T	C	0.4930280	0.0366061	0.0036697	4.6E-25
9	KANK1	rs10815197	546417	A	G	0.4929770	0.0367596	0.0036741	2.8E-25
9	KANK1	rs16919397	547399	A	G	0.2574160	0.0550648	0.0042000	3.6E-41
9	KANK1	rs16919430	550079	A	G	0.2830070	-0.0321826	0.0040483	7.4E-16
9	KANK1	rs2641989	552379	C	G	0.2614430	0.0551156	0.0041601	7.5E-42
9	KANK1	rs2641988	552783	A	G	0.4693370	-0.0362343	0.0036550	1.2E-24
9	KANK1	rs10975118	553032	C	G	0.4999890	0.0369926	0.0036509	1.1E-25
9	KANK1	rs10975119	553181	T	G	0.4707910	-0.0362106	0.0036552	1.4E-24
9	KANK1	rs10975120	553191	T	C	0.4710990	-0.0362330	0.0036534	1.2E-24
9	KANK1	rs78652864	553640	G	A	0.2654140	0.0558192	0.0041308	1.8E-43
9	KANK1	rs1874047	553794	G	A	0.2905630	-0.0334137	0.0040046	2.9E-17
9	KANK1	rs7851122	554261	G	C	0.2648300	0.0554266	0.0041338	6.2E-43
9	KANK1	rs7860794	554421	G	T	0.2757510	0.0544784	0.0040835	4.5E-42
9	KANK1	rs35613378	555140	A	G	0.2610300	0.0551092	0.0041450	2.2E-42
9	KANK1	rs35891812	555176	TA	T	0.2615060	0.0556534	0.0041457	4.1E-43
9	KANK1	rs12351767	555226	G	C	0.2615080	0.0556655	0.0041457	4.0E-43
9	KANK1	rs12353509	555332	G	A	0.2615020	0.0556784	0.0041456	3.8E-43
9	KANK1	rs34686847	555382	GCA	G	0.2615040	0.0556866	0.0041456	3.8E-43
9	KANK1	rs10815227	555456	G	A	0.2604010	0.0556086	0.0041562	1.0E-42
9	KANK1	rs10113890	555510	T	A	0.2601140	0.0557715	0.0041545	5.9E-43
9	KANK1	rs10113892	555528	T	A	0.2601140	0.0557715	0.0041545	5.9E-43
9	KANK1	rs10113911	555626	G	A	0.2601310	0.0558330	0.0041548	4.9E-43
9	KANK1	rs2641984	555653	C	T	0.4757160	0.0330177	0.0036550	7.7E-20
9	KANK1	rs10113966	555865	G	A	0.2597450	0.0554602	0.0041585	1.8E-42
9	KANK1	rs10114004	555983	T	A	0.2602030	0.0554944	0.0041584	1.4E-42
9	KANK1	rs11999231	556150	T	A	0.2608950	0.0553787	0.0041564	1.4E-42
9	KANK1	rs9632892	556399	T	C	0.2591700	0.0555204	0.0041632	1.7E-42
9	KANK1	rs1565793	556629	G	C	0.2588850	0.0549729	0.0041676	1.3E-41
9	KANK1	rs1565792	556677	C	G	0.2583570	0.0546908	0.0041702	3.6E-41
9	KANK1	rs2251373	556812	G	T	0.2959940	-0.0329557	0.0039745	3.3E-17
9	KANK1	rs10815231	557015	G	T	0.2946190	-0.0328651	0.0039780	4.8E-17
9	KANK1	rs3947468	557119	T	C	0.2583800	0.0550133	0.0041724	1.5E-41
9	KANK1	rs3028135	557205	C	A	0.2879440	-0.0334912	0.0040218	3.2E-17
9	KANK1	rs76927451	557260	C	T	0.2588570	0.0551045	0.0041686	9.0E-42
9	KANK1	rs10975130	557340	C	T	0.2952370	-0.0326934	0.0039741	5.5E-17
9	KANK1	rs3739592	557617	G	A	0.2934310	-0.0330033	0.0039763	2.5E-17
9	KANK1	rs3739591	557765	C	G	0.2895680	-0.0328330	0.0040016	7.9E-17
9	KANK1	rs3739590	557921	C	T	0.2867470	-0.0330348	0.0040127	5.3E-17
9	KANK1	rs113088943	557995	ACT	A	0.4735680	0.0333402	0.0036532	4.8E-20
9	KANK1	rs2804261	558343	G	A	0.4762180	0.0332038	0.0036525	7.1E-20
9	KANK1	rs3739589	559273	G	A	0.2663820	0.0555087	0.0041362	4.2E-43
9	KANK1	rs5002740	559403	G	A	0.2817460	-0.0330201	0.0040678	1.8E-16
9	KANK1	rs1908233	559434	C	T	0.2867550	-0.0321303	0.0040151	3.2E-16
9	KANK1	rs2804262	559714	C	A	0.2889610	-0.0325990	0.0040061	9.3E-17
9	KANK1	rs4742091	559867	C	G	0.4951810	-0.0364856	0.0036534	2.5E-25
9	KANK1	rs58029056	560308	G	A	0.2912710	-0.0324364	0.0039970	9.4E-17
9	KANK1	rs10975162	562441	C	A	0.2879350	-0.0332908	0.0040218	2.2E-17
9	KANK1	rs76958492	563532	T	C	0.2605310	0.0542610	0.0041688	8.6E-41
9	KANK1	rs4742101	564328	T	C	0.2804790	-0.0322159	0.0040559	5.0E-16
9	KANK1	rs7019523	564786	C	A	0.2641770	0.0547020	0.0041506	1.1E-41
9	KANK1	rs12552324	566105	G	C	0.3334470	-0.0301714	0.0038820	1.2E-15
9	KANK1	rs7021794	566509	T	C	0.2540940	0.0544153	0.0042275	7.8E-40
9	KANK1	rs2641978	566525	G	T	0.2607680	0.0542117	0.0041730	1.1E-40
9	KANK1	rs10815245	567046	G	C	0.3352100	-0.0323079	0.0038620	5.3E-18
9	KANK1	rs12345233	567615	C	T	0.2609800	0.0553471	0.0041627	2.3E-42
9	KANK1	rs60885769	567994	G	GT	0.2760990	0.0497954	0.0041442	7.0E-35
9	KANK1	rs881985	569992	G	T	0.3379570	-0.0323159	0.0038556	3.9E-18
9	KANK1	rs12684488	571582	A	T	0.2585570	0.0550560	0.0042100	6.1E-41
9	KANK1	rs2804271	574663	C	T	0.3434720	-0.0320395	0.0038475	6.2E-18
9	KANK1	rs2804272	575232	G	A	0.3441610	-0.0320627	0.0038423	5.7E-18
9	KANK1	rs73639373	576130	C	T	0.2668540	0.0546642	0.0041447	6.1E-42
9	KANK1	rs139124441	577213	G	T	0.2679700	0.0546106	0.0041314	3.3E-42
9	KANK1	rs111576106	577481	C	T	0.2681570	0.0546711	0.0041279	2.2E-42
9	KANK1	rs73639374	577841	G	A	0.2674850	0.0549767	0.0041305	8.9E-43
9	KANK1	rs2641973	580171	A	T	0.3385180	-0.0335152	0.0038409	3.3E-19
9	KANK1	rs58060168	580659	G	A	0.2698410	0.0553469	0.0041229	8.7E-44
9	KANK1	rs2804276	580725	T	C	0.3268570	-0.0341536	0.0038806	2.1E-19
9	KANK1	rs2361089	580868	C	T	0.3387050	-0.0333106	0.0038378	4.6E-19
9	KANK1	rs2641970	581453	C	T	0.3388560	-0.0330145	0.0038329	8.4E-19
9	KANK1	rs34194378	581521	T	TC	0.3384550	-0.0332341	0.0038365	5.1E-19
9	KANK1	rs2804278	582485	C	A	0.3749360	0.0408922	0.0037674	1.3E-29
9	KANK1	rs10491599	583025	G	T	0.2682820	0.0562689	0.0041198	6.2E-45
9	KANK1	rs1565789	583418	C	T	0.3763890	0.0403819	0.0037664	6.3E-29
9	KANK1	rs7028792	584087	G	A	0.2716180	0.0570286	0.0041060	2.5E-46
9	KANK1	rs73639378	585974	C	G	0.2655570	0.0552051	0.0041341	3.9E-43
9	KANK1	rs1494001	587663	A	G	0.3309020	-0.0332275	0.0038683	7.9E-19
9	KANK1	rs2804280	589511	C	T	0.3423970	-0.0331380	0.0038382	5.8E-19
9	KANK1	rs10975295	590078	G	C	0.2607050	0.0570239	0.0041831	1.9E-44
9	KANK1	rs16920619	590735	C	T	0.2698830	0.0573570	0.0041186	2.8E-46
9	KANK1	rs16920641	591610	A	G	0.2657230	0.0573404	0.0041441	4.7E-46
9	KANK1	rs12337439	591755	C	T	0.2659640	0.0573368	0.0041421	4.7E-46
9	KANK1	rs12349212	591816	A	G	0.2776490	0.0541303	0.0041279	1.4E-41

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	KANK1	rs10975307	592077	A	G	0.3261510	-0.0317892	0.0039035	3.1E-17
9	KANK1	rs7871641	592262	T	A	0.4051270	-0.0379278	0.0037228	1.1E-25
9	KANK1	rs12005187	592525	A	G	0.2769540	0.0582352	0.0040980	1.3E-48
9	KANK1	rs12000135	592526	A	T	0.2769540	0.0582352	0.0040980	1.3E-48
9	KANK1	rs2642002	592718	C	T	0.3202150	-0.0366244	0.0039128	1.8E-22
9	KANK1	rs12335853	592857	G	C	0.2778970	0.0581414	0.0040891	8.5E-49
9	KANK1	rs2642001	593229	T	C	0.3206210	-0.0364445	0.0039129	3.2E-22
9	KANK1	rs2641997	594697	G	T	0.3189380	-0.0364674	0.0039152	3.8E-22
9	KANK1	rs2804286	594716	C	T	0.3656380	0.0453959	0.0038012	1.6E-35
9	KANK1	rs2641996	595756	A	C	0.3183900	-0.0366633	0.0039153	1.8E-22
9	KANK1	rs10975337	597677	A	T	0.2786810	0.0572052	0.0040864	2.1E-47
9	KANK1	rs12346314	598223	C	T	0.2823580	0.0575412	0.0040694	2.9E-48
9	KANK1	rs12345378	598748	G	A	0.2795400	0.0576054	0.0041021	1.3E-47
9	KANK1	rs12347690	599535	C	T	0.2832640	0.0579463	0.0040606	4.7E-49
9	KANK1	rs12344866	599666	T	C	0.2807360	0.0580551	0.0040708	4.9E-49
9	KANK1	rs73639379	600204	T	C	0.2799840	0.0574958	0.0040792	7.7E-48
9	KANK1	rs57396250	600706	T	C	0.2793090	0.0578861	0.0040808	1.8E-48
9	KANK1	rs57643566	600804	G	T	0.2809360	0.0578909	0.0040700	8.9E-49
9	KANK1	rs57605578	602573 ATGAGA/	A	A	0.2834880	0.0571492	0.0040632	1.0E-47
9	KANK1	rs10975359	602949	A	G	0.2821180	0.0575150	0.0040706	3.3E-48
9	KANK1	rs10815316	603422	G	C	0.2810080	0.0580633	0.0040699	4.5E-49
9	KANK1	rs2804300	603836	G	A	0.3669600	0.0449143	0.0037989	7.8E-35
9	KANK1	rs2804301	603916	A	G	0.3656140	0.0447878	0.0038066	1.5E-34
9	KANK1	rs16924547	604072	G	A	0.2835740	0.0577840	0.0040634	1.0E-48
9	KANK1	rs10815341	609594	T	C	0.3281930	-0.0371094	0.0039021	5.8E-23
9	KANK1	rs35625797	611758	A	G	0.2766610	0.0586463	0.0040844	5.1E-50
9	KANK1	rs76191291	618226	T	C	0.2762600	0.0580446	0.0041150	4.4E-48
9	KANK1	rs10815352	620069	A	G	0.2817060	-0.0353448	0.0041211	3.4E-18
9	KANK1	rs10815354	622360	T	G	0.2736280	0.0581225	0.0040925	4.9E-49
9	KANK1	rs10815355	622523	T	G	0.2761610	0.0578693	0.0040550	1.2E-49
9	KANK1	rs1986564	622545	C	A	0.3452840	-0.0365541	0.0038281	3.5E-23
9	KANK1	rs10217450	622764	A	G	0.2732350	0.0578198	0.0040919	1.2E-48
9	KANK1	rs10124848	623485	A	T	0.2743940	0.0582285	0.0040873	2.5E-49
9	KANK1	rs10975466	624660	A	G	0.2731340	0.0581556	0.0040953	3.6E-49
9	KANK1	rs61697563	625041	CT	C	0.3455030	-0.0367581	0.0038171	1.4E-23
9	KANK1	rs10122143	625127	G	A	0.3454230	-0.0368134	0.0038180	1.3E-23
9	KANK1	rs10122327	625820	A	G	0.2738200	0.0585535	0.0040913	6.6E-50
9	KANK1	rs16921323	626096	A	G	0.2788730	0.0589093	0.0040808	1.2E-50
9	KANK1	rs72689696	627353	C	T	0.3306660	-0.0369273	0.0038812	3.6E-23
9	KANK1	rs62530062	627420	G	A	0.2904830	0.0547003	0.0040352	1.5E-44
9	KANK1	rs10815368	627953	C	A	0.2837300	0.0564723	0.0040736	8.4E-47
9	KANK1	rs10815369	628037	G	A	0.2755450	0.0587066	0.0040851	3.0E-50
9	KANK1	rs58845489	628519	G	C	0.2765860	0.0591488	0.0040815	4.9E-51
9	KANK1	rs58418306	628572	C	T	0.2815760	0.0568712	0.0040677	1.4E-47
9	KANK1	rs2078544	629245	C	A	0.3353220	-0.0378766	0.0038562	1.9E-24
9	KANK1	rs10975480	629437	T	C	0.2759990	0.0588863	0.0040839	2.6E-50
9	KANK1	rs12338412	629744	T	C	0.2756750	0.0587532	0.0040824	2.6E-50
9	KANK1	rs12353073	629791	T	G	0.2741930	0.0587606	0.0040912	3.6E-50
9	KANK1	rs10975485	630074	T	G	0.2754260	0.0585585	0.0040839	4.9E-50
9	KANK1	rs7043754	630424	A	G	0.3407680	-0.0380873	0.0038427	2.4E-25
9	KANK1	chr9:630954_C_CA	630954	CA	C	0.3302940	-0.0372152	0.0038766	1.2E-23
9	KANK1	rs10975496	631605	A	G	0.2842450	0.0563554	0.0040522	6.5E-47
9	KANK1	rs61288977	631809	C	T	0.2757190	0.0584973	0.0040835	6.3E-50
9	KANK1	rs9407325	632268	T	C	0.3203920	-0.0354636	0.0039035	2.2E-21
9	KANK1	rs9407326	632269	G	C	0.3226530	-0.0359936	0.0038952	4.6E-22
9	KANK1	rs55688828	632845	T	G	0.3322250	-0.0373219	0.0038627	7.0E-24
9	KANK1	rs12335565	632911	G	C	0.2762410	0.0589378	0.0040799	9.5E-51
9	KANK1	rs74307564	632996	T	A	0.2762530	0.0583323	0.0040849	1.0E-49
9	KANK1	rs148673360	633331	A	G	0.2714860	0.0572104	0.0041089	3.0E-47
9	KANK1	rs140749044	633390	T	G	0.3253920	-0.0354372	0.0038759	1.3E-21
9	KANK1	rs140656733	633394	C	G	0.3255270	-0.0353701	0.0038762	1.5E-21
9	KANK1	rs78482117	633500	T	C	0.2756830	0.0580183	0.0040728	1.9E-49
9	KANK1	rs9657628	633871	G	C	0.2756420	0.0578923	0.0040770	3.5E-49
9	KANK1	rs6477053	633911	G	A	0.3355140	-0.0369936	0.0038448	1.4E-23
9	KANK1	rs6477055	634094	T	A	0.3448580	-0.0374669	0.0038177	1.0E-24
9	KANK1	rs6477056	634160	G	A	0.3449030	-0.0373972	0.0038174	1.5E-24
9	KANK1	rs7048369	634269	G	A	0.3450940	-0.0374837	0.0038175	1.0E-24
9	KANK1	rs7030389	634405	C	G	0.3228560	-0.0347681	0.0038848	7.9E-21
9	KANK1	rs56342047	634416	C	A	0.2756030	0.0577001	0.0040790	9.9E-49
9	KANK1	rs7030430	634466	A	G	0.3420750	-0.0371142	0.0038289	3.5E-24
9	KANK1	rs59438577	635529	TA	T	0.3320900	-0.0372054	0.0038649	9.5E-24
9	KANK1	rs7026147	635585	C	T	0.3321390	-0.0369297	0.0038664	2.0E-23
9	KANK1	rs7047127	635677	T	C	0.3330490	-0.0367663	0.0038773	3.0E-23
9	KANK1	rs144456719	635779 3CTCTGC	A	A	0.2717680	0.0573914	0.0041185	2.6E-47
9	KANK1	rs12341226	635998	G	A	0.2750060	0.0577710	0.0040905	9.6E-49
9	KANK1	rs62530079	636887	A	G	0.2599310	0.0559195	0.0041693	4.2E-43
9	KANK1	rs12002249	637391	C	A	0.2530310	0.0558725	0.0042172	4.5E-43
9	KANK1	rs78948970	637886	A	T	0.2557480	0.0572184	0.0041882	2.1E-45
9	KANK1	rs9407328	641040	T	A	0.3287820	-0.0356956	0.0038854	1.5E-21
9	KANK1	rs16921551	641073	T	C	0.2585420	0.0584657	0.0041612	1.0E-47
9	KANK1	rs76869934	641450	G	A	0.2603050	0.0577829	0.0041481	6.9E-47
9	KANK1	rs62530087	642817	G	C	0.2697640	0.0566014	0.0041075	2.1E-45
9	KANK1	rs9407329	644079	T	A	0.3310600	-0.0368149	0.0038730	8.4E-23
9	KANK1	rs10975554	644936	G	C	0.3173220	-0.0344329	0.0039070	6.7E-20
9	KANK1	rs4742174	645243	T	C	0.4117790	-0.0362559	0.0037013	7.5E-24
9	KANK1	rs12237630	645380	C	T	0.2638510	0.0572343	0.0041675	6.9E-45
9	KANK1	rs10975559	645777	G	C	0.2689100	0.0568469	0.0041148	1.2E-45
9	KANK1	rs10975560	646078	C	T	0.2946600	0.0577755	0.0040030	2.6E-50
9	KANK1	rs58079949	647275	A	AATT	0.4139950	-0.0367402	0.0036962	1.4E-24
9	KANK1	rs60706357	647332	C	ATTCTTG	0.3152020	-0.0351992	0.0039313	1.3E-20
9	KANK1	rs10975570	648236	C	T	0.4120570	-0.0363170	0.0037001	4.4E-24
9	KANK1	rs10975571	648254	A	G	0.4124520	-0.0364259	0.0036992	3.2E-24
9	KANK1	rs10815427	648292	A	G	0.4143510	-0.0365739	0.0036957	2.2E-24
9	KANK1	rs10975572	648389	A	C	0.4134960	-0.0361046	0.0037025	8.9E-24
9	KANK1	rs10975573	648390	A	T	0.4135450	-0.0360940	0.0037029	9.1E-24
9	KANK1	rs7856915	648732	A	T	0.3187780	-0.0345559	0.0039008	4.1E-20
9	KANK1	rs12351209	648943	A	G	0.4239800	-0.0372672	0.0036831	1.2E-25
9	KANK1	rs7865421	648961	T	G	0.3175730	-0.0350085	0.0039060	1.8E-20
9	KANK1	rs12352349	648987	T	G	0.4233140	-0.0372021	0.0036837	1.6E-25
9	KANK1	rs10156623	649006	C	T	0.4147490	-0.0367565	0.0036932	1.2E-24

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	KANK1	rs6477081	649866	A	G	0.3168910	-0.0345329	0.0039115	7.0E-20
9	KANK1	rs7866461	651127	C	G	0.4147490	-0.0363704	0.0036925	4.2E-24
9	KANK1	rs9408648	651183	G	C	0.3204780	-0.0348503	0.0038929	2.3E-20
9	KANK1	rs9407331	651311	T	G	0.3195740	-0.0348109	0.0038957	2.7E-20
9	KANK1	rs9407332	651333	A	T	0.3212120	-0.0345804	0.0038911	4.0E-20
9	KANK1	rs9407333	651364	C	A	0.3203150	-0.0349034	0.0038927	2.0E-20
9	KANK1	rs9407334	651461	T	C	0.3203440	-0.0350291	0.0038924	1.4E-20
9	KANK1	rs2361096	651558	G	T	0.4259440	-0.0374460	0.0036753	6.1E-26
9	KANK1	rs2361097	651692	T	G	0.3202990	-0.0351094	0.0038895	1.1E-20
9	KANK1	rs2361098	651799	T	A	0.3204010	-0.0351290	0.0038885	1.0E-20
9	KANK1	rs2361102	652170	T	G	0.3204620	-0.0350749	0.0038877	1.2E-20
9	KANK1	rs11791156	652208	A	G	0.3198710	-0.0352057	0.0038935	9.9E-21
9	KANK1	rs76673482	652223	A	G	0.3192890	-0.0350391	0.0038980	1.5E-20
9	KANK1	rs75394351	652224	G	A	0.3192890	-0.0350391	0.0038980	1.5E-20
9	KANK1	rs74307570	652251	T	C	0.3189690	-0.0356564	0.0039000	3.1E-21
9	KANK1	rs4259462	652517	C	G	0.3206870	-0.0349760	0.0038889	1.7E-20
9	KANK1	rs4463482	652527	G	A	0.3205340	-0.0348818	0.0038876	2.0E-20
9	KANK1	rs4259463	652601	T	G	0.3205870	-0.0350271	0.0038868	1.4E-20
9	KANK1	rs4463483	652648	G	A	0.3206800	-0.0349678	0.0038860	1.5E-20
9	KANK1	rs7044387	652788	T	C	0.3198490	-0.0347608	0.0038937	2.5E-20
9	KANK1	rs10975590	652957	C	T	0.4255970	-0.0375047	0.0036762	5.7E-26
9	KANK1	rs79490619	653184	G	C	0.2468630	0.0599492	0.0042292	1.5E-48
9	KANK1	rs7851435	653262	G	A	0.3193740	-0.0353780	0.0038975	8.0E-21
9	KANK1	rs7863364	653263	A	G	0.3193740	-0.0353780	0.0038975	8.0E-21
9	KANK1	rs7863471	653304	T	G	0.3207520	-0.0350543	0.0038850	1.4E-20
9	KANK1	rs7875094	653313	T	C	0.3207460	-0.0349725	0.0038856	1.5E-20
9	KANK1	rs35445681	653494	AT	A	0.3200500	-0.0347643	0.0038909	2.9E-20
9	KANK1	rs7851766	653505	G	A	0.3207520	-0.0349410	0.0038855	1.7E-20
9	KANK1	rs7851799	653578	G	A	0.3207080	-0.0349574	0.0038861	1.6E-20
9	KANK1	rs7851886	653610	G	A	0.3207100	-0.0349761	0.0038862	1.6E-20
9	KANK1	rs7863869	653655	A	G	0.3207110	-0.0350886	0.0038863	1.3E-20
9	KANK1	rs9407335	653795	A	C	0.3120590	-0.0343256	0.0039157	1.4E-19
9	KANK1	rs7357820	653808	C	G	0.4169020	-0.0366599	0.0036884	7.9E-25
9	KANK1	rs16921959	653949	C	T	0.3211080	-0.0351801	0.0038846	1.1E-20
9	KANK1	rs72691349	653956	T	C	0.3211070	-0.0351813	0.0038846	1.1E-20
9	KANK1	rs7021495	654101	C	A	0.4254400	-0.0370481	0.0036822	4.8E-25
9	KANK1	rs6477082	654135	A	G	0.4210130	-0.0360789	0.0036791	8.8E-24
9	KANK1	rs6477083	654139	C	G	0.4209650	-0.0360567	0.0036788	9.2E-24
9	KANK1	rs6477084	654147	A	G	0.4124180	-0.0360299	0.0036881	7.7E-24
9	KANK1	rs36018076	654583	G	GT	0.4143840	-0.0369576	0.0036950	9.2E-25
9	KANK1	rs57085420	654602	C	T	0.4251980	-0.0380338	0.0036818	1.6E-26
9	KANK1	rs60397071	654608	C	T	0.4242530	-0.0378175	0.0036874	3.8E-26
9	KANK1	rs7028270	654626	A	C	0.4251280	-0.0380686	0.0036826	1.6E-26
9	KANK1	rs9408649	654671	A	T	0.3186860	-0.0347397	0.0038980	5.0E-20
9	KANK1	rs7028305	654681	A	G	0.4252120	-0.0378886	0.0036745	1.5E-26
9	KANK1	rs150685557	654812	T	3AGAGAC	0.4052630	-0.0351210	0.0037544	3.1E-22
9	KANK1	rs12003931	655108	G	A	0.4182230	-0.0367848	0.0036902	1.1E-24
9	KANK1	rs12005554	655165	C	T	0.4173240	-0.0366540	0.0036933	1.4E-24
9	KANK1	rs10975598	655227	C	T	0.4176220	-0.0368481	0.0036897	8.4E-25
9	KANK1	rs56349412	655309	T	C	0.4180920	-0.0367564	0.0036905	1.1E-24
9	KANK1	rs7863576	655409	T	A	0.3413560	-0.0349368	0.0039114	2.5E-20
9	KANK1	rs9408651	655962	G	T	0.4093550	-0.0359640	0.0037039	6.1E-24
9	KANK1	rs912170	656736	A	G	0.4244360	-0.0367719	0.0036850	4.1E-25
9	KANK1	rs4740843	656888	A	T	0.3118870	-0.0335118	0.0039249	6.5E-19
9	KANK1	rs35011466	657395	A	AG	0.3136200	-0.0341423	0.0039207	1.3E-19
9	KANK1	rs4742196	658393	G	A	0.3144920	-0.0339437	0.0039144	2.0E-19
9	KANK1	rs147565258	658471	G	GA	0.2456680	0.0603371	0.0042444	8.1E-49
9	KANK1	rs9407337	659171	G	C	0.3117740	-0.0337930	0.0039249	3.2E-19
9	KANK1	rs10815438	660315	G	C	0.3124730	-0.0338801	0.0039265	2.6E-19
9	KANK1	rs73639394	660798	G	T	0.4255610	-0.0371704	0.0036843	1.4E-25
9	KANK1	rs10739107	660851	T	C	0.4159900	-0.0368261	0.0036982	3.9E-25
9	KANK1	rs80201242	661132	C	A	0.4245290	-0.0370393	0.0036863	2.1E-25
9	KANK1	rs80293934	661188	G	A	0.4245110	-0.0370790	0.0036862	1.8E-25
9	KANK1	rs191206133	661754	G	C	0.4255210	-0.0369589	0.0036878	2.6E-25
9	KANK1	rs34001273	661951	T	C	0.2362030	0.0619140	0.0043427	1.0E-48
9	KANK1	rs35834559	661972	G	C	0.4318930	-0.0371853	0.0037208	4.0E-25
9	KANK1	rs9407341	662436	C	G	0.3202250	-0.0340870	0.0039024	1.1E-19
9	KANK1	rs9407343	663437	G	A	0.3162920	-0.0339199	0.0039130	2.4E-19
9	KANK1	rs10217169	663489	C	G	0.3556510	0.0421325	0.0038164	2.8E-30
9	KANK1	rs7865572	663617	G	C	0.3396820	0.0446127	0.0038560	8.9E-33
9	KANK1	rs4237165	663659	T	C	0.3479710	0.0437521	0.0038346	4.8E-32
9	KANK1	rs12682955	663775	G	C	0.2465940	0.0600058	0.0042303	1.1E-48
9	KANK1	rs7048080	664132	G	A	0.3158370	-0.0338593	0.0039162	2.6E-19
9	KANK1	rs10815442	664319	A	G	0.3472470	0.0429129	0.0038337	6.9E-31
9	KANK1	rs7042465	664444	T	C	0.3129220	-0.0336083	0.0039252	5.3E-19
9	KANK1	rs10815444	664731	T	C	0.3472900	0.0428716	0.0038332	7.5E-31
9	KANK1	rs7042833	664747	T	C	0.3134240	-0.0335646	0.0039235	5.4E-19
9	KANK1	rs7049049	664857	A	G	0.3484410	0.0436163	0.0038316	6.2E-32
9	KANK1	rs74307571	664936	T	C	0.2469450	0.0597346	0.0042265	2.1E-48
9	KANK1	rs7021494	665016	A	T	0.3484490	0.0436305	0.0038314	5.8E-32
9	KANK1	rs78033151	665281	G	A	0.2469580	0.0597565	0.0042263	2.0E-48
9	KANK1	rs9408659	665646	A	T	0.3157060	-0.0337952	0.0039149	2.8E-19
9	KANK1	rs9407348	665978	C	G	0.3190540	-0.0346390	0.0039077	3.3E-20
9	KANK1	rs10975651	666230	G	A	0.3501820	0.0413816	0.0038263	4.6E-29
9	KANK1	rs79947846	666279	T	A	0.2471020	0.0596646	0.0042250	2.5E-48
9	KANK1	rs10975652	666323	A	G	0.3494830	0.0416077	0.0038279	2.4E-29
9	KANK1	rs10975653	666389	C	T	0.3490050	0.0414153	0.0038305	4.0E-29
9	KANK1	rs76987374	666492	T	A	0.2471040	0.0596503	0.0042250	2.6E-48
9	KANK1	rs10975657	666970	A	C	0.3427810	0.0429229	0.0038482	1.1E-30
9	KANK1	chr9:667000_AT_A	667000	AT	A	0.3677380	0.0389718	0.0038183	4.5E-26
9	KANK1	rs9408661	667087	C	T	0.3155540	-0.0341248	0.0039282	1.7E-19
9	KANK1	rs7865660	668026	C	T	0.2486270	0.0588715	0.0042165	3.0E-47
9	KANK1	rs4742208	668240	A	T	0.3127420	-0.0335457	0.0039257	6.3E-19
9	KANK1	rs10975666	668388	G	T	0.3728430	0.0430711	0.0037746	1.2E-32
9	KANK1	rs4742209	668461	T	A	0.3594150	0.0400993	0.0038048	9.1E-28
9	KANK1	rs7035770	668887	A	C	0.3587660	0.0407689	0.0038090	1.3E-28
9	KANK1	rs9408665	669125	C	T	0.3587560	0.0407733	0.0038063	1.4E-28
9	KANK1	rs10815451	669259	G	C	0.3602750	0.0405758	0.0038029	2.9E-28
9	KANK1	chr9:669518_G_GT	669518	GT	G	0.3144690	-0.0344676	0.0039199	6.8E-20
9	KANK1	rs10975680	669533	G	A	0.3503270	0.0417666	0.0038253	1.7E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	KANK1	rs9407351	669852	G	A	0.3142690	-0.0343566	0.0039204	9.1E-20
9	KANK1	rs75233603	670969	G	T	0.3077430	-0.0341334	0.0039653	6.3E-19
9	KANK1	rs4584192	671053	G	A	0.3584260	0.0410503	0.0038132	7.5E-29
9	KANK1	rs7024725	671196	G	A	0.2474320	0.0593553	0.0042316	1.6E-47
9	KANK1	chr9:671225_GT_G	671225	G	GT	0.3594910	0.0407758	0.0038043	1.2E-28
9	KANK1	rs7037588	671330	G	C	0.3505480	0.0424210	0.0038262	1.2E-30
9	KANK1	rs9408667	671428	A	C	0.3512000	0.0426371	0.0038260	1.1E-30
9	KANK1	rs74307574	672254	C	A	0.2480850	0.0596084	0.0042234	2.6E-48
9	KANK1	rs56672067	672545	TCATAA1	C	0.3122200	-0.0336940	0.0039347	5.3E-19
9	KANK1	rs16922302	672920	C	G	0.2698010	0.0593839	0.0041094	2.6E-51
9	KANK1	rs7046490	673533	G	A	0.3818010	0.0421215	0.0037614	1.2E-31
9	KANK1	rs7027890	673545	C	T	0.3585070	0.0408271	0.0038104	1.1E-28
9	KANK1	rs9407352	673768	T	G	0.3592180	0.0403838	0.0038079	3.7E-28
9	KANK1	rs12684355	673981	A	C	0.2473790	0.0595046	0.0042268	4.4E-48
9	KANK1	rs4742215	674017	T	G	0.3517820	0.0418272	0.0038267	1.3E-29
9	KANK1	rs4742217	674428	A	G	0.3926820	0.0418559	0.0038047	1.3E-30
9	KANK1	rs55680746	674789	T	C	0.3072520	-0.0338610	0.0039478	3.8E-19
9	KANK1	rs11792599	674863	T	C	0.3810910	0.0422454	0.0037636	7.1E-32
9	KANK1	rs4742219	675377	T	C	0.3778980	0.0417496	0.0037689	6.8E-31
9	KANK1	rs4742220	675419	G	A	0.3816250	0.0419447	0.0037618	2.0E-31
9	KANK1	rs4742221	675430	G	A	0.3822480	0.0417439	0.0037660	5.2E-31
9	KANK1	rs4742222	675463	A	G	0.3780410	0.0418311	0.0037698	5.8E-31
9	KANK1	rs4742223	675600	C	T	0.3817720	0.0421653	0.0037616	1.1E-31
9	KANK1	rs34147505	676150	G	T	0.2670760	0.0588031	0.0041207	6.5E-50
9	KANK1	rs1570475	676569	C	T	0.4154010	-0.0362453	0.0036969	1.1E-24
9	KANK1	rs9407353	676571	C	T	0.3201720	-0.0348393	0.0039005	1.4E-20
9	KANK1	rs9407354	676692	C	T	0.3149210	-0.0342524	0.0039155	6.7E-20
9	KANK1	rs12685890	676704	C	T	0.2700870	0.0592253	0.0041079	4.7E-51
9	KANK1	rs12685605	676745	G	A	0.2679700	0.0594970	0.0041227	3.1E-51
9	KANK1	rs1570474	676820	A	G	0.4154120	-0.0362187	0.0036967	1.2E-24
9	KANK1	rs3831027	676837	T	TG	0.4154290	-0.0362366	0.0036968	1.1E-24
9	KANK1	rs2296055	676954	T	C	0.4162590	-0.0367584	0.0036970	2.6E-25
9	KANK1	rs2296054	677141	G	A	0.2461810	0.0593936	0.0042350	8.4E-48
9	KANK1	rs74386058	677864	G	C	0.2428670	0.0598825	0.0042530	6.7E-48
9	KANK1	rs4742225	677938	G	T	0.4153540	-0.0361966	0.0036969	1.3E-24
9	KANK1	rs4740851	677986	A	T	0.4161150	-0.0363749	0.0036969	7.1E-25
9	KANK1	rs4742226	678088	T	G	0.4175200	-0.0365717	0.0036929	4.3E-25
9	KANK1	rs4742227	679184	C	G	0.3225730	-0.0349402	0.0038916	1.3E-20
9	KANK1	rs141696483	679433	T	G	0.2395900	0.0593845	0.0042795	9.2E-47
9	KANK1	rs79341645	679916	G	A	0.2422240	0.0591386	0.0042553	8.4E-47
9	KANK1	rs7035584	680667	A	C	0.2728800	0.0571186	0.0040958	5.9E-48
9	KANK1	rs9408671	680763	T	C	0.3050500	-0.0325356	0.0039391	5.5E-18
9	KANK1	rs9408672	680768	A	G	0.3128270	-0.0332186	0.0039160	8.2E-19
9	KANK1	rs1323263	680905	T	C	0.3141820	-0.0339770	0.0039078	1.0E-19
9	KANK1	rs1853424	681150	T	C	0.3215620	-0.0339000	0.0038845	1.0E-19
9	KANK1	rs16922505	681688	C	T	0.2619010	0.0601604	0.0041647	3.5E-51
9	KANK1	rs9407357	682191	G	A	0.3139300	-0.0337648	0.0039254	2.6E-19
9	KANK1	rs60405463	682570	G	T	0.4263050	-0.0372641	0.0036914	7.3E-26
9	KANK1	rs16922514	682970	A	G	0.4264000	-0.0371990	0.0036977	1.2E-25
9	KANK1	rs72693403	683356	C	G	0.3122660	-0.0336810	0.0039345	3.7E-19
9	KANK1	rs73639400	683423	T	C	0.4156220	-0.0362217	0.0037080	1.5E-24
9	KANK1	rs12004436	683430	C	T	0.4156220	-0.0362258	0.0037080	1.5E-24
9	KANK1	rs10975820	684160	G	A	0.4186200	-0.0362989	0.0037043	1.1E-24
9	KANK1	rs35431822	684711	AT	A	0.3272590	-0.0344703	0.0038901	3.6E-20
9	KANK1	rs9408678	686170	C	A	0.4349230	-0.0382988	0.0037095	2.8E-26
9	KANK1	rs16922547	686301	T	C	0.2313500	0.0584202	0.0043899	2.8E-43
9	KANK1	chr9:687021_ATTTCT	687021	A	ATTTCT	0.4205270	-0.0358979	0.0037361	1.6E-23
9	KANK1	rs7034698	687205	C	T	0.4170710	-0.0360140	0.0037212	7.2E-24
9	KANK1	rs7044480	687265	T	G	0.4107900	-0.0355712	0.0037262	2.6E-23
9	KANK1	rs7044607	687333	T	G	0.4085010	-0.0353941	0.0037308	5.2E-23
9	KANK1	rs59858868	687719	G	A	0.2648310	0.0598945	0.0041800	1.5E-50
9	KANK1	rs9407360	688516	G	A	0.4199370	-0.0355902	0.0037245	2.2E-23
9	KANK1	rs9407361	688997	C	G	0.4122340	-0.0357810	0.0037396	1.4E-23
9	KANK1	rs9408680	689277	G	A	0.4161350	-0.0358562	0.0037198	7.1E-24
9	KANK1	rs9299038	689340	C	T	0.4155420	-0.0359350	0.0037219	5.7E-24
9	KANK1	rs140051557	689580	CT	C	0.4131600	-0.0355260	0.0037423	3.1E-23
9	KANK1	rs74579699	689586	T	C	0.4151930	-0.0356746	0.0037282	1.3E-23
9	KANK1	rs4742251	690053	T	C	0.3093310	-0.0330455	0.0039611	2.4E-18
9	KANK1	rs4742255	690237	C	G	0.3125390	-0.0331616	0.0039726	3.0E-18
9	KANK1	rs9299039	690460	T	C	0.3089820	-0.0333490	0.0039565	1.4E-18
9	KANK1	rs7031124	690580	A	G	0.3105390	-0.0332321	0.0039527	1.5E-18
9	KANK1	rs6477110	690837	G	T	0.3171050	-0.0337388	0.0039423	5.6E-19
9	KANK1	chr9:691301_AT_A	691301	AT	A	0.3288410	-0.0292761	0.0038853	3.1E-15
9	KANK1	rs7035433	691406	A	G	0.3299700	-0.0296744	0.0038729	1.2E-15
9	KANK1	rs4742257	691913	C	G	0.3226510	-0.0287836	0.0038857	8.1E-15
9	KANK1	rs2361112	692085	T	C	0.3175350	-0.0305179	0.0039051	4.8E-16
9	KANK1	rs4024265	692102	C	CAG	0.3174990	-0.0304209	0.0039060	6.3E-16
9	KANK1	rs3028241	692338	GGGCTT	T	0.3190840	-0.0303912	0.0039076	7.5E-16
9	KANK1	chr9:692714_GA_G	692714	GA	G	0.3231750	-0.0298126	0.0039368	6.4E-15
9	KANK1	rs7867295	692847	A	G	0.3180510	-0.0304372	0.0039021	5.4E-16
9	KANK1	rs912162	694453	C	T	0.3668940	-0.0301897	0.0037752	2.7E-16
9	KANK1	rs1475202	694826	G	C	0.3656670	-0.0306070	0.0037816	1.2E-16
9	KANK1	rs745875	695093	G	C	0.3162990	-0.0303116	0.0039044	7.2E-16
9	KANK1	rs745876	695143	T	A	0.3167950	-0.0303548	0.0038996	6.3E-16
9	KANK1	rs2018255	695293	A	G	0.3170010	-0.0301431	0.0038982	1.0E-15
9	KANK1	rs745877	695310	C	T	0.3169430	-0.0304131	0.0038991	6.1E-16
9	KANK1	rs3028271	695472	C	CTTGA	0.3166500	-0.0305029	0.0038995	5.2E-16
9	KANK1	rs732119	695607	G	A	0.3170710	-0.0302483	0.0038943	7.8E-16
9	KANK1	rs732118	695614	G	T	0.3164330	-0.0303981	0.0039012	7.0E-16
9	KANK1	rs1570473	695894	G	C	0.3167220	-0.0305259	0.0039001	5.6E-16
9	KANK1	rs7854502	696683	A	G	0.3292420	-0.0302240	0.0038711	4.4E-16
9	KANK1	rs10115726	697525	G	C	0.3161790	-0.0310730	0.0039128	2.2E-16
9	KANK1	rs912175	712137	C	G	0.2282510	0.0480421	0.0043523	3.0E-31
9	KANK1	rs912174	712156	G	T	0.2285310	0.0476221	0.0043498	8.2E-31
9	KANK1	rs79835909	712674	T	C	0.2275970	0.0480538	0.0043521	2.7E-31
9	KANK1	rs3824420	712766	A	G	0.2173600	0.0487656	0.0044316	3.0E-31
9	KANK1	rs4742277	713307	G	A	0.2547870	0.0481813	0.0041835	2.1E-34
9	KANK1	rs12684883	714040	G	A	0.2540410	0.0487276	0.0042051	9.6E-35
9	KANK1	rs144587480	714063	A	TTCTAA	0.2264030	0.0487215	0.0043829	1.6E-31
9	KANK1	rs12684909	714330	G	A	0.2277930	0.0480906	0.0043798	7.7E-31

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	KANK1	rs10481606	714479	T	C	0.3722480	0.0409382	0.0038075	1.7E-29
9	KANK1	rs12685176	714540	C	T	0.2287210	0.0481652	0.0043760	5.4E-31
9	KANK1	rs4740866	716570	T	G	0.3633610	-0.0217606	0.0037731	2.3E-09
9	KANK1	rs10976038	718835	A	G	0.1812490	-0.0274708	0.0047156	1.7E-08
9	KANK1	rs7861700	720583	T	C	0.1831830	0.0370400	0.0047608	4.1E-17
9	KANK1	rs4742292	720832	A	G	0.3458770	0.0245722	0.0038486	3.5E-11
9	KANK1	rs10815522	721431	T	C	0.3456610	0.0247995	0.0038440	2.2E-11
9	KANK1	rs7038561	721523	T	C	0.3666040	0.0258460	0.0038074	1.5E-12
9	KANK1	rs74736755	721865	A	G	0.1789450	0.0388633	0.0047513	2.5E-18
9	KANK1	rs12684491	722423	T	G	0.1789730	0.0384956	0.0047444	5.0E-18
9	KANK1	rs2885162	722756	T	C	0.1802180	0.0382238	0.0047275	6.0E-18
9	KANK1	rs2361114	722769	C	T	0.1802220	0.0381562	0.0047276	6.6E-18
9	KANK1	rs2885163	722946	G	A	0.1802200	0.0380779	0.0047285	7.4E-18
9	KANK1	rs7047065	723429	T	C	0.3331670	0.0252532	0.0038810	8.6E-12
9	KANK1	rs113202734	723504	TG	T	0.1782070	0.0375911	0.0047672	3.1E-17
9	KANK1	rs12345961	724011	A	G	0.1811540	0.0369149	0.0047716	3.3E-16
9	KANK1	rs6477166	724810	A	C	0.3358250	0.0256407	0.0038938	2.5E-11
9	KANK1	rs6477169	725008	T	G	0.3648440	0.0292793	0.0038143	7.6E-15
9	KANK1	rs12686171	725145	T	C	0.1978200	0.0418451	0.0045986	1.8E-21
9	KANK1	rs12685329	725147	A	G	0.1978250	0.0418536	0.0045987	1.8E-21
9	KANK1	rs12686200	725449	T	C	0.1968420	0.0419675	0.0046049	1.3E-21
9	KANK1	rs61426364	725577	T	C	0.1974320	0.0420563	0.0045992	9.1E-22
9	KANK1	rs57424346	725603	G	A	0.1977490	0.0422293	0.0045993	5.9E-22
9	KANK1	rs57866780	725705	G	T	0.2233800	0.0424181	0.0044052	3.5E-24
9	KANK1	rs72693437	725763	C	A	0.1974830	0.0421204	0.0045984	7.3E-22
9	KANK1	rs72693438	725780	C	T	0.1974750	0.0422129	0.0045986	6.1E-22
9	KANK1	rs72693439	725795	C	T	0.1975230	0.0420926	0.0045985	8.2E-22
9	KANK1	rs72693442	725877	G	A	0.1973570	0.0424743	0.0046005	3.7E-22
9	KANK1	rs72693444	725884	A	T	0.1973570	0.0424743	0.0046005	3.7E-22
9	KANK1	rs72693445	725893	A	G	0.1967240	0.0426643	0.0046096	2.9E-22
9	KANK1	rs59358367	725956	C	T	0.1974500	0.0424127	0.0046002	4.1E-22
9	KANK1	rs60673980	726074	T	C	0.1974170	0.0423694	0.0046000	4.6E-22
9	KANK1	rs61040206	726093	C	T	0.1974200	0.0423753	0.0046000	4.5E-22
9	KANK1	rs58887252	726162	T	A	0.1974200	0.0423768	0.0046000	4.4E-22
9	KANK1	rs60258495	726194	CTA	C	0.1974210	0.0423872	0.0046000	4.3E-22
9	KANK1	rs58950272	726197	A	G	0.1974360	0.0422873	0.0046000	5.4E-22
9	KANK1	rs10758843	726370	G	T	0.3669560	0.0292515	0.0038128	5.2E-15
9	KANK1	rs7029547	726531	T	C	0.3621250	0.0294625	0.0038368	5.7E-15
9	KANK1	rs12682774	726599	G	A	0.1981300	0.0432349	0.0046080	1.3E-22
9	KANK1	rs12685675	726610	C	G	0.1984370	0.0431576	0.0046036	1.3E-22
9	KANK1	rs10976090	726645	A	G	0.1970240	0.0429544	0.0046054	1.9E-22
9	KANK1	rs10815536	726686	A	G	0.1971670	0.0426852	0.0046050	3.3E-22
9	KANK1	rs10976091	726788	T	C	0.1952510	0.0425983	0.0046272	4.3E-22
9	KANK1	rs10758844	726901	G	A	0.3659790	0.0295490	0.0038161	2.9E-15
9	KANK1	rs10976097	727139	G	A	0.2229470	0.0430659	0.0044124	1.2E-24
9	KANK1	rs10976098	727145	C	A	0.2229220	0.0430964	0.0044123	1.1E-24
9	KANK1	rs12350091	727614	C	G	0.1973280	0.0429619	0.0046014	1.5E-22
9	KANK1	rs6477171	727962	G	A	0.3862140	0.0277734	0.0037806	1.1E-13
9	KANK1	rs55652202	728039	A	G	0.1975090	0.0427746	0.0046002	2.3E-22
9	KANK1	rs6477172	728070	G	C	0.3707020	0.0290204	0.0038103	8.1E-15
9	KANK1	rs56161822	728137	T	A	0.1975070	0.0427762	0.0046002	2.3E-22
9	KANK1	rs56142521	728224	A	C	0.1965790	0.0439298	0.0046120	2.8E-23
9	KANK1	rs55729803	728264	A	G	0.1975040	0.0428058	0.0046002	2.2E-22
9	KANK1	rs142693333	728288	TC	T	0.1975020	0.0428315	0.0046002	2.1E-22
9	KANK1	rs35729697	728297	A	G	0.1975020	0.0428315	0.0046002	2.1E-22
9	KANK1	rs35310071	728387	T	G	0.1973870	0.0428424	0.0046021	2.0E-22
9	KANK1	rs55882011	728419	A	G	0.1975000	0.0428540	0.0046004	2.0E-22
9	KANK1	rs35808800	728471	T	TA	0.1974970	0.0428472	0.0046004	2.1E-22
9	KANK1	rs35454342	728564	A	T	0.1974970	0.0428234	0.0046004	2.2E-22
9	KANK1	rs10815543	728716	T	C	0.1975000	0.0428578	0.0046005	2.1E-22
9	KANK1	rs10815548	729135	T	C	0.1975050	0.0429837	0.0045994	1.6E-22
9	KANK1	rs4742316	729758	A	G	0.2045840	0.0404211	0.0045445	1.8E-20
9	KANK1	rs141509381	729781	AG	A	0.2045840	0.0404211	0.0045445	1.8E-20
9	KANK1	rs115189612	729968	C	A	0.2044230	0.0403204	0.0045466	2.1E-20
9	KANK1	rs10125507	729972	A	G	0.2053080	0.0401435	0.0045409	3.4E-20
9	KANK1	rs12352313	730054	G	A	0.2045730	0.0404724	0.0045447	1.6E-20
9	KANK1	rs74343447	730460	G	A	0.3940040	0.0256247	0.0037772	6.7E-12
9	KANK1	rs10815555	730473	G	T	0.2044270	0.0405309	0.0045473	1.7E-20
9	KANK1	rs10815557	730777	C	T	0.2044580	0.0405097	0.0045475	1.7E-20
9	KANK1	rs10815563	732779	G	A	0.4198410	0.0294435	0.0037039	3.4E-16
9	KANK1	rs10429606	732892	C	G	0.3962150	0.0251989	0.0037367	5.4E-12
9	KANK1	rs10815567	733049	G	A	0.3978560	0.0275262	0.0037395	4.0E-14
9	KANK1	rs10739123	733358	C	A	0.4268720	0.0298897	0.0036949	6.9E-17
9	KANK1	rs10976142	733374	C	T	0.2402650	0.0422495	0.0042716	2.2E-25
9	KANK1	rs7874288	733971	C	T	0.3919110	0.0273221	0.0037648	2.0E-13
9	KANK1	rs2005123	734645	A	G	0.2093450	0.0387049	0.0045090	3.5E-19
9	KANK1	rs2296053	735089	A	G	0.3942010	0.0268104	0.0037470	4.0E-13
9	KANK1	rs7872783	735654	A	C	0.3735830	0.0287614	0.0037869	9.4E-15
9	KANK1	rs4742317	735900	T	C	0.2110600	0.0394144	0.0044746	4.6E-20
9	KANK1	rs4279657	736113	G	A	0.2103460	0.0397153	0.0044776	2.2E-20
9	KANK1	rs72693465	738055	C	T	0.2387990	0.0423030	0.0042657	2.4E-25
9	KANK1	rs2296052	738238	A	G	0.3698120	0.0227208	0.0037895	1.6E-09
9	KANK1	rs2296051	738434	T	C	0.2358100	0.0410849	0.0042910	1.2E-23
9	KANK1	rs10815589	739588	A	C	0.2341020	0.0414796	0.0043084	1.1E-23
9	KANK1	rs7869715	739913	G	T	0.4207500	0.0307399	0.0037137	3.5E-17
9	KANK1	rs10815591	740124	T	C	0.2100740	0.0410251	0.0044842	1.7E-21
9	KANK1	rs10758862	740472	A	G	0.3692930	0.0306598	0.0038095	2.9E-16
9	KANK1	rs2296049	740901	T	C	0.2079720	0.0384627	0.0045383	9.5E-19
9	KANK1	rs7048053	741084	T	C	0.2126430	0.0390039	0.0045019	8.6E-20
9	KANK1	rs7027313	741187	C	T	0.2426290	0.0328296	0.0042363	3.4E-16
9	KANK1	rs7048314	741224	G	C	0.4125150	0.0234446	0.0037481	1.1E-10
9	KANK1 *	rs10976465	772670	A	G	0.1882760	0.0227556	0.0046526	4.4E-08
9	KANK1 *	rs1407813	773376	C	G	0.1871870	0.0240421	0.0046768	9.8E-09
9	KANK1 *	rs1407812	773391	C	G	0.1784780	0.0239125	0.0047774	2.0E-08
9	GLIS3	rs10739039	4256066	G	A	0.2141460	-0.0253956	0.0045315	1.7E-08
9	GLIS3	rs10814901	4257627	C	G	0.1964540	-0.0279690	0.0046685	2.1E-09
9	GLIS3	rs7033923	4259455	A	G	0.1989570	-0.0267101	0.0046125	7.0E-09
9	GLIS3	rs34498325	4259531	C	G	0.2266800	-0.0251623	0.0043791	6.8E-09
9	GLIS3	rs10974417	4260491	A	C	0.3585490	0.0248535	0.0038210	1.2E-12
9	GLIS3	rs12378556	4261496	G	A	0.3773330	0.0262974	0.0037637	6.4E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	GLIS3	rs10974419	4261651	A	G	0.2076500	-0.0268194	0.0045103	2.7E-09
9	GLIS3	rs10974420	4262137	T	C	0.2061690	-0.0272889	0.0045272	1.5E-09
9	GLIS3	rs7023829	4262424	A	G	0.2111920	-0.0264682	0.0044821	3.9E-09
9	GLIS3	rs7024735	4262430	T	C	0.2111900	-0.0264865	0.0044821	3.8E-09
9	GLIS3	rs7043929	4262497	C	T	0.2107840	-0.0264648	0.0044788	3.9E-09
9	GLIS3	rs12380197	4262516	A	G	0.2108200	-0.0264602	0.0044787	3.9E-09
9	GLIS3	rs7040913	4262666	T	A	0.2113900	-0.0261759	0.0044722	5.2E-09
9	GLIS3	rs12684245	4262697	T	C	0.3770550	0.0267578	0.0037585	3.3E-14
9	GLIS3	rs7025288	4262820	A	C	0.2115000	-0.0260024	0.0044701	6.6E-09
9	GLIS3	rs7028616	4263055	C	T	0.3955840	0.0259677	0.0037241	1.3E-13
9	GLIS3	rs17717029	4263378	C	T	0.2112360	-0.0254989	0.0044707	1.2E-08
9	GLIS3	chr9:4263513_C_CA	4263513	C	CA	0.3849860	0.0267901	0.0037740	3.4E-14
9	GLIS3	rs4111491	4264425	A	C	0.3757650	0.0262197	0.0037550	7.0E-14
9	GLIS3	rs66530158	4264562	G	C	0.2123790	-0.0266168	0.0044561	2.5E-09
9	GLIS3	rs72690058	4265148	A	G	0.2105060	-0.0256450	0.0044871	1.0E-08
9	GLIS3	rs13290535	4265151	G	A	0.3719410	0.0276025	0.0037870	8.6E-15
9	GLIS3	rs7037716	4265363	C	T	0.3965570	0.0258398	0.0037150	1.1E-13
9	GLIS3	rs10974423	4265865	A	G	0.3749130	0.0261604	0.0037522	8.5E-14
9	GLIS3	rs1571583	4267209	A	G	0.3786500	0.0269759	0.0037363	1.0E-14
9	GLIS3	rs12336304	4268004	A	T	0.3798080	0.0263738	0.0037439	3.4E-14
9	GLIS3	rs13440020	4268029	G	A	0.3802150	0.0264344	0.0037436	3.0E-14
9	GLIS3	rs72690059	4268055	G	A	0.2156120	-0.0261964	0.0044359	5.1E-09
9	GLIS3	rs7019761	4268175	C	G	0.3808310	0.0264342	0.0037435	3.4E-14
9	GLIS3	rs12377056	4268575	A	G	0.2127620	-0.0262817	0.0044536	4.3E-09
9	GLIS3	rs4548236	4268785	T	C	0.3796800	0.0268452	0.0037467	1.4E-14
9	GLIS3	rs10974424	4268887	A	G	0.2137480	-0.0267786	0.0044441	1.8E-09
9	GLIS3	rs10511458	4269407	G	A	0.2320770	-0.0255905	0.0043167	2.6E-09
9	GLIS3	rs10814904	4269477	T	C	0.2105610	-0.0272883	0.0044720	9.1E-10
9	GLIS3	rs10974425	4269636	C	A	0.3810250	0.0272442	0.0037558	8.9E-15
9	GLIS3	rs10124633	4269765	C	T	0.2323740	-0.0255652	0.0043149	2.6E-09
9	GLIS3	rs12238142	4270051	G	A	0.2161080	-0.0265987	0.0044345	2.1E-09
9	GLIS3	rs10120752	4270074	T	C	0.3801310	0.0275663	0.0037577	5.6E-15
9	GLIS3	rs10814905	4270580	C	T	0.2323570	-0.0256207	0.0043137	2.3E-09
9	GLIS3	rs10814906	4270669	G	A	0.2156700	-0.0269556	0.0044295	1.6E-09
9	GLIS3	rs10758589	4270682	C	T	0.2323430	-0.0257204	0.0043132	2.0E-09
9	GLIS3	rs10814907	4271910	T	C	0.2136690	-0.0264042	0.0044340	2.4E-09
9	GLIS3	rs4740761	4271954	C	T	0.2320830	-0.0251519	0.0043056	3.7E-09
9	GLIS3	rs4741933	4271970	T	C	0.2320790	-0.0251555	0.0043056	3.7E-09
9	GLIS3	rs4740762	4272041	T	C	0.2320140	-0.0251226	0.0043063	3.8E-09
9	GLIS3	rs4740763	4272086	C	T	0.2151390	-0.0263248	0.0044238	2.2E-09
9	GLIS3	rs10814908	4272449	C	T	0.2138550	-0.0263242	0.0044315	2.7E-09
9	GLIS3	rs34523277	4273577	G	A	0.2335350	-0.0251690	0.0043083	3.7E-09
9	GLIS3	rs10814909	4274786	T	C	0.1917990	-0.0272954	0.0046831	6.2E-09
9	GLIS3	rs10814910	4275493	G	C	0.2330370	-0.0296471	0.0043636	5.4E-12
9	GLIS3	chr9:4275603_T_TA	4275603	TA	T	0.2382250	-0.0283860	0.0043425	2.4E-11
9	GLIS3	rs192898048	4276491	G	C	0.2300650	-0.0297385	0.0044020	6.2E-12
9	GLIS3	rs12236950	4276564	A	G	0.2299440	-0.0298228	0.0043982	6.6E-12
9	GLIS3	rs10974428	4277102	A	G	0.2273750	-0.0301146	0.0044040	4.1E-12
9	GLIS3	rs7035948	4277839	C	G	0.4463050	0.0333430	0.0037231	5.4E-21
9	GLIS3	rs10974429	4278537	C	T	0.2380490	-0.0306107	0.0043526	7.6E-13
9	GLIS3	rs10814911	4278997	G	A	0.2388620	-0.0304916	0.0043514	9.1E-13
9	GLIS3	rs10814912	4279145	T	C	0.2330430	-0.0311034	0.0044021	5.2E-13
9	GLIS3	rs10814913	4279156	T	G	0.2320430	-0.0315470	0.0044139	3.2E-13
9	GLIS3	rs4380994	4282536	A	G	0.4685540	0.0383321	0.0036718	7.1E-28
9	GLIS3	rs10974434	4282782	C	T	0.2463230	-0.0348002	0.0042446	5.9E-17
9	GLIS3	rs3892354	4282942	T	G	0.4732240	0.0391356	0.0036453	2.9E-29
9	GLIS3	rs1574285	4283137	G	T	0.4560630	0.0407083	0.0036482	3.4E-31
9	GLIS3	rs10974435	4283682	T	C	0.4865100	0.0387418	0.0036398	7.4E-29
9	GLIS3	chr9:4284961_AT_A	4284961	A	AT	0.4570980	0.0414773	0.0036888	7.9E-32
9	GLIS3	rs3934283	4285119	G	C	0.4538260	0.0429567	0.0036544	3.5E-34
9	GLIS3	rs10758591	4285986	G	C	0.4798080	0.0398239	0.0036440	4.5E-30
9	GLIS3	rs7024686	4287211	G	C	0.4783890	0.0407468	0.0036382	2.2E-31
9	GLIS3	rs7041847	4287466	A	G	0.4777520	0.0407127	0.0036365	1.7E-31
9	GLIS3	rs7034200	4289050	A	C	0.4556900	0.0416710	0.0036467	1.8E-32
9	GLIS3	rs10814914	4289196	T	C	0.4800100	0.0394339	0.0036376	1.2E-29
9	GLIS3	rs4237150	4290085	C	G	0.4482070	0.0428805	0.0036508	2.4E-34
9	GLIS3	rs10116772	4290541	A	C	0.4403290	0.0418766	0.0036634	2.0E-32
9	GLIS3	rs10814915	4290544	T	C	0.4700000	0.0400051	0.0036424	1.9E-30
9	GLIS3	rs6476839	4290823	T	A	0.4490000	0.0407087	0.0036561	6.0E-31
9	GLIS3	rs6476842	4291268	T	C	0.4270440	-0.0353843	0.0036895	3.1E-23
9	GLIS3	rs7020673	4291747	G	C	0.4831040	0.0393734	0.0036345	1.2E-29
9	GLIS3	rs10974438	4291928	C	A	0.3823660	0.0422249	0.0037679	7.7E-32
9	GLIS3	rs7043265	4292012	C	T	0.2541530	-0.0341191	0.0041926	1.1E-16
9	GLIS3	rs10758593	4292083	A	G	0.4406700	0.0413925	0.0036593	8.6E-32
9	GLIS3	rs7867224	4292152	A	G	0.4816540	0.0387240	0.0036433	1.1E-28
9	GLIS3	rs10814916	4293150	C	A	0.4708490	0.0407159	0.0036386	1.8E-31
9	GLIS3	rs34706136	4294707	TG	T	0.4814570	0.0366132	0.0036716	2.4E-25
9	GLIS3	rs10758594	4295583	G	A	0.4394220	-0.0359343	0.0036710	3.4E-24
9	GLIS3	rs4339696	4295880	T	G	0.4263320	-0.0360720	0.0036685	1.8E-24
9	GLIS3	rs10814917	4296430	A	G	0.4811980	0.0391150	0.0036806	1.7E-28
9	CDKN2B *	rs12379111	22128181	G	C	0.1511710	-0.0388611	0.0051842	6.0E-15
9	CDKN2B *	rs7020996	22129580	T	C	0.3940060	-0.0481540	0.0037218	3.4E-40
9	CDKN2B *	rs10965243	22130066	G	A	0.3899120	-0.0495902	0.0037790	6.8E-41
9	CDKN2B *	rs10965245	22130516	A	G	0.3897540	-0.0497887	0.0037868	3.9E-41
9	CDKN2B *	rs2383208	22132077	G	A	0.3959180	-0.0545606	0.0037225	8.6E-50
9	CDKN2B *	rs10965246	22132699	C	T	0.4175820	-0.0631932	0.0037102	1.9E-66
9	CDKN2B *	rs10965247	22132730	G	A	0.4187140	-0.0625472	0.0037095	4.4E-65
9	CDKN2B *	rs10965248	22132879	C	T	0.4192440	-0.0623773	0.0037098	1.3E-64
9	CDKN2B *	rs10965249	22133132	C	T	0.0838247	-0.0430363	0.0066037	1.0E-10
9	CDKN2B *	rs10965250	22133285	A	G	0.4161630	-0.0637413	0.0036927	6.1E-68
9	CDKN2B *	rs10217762	22133646	T	C	0.3968470	0.0278130	0.0037195	1.2E-13
9	CDKN2B *	rs10811659	22133717	C	T	0.1049910	0.0345482	0.0059195	6.0E-09
9	CDKN2B *	rs10757282	22133985	T	C	0.3959760	0.0268602	0.0037175	9.6E-13
9	CDKN2B *	rs10965251	22134030	A	G	0.0804074	-0.0485388	0.0067125	6.7E-13
9	CDKN2B *	rs10811660	22134069	A	G	0.4151930	-0.0638237	0.0036946	5.4E-68
9	CDKN2B *	rs10811661	22134095	C	T	0.4151890	-0.0638352	0.0036943	5.1E-68
9	CDKN2B *	rs10757283	22134173	C	T	0.3982870	0.0274021	0.0037151	3.8E-13
9	CDKN2B *	rs10811662	22134254	A	G	0.4150830	-0.0637647	0.0036958	8.6E-68
9	CDKN2B *	rs7019437	22134303	C	G	0.3966120	0.0268602	0.0037163	9.3E-13
9	CDKN2B *	rs7019778	22134652	A	C	0.3971360	0.0267038	0.0037208	1.4E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	CDKN2B *	rs10965252	22135920	G	A	0.0803672	-0.0479177	0.0066993	9.9E-13
9	CDKN2B *	rs1333051	22136490	T	A	0.1427460	-0.0361671	0.0051941	2.3E-12
9	CDKN2B *	rs201556756	22136666	CA	C	0.0822084	-0.0442380	0.0066214	3.0E-11
9	CDKN2B *	rs10965253	22136688	G	T	0.0819608	-0.0450615	0.0066319	1.3E-11
10	KLF6 *	rs11252157	3886272	A	C	0.2501650	0.0238757	0.0042306	2.0E-08
10	KLF6 *	rs10795086	3887334	C	T	0.3831800	0.0218947	0.0037535	1.3E-08
10	MIR6078 *	rs11252171	3896178	A	G	0.1791610	0.0279999	0.0047632	3.5E-09
10	MIR6078 *	rs7900884	3901025	G	A	0.4796040	-0.0201700	0.0036747	2.4E-08
10	MIR6078 *	rs7076800	3901557	A	T	0.4774210	-0.0199993	0.0036759	2.9E-08
10	MIR6078 *	rs7092293	3901571	G	A	0.4774190	-0.0199918	0.0036759	3.0E-08
10	MIR6078 *	rs7917483	3902861	G	A	0.4245710	0.0243718	0.0037028	6.5E-11
10	MIR6078 *	rs4881232	3903208	C	A	0.4244700	0.0246111	0.0036983	4.1E-11
10	MIR6078 *	rs4880637	3903293	C	A	0.4245350	0.0244831	0.0036958	4.8E-11
10	MIR6078 *	rs10904131	3903789	G	A	0.4254360	0.0244492	0.0036773	3.3E-11
10	MIR6078 *	rs11252179	3904119	A	G	0.1538640	0.0293042	0.0050649	5.2E-09
10	MIR6078 *	rs10736980	3904275	C	A	0.4260550	0.0236766	0.0036798	1.2E-10
10	MIR6078 *	rs10751943	3904313	C	T	0.4247390	0.0242402	0.0036751	4.3E-11
10	MIR6078 *	rs10732922	3904418	T	C	0.4775430	-0.0197117	0.0036349	2.6E-08
10	MIR6078 *	rs10736981	3904538	T	C	0.4783340	-0.0194815	0.0036347	3.8E-08
10	MIR6078 *	rs10736982	3904552	T	G	0.4783810	-0.0194765	0.0036351	3.8E-08
10	MIR6078 *	rs10732923	3904616	A	G	0.4785080	-0.0194612	0.0036357	4.0E-08
10	MIR6078 *	rs10732924	3904783	T	G	0.4783690	-0.0194391	0.0036374	4.3E-08
10	MIR6078 *	rs11388777	3905251	T	TA	0.4848560	-0.0207571	0.0036651	8.9E-09
10	MIR6078 *	rs7085649	3905287	G	A	0.4815760	-0.0200709	0.0036654	2.5E-08
10	MIR6078 *	rs7086671	3905296	C	T	0.4813540	-0.0201212	0.0036645	2.3E-08
10	MIR6078 *	rs7086674	3905298	C	T	0.4813540	-0.0201210	0.0036645	2.3E-08
10	MIR6078 *	rs7085797	3905390	G	A	0.4796200	-0.0198151	0.0036472	2.8E-08
10	MIR6078 *	rs7915142	3906237	T	C	0.2251980	0.0263390	0.0043785	2.0E-09
10	SEC61A2	rs7897731	12148322	C	T	0.4570120	-0.0212404	0.0036719	2.7E-09
10	SEC61A2	rs11257565	12148526	T	C	0.4568160	-0.0200072	0.0036615	2.1E-08
10	SEC61A2	rs11257566	12148897	C	A	0.4537950	-0.0205530	0.0036561	7.7E-09
10	SEC61A2	rs7072486	12148912	G	T	0.4540550	-0.0205569	0.0036536	8.4E-09
10	SEC61A2	rs7077306	12149238	C	T	0.4543080	-0.0205345	0.0036528	8.6E-09
10	SEC61A2	rs7077434	12149308	C	T	0.4542160	-0.0205640	0.0036525	8.0E-09
10	SEC61A2	rs10466280	12149934	C	T	0.4540810	-0.0204895	0.0036513	9.2E-09
10	SEC61A2	rs9329337	12150318	C	T	0.4542200	-0.0205644	0.0036525	8.0E-09
10	SEC61A2	rs7914422	12152280	G	A	0.4542170	-0.0206128	0.0036526	7.4E-09
10	SEC61A2	rs10906088	12152990	C	T	0.4540230	-0.0206288	0.0036543	7.0E-09
10	SEC61A2	rs2895501	12153882	G	A	0.4537470	-0.0206521	0.0036539	7.4E-09
10	SEC61A2	rs3758375	12154691	A	G	0.4538860	-0.0206964	0.0036550	7.3E-09
10	SEC61A2	rs3758376	12156020	G	A	0.4540970	-0.0206299	0.0036552	7.7E-09
10	SEC61A2	rs4750174	12157743	T	C	0.4521280	-0.0206729	0.0036592	7.0E-09
10	SEC61A2	rs4750175	12158126	C	T	0.4534970	-0.0207838	0.0036558	5.8E-09
10	SEC61A2	rs4589194	12158407	A	G	0.4536510	-0.0207810	0.0036571	5.8E-09
10	SEC61A2	rs12267387	12158906	C	T	0.4546030	-0.0205121	0.0036559	9.1E-09
10	SEC61A2	rs2399782	12159595	T	G	0.4540610	-0.0206747	0.0036552	6.5E-09
10	SEC61A2	rs10906090	12160409	T	C	0.4540360	-0.0204678	0.0036641	8.3E-09
10	SEC61A2	rs10906091	12160497	G	C	0.4548350	-0.0205692	0.0036670	7.5E-09
10	SEC61A2	rs34165047	12160709	CAA	C	0.4540440	-0.0206876	0.0036552	6.4E-09
10	SEC61A2	rs10906092	12160867	A	T	0.4540890	-0.0206758	0.0036555	6.6E-09
10	SEC61A2	rs1573986	12161322	G	A	0.4540440	-0.0206816	0.0036552	6.5E-09
10	SEC61A2	rs1573987	12161357	G	T	0.4536600	-0.0207443	0.0036550	5.6E-09
10	SEC61A2	rs4750179	12165888	A	T	0.4544920	-0.0209396	0.0036558	3.8E-09
10	SEC61A2	rs1053403	12166308	G	A	0.4542070	-0.0205967	0.0036554	6.8E-09
10	SEC61A2	rs2280619	12167400	C	G	0.4538350	-0.0206826	0.0036535	5.4E-09
10	NUDT5, SEC61A2	rs6686	12167753	T	C	0.4324820	-0.0196288	0.0036680	3.8E-08
10	NUDT5, SEC61A2	rs71513318	12167937	GT	G	0.4528220	-0.0206003	0.0036535	6.0E-09
10	NUDT5, SEC61A2	rs4747967	12168405	G	A	0.4538830	-0.0208008	0.0036547	4.7E-09
10	NUDT5, SEC61A2	rs9633765	12169591	T	C	0.4532520	-0.0205944	0.0036559	6.6E-09
10	NUDT5, SEC61A2	rs1054067	12169762	A	T	0.4536890	-0.0206834	0.0036529	5.4E-09
10	NUDT5	rs11257577	12170187	A	T	0.4328000	-0.0196552	0.0036684	3.7E-08
10	NUDT5	rs2399786	12173181	C	T	0.4334900	-0.0196945	0.0036706	3.6E-08
10	NUDT5	rs71382687	12174931	TA	T	0.4320830	-0.0199056	0.0036781	2.8E-08
10	CDC123	rs12414441	12207006	A	G	0.3097230	-0.0226395	0.0040057	1.9E-09
10	CDC123	rs12411838	12207007	A	C	0.3099480	-0.0226595	0.0040036	1.9E-09
10	CDC123	rs12773913	12207225	T	G	0.3083260	-0.0230081	0.0039994	1.4E-09
10	CDC123	rs12413792	12207290	C	T	0.3083480	-0.0230255	0.0039991	1.4E-09
10	CDC123	rs12775830	12207446	G	C	0.3077320	-0.0226579	0.0040008	2.6E-09
10	CDC123	rs4747968	12207798	T	C	0.3087500	-0.0232211	0.0039884	9.6E-10
10	CDC123	rs7100710	12208862	G	A	0.4164350	-0.0308095	0.0036988	1.1E-18
10	CDC123	rs2271804	12210218	A	G	0.3136980	-0.0236787	0.0039219	2.2E-10
10	CDC123	rs12221133	12211598	G	A	0.4464590	-0.0349692	0.0036454	8.6E-24
10	CDC123	rs7896600	12213176	G	C	0.4422400	-0.0347467	0.0036487	1.5E-23
10	CDC123	rs11257600	12213658	G	T	0.4423350	-0.0347441	0.0036494	1.5E-23
10	CDC123	rs2399796	12214560	G	A	0.3133740	-0.0238536	0.0039191	1.7E-10
10	CDC123	rs10906100	12218020	C	T	0.4417180	-0.0349444	0.0036547	7.3E-24
10	CDC123	rs35674932	12219811	A	T	0.4417010	-0.0347365	0.0036550	1.5E-23
10	CDC123	rs12780155	12219853	T	A	0.4417160	-0.0347452	0.0036549	1.5E-23
10	CDC123	rs4478891	12225655	G	A	0.3873180	-0.0303639	0.0037381	1.7E-17
10	CDC123	rs35828869	12226538	A	G	0.3083310	-0.0233736	0.0039608	4.1E-10
10	CDC123	rs7897432	12226995	C	T	0.3141100	-0.0234548	0.0039158	2.9E-10
10	CDC123	rs61848333	12231970	T	C	0.3599700	0.0211007	0.0037977	5.0E-10
10	CDC123	chr10:12232788_C_CT	12232788	CT	C	0.2972840	-0.0226658	0.0040464	1.9E-09
10	CDC123	rs17566555	12233948	A	G	0.3115900	-0.0236153	0.0039206	2.2E-10
10	CDC123	rs7068966	12235993	T	C	0.3114110	-0.0238864	0.0039184	1.4E-10
10	CDC123	rs7090277	12236022	A	T	0.3116400	-0.0237904	0.0039182	1.8E-10
10	CDC123	rs57062879	12236526	G	A	0.3123460	-0.0245685	0.0039157	4.9E-11
10	CDC123	rs111719683	12237639	T	TG	0.3109210	-0.0239745	0.0039248	1.3E-10
10	CDC123	rs10906104	12238297	G	A	0.4004890	-0.0217131	0.0037128	2.4E-10
10	CDC123	rs34428576	12239112	A	G	0.3629760	0.0208411	0.0037847	8.0E-10
10	CDC123	rs7071305	12239633	G	A	0.3650220	-0.0265696	0.0037805	7.6E-14
10	CDC123	rs7075724	12240462	G	A	0.3658130	-0.0270504	0.0037709	2.2E-14
10	CDC123	rs71513320	12241162	TAGTA	T	0.4416580	-0.0343745	0.0036579	4.2E-23
10	CDC123	rs35117583	12241966	GTTC	G	0.3926570	-0.0301092	0.0037250	1.8E-17
10	CDC123	rs147105908	12241969	CTTT	C	0.3903360	-0.0304984	0.0037492	1.0E-17
10	CDC123	rs35475841	12242083	AC	A	0.3138470	-0.0238547	0.0039128	1.2E-10
10	CDC123	rs11257613	12242393	A	G	0.3121530	-0.0242482	0.0039166	6.8E-11
10	CDC123	rs5783244	12243129	T	TG	0.3141220	-0.0240660	0.0039131	7.6E-11
10	CDC123	rs146552456	12243628	CA	C	0.3126380	-0.0237411	0.0039244	1.6E-10
10	CDC123	rs2001546	12243736	T	A	0.3130730	-0.0243175	0.0039251	6.0E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	CDC123	rs10906106	12245403	C	G	0.3611290	0.0206121	0.0037909	1.1E-09
10	CDC123	rs36042706	12246303	G	A	0.3119450	-0.0244748	0.0039247	3.6E-11
10	CDC123	rs4469792	12246781	G	A	0.3106050	-0.0246570	0.0039249	3.1E-11
10	CDC123	rs4372354	12246991	C	T	0.3071830	-0.0235514	0.0039544	1.7E-10
10	CDC123	rs2399797	12247619	T	C	0.3092340	-0.0247392	0.0039338	3.3E-11
10	CDC123	rs11257615	12247776	A	G	0.3634980	0.0205755	0.0037872	1.2E-09
10	CDC123	rs4750193	12248731	C	G	0.3094080	-0.0246317	0.0039319	3.4E-11
10	CDC123 *	rs35930121	12251683	A	ATT	0.3072030	-0.0248978	0.0039452	2.7E-11
10	CDC123 *	rs11257621	12251769	G	A	0.3829400	-0.0315049	0.0037431	1.4E-18
10	CDC123 *	rs12241367	12252091	G	A	0.3831430	-0.0314110	0.0037450	1.8E-18
10	CDC123 *	rs12767576	12252284	T	G	0.3072190	-0.0248607	0.0039453	2.9E-11
10	CDC123 *	rs4511202	12252662	C	T	0.3858120	-0.0323005	0.0037404	1.6E-19
10	CDC123 *	rs4545446	12252967	T	C	0.3098080	-0.0255684	0.0039393	6.8E-12
10	CDC123 *	rs11257622	12253340	C	T	0.3651780	0.0204373	0.0037814	1.5E-09
10	CDC123 *	rs12783654	12254622	G	C	0.3683740	-0.0311326	0.0038442	3.2E-17
10	CDC123 *	rs11257627	12254800	G	A	0.3828660	-0.0319490	0.0037535	4.8E-19
10	CDC123 *	rs4747969	12255231	C	T	0.3633690	0.0211201	0.0037987	5.7E-10
10	CDC123 *	rs11817797	12256445	T	C	0.2979360	-0.0255793	0.0040105	2.7E-11
10	CDC123 *	rs11593214	12256596	C	G	0.3070740	-0.0254402	0.0039558	1.2E-11
10	CDC123 *	rs12098287	12257504	T	A	0.3061450	-0.0252295	0.0039651	1.9E-11
10	CDC123 *	chr10:12257624_CA_C	12257624	C	CA	0.3109200	-0.0249351	0.0039734	3.6E-11
10	CDC123 *	rs7916879	12258791	G	A	0.3890040	-0.0302588	0.0037590	2.8E-17
10	CDC123 *	rs11599700	12260061	A	C	0.3120610	-0.0239813	0.0039452	1.4E-10
10	CDC123 *	rs10906111	12260358	C	T	0.4437290	-0.0348455	0.0036698	1.1E-23
10	CDC123 *	rs10795945	12260608	C	T	0.4421290	-0.0346645	0.0036701	1.8E-23
10	CDC123 *	rs4747971	12261372	C	T	0.4422910	-0.0346561	0.0036685	1.9E-23
10	CDC123 *	rs61848342	12261814	T	C	0.3823570	-0.0296881	0.0037702	1.1E-16
10	CDC123 *	rs55713253	12263359	T	C	0.2850120	0.0288048	0.0040320	3.2E-12
10	CDC123 *	rs4747972	12263649	C	G	0.3120850	-0.0238392	0.0039358	1.6E-10
10	CDC123 *	chr10:12264522_C_CT	12264522	CT	C	0.3122660	-0.0236383	0.0039310	2.0E-10
10	CDC123 *	rs34465514	12264720	A	AT	0.3108120	-0.0235493	0.0039453	2.6E-10
10	CDC123 *	rs35465721	12265089	A	AC	0.3115950	-0.0236943	0.0039359	2.0E-10
10	CDC123 *	rs11257654	12265612	T	C	0.2854050	0.0287630	0.0040173	3.3E-12
10	CDC123 *	rs36062557	12265828	T	C	0.3132420	-0.0239971	0.0039238	1.1E-10
10	CDC123 *	rs11257655	12265895	C	T	0.4431170	-0.0348181	0.0036445	1.0E-23
10	CDC123 *	rs11593567	12265964	G	A	0.3132510	-0.0239959	0.0039238	1.1E-10
10	CDC123 *	rs11594076	12266435	G	A	0.3131050	-0.0240123	0.0039259	1.2E-10
10	CDC123 *	rs7072473	12266890	A	G	0.3127160	-0.0239563	0.0039303	1.4E-10
10	CDC123 *	rs11257657	12267140	C	G	0.4432620	-0.0349830	0.0036533	7.8E-24
10	CDC123 *	rs11257658	12267269	G	A	0.3670380	-0.0264009	0.0037810	1.5E-13
10	CDC123 *	rs11257659	12267270	C	T	0.3670380	-0.0264009	0.0037810	1.5E-13
10	CDC123 *	rs79174237	12267509	T	C	0.2545940	-0.0235489	0.0042008	5.2E-09
10	CDC123 *	rs112790657	12268285	A	G	0.2568470	-0.0229162	0.0041755	1.2E-08
10	CDC123 *	rs7895410	12268738	C	T	0.3377940	0.0231662	0.0038529	1.2E-08
10	CDC123 *	rs33932777	12269466	G	A	0.3873850	-0.0330729	0.0037297	2.5E-20
10	CDC123 *	rs11257671	12269614	G	C	0.3383570	0.0232143	0.0038537	1.1E-08
10	CDC123 *	rs56184232	12269689	TTTAA	T	0.3885690	-0.0335769	0.0037335	7.1E-21
10	CDC123 *	rs58891143	12270047	C	T	0.2517650	-0.0229674	0.0042357	2.0E-08
10	CDC123 *	rs34464447	12270204	G	A	0.2571730	-0.0231164	0.0041723	9.1E-09
10	CDC123 *	rs12415897	12270303	A	G	0.2571760	-0.0230964	0.0041721	9.3E-09
10	CDC123 *	rs10906114	12270426	A	C	0.3370760	-0.0289896	0.0038490	7.0E-15
10	CDC123 *	rs34464354	12271137	TC	T	0.3097540	-0.0259081	0.0039361	6.7E-12
10	CDC123 *	rs75362664	12271826	G	A	0.3893660	-0.0317275	0.0037656	5.9E-19
10	CDC123 *	rs12779959	12272069	T	C	0.2466730	-0.0233892	0.0042461	1.5E-08
10	CDC123 *	rs11597664	12272198	T	A	0.2530770	-0.0226774	0.0041924	2.3E-08
10	CDC123 *	rs11257676	12272474	A	G	0.3832230	-0.0329171	0.0037294	4.7E-20
10	CDC123 *	rs17151496	12272704	T	A	0.2532450	-0.0230275	0.0041895	1.4E-08
10	CDC123 *	rs10906115	12272998	G	A	0.3832700	-0.0329703	0.0037285	4.0E-20
10	CDC123 *	rs7076900	12274860	T	G	0.3051720	-0.0257618	0.0039507	1.3E-11
10	CDC123 *	rs11257678	12275139	C	T	0.3055360	-0.0257259	0.0039483	1.4E-11
10	CDC123 *	rs10906116	12275719	G	T	0.3983290	-0.0306046	0.0037321	1.1E-17
10	MYO3A	rs36024300	26014656	T	G	0.2462810	-0.0226156	0.0042561	1.0E-08
10	MYO3A	rs35769796	26014785	A	C	0.2462810	-0.0226156	0.0042561	1.0E-08
10	MYO3A	rs67764971	26017802	ATAAAG	A	0.2417370	-0.0223896	0.0043040	2.1E-08
10	MYO3A	rs17666079	26021750	C	A	0.2476830	-0.0234668	0.0042591	2.8E-09
10	MYO3A	rs1339816	26023496	T	C	0.2489920	-0.0242185	0.0042441	8.0E-10
10	MYO3A	rs1339815	26023529	C	G	0.2490490	-0.0243713	0.0042433	6.1E-10
10	MYO3A	rs12572400	26023546	A	G	0.2481060	-0.0240973	0.0042329	8.8E-10
10	MYO3A	rs1339814	26023895	A	G	0.2481060	-0.0240973	0.0042329	8.8E-10
10	MYO3A	rs1416860	26024408	A	G	0.2482280	-0.0240167	0.0042340	9.9E-10
10	MYO3A	rs1339813	26025051	A	G	0.2481080	-0.0241489	0.0042325	8.3E-10
10	MYO3A	rs1339812	26029232	T	C	0.2577300	-0.0211495	0.0041583	2.5E-08
10	MYO3A	rs35063376	26029290	AT	A	0.2576080	-0.0209450	0.0041582	3.3E-08
10	MYO3A	rs17813720	26029866	A	G	0.2571090	-0.0211845	0.0041597	2.4E-08
10	MYO3A	rs1361376	26030956	G	A	0.2566660	-0.0212722	0.0041636	2.4E-08
10	MYO3A	rs12267297	26031879	T	G	0.2559400	-0.0211381	0.0041682	3.0E-08
10	MYO3A	rs11598907	26033854	C	T	0.2372390	-0.0285762	0.0043101	1.6E-12
10	MYO3A	rs1339810	26035034	T	A	0.2594490	-0.0208298	0.0041634	3.7E-08
10	MYO3A	rs1339809	26035121	A	C	0.2572350	-0.0212728	0.0041756	2.4E-08
10	MYO3A	rs1339808	26035181	C	T	0.2572350	-0.0212728	0.0041756	2.4E-08
10	MYO3A	chr10:26036249_AT_A	26036249	A	AT	0.2594490	-0.0208298	0.0041634	3.7E-08
10	MYO3A	rs34513929	26036285	AC	A	0.2590730	-0.0207442	0.0041663	4.8E-08
10	MYO3A	rs949896	26037508	C	T	0.2572350	-0.0212728	0.0041756	2.4E-08
10	MYO3A	rs1856603	26038538	A	G	0.2562110	-0.0210803	0.0041653	3.2E-08
10	MYO3A	rs11014923	26039200	C	T	0.2563570	-0.0207761	0.0041734	3.8E-08
10	MYO3A	rs11014924	26039546	T	C	0.2559370	-0.0208889	0.0041685	4.1E-08
10	MYO3A	rs12262670	26040036	T	G	0.2560910	-0.0212188	0.0041664	2.8E-08
10	MYO3A	rs1915478	26041289	G	T	0.2562580	-0.0210804	0.0041653	3.1E-08
10	MYO3A	rs1949616	26041652	T	G	0.2562140	-0.0210799	0.0041653	3.2E-08
10	MYO3A	rs6482528	26041698	G	A	0.2584600	-0.0206197	0.0041531	4.8E-08
10	MYO3A	rs1402436	26045011	A	G	0.2592660	-0.0207317	0.0041475	3.9E-08
10	MYO3A	rs12572695	26048269	C	A	0.2576050	-0.0209436	0.0041581	3.3E-08
10	MYO3A	rs11014925	26048446	T	C	0.2567530	-0.0208312	0.0041638	4.2E-08
10	MYO3A	rs12247650	26052652	T	G	0.2571450	-0.0212123	0.0041606	2.5E-08
10	MYO3A	rs12766250	26052905	C	G	0.2576970	-0.0209553	0.0041587	3.2E-08
10	MYO3A	rs12768268	26053241	T	C	0.2576050	-0.0209436	0.0041581	3.3E-08
10	MYO3A	rs7899450	26054235	A	G	0.2570610	-0.0211917	0.0041596	2.5E-08
10	MYO3A	rs7899567	26054268	A	G	0.2570610	-0.0211917	0.0041596	2.5E-08
10	MYO3A	rs2368120	26055249	G	A	0.2590640	-0.0206161	0.0041496	4.5E-08
10	MYO3A	rs1591906	26055578	A	G	0.2593190	-0.0206130	0.0041477	4.5E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	MYO3A	rs11014928	26055997	T	G	0.2594090	-0.0208064	0.0041371	3.5E-08
10	MYO3A	rs11014929	26056010	G	A	0.2593970	-0.0207869	0.0041369	3.6E-08
10	MYO3A	rs11014931	26056085	G	C	0.2593950	-0.0207693	0.0041369	3.7E-08
10	MYO3A	rs11014932	26056141	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014933	26056236	G	A	0.2592220	-0.0208159	0.0041388	3.5E-08
10	MYO3A	rs11014934	26056329	G	A	0.2572070	-0.0212069	0.0041488	2.5E-08
10	MYO3A	rs11014935	26056344	T	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014936	26056487	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs34089187	26056552	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs17738967	26056581	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs17666328	26056661	G	C	0.2593310	-0.0207811	0.0041377	3.7E-08
10	MYO3A	rs34669089	26056682	A	AG	0.2593310	-0.0207811	0.0041377	3.7E-08
10	MYO3A	rs7917879	26056706	T	C	0.2593250	-0.0207885	0.0041376	3.7E-08
10	MYO3A	rs34311739	26056741	A	G	0.2593250	-0.0207885	0.0041376	3.7E-08
10	MYO3A	rs17738985	26056770	G	C	0.2593250	-0.0207885	0.0041376	3.7E-08
10	MYO3A	chr10:26056960_GA_G	26056960	G	GA	0.2598150	-0.0206779	0.0041406	4.2E-08
10	MYO3A	rs59180311	26056978	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs35000419	26057118	A	G	0.2594500	-0.0206799	0.0041371	4.2E-08
10	MYO3A	rs35251452	26057157	G	T	0.2593070	-0.0207079	0.0041387	3.9E-08
10	MYO3A	rs34353852	26057161	C	A	0.2593070	-0.0207079	0.0041387	3.9E-08
10	MYO3A	rs12784526	26057223	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12784683	26057250	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12784717	26057325	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12784877	26057386	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12241851	26057551	G	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12240279	26057612	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014938	26057716	C	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014939	26057722	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014940	26057788	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs7894301	26057851	G	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs34607240	26057956	TG	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs7910497	26058019	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12263847	26058120	T	C	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs11814295	26058126	A	G	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs12248769	26058174	C	G	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs7893838	26058219	A	G	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs12263998	26058335	T	C	0.2588080	-0.0214785	0.0041456	1.4E-08
10	MYO3A	rs12243741	26058384	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12242258	26058536	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12249006	26058605	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12264250	26058662	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12242396	26058668	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs34756309	26058934	T	C	0.2593290	-0.0209742	0.0041389	2.9E-08
10	MYO3A	rs34192722	26058940	GA	G	0.2593290	-0.0209742	0.0041389	2.9E-08
10	MYO3A	rs7914972	26058947	T	A	0.2593290	-0.0209742	0.0041389	2.9E-08
10	MYO3A	rs34817852	26059017	A	AC	0.2593230	-0.0208636	0.0041375	3.3E-08
10	MYO3A	rs138540702	26059206	AT	A	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs7915315	26059244	G	A	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs61849329	26059452	C	T	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs61849330	26059453	C	A	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs34558407	26059479	T	A	0.2593190	-0.0209394	0.0041379	2.9E-08
10	MYO3A	rs35158540	26059601	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs17666400	26059772	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs71492521	26059887	C	T	0.2592840	-0.0207793	0.0041379	3.8E-08
10	MYO3A	rs71492522	26059892	T	C	0.2594540	-0.0206955	0.0041370	4.1E-08
10	MYO3A	rs71492523	26059897	A	G	0.2595030	-0.0209841	0.0041373	2.8E-08
10	MYO3A	rs71492524	26059987	G	A	0.2580850	-0.0210231	0.0041486	2.6E-08
10	MYO3A	rs71492525	26060024	G	A	0.2566360	-0.0217715	0.0041641	1.0E-08
10	MYO3A	rs71492526	26060074	A	G	0.2586710	-0.0208595	0.0041439	3.2E-08
10	MYO3A	rs71492527	26060084	C	T	0.2586710	-0.0208595	0.0041439	3.2E-08
10	MYO3A	rs71492528	26060115	T	C	0.2554810	-0.0215433	0.0041714	1.8E-08
10	MYO3A	rs77873717	26060174	G	A	0.2523460	-0.0227717	0.0042039	2.9E-09
10	MYO3A	rs79944150	26060202	A	T	0.2586330	-0.0216445	0.0041472	9.4E-09
10	MYO3A	rs76725843	26060214	G	A	0.2585890	-0.0215476	0.0041476	1.1E-08
10	MYO3A	rs12778820	26060338	A	G	0.2571530	-0.0208062	0.0041572	4.2E-08
10	MYO3A	rs12781231	26060439	G	A	0.2595170	-0.0209448	0.0041370	3.0E-08
10	MYO3A	rs12781392	26060477	C	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12780744	26060544	A	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs76455277	26060561	TTATTTT	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs377504397	26060562	C	CCA	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12781790	26060659	C	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12779671	26060734	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs5012431	26060758	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs200468971	26060937	A	AT	0.2577640	-0.0207772	0.0041523	3.7E-08
10	MYO3A	rs58595215	26060951	T	C	0.2577640	-0.0207772	0.0041523	3.7E-08
10	MYO3A	rs35321191	26060998	G	A	0.2581490	-0.0207730	0.0041565	3.7E-08
10	MYO3A	rs35221748	26061015	A	G	0.2577640	-0.0207772	0.0041523	3.7E-08
10	MYO3A	rs61849334	26061158	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61849335	26061172	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61849336	26061234	G	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs17739106	26061247	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs17666458	26061422	C	A	0.2584340	-0.0210384	0.0041469	3.0E-08
10	MYO3A	rs61849337	26061452	C	T	0.2494860	-0.0215411	0.0042382	2.5E-08
10	MYO3A	rs61849338	26061456	T	C	0.2494860	-0.0215411	0.0042382	2.5E-08
10	MYO3A	rs35740796	26061471	A	AT	0.2572500	-0.0210437	0.0041570	3.3E-08
10	MYO3A	rs4998836	26062698	G	C	0.2587080	-0.0207983	0.0041441	3.3E-08
10	MYO3A	rs4998837	26062831	T	A	0.2595820	-0.0205642	0.0041385	4.9E-08
10	MYO3A	rs4998838	26062850	T	G	0.2595820	-0.0205642	0.0041385	4.9E-08
10	MYO3A	rs5783959	26062888	T	TGAG	0.2596350	-0.0205905	0.0041389	4.8E-08
10	MYO3A	rs2176942	26062963	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs4998839	26063083	T	C	0.2593340	-0.0206631	0.0041374	4.2E-08
10	MYO3A	rs4998840	26063119	T	G	0.2593340	-0.0206631	0.0041374	4.2E-08
10	MYO3A	rs12252534	26063140	G	A	0.2571440	-0.0211334	0.0041494	2.7E-08
10	MYO3A	rs12244889	26063150	T	C	0.2593340	-0.0206631	0.0041374	4.2E-08
10	MYO3A	rs61849340	26063258	T	A	0.2593340	-0.0206631	0.0041374	4.2E-08
10	MYO3A	rs34135459	26063288	T	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61849341	26063340	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61849342	26063341	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12775228	26063424	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12776958	26063480	G	C	0.2593950	-0.0207424	0.0041368	3.8E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	MYO3A	rs4631780	26063747	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs10508710	26063842	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11593128	26064023	A	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61849343	26064266	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61849344	26064318	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11595393	26064402	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs7097468	26064467	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs1521031	26064747	G	C	0.2596590	-0.0212357	0.0041405	2.2E-08
10	MYO3A	rs1521030	26064822	G	A	0.2592190	-0.0207930	0.0041383	3.6E-08
10	MYO3A	rs1521029	26064915	C	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs10828945	26065067	A	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs10828946	26065172	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014944	26065264	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014945	26065305	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014946	26065416	T	A	0.2595860	-0.0206690	0.0041376	4.3E-08
10	MYO3A	rs11014947	26065703	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11014948	26065725	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs11593320	26065827	G	A	0.2454040	-0.0233967	0.0042723	3.9E-09
10	MYO3A	rs12761327	26066170	G	A	0.2595650	-0.0207662	0.0041383	3.7E-08
10	MYO3A	rs12785093	26066298	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12761590	26066301	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12785116	26066343	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12569363	26066412	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12570534	26066647	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824705	26066792	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824704	26066805	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824703	26066842	A	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824702	26066933	T	G	0.2593150	-0.0207132	0.0041377	4.1E-08
10	MYO3A	rs3824701	26066943	G	A	0.2593150	-0.0207132	0.0041377	4.1E-08
10	MYO3A	rs3824700	26066977	A	G	0.2593360	-0.0206736	0.0041374	4.4E-08
10	MYO3A	rs3824698	26067085	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824697	26067086	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824696	26067108	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3824695	26067137	T	C	0.2594420	-0.0208273	0.0041369	3.4E-08
10	MYO3A	rs61846589	26067265	T	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs61846590	26067348	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs34834344	26067513	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs35910374	26067682	AT	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs34879813	26067697	C	G	0.2590480	-0.0211724	0.0041405	2.3E-08
10	MYO3A	rs34580592	26067730	C	A	0.2587100	-0.0212342	0.0041438	2.1E-08
10	MYO3A	rs12768454	26067740	T	C	0.2587100	-0.0212342	0.0041438	2.1E-08
10	MYO3A	rs34967200	26067751	A	G	0.2587100	-0.0212342	0.0041438	2.1E-08
10	MYO3A	rs35895855	26067854	CT	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12772112	26067869	A	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12773856	26068006	T	C	0.2592030	-0.0206625	0.0041386	4.2E-08
10	MYO3A	rs12772553	26068128	T	G	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12775421	26068409	G	A	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs12773390	26068469	C	G	0.2595260	-0.0206120	0.0041379	4.4E-08
10	MYO3A	rs12774889	26068521	T	C	0.2595260	-0.0206120	0.0041379	4.4E-08
10	MYO3A	rs7477386	26068630	A	G	0.2591080	-0.0208022	0.0041387	3.4E-08
10	MYO3A	rs35636005	26068644	A	G	0.2580790	-0.0208819	0.0041501	3.1E-08
10	MYO3A	rs3817421	26068696	C	T	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs35379457	26068818	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3817419	26068891	T	C	0.2593950	-0.0207424	0.0041368	3.8E-08
10	MYO3A	rs3817418	26069042	G	A	0.2594160	-0.0207402	0.0041370	3.8E-08
10	MYO3A	rs7095515	26069072	C	G	0.2594160	-0.0207402	0.0041370	3.8E-08
10	MYO3A	rs3817417	26069181	G	A	0.2594160	-0.0207402	0.0041370	3.8E-08
10	MYO3A	rs7095668	26069212	T	G	0.2593700	-0.0206660	0.0041375	4.2E-08
10	MYO3A	rs11289890	26069229	G	GT	0.2593700	-0.0206660	0.0041375	4.2E-08
10	MYO3A	rs7095982	26069444	C	G	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs7096274	26069636	A	G	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs7084483	26069645	C	T	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs7097387	26069705	T	C	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs12248210	26069769	G	C	0.2592530	-0.0207479	0.0041383	3.6E-08
10	MYO3A	rs3758444	26069943	C	T	0.2594950	-0.0206202	0.0041376	4.6E-08
10	MYO3A	rs3758443	26069984	A	G	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs3758441	26070251	G	T	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs3834403	26070271	TA	T	0.2595320	-0.0209476	0.0041369	3.0E-08
10	MYO3A	rs12770421	26070637	G	T	0.2568150	-0.0208461	0.0041532	3.8E-08
10	MYO3A	rs12765553	26070714	G	A	0.2586910	-0.0211364	0.0041455	2.1E-08
10	MYO3A	rs12765561	26070726	T	A	0.2583400	-0.0212572	0.0041484	1.9E-08
10	MYO3A	rs12770618	26070925	T	A	0.2592530	-0.0207854	0.0041388	3.6E-08
10	MYO3A	chr10:26071023_A_AT	26071023	AT	A	0.2485740	-0.0219661	0.0042295	1.5E-08
10	MYO3A	rs12768879	26071083	A	G	0.2595700	-0.0207145	0.0041388	3.9E-08
10	MYO3A	rs12776584	26071198	C	T	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs12770526	26071236	T	C	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs12771414	26071263	G	A	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs4378287	26071390	A	G	0.2595700	-0.0207145	0.0041388	3.9E-08
10	MYO3A	rs4313469	26071445	A	G	0.2596080	-0.0207184	0.0041370	3.8E-08
10	MYO3A	rs4581343	26071486	A	C	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs4581344	26071517	A	C	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs4548528	26071816	G	T	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs56011042	26071902	G	C	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs56403024	26071906	T	C	0.2594120	-0.0207408	0.0041371	3.8E-08
10	MYO3A	rs58759321	26072039	G	ACCCTCT	0.2574720	-0.0212875	0.0041568	2.0E-08
10	MYO3A	rs59075175	26072070	G	C	0.2580470	-0.0211079	0.0041513	2.5E-08
10	MYO3A	rs58217723	26072195	C	T	0.2594110	-0.0207280	0.0041371	3.9E-08
10	MYO3A	rs55752594	26072231	T	C	0.2608350	-0.0206532	0.0041360	4.2E-08
10	MYO3A	rs59764643	26072301	G	A	0.2594250	-0.0207355	0.0041373	3.9E-08
10	MYO3A	rs12267024	26072345	A	G	0.2591310	-0.0209542	0.0041406	3.0E-08
10	MYO3A	rs12260321	26072347	G	A	0.2591310	-0.0209542	0.0041406	3.0E-08
10	MYO3A	rs12252825	26072382	A	C	0.2594250	-0.0207355	0.0041373	3.9E-08
10	MYO3A	rs12267071	26072395	T	G	0.2589380	-0.0213329	0.0041423	1.9E-08
10	MYO3A	rs12267078	26072417	A	G	0.2573940	-0.0210580	0.0041495	3.0E-08
10	MYO3A	rs12253015	26072670	T	C	0.2578020	-0.0207664	0.0041486	3.8E-08
10	MYO3A	rs12263561	26072757	A	T	0.2590120	-0.0209585	0.0041412	3.0E-08
10	MYO3A	rs12263812	26073161	C	T	0.2594110	-0.0207280	0.0041371	3.9E-08
10	MYO3A	rs12262265	26073168	G	A	0.2594110	-0.0207280	0.0041371	3.9E-08
10	MYO3A	rs12269051	26073288	A	G	0.2590510	-0.0205872	0.0041399	4.5E-08
10	MYO3A	rs66657341	26073342	T	C	0.2594820	-0.0207715	0.0041379	3.7E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	MYO3A	rs67216996	26073397	A	G	0.2594110	-0.0207280	0.0041371	3.9E-08
10	MYO3A	rs61840796	26073541	T	C	0.2594110	-0.0207280	0.0041371	3.9E-08
10	MYO3A	rs37756647	26073666	A	AT	0.2553640	-0.0209440	0.0041756	3.7E-08
10	MYO3A	rs61840797	26073682	G	A	0.2553640	-0.0209440	0.0041756	3.7E-08
10	MYO3A	rs12767114	26073905	G	A	0.2594110	-0.0207280	0.0041371	3.9E-08
10	MYO3A	rs11287744	26074564	A	AT	0.2565190	-0.0209224	0.0041552	4.0E-08
10	MYO3A	rs2090797	26085157	T	C	0.2565560	-0.0209721	0.0041591	3.7E-08
10	MYO3A	rs34986792	26085186	AT	A	0.2587610	-0.0206457	0.0041449	4.9E-08
10	MYO3A	rs1539323	26085670	T	C	0.2567300	-0.0209446	0.0041572	3.9E-08
10	MYO3A	rs2176937	26086208	G	A	0.2587590	-0.0206406	0.0041449	4.9E-08
10	MYO3A	rs1546701	26086729	A	G	0.2567360	-0.0209259	0.0041539	4.3E-08
10	MYO3A	rs3057676	26086984	GTA	G	0.2587750	-0.0207114	0.0041430	4.6E-08
10	MYO3A	rs7898544	26086919	A	G	0.2550490	-0.0209576	0.0041714	4.9E-08
10	MYO3A	rs12246202	26090124	C	A	0.2568130	-0.0210774	0.0041536	3.6E-08
10	MYO3A	rs12261502	26094718	A	G	0.2569160	-0.0208724	0.0041539	4.5E-08
10	MYO3A	rs1818747	26097501	T	A	0.2567180	-0.0210045	0.0041659	4.4E-08
10	MYO3A	rs11498243	26099805	T	C	0.2850400	-0.0202696	0.0040650	4.4E-08
10	MYO3A	rs11498424	26100081	G	A	0.2566450	-0.0212126	0.0041686	3.4E-08
10	MYO3A	rs61840836	26103183	T	C	0.2569010	-0.0210004	0.0041675	4.4E-08
10	MYO3A	rs35137356	26103253	A	G	0.2566480	-0.0212349	0.0041692	3.3E-08
10	MYO3A	rs11014959	26103895	A	G	0.2569490	-0.0210257	0.0041663	4.4E-08
10	MYO3A	rs12774270	26106176	C	T	0.2569500	-0.0210451	0.0041663	4.3E-08
10	MYO3A	rs1402437	26109457	A	T	0.2566870	-0.0212575	0.0041682	3.3E-08
10	MYO3A	rs7912435	26109880	A	G	0.2569500	-0.0210451	0.0041663	4.3E-08
10	MYO3A	rs7913502	26110719	C	G	0.2566870	-0.0212575	0.0041682	3.3E-08
10	MYO3A	rs10828953	26111816	C	A	0.2566850	-0.0212271	0.0041682	3.4E-08
10	MYO3A	rs12569739	26112662	C	T	0.2569540	-0.0210368	0.0041662	4.3E-08
10	MYO3A	rs5783962	26114586	T	TA	0.2566960	-0.0212300	0.0041681	3.4E-08
10	MYO3A	rs2176941	26114744	C	G	0.2566960	-0.0212300	0.0041681	3.4E-08
10	MYO3A	rs12263990	26118479	G	C	0.2566710	-0.0212571	0.0041684	3.4E-08
10	MYO3A	rs7907187	26121513	C	G	0.2569350	-0.0210448	0.0041665	4.4E-08
10	MYO3A	chr10:26123924_TAAACAA_T	26123924	T	'AAAAA	0.2552080	-0.0214871	0.0041967	2.2E-08
10	MYO3A	rs17739425	26128602	G	T	0.2570590	-0.0210411	0.0041665	4.5E-08
10	MYO3A	rs11819592	26133478	A	G	0.2567880	-0.0212870	0.0041687	3.3E-08
10	MYO3A	rs7895318	26134162	G	A	0.2567880	-0.0212870	0.0041687	3.3E-08
10	MYO3A	rs10718017	26134474	C	CT	0.2563930	-0.0210707	0.0041716	4.0E-08
10	MYO3A	rs7903895	26135771	C	G	0.2570480	-0.0210949	0.0041666	4.2E-08
10	MYO3A	rs7085136	26136748	T	C	0.2579160	-0.0211027	0.0041631	3.4E-08
10	MYO3A	rs7068611	26136749	G	A	0.2583070	-0.0211507	0.0041612	3.2E-08
10	MYO3A	rs7068633	26136790	G	A	0.2587100	-0.0210304	0.0041564	3.8E-08
10	MYO3A	rs4548529	26137847	G	A	0.2587550	-0.0210100	0.0041563	4.0E-08
10	MYO3A	rs12772392	26138248	T	C	0.2587640	-0.0210269	0.0041562	3.9E-08
10	MYO3A	rs10082469	26139386	A	T	0.2567820	-0.0213381	0.0041679	2.9E-08
10	MYO3A	rs12247680	26139851	T	C	0.2570530	-0.0211580	0.0041659	3.7E-08
10	MYO3A	rs7908466	26140614	G	A	0.2588460	-0.0210626	0.0041557	3.5E-08
10	MYO3A	rs2368157	26141605	G	A	0.2571430	-0.0213469	0.0041648	2.6E-08
10	MYO3A	rs2096176	26144437	T	C	0.3030150	-0.0244475	0.0039519	4.6E-11
10	MYO3A	rs7085103	26144744	A	G	0.3028070	-0.0245913	0.0039526	3.5E-11
10	MYO3A	rs10828955	26144942	A	G	0.3028070	-0.0245913	0.0039526	3.5E-11
10	MYO3A	rs2226129	26146401	C	T	0.3029510	-0.0245015	0.0039521	4.4E-11
10	MYO3A	rs7091566	26146980	G	A	0.3029510	-0.0245015	0.0039521	4.4E-11
10	MYO3A	rs11273792	26147231	C	'AAGGAG	0.3026480	-0.0244864	0.0039592	4.8E-11
10	MYO3A	rs2368158	26147358	T	G	0.3027320	-0.0245904	0.0039532	3.5E-11
10	MYO3A	rs7079780	26148577	T	C	0.3027980	-0.0245272	0.0039534	4.1E-11
10	MYO3A	rs7082411	26148840	A	G	0.3042910	-0.0242773	0.0039463	5.6E-11
10	MYO3A	rs1342319	26149220	T	C	0.3043480	-0.0242920	0.0039466	5.6E-11
10	MYO3A	chr10:26149611_CT_C	26149611	C	CT	0.3047510	-0.0240976	0.0039453	7.2E-11
10	MYO3A	rs7093989	26151483	T	C	0.3029430	-0.0244599	0.0039522	4.7E-11
10	MYO3A	rs7081905	26152169	G	A	0.3026920	-0.0246521	0.0039536	3.5E-11
10	MYO3A	rs7476324	26152501	G	A	0.3026840	-0.0246663	0.0039537	3.4E-11
10	MYO3A	rs7079125	26155357	T	C	0.3022350	-0.0238918	0.0039617	1.4E-10
10	MYO3A	rs4575167	26155558	C	T	0.3028740	-0.0242998	0.0039548	6.9E-11
10	MYO3A	rs7084000	26157105	A	T	0.3027390	-0.0241422	0.0039605	9.3E-11
10	MYO3A	rs3758449	26157383	A	G	0.3039990	-0.0238895	0.0039543	1.2E-10
10	MYO3A	rs7096646	26157740	A	G	0.3025670	-0.0240264	0.0039618	1.1E-10
10	MYO3A	rs11014974	26158259	A	T	0.3069630	-0.0248492	0.0039878	3.0E-11
10	MYO3A	rs12247347	26160429	G	T	0.3039630	-0.0239674	0.0039621	1.2E-10
10	MYO3A	rs11014976	26162030	T	C	0.3011450	-0.0240601	0.0039783	1.5E-10
10	MYO3A	rs12258401	26162973	A	G	0.3008060	-0.0243669	0.0039809	1.0E-10
10	MYO3A	rs11278135	26164136	A	AGTGAA	0.3012030	-0.0248222	0.0039950	5.8E-11
10	MYO3A	rs7095559	26164239	A	G	0.3007910	-0.0244338	0.0039820	9.0E-11
10	MYO3A	rs79404147	26164378	T	TCTC	0.3010220	-0.0242316	0.0039807	1.2E-10
10	MYO3A	rs11593041	26164463	T	C	0.3007870	-0.0244047	0.0039823	9.3E-11
10	MYO3A	rs11014979	26164506	T	C	0.3007850	-0.0244041	0.0039823	9.4E-11
10	MYO3A	rs6482531	26164870	G	A	0.3027660	-0.0240999	0.0039738	1.3E-10
10	MYO3A	rs12262728	26165259	A	G	0.3007720	-0.0244605	0.0039829	8.8E-11
10	MYO3A	rs1935484	26165561	C	A	0.3009880	-0.0242355	0.0039817	1.2E-10
10	MYO3A	rs57140516	26165682	TA	T	0.3007240	-0.0239168	0.0039922	2.0E-10
10	MYO3A	rs6482532	26166936	T	C	0.3008820	-0.0241239	0.0039836	1.5E-10
10	MYO3A	rs7072451	26167004	C	T	0.3007150	-0.0240969	0.0039853	1.5E-10
10	MYO3A	rs12411554	26167273	T	C	0.2999300	-0.0242468	0.0039912	1.3E-10
10	MYO3A	rs1342320	26168607	T	C	0.3004110	-0.0242569	0.0039879	1.2E-10
10	MYO3A	rs12266309	26172303	A	G	0.3003980	-0.0244185	0.0039897	1.1E-10
10	MYO3A	rs7920488	26172632	C	T	0.3017360	-0.0240379	0.0039840	1.7E-10
10	MYO3A	rs3740232	26173861	A	G	0.3001430	-0.0245635	0.0039914	8.6E-11
10	MYO3A	rs3740231	26174114	T	A	0.3003770	-0.0244166	0.0039898	1.1E-10
10	MYO3A	rs3758448	26174640	A	G	0.2999800	-0.0245735	0.0039929	8.3E-11
10	MYO3A	rs3758447	26174658	G	C	0.3002150	-0.0244264	0.0039914	1.0E-10
10	MYO3A	chr10:26174880_T_TA	26174880	TA	T	0.2904890	-0.0247058	0.0040778	1.6E-10
10	MYO3A	rs11014984	26174951	C	A	0.2999720	-0.0245248	0.0039939	8.8E-11
10	MYO3A	rs12258453	26175593	T	C	0.2998670	-0.0247316	0.0039952	6.3E-11
10	MYO3A	rs10764598	26176021	A	G	0.2998610	-0.0247109	0.0039953	6.6E-11
10	MYO3A	rs4539209	26178388	A	C	0.2995020	-0.0249254	0.0040008	5.1E-11
10	MYO3A	rs10508714	26181507	A	G	0.2678750	-0.0277966	0.0041515	3.2E-12
10	MYO3A	rs35345606	26182961	G	GGT	0.2682950	-0.0279297	0.0041497	2.2E-12
10	MYO3A	rs35115855	26189048	G	GA	0.2446960	-0.0340330	0.0042952	4.9E-16
10	MYO3A	rs11014993	26194254	C	T	0.2415350	-0.0360817	0.0043099	8.0E-18
10	MYO3A	rs11014995	26201627	A	C	0.2732010	-0.0350043	0.0041218	7.8E-19
10	MYO3A	rs11014996	26202223	C	G	0.2746430	-0.0350863	0.0041116	4.9E-19
10	MYO3A	rs11819063	26204863	G	T	0.2743570	-0.0350756	0.0041034	4.0E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	MYO3A	rs12243193	26205574	A	G	0.2700310	-0.0359901	0.0041590	1.3E-19
10	MYO3A	rs7073982	26205583	T	A	0.3313030	-0.0278276	0.0039256	4.0E-14
10	MYO3A	rs12266027	26205678	G	A	0.2689880	-0.0355929	0.0041439	3.1E-19
10	MYO3A	rs11014997	26205715	A	C	0.2717610	-0.0345752	0.0041222	2.4E-18
10	MYO3A	rs78507306	26206368	C	CT	0.2729800	-0.0358723	0.0040997	7.1E-20
10	MYO3A	rs28838032	26206741	T	G	0.2730240	-0.0357539	0.0040988	9.0E-20
10	MYO3A	rs995683	26207454	T	A	0.2730590	-0.0356860	0.0040976	1.0E-19
10	MYO3A	rs7099347	26207814	C	T	0.2730530	-0.0357188	0.0040969	9.3E-20
10	MYO3A	chr10:26210133_GGGAA_G	26208052	AT	A	0.2710200	-0.0350429	0.0041199	7.4E-19
10	MYO3A	rs11014998	26208216	A	G	0.3349850	-0.0278756	0.0038719	3.3E-14
10	MYO3A	rs1330572	26208490	G	A	0.2730690	-0.0358513	0.0040951	6.5E-20
10	MYO3A	rs7923442	26208775	G	A	0.2731030	-0.0358938	0.0040945	5.8E-20
10	MYO3A	rs1330573	26208970	G	C	0.3348540	-0.0276612	0.0038684	4.4E-14
10	MYO3A	chr10:26210133_GGGAA_G	26210133	G	GGGAA	0.2634230	-0.0371557	0.0041821	3.3E-20
10	MYO3A	chr10:26210982_G_GCA	26210982	GCA	G	0.2728260	-0.0346632	0.0041123	1.1E-18
10	MYO3A	rs994502	26211237	C	T	0.2731750	-0.0357497	0.0040821	6.2E-20
10	MYO3A	rs10508715	26211729	G	A	0.2730760	-0.0355388	0.0040809	9.9E-20
10	MYO3A *	rs7072136	26213780	A	G	0.2733220	-0.0355652	0.0040751	8.3E-20
10	GAD2 *	rs8190582	26214806	T	A	0.2731720	-0.0354051	0.0040712	1.1E-19
10	GAD2 *	rs2839669	26214873	T	C	0.2731740	-0.0354200	0.0040712	1.1E-19
10	GAD2 *	rs3758446	26215210	A	G	0.2731720	-0.0354101	0.0040711	1.1E-19
10	GAD2 *	rs2839670	26215411	A	C	0.2731640	-0.0354010	0.0040712	1.1E-19
10	GAD2 *	rs2236417	26216285	C	G	0.2732560	-0.0354103	0.0040709	9.6E-20
10	GAD2	rs2236418	26216567	G	A	0.2734480	-0.0354327	0.0040696	9.3E-20
10	GAD2	rs2839671	26216893	A	G	0.2734060	-0.0353499	0.0040699	1.1E-19
10	GAD2	rs57204137	26218555	T	A	0.2613650	-0.0360358	0.0042153	1.7E-19
10	GAD2	rs8190598	26218666	G	A	0.2731220	-0.0352888	0.0040754	1.3E-19
10	GAD2	rs7071922	26218918	G	C	0.3343360	-0.0272042	0.0038487	6.3E-14
10	GAD2	rs61839365	26226737	A	G	0.2738430	-0.0355005	0.0040766	7.9E-20
10	GAD2	rs3847378	26231023	G	A	0.3287680	-0.0271177	0.0038738	1.1E-13
10	GAD2	rs8190647	26231584	T	C	0.2707910	-0.0357590	0.0040952	9.8E-20
10	GAD2	rs12243037	26235445	A	G	0.2692800	-0.0358061	0.0040970	8.0E-20
10	GAD2	rs1330581	26239906	G	A	0.3363160	-0.0267917	0.0038976	2.3E-13
10	GAD2	rs4749100	26248701	C	A	0.2620200	-0.0302341	0.0041839	4.9E-14
10	GAD2	rs11015014	26249690	A	G	0.2628360	-0.0307420	0.0041805	1.7E-14
10	GAD2	rs11015015	26250566	G	A	0.2628350	-0.0302305	0.0041729	4.1E-14
10	GAD2	rs7074897	26250754	T	A	0.2544730	-0.0300084	0.0042366	1.7E-13
10	GAD2	rs2368159	26251800	C	T	0.3237890	-0.0226936	0.0039124	8.0E-10
10	GAD2	rs2368160	26251842	A	G	0.3237820	-0.0226964	0.0039124	8.0E-10
10	GAD2	rs10828964	26252355	T	C	0.3174130	-0.0232784	0.0039556	4.2E-10
10	GAD2	rs8190678	26254190	C	G	0.3237640	-0.0224097	0.0039083	1.3E-09
10	GAD2	rs8190683	26254515	T	C	0.3238170	-0.0224009	0.0039077	1.3E-09
10	GAD2	rs7900739	26254929	A	G	0.3238300	-0.0224896	0.0039075	1.1E-09
10	GAD2	rs58116757	26255600	GGAAA	G	0.3223150	-0.0223768	0.0039220	1.3E-09
10	GAD2	rs71908996	26255646	A	AGGGGAC	0.3195820	-0.0221106	0.0039388	2.1E-09
10	GAD2	rs7089218	26255858	A	G	0.3239060	-0.0223785	0.0039067	1.3E-09
10	GAD2	rs12414701	26256474	T	C	0.3241860	-0.0223276	0.0039071	1.5E-09
10	GAD2	rs7918935	26257342	A	C	0.3239310	-0.0222983	0.0039059	1.4E-09
10	GAD2	rs79108813	26257634	A	AC	0.3239680	-0.0222847	0.0039059	1.5E-09
10	GAD2	rs1935996	26259517	A	T	0.2625980	-0.0299951	0.0041621	6.7E-14
10	GAD2	rs7893400	26261214	C	T	0.2629830	-0.0297743	0.0041601	9.7E-14
10	GAD2	rs1330582	26263185	T	C	0.2628160	-0.0296961	0.0041584	1.0E-13
10	GAD2	rs4749101	26263648	T	C	0.3239430	-0.0219530	0.0039044	2.7E-09
10	GAD2	rs4749102	26263794	A	G	0.3243480	-0.0221032	0.0039022	2.2E-09
10	GAD2	rs4747547	26264631	G	A	0.2611890	-0.0300906	0.0041646	6.1E-14
10	GAD2	rs8190704	26268384	C	T	0.3227790	-0.0224889	0.0039009	1.3E-09
10	GAD2	rs7073119	26268681	G	A	0.3233790	-0.0223914	0.0038991	1.5E-09
10	GAD2	rs7076544	26268796	G	A	0.2615610	-0.0300962	0.0041574	6.1E-14
10	GAD2	rs8190706	26268841	A	C	0.2615500	-0.0300897	0.0041574	6.1E-14
10	GAD2	rs4749103	26271001	C	A	0.2621290	-0.0298835	0.0041450	8.0E-14
10	GAD2	rs3781114	26271711	A	G	0.2624360	-0.0295484	0.0041374	1.3E-13
10	GAD2	rs7095327	26272292	C	T	0.3237580	-0.0221041	0.0038772	1.7E-09
10	GAD2	rs7074235	26272333	T	C	0.2627860	-0.0299112	0.0041302	5.7E-14
10	GAD2	rs8190722	26272554	CAG	C	0.3237950	-0.0221153	0.0038765	1.7E-09
10	GAD2	rs6482548	26272950	G	A	0.3236340	-0.0221340	0.0038777	1.7E-09
10	GAD2	rs7906725	26273968	A	G	0.3238370	-0.0219918	0.0038755	2.1E-09
10	GAD2	rs4749105	26274041	T	A	0.3238380	-0.0219877	0.0038755	2.1E-09
10	GAD2	rs7900976	26275504	G	T	0.2628660	-0.0298635	0.0041283	6.1E-14
10	GAD2	rs6482550	26275598	C	T	0.3237940	-0.0219968	0.0038748	2.0E-09
10	GAD2	rs7909127	26275922	G	A	0.2628660	-0.0298742	0.0041283	5.9E-14
10	GAD2	rs56405990	26276309	A	G	0.2628630	-0.0298844	0.0041283	5.8E-14
10	GAD2	rs59350339	26276457	CT	C	0.2628660	-0.0298765	0.0041283	5.9E-14
10	GAD2	rs7067571	26276705	T	G	0.3237910	-0.0219717	0.0038747	2.1E-09
10	GAD2	rs11015024	26276893	G	A	0.2628620	-0.0298535	0.0041283	6.1E-14
10	GAD2	rs913962	26277306	C	T	0.2629030	-0.0297952	0.0041277	6.7E-14
10	GAD2	rs913963	26277363	T	C	0.2629030	-0.0297952	0.0041277	6.7E-14
10	GAD2	rs1999241	26277498	G	A	0.3238040	-0.0219084	0.0038743	2.3E-09
10	GAD2	rs11015026	26277678	C	G	0.2607570	-0.0294857	0.0041404	9.9E-14
10	GAD2	rs992990	26278252	A	C	0.3214070	-0.0213650	0.0038850	4.4E-09
10	GAD2	rs3781113	26278759	C	T	0.2606980	-0.0294007	0.0041411	1.2E-13
10	GAD2	rs3781112	26278932	G	A	0.3217910	-0.0215488	0.0038852	3.5E-09
10	GAD2	rs3781111	26278986	G	A	0.3215960	-0.0213901	0.0038834	4.3E-09
10	GAD2	rs3781109	26279433	G	C	0.3216190	-0.0214686	0.0038851	3.8E-09
10	GAD2	rs4144102	26279776	G	A	0.2606880	-0.0295357	0.0041426	8.8E-14
10	GAD2	rs8190748	26280826	G	A	0.3217610	-0.0217629	0.0038850	2.4E-09
10	GAD2	rs8190754	26281792	T	G	0.2608460	-0.0298259	0.0041423	5.4E-14
10	GAD2	rs8190756	26281996	A	G	0.2608460	-0.0298259	0.0041423	5.4E-14
10	GAD2	rs8190757	26282080	C	A	0.3218190	-0.0218377	0.0038854	2.1E-09
10	GAD2	rs8190758	26282135	G	GT	0.3218190	-0.0218377	0.0038854	2.1E-09
10	GAD2	rs4749107	26283913	G	A	0.3217380	-0.0218124	0.0038851	2.2E-09
10	GAD2	rs4749108	26284109	T	C	0.2608390	-0.0298552	0.0041425	5.1E-14
10	GAD2	rs11594057	26284147	A	G	0.2608390	-0.0298552	0.0041425	5.1E-14
10	GAD2	rs11594128	26284628	A	G	0.2592760	-0.0294960	0.0041524	1.2E-13
10	GAD2	rs4749109	26284820	T	C	0.2582890	-0.0300702	0.0041569	5.1E-14
10	GAD2	rs4747548	26285001	G	T	0.2582420	-0.0303725	0.0041578	2.6E-14
10	GAD2	rs8190764	26285330	C	G	0.3210820	-0.0216494	0.0038899	2.8E-09
10	GAD2	rs7913676	26285818	T	C	0.2558970	-0.0301261	0.0041763	6.6E-14
10	GAD2	rs7902107	26285964	C	T	0.3199720	-0.0211876	0.0038935	6.4E-09
10	GAD2	rs4747549	26287097	G	A	0.2587730	-0.0302201	0.0041520	3.4E-14
10	GAD2	rs3847379	26287905	A	G	0.2587280	-0.0302538	0.0041521	3.2E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	GAD2	rs55878324	26288742	A	G	0.2588770	-0.0305317	0.0041515	2.0E-14
10	GAD2	rs3847380	26289015	T	G	0.3209310	-0.0217134	0.0038884	2.4E-09
10	GAD2	rs11015028	26289408	T	C	0.2587300	-0.0302580	0.0041520	3.2E-14
10	GAD2	rs8190780	26291107	G	T	0.3209290	-0.0216868	0.0038883	2.5E-09
10	GAD2	rs8190782	26291455	C	G	0.2587280	-0.0302545	0.0041520	3.2E-14
10	GAD2	rs3781108	26292164	C	T	0.2587490	-0.0302875	0.0041520	3.1E-14
10	GAD2	rs3824694	26292392	C	G	0.2587310	-0.0302921	0.0041520	3.1E-14
10	GAD2	rs57685594	26294449	C	T	0.2587310	-0.0302921	0.0041520	3.1E-14
10	GAD2	rs58143184	26295041	T	TG	0.2587310	-0.0302921	0.0041520	3.1E-14
10	GAD2	rs56086837	26295073	A	G	0.2587310	-0.0302921	0.0041520	3.1E-14
10	GAD2	rs4747550	26296673	G	A	0.2587500	-0.0303265	0.0041521	2.9E-14
10	GAD2	chr10:26296920_AT_A	26296920	A	AT	0.2574470	-0.0304443	0.0041738	3.3E-14
10	GAD2	rs12248404	26297174	G	A	0.2577280	-0.0301271	0.0041624	4.1E-14
10	GAD2	rs12240863	26297176	G	C	0.2577280	-0.0301271	0.0041624	4.1E-14
10	GAD2	rs61839388	26298225	A	G	0.2587030	-0.0304160	0.0041529	2.5E-14
10	GAD2	rs913964	26298612	G	A	0.2587000	-0.0304209	0.0041529	2.5E-14
10	GAD2	rs913965	26299434	C	A	0.2586960	-0.0304367	0.0041529	2.4E-14
10	GAD2	rs928197	26300696	A	T	0.2585030	-0.0303796	0.0041553	2.8E-14
10	GAD2	rs3781106	26302081	G	A	0.2586000	-0.0302225	0.0041538	3.4E-14
10	GAD2	rs1335547	26302650	A	G	0.2585960	-0.0301781	0.0041537	3.6E-14
10	GAD2	rs8190809	26303059	T	G	0.2584900	-0.0301451	0.0041555	3.9E-14
10	GAD2	rs147225410	26303980	T	TTCTCTC	0.2573080	-0.0303898	0.0041663	3.0E-14
10	GAD2 *	rs4749110	26304596	G	A	0.2586520	-0.0301127	0.0041522	3.8E-14
10	GAD2 *	rs4749111	26304777	A	T	0.2590060	-0.0298786	0.0041526	5.6E-14
10	GAD2 *	rs4747551	26304794	C	T	0.2582260	-0.0297690	0.0041609	7.9E-14
10	GAD2 *	rs4747552	26304795	A	G	0.2585450	-0.0296478	0.0041576	9.3E-14
10	GAD2 *	rs4747553	26304945	T	C	0.2586430	-0.0300546	0.0041516	4.1E-14
10	GAD2 *	rs144491599	26304973	TG	T	0.2587130	-0.0300936	0.0041524	3.8E-14
10	GAD2 *	rs11812647	26305230	A	G	0.2587320	-0.0300846	0.0041504	3.8E-14
10	GAD2 *	rs11816486	26305244	T	C	0.2586900	-0.0300252	0.0041508	4.4E-14
10	GAD2 *	rs11816500	26305255	T	C	0.2587320	-0.0300846	0.0041504	3.8E-14
10	GAD2 *	rs34495911	26305310	GT	G	0.2557180	-0.0309633	0.0041743	1.0E-14
10	GAD2 *	rs11816523	26305391	T	C	0.2587020	-0.0305358	0.0041519	2.0E-14
10	GAD2 *	rs11818976	26305392	C	T	0.2587020	-0.0305358	0.0041519	2.0E-14
10	GAD2 *	rs148314348	26305459	AT	A	0.2586050	-0.0300713	0.0041559	4.4E-14
10	GAD2 *	rs2017306	26306329	C	A	0.2586830	-0.0300118	0.0041500	4.2E-14
10	GAD2 *	rs1831432	26306376	G	A	0.2586840	-0.0300202	0.0041500	4.2E-14
10	GAD2 *	rs1888251	26308387	T	C	0.3204540	-0.0214914	0.0038881	3.4E-09
10	GAD2 *	rs913961	26308420	T	C	0.3157910	-0.0218272	0.0039181	2.4E-09
10	GAD2 *	rs882139	26308486	T	C	0.3194490	-0.0210902	0.0038966	7.4E-09
10	GAD2 *	rs5783969	26308753	AT	A	0.3211820	-0.0214461	0.0038842	3.7E-09
10	GAD2 *	rs882138	26308804	C	T	0.2588540	-0.0298776	0.0041463	5.3E-14
10	GAD2 *	rs4749112	26312430	G	A	0.3289620	-0.0226904	0.0038711	6.6E-10
10	GAD2 *	rs12248143	26313498	A	G	0.2585180	-0.0298564	0.0041502	5.7E-14
10	GAD2 *	rs2150158	26314421	T	C	0.3208330	-0.0215369	0.0038870	3.4E-09
10	GAD2 *	rs12265385	26314508	T	C	0.3208280	-0.0215554	0.0038870	3.3E-09
10	GAD2 *	rs60023298	26314569	C	CGTGG	0.3207910	-0.0215168	0.0038873	3.5E-09
10	GAD2 *	rs10828968	26314785	A	G	0.2584760	-0.0299139	0.0041509	5.1E-14
10	GAD2 *	rs10828969	26315141	A	G	0.2586150	-0.0299766	0.0041518	4.6E-14
10	GAD2 *	rs12260721	26317687	T	C	0.2584900	-0.0298367	0.0041538	5.1E-14
10	GAD2 *	rs12247267	26317994	A	G	0.2583730	-0.0298197	0.0041532	5.5E-14
10	GAD2 *	rs12572822	26318439	A	C	0.2583680	-0.0298130	0.0041533	5.6E-14
10	GAD2 *	rs61838362	26318622	G	A	0.3095720	-0.0226517	0.0039773	1.6E-09
10	GAD2 *	rs61838363	26319036	C	T	0.2585120	-0.0298325	0.0041519	5.9E-14
10	GAD2 *	rs4749113	26320450	C	A	0.3212850	-0.0214306	0.0038964	4.2E-09
10	GAD2 *	rs7079553	26321314	A	G	0.3209470	-0.0214429	0.0039018	3.7E-09
10	GAD2 *	rs7079848	26321528	A	G	0.3209460	-0.0214763	0.0039022	3.5E-09
10	GAD2 *	rs7080952	26321550	T	C	0.3209120	-0.0215536	0.0039022	3.1E-09
10	GAD2 *	rs7068091	26321586	C	T	0.3210510	-0.0216801	0.0039012	2.7E-09
10	GAD2 *	rs7080128	26321735	A	G	0.2587630	-0.0299394	0.0041649	4.9E-14
10	GAD2 *	rs12241667	26322609	A	C	0.3213430	-0.0219230	0.0039050	1.8E-09
10	GAD2 *	rs12250822	26322636	C	T	0.2588430	-0.0300752	0.0041668	4.1E-14
10	GAD2 *	rs12245460	26323987	A	C	0.3207640	-0.0217969	0.0039138	2.2E-09
10	GAD2 *	rs6482555	26325159	T	C	0.2536240	-0.0304310	0.0042227	3.9E-14
10	GAD2 *	rs989118	26326902	T	C	0.2564060	-0.0306137	0.0042059	2.5E-14
10	GAD2 *	rs10828972	26333318	G	A	0.2453800	-0.0281811	0.0043122	5.4E-12
10	GAD2 *	rs11015040	26335958	C	A	0.2442540	-0.0278531	0.0043233	1.1E-11
10	GAD2 *	rs10828974	26339846	T	C	0.2732760	-0.0217508	0.0041008	3.7E-08
10	PAPSS2	rs116984245	87721910	C	T	0.0670147	0.0421519	0.0073512	3.4E-08
10	PAPSS2	rs117699393	87735100	T	C	0.0644453	0.0419087	0.0074586	4.8E-08
10	ATAD1	rs117726160	87793220	C	G	0.0612526	0.0437322	0.0075982	2.9E-08
10	ATAD1	rs117347219	87812543	A	G	0.0606264	0.0435906	0.0076422	3.7E-08
10	HHEX *	rs10786053	92714340	G	A	0.1864140	0.0267197	0.0046745	1.9E-08
10	HHEX *	rs10882105	92714354	C	T	0.1864140	0.0267197	0.0046745	1.9E-08
10	HHEX *	rs2901609	92715354	G	A	0.1850390	0.0268633	0.0047707	2.1E-08
10	HHEX *	rs10748582	92717462	T	A	0.1908890	0.0265855	0.0046326	1.1E-08
10	HHEX *	rs1832886	92717782	G	A	0.1909500	0.0268264	0.0046336	8.8E-09
10	HHEX *	rs7898054	92718113	C	T	0.1908930	0.0265188	0.0046323	1.3E-08
10	HHEX *	rs10882106	92720577	C	T	0.1910320	0.0268465	0.0046280	9.2E-09
10	HHEX *	rs7923837	92722160	G	A	0.1920670	0.0259141	0.0046029	2.4E-08
10	HHEX *	rs7923866	92722319	C	T	0.1910480	0.0265401	0.0046257	1.2E-08
10	HHEX *	rs11187149	92726006	G	A	0.1898780	0.0268443	0.0046375	9.5E-09
10	PDE6C	rs2857293	93621212	A	G	0.3615520	-0.0208356	0.0037803	2.7E-08
10	PDE6C	rs701865	93622016	A	T	0.4759640	-0.0273963	0.0036611	1.2E-13
10	PDE6C	rs68054705	93622807	G	A	0.4764390	-0.0279259	0.0036689	5.6E-14
10	PDE6C	rs4919314	93623845	C	T	0.4752480	-0.0277938	0.0036645	5.2E-14
10	PDE6C	rs7903992	93624100	C	T	0.4064340	-0.0240535	0.0037207	3.8E-11
10	PDE6C	rs7095788	93624395	T	C	0.4750410	-0.0277884	0.0036626	5.7E-14
10	PDE6C	rs72822861	93624434	T	C	0.3628310	-0.0212111	0.0037986	1.5E-08
10	PDE6C	rs2785137	93626450	A	G	0.4601550	-0.0292197	0.0036652	3.1E-15
10	PDE6C	rs2765828	93626511	C	T	0.4601860	-0.0293156	0.0036650	2.5E-15
10	PDE6C	rs2785138	93626983	A	C	0.3480630	-0.0227322	0.0038359	2.1E-09
10	PDE6C	rs2785139	93627037	T	C	0.3481230	-0.0227828	0.0038358	2.0E-09
10	PDE6C	rs72822864	93627543	A	G	0.3481200	-0.0229393	0.0038336	1.5E-09
10	PDE6C	rs10882287	93628570	G	A	0.4604120	-0.0296265	0.0036587	1.2E-15
10	PDE6C	rs2857300	93629157	G	A	0.4595010	-0.0293062	0.0036475	2.2E-15
10	PDE6C	rs714550	93629284	A	G	0.4590750	-0.0294309	0.0036482	1.4E-15
10	PDE6C	rs714549	93629326	G	A	0.4590810	-0.0293384	0.0036480	1.7E-15
10	PDE6C	rs714551	93629367	A	G	0.4590670	-0.0293946	0.0036480	1.5E-15
10	PDE6C	rs1409335	93629492	A	G	0.4590930	-0.0294220	0.0036477	1.3E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	PDE6C	rs1409334	93629494	A	T	0.4590900	-0.0294487	0.0036477	1.3E-15
10	PDE6C	rs4919339	93629924	C	T	0.4591330	-0.0293311	0.0036473	1.7E-15
10	PDE6C	rs4917871	93629971	G	A	0.4545090	-0.0298929	0.0036448	5.3E-16
10	PDE6C	rs4919340	93630024	G	C	0.3425620	-0.0232561	0.0038280	8.7E-10
10	PDE6C	rs72822871	93630117	A	G	0.3425140	-0.0233788	0.0038278	7.2E-10
10	PDE6C	rs10882288	93630119	T	C	0.4544450	-0.0298145	0.0036449	6.1E-16
10	PDE6C	rs72822872	93630206	T	C	0.3425150	-0.0233791	0.0038278	7.3E-10
10	PDE6C	rs3824752	93630259	G	C	0.4544240	-0.0298315	0.0036451	6.0E-16
10	PDE6C	rs716333	93630984	A	T	0.4553960	-0.0297717	0.0036445	6.4E-16
10	PDE6C	rs716332	93631058	C	G	0.3429030	-0.0230926	0.0038294	1.1E-09
10	PDE6C	rs1409333	93631162	T	C	0.4547370	-0.0296517	0.0036496	9.2E-16
10	PDE6C	rs11187560	93631600	G	A	0.4389340	0.0231158	0.0036834	3.6E-10
10	PDE6C	rs11187561	93631602	C	T	0.4389340	0.0231176	0.0036834	3.6E-10
10	PDE6C	rs473934	93632179	T	A	0.4402710	0.0224819	0.0036695	8.5E-10
10	PDE6C	rs11187562	93632274	C	G	0.4402570	0.0224629	0.0036694	8.7E-10
10	PDE6C	rs4919344	93632334	G	A	0.4402480	0.0225056	0.0036694	8.3E-10
10	PDE6C	rs1326219	93632627	C	G	0.4403190	0.0223998	0.0036688	9.9E-10
10	PDE6C	rs1326218	93632628	G	A	0.4403190	0.0223998	0.0036688	9.9E-10
10	PDE6C	rs199932924	93633475	T	A	0.3160160	-0.0240588	0.0040022	1.9E-09
10	PDE6C	rs1147642	93633481	A	T	0.4459800	0.0222749	0.0036723	1.4E-09
10	PDE6C	rs547759	93633864	G	A	0.4472790	0.0229024	0.0036730	5.3E-10
10	PDE6C	rs583830	93634171	G	C	0.4459520	0.0224820	0.0036724	1.0E-09
10	ADRA2A *	rs17189569	111211193	T	G	0.0366726	-0.0583579	0.0096978	2.5E-09
10	ADRA2A *	rs7099830	111211799	T	C	0.0366721	-0.0584514	0.0096978	2.4E-09
10	ADRA2A *	rs12780861	111212053	A	C	0.0365279	-0.0576037	0.0097147	4.2E-09
10	ADRA2A *	rs11595612	111212747	T	C	0.0365079	-0.0577031	0.0097173	3.9E-09
10	ADRA2A *	rs4369325	111215419	A	G	0.0365306	-0.0571185	0.0097198	5.8E-09
10	ADRA2A *	rs34879213	111217275	G	T	0.0365706	-0.0588244	0.0097124	1.8E-09
10	ADRA2A *	rs17775480	111219324	A	G	0.0415840	-0.0531947	0.0091625	6.8E-09
10	ADRA2A *	rs35990311	111220933	CA	C	0.0415898	-0.0529668	0.0091618	7.8E-09
10	ADRA2A *	rs11598008	111221933	A	G	0.0414570	-0.0522617	0.0091743	1.2E-08
10	ADRA2A *	rs1335715	111222319	T	C	0.0414567	-0.0522594	0.0091743	1.2E-08
10	ADRA2A *	rs11598724	111223231	A	G	0.0364653	-0.0581088	0.0097234	2.8E-09
10	ADRA2A *	rs12769195	111226630	A	G	0.0366419	-0.0586283	0.0097012	2.0E-09
10	ADRA2A *	rs11817468	111227839	G	A	0.0366483	-0.0583940	0.0097004	2.2E-09
10	ADRA2A *	rs1889746	111228166	A	G	0.0366459	-0.0583986	0.0097004	2.2E-09
10	ADRA2A *	rs12263303	111229260	C	A	0.0366484	-0.0586764	0.0096999	1.9E-09
10	ADRA2A *	rs34083578	111229853	T	C	0.0366735	-0.0585062	0.0096979	2.1E-09
10	ADRA2A *	rs12771311	111230167	A	G	0.0366717	-0.0585368	0.0096969	2.0E-09
10	ADRA2A *	rs75491596	111233242	G	C	0.0365734	-0.0579704	0.0097069	2.9E-09
10	ADRA2A *	rs58799675	111233351	C	CTCAGA1	0.0365767	-0.0579177	0.0097064	3.0E-09
10	ADRA2A *	rs36121579	111234277	G	A	0.0367208	-0.0584291	0.0096896	2.1E-09
10	ADRA2A *	rs17128623	111237115	A	G	0.0369514	-0.0579446	0.0096619	2.5E-09
10	ADRA2A *	rs2078596	111237410	C	T	0.0369578	-0.0577588	0.0096611	2.8E-09
10	ADRA2A *	rs77262937	111240659	C	T	0.0370586	-0.0578325	0.0096485	2.9E-09
10	ADRA2A *	rs865858825	111242150	T	C	0.0363248	-0.0595171	0.0097442	1.4E-09
10	ADRA2A *	rs190656732	111242270	C	T	0.0328349	-0.0577312	0.0102519	1.6E-08
10	ADRA2A *	rs868056697	111242279	A	T	0.0359395	-0.0597049	0.0097928	1.5E-09
10	ADRA2A *	rs199751672	111242674	T	TAA	0.0371074	-0.0578865	0.0096413	2.7E-09
10	ADRA2A *	rs12769814	111243819	T	G	0.0369587	-0.0593846	0.0096606	1.1E-09
10	ADRA2A *	rs12770960	111243867	G	T	0.0371101	-0.0580088	0.0096409	2.5E-09
10	ADRA2A *	rs71481125	111245039	G	A	0.0371196	-0.0582972	0.0096397	2.1E-09
10	ADRA2A *	rs34045903	111246355	T	C	0.0371579	-0.0585757	0.0096356	1.7E-09
10	ADRA2A *	rs150853619	111247639	T	TATATA	0.0371496	-0.0583369	0.0096355	2.0E-09
10	ADRA2A *	rs12780993	111249500	T	C	0.0372218	-0.0593665	0.0096245	1.0E-09
10	ADRA2A *	rs7100417	111249666	G	A	0.0372210	-0.0593578	0.0096244	1.0E-09
10	ADRA2A *	rs58899740	111249859	G	A	0.0372307	-0.0593456	0.0096232	1.1E-09
10	ADRA2A *	rs12768852	111250758	T	C	0.0372615	-0.0591999	0.0096171	1.2E-09
10	ADRA2A *	rs34294586	111253094	T	TA	0.0385141	-0.0552589	0.0094763	6.8E-09
10	ADRA2A *	rs35095809	111254014	T	C	0.0370397	-0.0586390	0.0096426	1.4E-09
10	ADRA2A *	rs7098315	111254105	G	A	0.0374109	-0.0585096	0.0095949	1.7E-09
10	ADRA2A *	rs7098858	111254278	A	G	0.0374139	-0.0585806	0.0095945	1.6E-09
10	ADRA2A *	rs11599394	111254379	A	G	0.0374131	-0.0585674	0.0095945	1.6E-09
10	ADRA2A *	rs11592908	111254510	C	T	0.0374159	-0.0587262	0.0095941	1.5E-09
10	ADRA2A *	rs17128645	111255551	A	G	0.0376125	-0.0604165	0.0095687	4.3E-10
10	ADRA2A *	rs76385632	111255844	G	C	0.0376655	-0.0605303	0.0095608	3.6E-10
10	ADRA2A *	rs71481128	111257344	A	C	0.0379211	-0.0619545	0.0095284	1.4E-10
10	ADRA2A *	rs12775580	111257644	T	C	0.0379577	-0.0616184	0.0095270	1.7E-10
10	ADRA2A *	rs56046350	111258401	T	C	0.0379413	-0.0621398	0.0095260	1.3E-10
10	ADRA2A *	rs34211312	111261215	T	C	0.0378537	-0.0609745	0.0095369	2.6E-10
10	ADRA2A *	rs9804290	111261305	A	G	0.0380106	-0.0619023	0.0095175	1.4E-10
10	ADRA2A *	rs11195496	111261773	T	G	0.0378697	-0.0610391	0.0095349	2.4E-10
10	ADRA2A *	rs4287275	111262555	C	T	0.0380632	-0.0620650	0.0095103	1.2E-10
10	ADRA2A *	rs57929635	111264756	A	G	0.0380801	-0.0622599	0.0095078	1.1E-10
10	ADRA2A *	rs11594653	111266128	A	G	0.0375796	-0.0608596	0.0095655	3.1E-10
10	ADRA2A *	rs11599188	111266699	G	A	0.0377370	-0.0618017	0.0095460	1.7E-10
10	ADRA2A *	rs10509938	111268859	T	C	0.0377902	-0.0614167	0.0095382	2.2E-10
10	ADRA2A *	rs10885119	111269201	T	C	0.0377958	-0.0618732	0.0095364	1.6E-10
10	ADRA2A *	rs35011531	111272337	T	C	0.0380231	-0.0621793	0.0095055	1.1E-10
10	ADRA2A *	rs4258313	111272640	T	G	0.0378830	-0.0619581	0.0095243	1.4E-10
10	ADRA2A *	rs7071574	111273370	A	G	0.0378792	-0.0619303	0.0095247	1.4E-10
10	ADRA2A *	rs12255945	111273466	A	G	0.0378792	-0.0619303	0.0095247	1.4E-10
10	ADRA2A *	rs11358281	111274806	T	TG	0.0374851	-0.0625070	0.0095756	1.4E-10
10	ADRA2A *	rs12784552	111276596	G	A	0.0378814	-0.0616173	0.0095248	1.8E-10
10	ADRA2A *	rs35255813	111277219	T	C	0.0378820	-0.0616221	0.0095244	1.8E-10
10	ADRA2A *	rs10885120	111278466	T	A	0.0384192	-0.0601273	0.0094645	3.9E-10
10	ADRA2A *	rs35824917	111279462	T	A	0.0379936	-0.0610944	0.0095072	2.3E-10
10	ADRA2A *	rs11195502	111279909	T	C	0.0379988	-0.0612912	0.0095064	2.0E-10
10	ADRA2A *	rs58338647	111280502	A	G	0.0380198	-0.0617218	0.0095027	1.5E-10
10	ADRA2A *	rs35736754	111281041	C	T	0.0380223	-0.0614808	0.0095023	1.7E-10
10	ADRA2A *	rs35126798	111281068	G	A	0.0380221	-0.0614791	0.0095023	1.7E-10
10	ADRA2A *	rs12771749	111283511	T	C	0.0277792	-0.0691372	0.0110525	5.4E-10
10	ADRA2A *	rs35370618	111284472	C	G	0.0276687	-0.0695798	0.0110792	4.9E-10
10	ADRA2A *	rs34667359	111284621	G	A	0.0276586	-0.0695912	0.0110812	4.8E-10
10	ADRA2A *	rs11195508	111286621	G	C	0.0273326	-0.0646638	0.0111711	7.9E-09
10	ADRA2A *	rs11592309	111286766	A	G	0.0273929	-0.0647903	0.0111522	6.0E-09
10	KCNK18 *	rs363317	117222309	A	C	0.2309640	0.0241495	0.0043489	3.5E-09
10	KCNK18 *	rs363365	117222454	C	A	0.2308450	0.0234447	0.0043436	8.4E-09
10	KCNK18 *	rs363366	117222891	G	A	0.2340360	0.0228383	0.0043292	1.3E-08
10	SLC18A2 *	rs363323	117227202	T	A	0.2334300	0.0236308	0.0043081	5.1E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	SLC18A2 *	rs2803818	117227828	C	A	0.2335430	0.0237377	0.0043059	4.5E-09
10	SLC18A2 *	rs59422041	117228928	A	ATTATAT	0.2342870	0.0233780	0.0042945	7.5E-09
10	SLC18A2 *	rs3981210	117230093	A	G	0.2338400	0.0236074	0.0042965	5.9E-09
10	SLC18A2 *	rs363325	117230786	A	G	0.2343800	0.0233254	0.0042904	8.0E-09
10	SLC18A2 *	rs363326	117231005	A	G	0.2344010	0.0232678	0.0042899	8.6E-09
10	SLC18A2 *	rs363327	117231271	A	G	0.2343000	0.0233230	0.0042889	8.3E-09
10	SLC18A2 *	rs363328	117231615	C	T	0.2342320	0.0234070	0.0042910	8.3E-09
10	SLC18A2 *	rs363329	117232071	T	C	0.2340100	0.0236402	0.0042957	6.0E-09
10	SLC18A2 *	rs12414934	117232263	A	G	0.2340050	0.0235892	0.0042958	6.4E-09
10	SLC18A2 *	rs2619097	117233073	C	A	0.2325840	0.0244966	0.0043051	2.2E-09
10	SLC18A2 *	rs363330	117235327	G	A	0.2326490	0.0250100	0.0043071	1.1E-09
10	SLC18A2 *	rs60543597	117241061	G	A	0.4250670	0.0192663	0.0037031	2.0E-08
10	WDR11 *	rs1907240	121138445	G	A	0.4138100	-0.0226084	0.0036872	1.4E-10
10	WDR11 *	rs1907241	121138470	G	T	0.4133020	-0.0225756	0.0036871	1.6E-10
10	WDR11 *	rs2257129	121139183	T	C	0.4108400	-0.0232170	0.0036912	3.6E-11
10	WDR11 *	rs2263985	121143992	C	T	0.4108580	-0.0235170	0.0036929	2.1E-11
10	WDR11 *	rs2451876	121144368	T	C	0.4107700	-0.0234311	0.0036923	2.4E-11
10	WDR11 *	rs2263983	121145186	T	C	0.4107640	-0.0233939	0.0036923	2.6E-11
10	WDR11 *	rs2220607	121146746	C	A	0.4123120	-0.0234327	0.0036902	2.3E-11
10	WDR11 *	rs2172073	121150111	C	A	0.4124850	-0.0235268	0.0036901	2.0E-11
10	WDR11 *	rs1907256	121150416	A	G	0.3712210	0.0201300	0.0037597	4.5E-08
10	WDR11 *	rs7098433	121153961	C	T	0.4125890	-0.0237736	0.0036885	1.1E-11
10	WDR11 *	rs17101518	121155455	G	A	0.3658190	-0.0226810	0.0037709	3.2E-10
10	WDR11 *	rs72631105	121155831	A	G	0.3526420	0.0203174	0.0038006	4.8E-08
10	WDR11 *	rs56351107	121155983	G	C	0.3656630	-0.0227999	0.0037697	2.5E-10
10	WDR11 *	rs17101521	121156039	C	T	0.3647360	-0.0230374	0.0037755	1.8E-10
10	WDR11 *	rs59313277	121156141	T	G	0.3654970	-0.0226303	0.0037709	3.4E-10
10	WDR11 *	chr10:121156208_T_TA	121156208	TA	T	0.3578480	-0.0212171	0.0038300	5.0E-09
10	WDR11 *	rs73366917	121156240	A	G	0.3651180	-0.0229331	0.0037719	2.2E-10
10	WDR11 *	rs17101524	121156265	A	C	0.3656630	-0.0227999	0.0037697	2.5E-10
10	WDR11 *	rs59082214	121156440	A	CACACAC	0.3595140	-0.0226842	0.0038152	2.8E-10
10	WDR11 *	rs4752500	121156448	T	A	0.3680170	-0.0227050	0.0037762	3.4E-10
10	WDR11 *	rs1907266	121156628	T	C	0.4123640	-0.0236272	0.0036881	1.7E-11
10	WDR11 *	rs7920116	121156957	C	T	0.3656630	-0.0227999	0.0037697	2.5E-10
10	WDR11 *	rs7903585	121157114	G	A	0.3641030	-0.0223157	0.0037766	8.0E-10
10	WDR11 *	rs7903948	121157125	A	G	0.3655370	-0.0227490	0.0037702	2.8E-10
10	WDR11 *	rs10710843	121157294	C	CA	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs7904102	121157377	G	C	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs59754371	121157811	C	T	0.3649680	-0.0225460	0.0037743	4.4E-10
10	WDR11 *	rs57615383	121157842	A	G	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs112209982	121158067	A	G	0.3616010	-0.0222877	0.0037925	7.7E-10
10	WDR11 *	rs58324269	121158215	G	A	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs60089052	121158221	C	T	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs58217496	121158313	C	T	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs60711290	121158469	T	G	0.3656580	-0.0227406	0.0037693	2.8E-10
10	WDR11 *	rs57142282	121158561	T	C	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs17101530	121158601	C	T	0.3657080	-0.0227151	0.0037695	2.9E-10
10	WDR11 *	rs71945618	121158703	AG	A	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs73366943	121158995	G	A	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs17101534	121159361	C	T	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs11199803	121159565	G	A	0.3656610	-0.0227696	0.0037692	2.7E-10
10	WDR11 *	rs11199804	121159660	G	C	0.3656600	-0.0227691	0.0037692	2.7E-10
10	WDR11 *	rs11199805	121159692	T	C	0.3656600	-0.0227691	0.0037692	2.7E-10
10	WDR11 *	rs11199806	121159795	A	G	0.3656640	-0.0227813	0.0037693	2.6E-10
10	WDR11 *	rs7917346	121160328	G	A	0.3657790	-0.0228496	0.0037697	2.3E-10
10	WDR11 *	rs7902919	121160588	C	T	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs7917833	121160641	A	C	0.3656700	-0.0227370	0.0037694	2.8E-10
10	WDR11 *	rs2130786	121161069	C	T	0.4123980	-0.0236779	0.0036877	1.5E-11
10	WDR11 *	rs1907267	121161442	T	C	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs1907268	121161733	C	T	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs1907269	121161835	C	A	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs6585696	121162049	G	A	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs6585697	121162083	T	C	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs6585698	121162088	G	T	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs6585699	121162146	C	T	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs6585700	121162243	C	G	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs6585701	121162277	C	T	0.3656630	-0.0227826	0.0037693	2.6E-10
10	WDR11 *	rs7920041	121162857	C	T	0.3656680	-0.0227858	0.0037693	2.6E-10
10	WDR11 *	rs7906567	121162944	C	A	0.3656680	-0.0227858	0.0037693	2.6E-10
10	WDR11 *	rs59296617	121163320	A	T	0.3656680	-0.0227858	0.0037693	2.6E-10
10	WDR11 *	rs11199810	121164064	C	T	0.3656680	-0.0227858	0.0037693	2.6E-10
10	WDR11 *	rs60590589	121164227	AAAAAC	A	0.3657140	-0.0227671	0.0037696	2.7E-10
10	WDR11 *	rs7087606	121164303	T	C	0.3656230	-0.0228837	0.0037693	2.3E-10
10	WDR11 *	rs6585702	121164396	T	G	0.3656230	-0.0228837	0.0037693	2.3E-10
10	WDR11 *	rs6585703	121164626	A	G	0.3656700	-0.0227899	0.0037693	2.6E-10
10	WDR11 *	rs7915733	121165125	A	C	0.3656820	-0.0228197	0.0037694	2.5E-10
10	WDR11 *	rs10788141	121165340	G	T	0.4124520	-0.0237206	0.0036876	1.4E-11
10	WDR11 *	rs1907274	121165824	T	G	0.3656790	-0.0228952	0.0037695	2.2E-10
10	WDR11 *	rs6585708	121167429	T	C	0.3656590	-0.0229288	0.0037702	2.2E-10
10	WDR11 *	rs10886862	121169894	C	T	0.4121420	-0.0236026	0.0036902	1.8E-11
10	WDR11 *	rs35326857	121169898	G	T	0.3706630	0.0201942	0.0037606	4.3E-08
10	WDR11 *	rs10886863	121169979	T	C	0.4121420	-0.0236026	0.0036902	1.8E-11
10	WDR11 *	rs10886864	121170023	C	T	0.4121420	-0.0236026	0.0036902	1.8E-11
10	WDR11 *	rs7071036	121171054	C	T	0.3654460	-0.0226919	0.0037718	3.1E-10
10	WDR11 *	rs7071062	121171098	C	T	0.3654460	-0.0226919	0.0037718	3.1E-10
10	WDR11 *	rs1873449	121172138	T	G	0.3620780	-0.0223475	0.0037861	6.1E-10
10	WDR11 *	rs754227	121172490	C	T	0.3684400	-0.0222904	0.0037751	6.0E-10
10	WDR11 *	rs3962180	121177844	A	C	0.3625370	-0.0222726	0.0038316	1.1E-09
11	KCNQ1, KCNQ1OT1	rs231361	2670270	G	A	0.1863170	-0.0316674	0.0046613	2.3E-11
11	KCNQ1, KCNQ1OT1	rs231359	2673376	C	A	0.1815660	-0.0323869	0.0047077	1.0E-11
11	KCNQ1, KCNQ1OT1	rs111698879	2678651	C	CA	0.1400050	-0.0368277	0.0052391	1.7E-12
11	KCNQ1, KCNQ1OT1	rs231356	2684113	A	T	0.1853310	-0.0327585	0.0046773	3.3E-12
11	KCNQ1, KCNQ1OT1	rs231353	2687789	A	G	0.1777130	-0.0324689	0.0047645	7.9E-12
11	KCNQ1, KCNQ1OT1	rs7927129	2694302	G	T	0.1724640	-0.0314514	0.0048263	9.7E-11
11	KCNQ1, KCNQ1OT1	rs463924	2696450	C	T	0.1798430	-0.0307476	0.0047245	9.3E-11
11	KCNQ1, KCNQ1OT1	rs2283193	2696598	T	C	0.1691730	-0.0317421	0.0048430	7.8E-11
11	KCNQ1, KCNQ1OT1	rs10832548	2697747	T	C	0.1636480	-0.0339559	0.0049210	8.4E-12
11	KCNQ1, KCNQ1OT1	rs35957135	2698444	AC	A	0.1833320	-0.0310860	0.0047024	6.2E-11
11	KCNQ1, KCNQ1OT1	rs12277353	2699445	G	A	0.1632590	-0.0333541	0.0049662	2.4E-11
11	KCNQ1	rs11023840	2700338	T	C	0.1711340	-0.0329028	0.0048513	1.5E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	KCNQ1	rs231840	2702900	C	T	0.1739780	-0.0304525	0.0048111	4.7E-10
11	KCNQ1	rs2283196	2704522	C	A	0.1477000	-0.0347000	0.0051399	9.2E-12
11	KCNQ1	rs2283200	2708110	T	C	0.1331750	-0.0372440	0.0053647	2.3E-12
11	KCNQ1	rs129074	2712895	G	A	0.1459470	-0.0358407	0.0051948	6.4E-12
11	KCNQ1	rs11601574	2807569	T	C	0.3973080	-0.0315593	0.0037583	8.9E-17
11	KCNQ1	rs11024175	2809335	T	C	0.4086170	-0.0304293	0.0037241	5.2E-16
11	KCNQ1	rs8181588	2810311	C	T	0.4022490	-0.0292731	0.0036979	2.9E-15
11	KCNQ1	rs163177	2817183	C	T	0.4629980	0.0375433	0.0036364	1.0E-24
11	KCNQ1	rs2237892	2818521	T	C	0.3249930	-0.0410469	0.0038676	1.5E-25
11	KCNQ1	rs163182	2822986	C	G	0.3743980	0.0329857	0.0037619	8.9E-18
11	KCNQ1	rs5680306	2825176 CGGGAC	C	C	0.3640650	-0.0359166	0.0038068	1.9E-20
11	KCNQ1	rs163184	2825839	G	T	0.4414780	0.0377006	0.0036655	1.5E-24
11	KCNQ1	rs2283228	2828300	C	A	0.3599390	-0.0387042	0.0037855	6.4E-24
11	KCNQ1	rs234852	2829552	T	C	0.3668800	-0.0391409	0.0037778	4.2E-24
11	KCNQ1	rs234853	2829598	G	A	0.3733240	-0.0383737	0.0037720	1.7E-23
11	KCNQ1	rs234854	2829740	G	A	0.3716060	-0.0385937	0.0037783	1.5E-23
11	KCNQ1	rs234855	2829883	T	C	0.3672860	-0.0391363	0.0037934	8.8E-24
11	KCNQ1	rs4930011	2835428	G	C	0.3487950	0.0398095	0.0038298	3.2E-24
11	KCNQ1	rs2237895	2835964	C	A	0.3503880	0.0391821	0.0038070	8.0E-24
11	KCNQ1	rs234864	2836067	G	A	0.3511640	0.0398922	0.0038202	1.8E-24
11	KCNQ1	rs2237897	2837316	T	C	0.3343610	-0.0485511	0.0039071	5.5E-34
11	LMO1	chr11:8226338_TATAAAA_T	8226338	T	TATAAAA	0.4348670	-0.0195709	0.0037172	4.6E-08
11	LMO1	rs12797723	8226437	T	C	0.4351370	-0.0218583	0.0036979	1.3E-09
11	LMO1	rs4758317	8229264	A	C	0.4378610	-0.0200201	0.0036599	1.4E-08
11	LMO1	rs110419	8231306	G	A	0.4387270	-0.0209034	0.0036482	3.3E-09
11	LMO1	rs110420	8231502	C	T	0.4395360	-0.0202575	0.0036575	1.1E-08
11	LMO1	rs204928	8232886	G	A	0.4341600	-0.0215065	0.0036838	1.6E-09
11	CRY2 *	rs11038678	45836971	A	C	0.2944520	-0.0225505	0.0039870	7.8E-09
11	CRY2 *	rs12419690	45837033	A	G	0.2946600	-0.0226003	0.0039865	7.0E-09
11	CRY2 *	rs7121611	45842591	A	T	0.2579860	-0.0246862	0.0041481	2.6E-09
11	CRY2 *	rs6485646	45844213	A	G	0.2579940	-0.0246663	0.0041478	2.7E-09
11	CRY2 *	rs12807179	45844588	A	G	0.2530900	-0.0227860	0.0041978	4.8E-08
11	CRY2	rs10838524	45848626	G	A	0.2585970	-0.0247611	0.0041427	2.2E-09
11	CRY2	rs111525306	45850014	G	T	0.2392660	-0.0247246	0.0043218	1.1E-08
11	CRY2	rs12794698	45850310	A	G	0.2583910	-0.0247129	0.0041436	2.5E-09
11	CRY2	rs11605924	45851540	C	A	0.2583840	-0.0247284	0.0041431	2.4E-09
11	CRY2	rs11038694	45856572	A	G	0.2584410	-0.0246829	0.0041436	2.5E-09
11	CRY2	rs7945565	45857441	G	A	0.2584260	-0.0246890	0.0041439	2.5E-09
11	CRY2	rs7945689	45857455	T	C	0.2584260	-0.0246890	0.0041439	2.5E-09
11	CRY2	rs1401419	45858188	C	T	0.2584240	-0.0246776	0.0041439	2.5E-09
11	CRY2	rs7933420	45875246	A	T	0.2580710	-0.0247270	0.0041479	2.5E-09
11	CRY2	rs2292910	45882062	C	A	0.3106300	-0.0230118	0.0039687	6.0E-09
11	DAGLA *	rs7925523	61675020	A	G	0.2533580	0.0230721	0.0041956	4.5E-09
11	DAGLA *	rs60399071	61675683	A	G	0.2534810	0.0229203	0.0041961	5.5E-09
11	DAGLA *	rs151242175	61679851	T	C	0.2529410	0.0230284	0.0042056	5.1E-09
11	DAGLA *	rs115702847	61679884	A	T	0.2529440	0.0230559	0.0042056	4.9E-09
11	DAGLA	rs59200224	61682665	G	A	0.2534580	0.0230950	0.0042009	4.7E-09
11	DAGLA	rs59371352	61682823	A	G	0.2536530	0.0232548	0.0042074	4.3E-09
11	DAGLA	rs72918042	61684076	G	C	0.2534670	0.0231310	0.0042009	4.4E-09
11	DAGLA	rs35404524	61687658	C	CTT	0.2534770	0.0232178	0.0042013	3.7E-09
11	DAGLA	rs4963308	61688954	A	G	0.2534730	0.0230982	0.0042020	4.5E-09
11	DAGLA	rs883724	61690385	T	C	0.2530860	0.0233323	0.0042051	3.4E-09
11	DAGLA	rs11827215	61691123	A	G	0.2538270	0.0231542	0.0041990	3.8E-09
11	DAGLA	rs72315101	61695289	C	CTCTG	0.2534520	0.0233034	0.0042033	3.5E-09
11	DAGLA	rs60507107	61696297	T	C	0.2534170	0.0232088	0.0042036	4.2E-09
11	DAGLA	rs2097853	61698795	T	G	0.2535780	0.0233215	0.0042037	3.5E-09
11	DAGLA	rs58217294	61702031	A	T	0.2536030	0.0234180	0.0042045	3.1E-09
11	DAGLA	rs12274157	61710175	C	A	0.2537390	0.0232557	0.0042066	3.9E-09
11	DAGLA	rs731842	61712719	C	T	0.2538500	0.0234207	0.0042060	3.1E-09
11	DAGLA	rs17156244	61714923	G	T	0.2539370	0.0237023	0.0042051	2.0E-09
11	DAGLA	rs198435	61715852	C	G	0.2509380	0.0251080	0.0042266	3.6E-10
11	DAGLA	rs2903825	61721496	T	C	0.2611030	0.0243141	0.0041705	4.8E-10
11	DAGLA	rs9735635	61723408	A	C	0.2604940	0.0246563	0.0041738	3.0E-10
11	DAGLA	rs4963243	61726855	A	G	0.2615090	0.0241070	0.0041660	6.3E-10
11	DAGLA	rs2240287	61738111	A	G	0.2639360	0.0251358	0.0041605	1.3E-10
11	DAGLA	rs2240286	61738982	C	T	0.2639520	0.0249237	0.0041613	1.7E-10
11	DAGLA	rs4963255	61740134	A	G	0.2639740	0.0248921	0.0041621	1.8E-10
11	DAGLA	rs3741252	61744026	T	C	0.2613330	0.0254287	0.0041864	1.2E-10
11	MYRF	rs174528	61776027	T	C	0.4016770	0.0377638	0.0037380	2.9E-26
11	MYRF	rs174529	61776489	T	C	0.4017800	0.0378754	0.0037396	2.6E-26
11	MYRF	rs174530	61779120	A	G	0.4111780	0.0387053	0.0037205	1.0E-27
11	MYRF	rs108499	61779765	C	T	0.4145710	0.0389652	0.0037158	4.5E-28
11	MYRF	rs509360	61781087	A	G	0.4016550	0.0382466	0.0037409	1.2E-26
11	MYRF	rs174533	61781553	G	A	0.4142210	0.0384084	0.0037195	3.4E-27
11	MYRF	rs174534	61781986	A	G	0.4109900	0.0389737	0.0037234	6.2E-28
11	MYRF	rs174535	61783884	T	C	0.4101170	0.0388787	0.0037206	5.9E-28
11	MYRF	rs174536	61784455	A	C	0.4126810	0.0386691	0.0037196	1.4E-27
11	MYRF	rs174537	61785208	G	T	0.4135830	0.0386969	0.0037159	1.0E-27
11	TMEM258	rs102275	61790331	T	C	0.4131740	0.0387991	0.0037156	7.9E-28
11	TMEM258	rs102274	61790354	T	C	0.4133370	0.0387423	0.0037162	9.4E-28
11	TMEM258	rs174538	61792609	G	A	0.4157320	0.0390528	0.0037129	2.8E-28
11	FEN1	rs4246215	61796827	G	T	0.4136410	0.0389106	0.0037154	4.8E-28
11	FADS1 *	rs174541	61798436	T	C	0.4134490	0.0390864	0.0037176	3.4E-28
11	FADS1	rs174544	61800281	C	A	0.4225720	0.0402060	0.0037154	6.9E-30
11	FADS1	rs174545	61801834	C	G	0.4138880	0.0388217	0.0037151	6.0E-28
11	FADS1	rs174546	61802358	C	T	0.4139270	0.0388164	0.0037154	6.4E-28
11	FADS1	rs174547	61803311	T	C	0.4138160	0.0389127	0.0037165	4.5E-28
11	FADS1	rs174548	61803876	C	G	0.4216170	0.0398712	0.0037075	1.8E-29
11	FADS1	rs174549	61803910	G	A	0.4221030	0.0397992	0.0037090	2.5E-29
11	FADS1	rs174550	61804006	T	C	0.4138630	0.0387576	0.0037151	7.3E-28
11	FADS1	rs174553	61807686	A	G	0.4142020	0.0388973	0.0037152	5.6E-28
11	FADS1	rs72643557	61811955	T	C	0.4106900	0.0382673	0.0037322	6.3E-27
11	FADS1	rs174554	61811991	A	G	0.4142220	0.0387883	0.0037149	7.7E-28
11	FADS1	rs174555	61812288	T	C	0.4214990	0.0397630	0.0037077	2.5E-29
11	FADS1	rs174556	61813163	C	T	0.4215450	0.0397213	0.0037078	3.0E-29
11	FADS1	rs174559	61814184	G	A	0.4232480	0.0398840	0.0037068	1.8E-29
11	FADS1	rs174560	61814292	T	C	0.4215310	0.0396721	0.0037079	3.4E-29
11	FADS1, MIR1908	rs174561	61815236	T	C	0.4215050	0.0396394	0.0037086	4.0E-29
11	FADS2	rs174562	61817672	A	G	0.4134240	0.0385173	0.0037189	1.8E-27
11	FADS2	rs35473591	61818856	C	CT	0.4136430	0.0387549	0.0037186	9.8E-28

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	FADS2	rs174564	61820833	A	G	0.4125100	0.0388919	0.0037234	6.8E-28
11	FADS2	rs28456	61822009	A	G	0.4202200	0.0397929	0.0037191	3.1E-29
11	FADS2	rs174565	61824164	C	G	0.4144680	0.0390923	0.0037219	3.7E-28
11	FADS2	chr11:61824525_A_AAG	61824525	A	AAG	0.4167450	0.0386144	0.0037321	2.7E-27
11	FADS2	rs174566	61824890	A	G	0.4125100	0.0389209	0.0037234	6.3E-28
11	FADS2	rs174567	61825533	A	G	0.4154280	0.0384656	0.0037184	2.5E-27
11	FADS2	rs174568	61826344	C	T	0.4144490	0.0386845	0.0037172	1.3E-27
11	FADS2	rs174569	61826692	C	T	0.1423640	-0.0308207	0.0053109	3.7E-09
11	FADS2	rs3834458	61827448	CT	C	0.4136220	0.0386205	0.0037201	1.6E-27
11	FADS2	rs5792235	61828850	CA	C	0.4125750	0.0384196	0.0037179	2.3E-27
11	FADS2	rs99780	61829161	C	T	0.4125800	0.0384119	0.0037180	2.3E-27
11	FADS2	rs174570	61829740	C	T	0.4145970	0.0382485	0.0037153	3.2E-27
11	FADS2	rs1535	61830500	A	G	0.4125110	0.0383786	0.0037174	2.6E-27
11	FADS2	rs174574	61832870	C	A	0.4125820	0.0380693	0.0037195	6.7E-27
11	FADS2	rs2524296	61833906	T	C	0.4392020	-0.0238081	0.0036899	4.3E-12
11	FADS2	rs2845574	61834400	T	C	0.4440280	-0.0238262	0.0036723	2.7E-12
11	FADS2	rs2845573	61834436	G	A	0.4494180	-0.0237138	0.0036718	3.8E-12
11	FADS2	rs199649489	61834989	A	C	0.4311520	0.0372416	0.0037777	4.1E-25
11	FADS2	rs2727270	61835765	T	C	0.4463010	-0.0232365	0.0036704	8.5E-12
11	FADS2	rs2727271	61835886	T	A	0.4463260	-0.0232113	0.0036705	8.4E-12
11	FADS2	rs174576	61836038	C	A	0.4121300	0.0379824	0.0037197	7.8E-27
11	FADS2	rs2524299	61837310	T	A	0.4465630	-0.0233435	0.0036691	7.1E-12
11	FADS2	rs174577	61837342	C	A	0.4122610	0.0379678	0.0037189	8.5E-27
11	FADS2	rs2072113	61837495	T	C	0.4462830	-0.0235025	0.0036710	5.6E-12
11	FADS2	rs2072114	61837743	G	A	0.4462390	-0.0235495	0.0036705	4.7E-12
11	FADS2	rs174578	61838027	T	A	0.4124990	0.0376985	0.0037203	1.9E-26
11	FADS2	rs174580	61839170	A	G	0.4118640	0.0379124	0.0037223	1.2E-26
11	FADS2	rs174581	61839211	G	A	0.4119940	0.0379276	0.0037228	1.2E-26
11	FADS2	rs2727265	61841532	A	C	0.4467810	-0.0236805	0.0036932	5.3E-12
11	FADS2	rs174583	61842278	C	T	0.4115230	0.0374452	0.0037207	3.6E-26
11	FADS2	rs174584	61843278	G	A	0.4112140	0.0377174	0.0037230	2.3E-26
11	FADS2	rs2526680	61843744	T	C	0.4487230	-0.0236284	0.0036772	4.1E-12
11	FADS2	rs2845572	61847123	A	G	0.4451740	-0.0236919	0.0036773	4.3E-12
11	FADS2	rs2851682	61848540	G	A	0.4456180	-0.0238346	0.0036721	3.3E-12
11	FADS2	rs2727263	61850540	T	C	0.4466190	-0.0231756	0.0036864	1.5E-11
11	FADS2	rs174592	61851136	A	G	0.4084480	0.0373686	0.0037214	7.5E-26
11	FADS2	rs174594	61852357	A	C	0.4083660	0.0370405	0.0037275	2.7E-25
11	FADS2	rs72643559	61852802	C	T	0.4046670	0.0368575	0.0037475	9.1E-25
11	FADS2	chr11:61853156_AAACAAC_A	61853156	AAACAAC	A	0.4084490	0.0377201	0.0037421	8.1E-26
11	FADS2	rs174598	61853722	G	A	0.4097350	0.0371927	0.0037225	1.5E-25
11	FADS2	rs174599	61854084	G	C	0.4075950	0.0366322	0.0037267	8.4E-25
11	FADS2	rs174600	61854755	T	C	0.4091280	0.0371519	0.0037288	2.1E-25
11	FADS2	rs174601	61855668	C	T	0.4038900	0.0360509	0.0037301	6.4E-24
11	ARAP1	rs11605691	72708469	T	C	0.0801643	-0.0453661	0.0067796	3.3E-11
11	ARAP1	rs9667947	72713589	C	T	0.0847945	-0.0504991	0.0066255	3.7E-14
11	ARAP1	rs73541184	72717103	A	G	0.0759415	-0.0559267	0.0069625	1.9E-15
11	ARAP1	rs76550717	72717127	G	A	0.0782675	-0.0564261	0.0068613	5.2E-16
11	ARAP1	rs75896506	72718534	A	G	0.0606291	-0.0621618	0.0076711	5.2E-16
11	ARAP1	rs140717197	72718751	T	TGCA	0.0654744	-0.0608472	0.0073709	1.9E-16
11	ARAP1	rs143429404	72719152	A	C	0.0351557	-0.0579984	0.0098985	1.6E-08
11	ARAP1	rs11603334	72721940	A	G	0.0662420	-0.0609824	0.0073215	8.1E-17
11	ARAP1	rs1552224	72722053	C	A	0.0662027	-0.0610166	0.0073228	8.3E-17
11	ARAP1	rs7129793	72744840	T	C	0.0651338	-0.0615999	0.0074038	8.4E-17
11	ARAP1	rs74333814	72744642	T	C	0.0650632	-0.0617269	0.0074078	7.3E-17
11	ARAP1	rs77464186	72749353	C	A	0.0656037	-0.0609968	0.0073872	1.4E-16
11	ARAP1	rs11603349	72749649	C	T	0.0656039	-0.0609739	0.0073874	1.4E-16
11	ARAP1	rs11602873	72749717	T	A	0.0656039	-0.0609739	0.0073874	1.4E-16
11	ARAP1	rs148527516	72750767	AG	A	0.0655457	-0.0613561	0.0073912	9.9E-17
11	ARAP1	rs77198110	72751013	C	G	0.0638446	-0.0641761	0.0074926	1.4E-17
11	ARAP1 *	rs7109575	72752390	A	G	0.0640363	-0.0620917	0.0074831	7.0E-17
11	STARD10	rs140130268	72759870	G	GGTTT	0.0677865	-0.0610179	0.0073051	7.0E-17
11	STARD10	rs79430446	72762959	T	G	0.0667692	-0.0611206	0.0073271	7.4E-17
11	STARD10	rs140735484	72763136	C	CA	0.0670313	-0.0605382	0.0073149	1.4E-16
11	STARD10	rs7103836	72763526	C	G	0.0670335	-0.0607429	0.0073075	9.8E-17
11	STARD10	rs613937	72763794	G	A	0.0751532	-0.0555808	0.0069522	1.6E-15
11	STARD10	rs77106637	72767275	A	G	0.0687245	-0.0593094	0.0072022	2.2E-16
11	STARD10	rs74495520	72768017	T	C	0.0365855	-0.0560611	0.0097301	2.8E-08
11	STARD10	rs3862791	72789957	T	C	0.0671825	-0.0546504	0.0072926	4.8E-14
11	STARD10 *	rs1059000	72793927	C	G	0.0673492	-0.0544610	0.0072829	5.1E-14
11	STARD10 *	rs139534838	72795835	C	T	0.0671473	-0.0546901	0.0072948	4.8E-14
11	STARD10 *	chr11:72800100_C_CT	72800100	CT	C	0.0575085	-0.0576091	0.0079065	1.5E-13
11	STARD10 *	rs76724404	72800476	C	A	0.0650329	-0.0546010	0.0074143	1.0E-13
11	STARD10 *	rs117819392	72803458	T	C	0.0659131	-0.0566966	0.0073576	1.4E-14
11	ATG16L2 *	rs145398037	72811097	C	G	0.0642729	-0.0564591	0.0074612	4.6E-14
11	ATG16L2	rs2303969	72825227	A	G	0.4481410	-0.0208270	0.0036822	3.5E-08
11	FCHSD2	rs3814730	72844508	A	G	0.0657674	-0.0519723	0.0073590	6.2E-12
11	FCHSD2	rs11603313	72877132	A	G	0.0645000	-0.0518296	0.0074370	7.2E-12
11	FCHSD2	rs11602858	72904024	G	C	0.0592457	-0.0520386	0.0077138	4.4E-11
11	FCHSD2	rs76793820	72908815	A	G	0.0620973	-0.0537430	0.0075378	2.6E-12
11	FCHSD2	rs17244499	72918901	G	A	0.0624300	-0.0539903	0.0075173	2.2E-12
11	FCHSD2	rs74439784	72938351	T	A	0.0619135	-0.0547810	0.0075479	1.4E-12
11	FCHSD2	rs11605166	72958732	C	T	0.0617758	-0.0549446	0.0075558	1.2E-12
11	FCHSD2	rs7109082	72996396	C	A	0.0619593	-0.0548567	0.0075462	1.2E-12
11	FCHSD2	rs2886599	73010226	A	C	0.0615410	-0.0554808	0.0075718	7.8E-13
11	FCHSD2	rs11600585	73016795	G	A	0.0619175	-0.0549927	0.0075475	1.2E-12
11	FCHSD2	rs144064911	73099280	C	CA	0.0616703	-0.0546207	0.0075661	1.6E-12
11	FAT3	rs7118248	92890183	G	T	0.4410930	0.0221972	0.0037240	8.6E-09
11	FAT3	rs7101609	92890327	C	G	0.4404010	0.0220952	0.0037257	9.6E-09
11	FAT3 *	rs7120048	92923023	G	C	0.4664390	0.0250148	0.0036651	5.5E-12
11	FAT3 *	rs11020102	92924049	A	G	0.4650760	0.0252073	0.0036630	3.9E-12
11	FAT3 *	rs2399548	92928400	G	A	0.4662860	0.0249413	0.0036495	6.2E-12
11	FAT3 *	rs1158885	92928777	A	G	0.4657080	0.0252222	0.0036452	3.7E-12
11	FAT3 *	rs4466787	92929842	C	T	0.4653060	0.0250352	0.0036479	5.2E-12
11	FAT3 *	rs12274325	92931981	C	T	0.0366938	-0.0568095	0.0098343	5.8E-10
11	MTNR1B *	rs3847554	92935660	C	T	0.4588750	-0.0583053	0.0036429	6.7E-58
11	MTNR1B *	rs6483204	92936246	A	T	0.4592950	-0.0596521	0.0036689	5.7E-60
11	MTNR1B *	rs6483205	92936742	T	A	0.4558060	-0.0610155	0.0036737	2.5E-62
11	MTNR1B *	rs7112766	92938855	T	G	0.4552290	0.0715530	0.0036641	7.5E-87
11	MTNR1B *	rs2895443	92939635	G	A	0.4833740	-0.0679361	0.0036895	4.4E-76
11	MTNR1B *	rs724030	92940406	G	A	0.4595370	0.0724175	0.0036472	9.8E-90

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	MTNR1B *	rs1387153	92940662	T	C	0.4572810	0.0728942	0.0036474	7.7E-91
11	MTNR1B *	rs2121651	92944532	G	T	0.4576830	0.0731449	0.0036491	2.7E-91
11	MTNR1B *	rs6483206	92945231	T	C	0.4575140	0.0729185	0.0036492	9.4E-91
11	MTNR1B *	rs2121650	92945972	A	G	0.4597860	0.0724143	0.0036499	9.5E-90
11	MTNR1B *	rs2121649	92946032	T	C	0.4587100	0.0723013	0.0036489	1.9E-89
11	MTNR1B *	rs2121648	92946267	T	G	0.4562040	0.0729517	0.0036518	1.3E-90
11	MTNR1B *	rs2121647	92946273	C	G	0.4566540	0.0727757	0.0036507	2.5E-90
11	MTNR1B *	rs1985254	92946547	C	T	0.4594560	0.0725427	0.0036468	4.0E-90
11	MTNR1B *	rs11523890	92946612	T	C	0.4575670	0.0729765	0.0036475	5.4E-91
11	MTNR1B *	rs2166704	92947448	A	T	0.4594970	0.0724906	0.0036457	4.5E-90
11	MTNR1B *	rs10830956	92947847	T	C	0.4569030	0.0716513	0.0036520	1.3E-87
11	MTNR1B *	rs10765572	92948068	C	T	0.4575670	0.0728348	0.0036461	9.5E-91
11	MTNR1B *	rs11020114	92949438	C	T	0.4575660	0.0728330	0.0036461	9.6E-91
11	MTNR1B *	rs11020115	92949576	A	G	0.4594890	0.0725389	0.0036460	3.5E-90
11	MTNR1B *	rs11020116	92949848	C	A	0.4597130	0.0725908	0.0036467	3.0E-90
11	MTNR1B *	rs10830957	92949907	T	C	0.4564260	0.0728941	0.0036483	6.3E-91
11	MTNR1B *	rs10765573	92950166	A	T	0.4573480	0.0726806	0.0036465	2.0E-90
11	MTNR1B *	rs10830958	92950789	G	T	0.4576210	0.0727756	0.0036467	1.4E-90
11	MTNR1B *	rs7933855	92951156	A	G	0.4595720	0.0724993	0.0036462	4.4E-90
11	MTNR1B *	rs10830959	92951950	G	A	0.4576300	0.0727858	0.0036466	1.3E-90
11	MTNR1B *	rs10830960	92954846	T	A	0.4585000	0.0728317	0.0036516	1.5E-90
11	MTNR1B *	rs11020123	92956112	T	C	0.4596500	0.0724382	0.0036459	5.9E-90
11	MTNR1B *	rs10765575	92956120	C	A	0.4596270	0.0724087	0.0036461	7.1E-90
11	MTNR1B *	rs10741452	92956184	G	A	0.4577040	0.0727729	0.0036465	1.4E-90
11	MTNR1B *	rs7936247	92956866	T	G	0.4577610	0.0728051	0.0036457	1.1E-90
11	MTNR1B *	chr11:92956929_C_CT	92956929	CT	C	0.4693050	0.0693952	0.0036951	1.7E-81
11	MTNR1B *	rs11020124	92957495	C	T	0.4578260	0.0730036	0.0036467	4.0E-91
11	MTNR1B *	rs2166706	92958366	C	T	0.4597350	0.0728021	0.0036439	5.6E-91
11	MTNR1B *	rs7948632	92959380	T	C	0.4527810	0.0728478	0.0036911	2.7E-89
11	MTNR1B *	rs7948640	92959391	T	C	0.4559720	0.0723228	0.0036759	1.9E-88
11	MTNR1B *	rs10830961	92961591	G	A	0.4739130	0.0809931	0.0036951	9.6E-110
11	MTNR1B *	rs4331050	92962848	T	G	0.4385100	0.0886799	0.0037015	6.3E-131
11	MTNR1B *	rs10466351	92964815	T	C	0.4395650	0.0894082	0.0036576	4.5E-136
11	MTNR1B *	rs10830962	92965261	G	C	0.4401100	0.0893201	0.0036586	1.1E-135
11	MTNR1B *	rs7941837	92966500	T	A	0.4405510	0.0904345	0.0036689	2.1E-138
11	MTNR1B *	rs7945617	92967121	C	T	0.4735450	0.0841723	0.0036535	8.7E-121
11	MTNR1B *	rs4753426	92968430	T	C	0.3028290	-0.0541753	0.0039514	3.3E-43
11	MTNR1B *	rs7951037	92973009	G	A	0.2977790	-0.0551788	0.0039877	3.9E-44
11	MTNR1B *	rs10765576	92973778	A	G	0.2975920	-0.0551824	0.0039900	4.1E-44
11	MTNR1B *	rs11020127	92974394	A	C	0.3009530	-0.0556778	0.0039893	5.8E-45
11	MTNR1B *	rs10830963	92975544	G	C	0.4333730	0.0924650	0.0036648	5.5E-144
11	MTNR1B *	rs11369429	92976524	C	CA	0.3106170	-0.0554926	0.0039450	7.3E-46
11	MTNR1B *	rs3781638	92980341	G	T	0.3124580	-0.0550884	0.0039457	4.2E-45
11	MTNR1B *	rs1562444	92982683	G	A	0.3119860	-0.0546125	0.0039498	1.3E-44
11	MTNR1B *	rs12792653	92982750	G	A	0.3133650	-0.0560142	0.0039361	5.6E-47
11	MTNR1B *	rs10765578	92983450	C	G	0.3143090	-0.0559921	0.0039335	5.1E-47
11	MTNR1B *	rs4753072	92984239	C	A	0.3129560	-0.0560283	0.0039289	4.0E-47
11	MTNR1B *	rs4753073	92984309	G	A	0.3129570	-0.0560392	0.0039289	3.8E-47
11	MTNR1B *	rs113887439	92984467	C	CTTTGAC	0.3173600	-0.0553857	0.0039435	1.1E-45
11	MTNR1B *	rs1447350	92984961	G	C	0.3132620	-0.0559123	0.0039209	5.2E-47
11	MTNR1B *	rs1447351	92984997	A	G	0.3132800	-0.0559929	0.0039198	3.9E-47
11	MTNR1B *	rs12225378	92985483	C	T	0.0940949	-0.0370828	0.0062374	1.1E-09
11	MTNR1B *	rs4611171	92986041	T	G	0.3126720	-0.0557985	0.0039225	1.0E-46
11	MTNR1B *	rs10830964	92986515	T	C	0.2130400	-0.0533020	0.0044351	1.3E-34
11	MTNR1B *	rs4612758	92986549	T	G	0.3124280	-0.0560247	0.0039229	5.1E-47
11	MTNR1B *	rs7930067	92987568	T	C	0.3140830	-0.0557364	0.0039173	9.0E-47
11	MTNR1B *	rs7930592	92988001	T	G	0.3144370	-0.0554698	0.0039147	1.9E-46
11	MTNR1B *	rs1597023	92988153	G	A	0.3145790	-0.0554945	0.0039136	1.7E-46
11	MTNR1B *	rs4406791	92988621	A	C	0.3139450	-0.0555270	0.0039146	1.3E-46
11	MTNR1B *	rs4753428	92988900	T	C	0.3135240	-0.0556509	0.0039165	9.7E-47
11	MTNR1B *	rs1447352	92989595	G	A	0.3140540	-0.0554240	0.0039129	2.1E-46
11	MTNR1B *	rs1447353	92989629	C	A	0.3139660	-0.0553996	0.0039135	2.0E-46
11	MTNR1B *	rs71064730	92990291	T	TA	0.3136910	-0.0555548	0.0039151	1.4E-46
11	MTNR1B *	rs1971186	92990522	C	T	0.3113520	-0.0555497	0.0039300	3.1E-46
11	MTNR1B *	rs11020133	92991154	G	A	0.3134790	-0.0558745	0.0039159	4.5E-47
11	MTNR1B *	rs7121092	92991185	T	C	0.3134790	-0.0558745	0.0039159	4.5E-47
11	MTNR1B *	rs6483212	92992074	A	G	0.3134710	-0.0558966	0.0039160	4.2E-47
11	MTNR1B *	rs6483213	92992155	A	G	0.3134650	-0.0559351	0.0039160	3.6E-47
11	MTNR1B *	rs271035	92998312	A	T	0.2562090	0.0251792	0.0041982	2.3E-09
11	MTNR1B *	rs271038	93002638	A	C	0.2543170	0.0245279	0.0041830	6.6E-09
11	DDX6 *	rs501656	118798873	T	C	0.1215960	0.0348313	0.0056591	3.1E-10
12	KLHL42 *	rs12423100	27812936	G	A	0.4795950	0.0198437	0.0036830	4.6E-08
12	KLHL42 *	rs10842998	27813113	C	T	0.4801610	0.0201611	0.0036742	3.2E-08
12	KLHL42 *	chr12:27813191_C_CT	27813191	C	CT	0.4909770	0.0208495	0.0037091	1.3E-08
12	KLHL42 *	rs1971733	27813245	T	C	0.4802340	0.0201820	0.0036746	3.0E-08
12	KLHL42 *	rs1544860	27813520	A	G	0.4883370	0.0207303	0.0036416	1.0E-08
12	RMST *	rs17026787	97335254	A	G	0.4272050	0.0202243	0.0037093	1.7E-08
12	RMST *	rs1833214	97336425	A	T	0.4308190	0.0195365	0.0037069	4.5E-08
12	FBRSL1 *	rs11614840	132476443	A	G	0.1177790	0.0365653	0.0057545	6.3E-11
12	FBRSL1 *	rs7296889	132478070	C	T	0.1445370	0.0315469	0.0052581	1.5E-09
12	FBRSL1 *	rs11147192	132483963	A	G	0.1150300	0.0405697	0.0057629	1.3E-12
12	FBRSL1 *	rs61951158	132484495	A	G	0.1102940	0.0394481	0.0058705	9.7E-12
12	FBRSL1 *	rs28435470	132490887	A	G	0.1494090	0.0303195	0.0051138	1.7E-09
12	FBRSL1 *	rs7295014	132491403	A	G	0.1493560	0.0301792	0.0051145	2.2E-09
12	FBRSL1 *	rs3751297	132511579	A	G	0.1014800	0.0389825	0.0060726	4.4E-11
12	FBRSL1 *	rs35653050	132518451	T	C	0.1114510	0.0362141	0.0058331	1.3E-10
12	FBRSL1 *	rs11146914	132530938	T	C	0.1324540	0.0286155	0.0054436	4.6E-08
12	FBRSL1 *	rs11297441	132532166	G	GA	0.1131900	0.0353186	0.0057951	2.1E-10
12	FBRSL1 *	rs34729699	132538825	AT	A	0.1126700	0.0359778	0.0058091	1.3E-10
13	RNF6 *	rs34238147	26202118	A	G	0.3924420	0.0289755	0.0037439	5.7E-15
13	RNF6 *	rs5802366	26202629	T	TA	0.3957970	0.0290900	0.0037207	3.4E-15
13	RNF6 *	rs34584161	26202862	G	A	0.3917310	0.0289578	0.0037185	3.2E-15
13	RNF6 *	rs9581587	26202946	C	A	0.3966050	0.0287033	0.0037101	6.6E-15
13	RNF6 *	rs9581588	26203162	G	C	0.3957470	0.0288764	0.0037164	5.3E-15
13	RNF6 *	rs76154673	26203351	C	T	0.3918010	0.0288431	0.0037181	4.3E-15
13	RNF6 *	rs34897738	26203574	T	A	0.3966160	0.0287073	0.0037099	6.6E-15
13	RNF6 *	rs4545656	26203604	G	A	0.3966140	0.0287020	0.0037099	6.6E-15
13	RNF6 *	rs4630391	26203687	T	C	0.3917730	0.0288639	0.0037180	4.0E-15
13	RNF6 *	rs7317124	26204116	G	T	0.3737280	-0.0289506	0.0037964	9.2E-14
13	RNF6 *	rs9319280	26204824	G	T	0.3966270	0.0286277	0.0037098	7.6E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
13	RNF6 *	rs9581589	26205115	T	C	0.3966310	0.0286629	0.0037097	7.1E-15
13	RNF6 *	rs71771342	26205195	G	ACATGGA	0.3924900	0.0281728	0.0037371	3.6E-14
13	RNF6 *	rs34015717	26205290	A	AG	0.3915330	0.0288237	0.0037198	4.2E-15
13	RNF6 *	rs34701644	26205293	T	C	0.3915380	0.0288407	0.0037198	4.1E-15
13	RNF6 *	rs12873948	26205639	G	A	0.3909550	0.0287841	0.0037224	5.4E-15
13	RNF6 *	rs35328831	26206204	C	T	0.3934730	0.0283244	0.0037422	3.2E-14
13	RNF6 *	rs10467680	26206283	T	C	0.3966450	0.0286053	0.0037096	7.9E-15
13	RNF6 *	rs11617826	26206304	T	C	0.3739140	-0.0286724	0.0037931	1.5E-13
13	RNF6 *	rs12869931	26206528	G	A	0.3966950	0.0287034	0.0037093	6.2E-15
13	RNF6 *	chr13:26206916_TA_T	26206916	T	TA	0.3737350	-0.0284415	0.0037975	2.4E-13
13	RNF6 *	rs10507349	26207391	A	G	0.3924480	0.0289795	0.0037154	3.2E-15
13	RNF6 *	rs12874929	26207470	G	A	0.3923390	0.0289946	0.0037162	3.1E-15
13	RNF6 *	rs34921709	26207477	G	GT	0.3923510	0.0288764	0.0037163	3.9E-15
13	RNF6 *	rs12429453	26207882	C	T	0.4908260	-0.0291490	0.0036603	3.9E-15
13	RNF6 *	rs4770958	26208106	G	A	0.3738520	-0.0286660	0.0037931	1.5E-13
13	RNF6 *	rs35855043	26208296	A	G	0.4857610	-0.0288060	0.0036605	1.0E-14
13	RNF6 *	rs9319281	26208750	G	T	0.3573000	-0.0266453	0.0038319	1.1E-11
13	RNF6 *	rs4769486	26208959	G	A	0.3736700	-0.0287751	0.0037947	1.2E-13
13	RNF6 *	rs4100617	26209445	C	T	0.3737370	-0.0286966	0.0037954	1.4E-13
13	RNF6 *	rs9581591	26210802	C	T	0.3920500	0.0289365	0.0037194	3.6E-15
13	RNF6 *	rs11839581	26211694	A	G	0.3731240	-0.0275478	0.0038039	1.6E-12
13	RNF6 *	rs34068231	26211702	A	G	0.3720770	-0.0273422	0.0038091	2.2E-12
13	RNF6	rs1830	26212948	G	A	0.3736220	-0.0279038	0.0038065	7.6E-13
13	RNF6	rs9319282	26216037	A	C	0.4326890	0.0302352	0.0036814	1.4E-16
13	RNF6	rs4770960	26216997	G	A	0.3734520	-0.0280085	0.0038046	6.7E-13
13	RNF6	rs11558132	26221326	A	C	0.3753970	-0.0275105	0.0037937	1.5E-12
13	RNF6	rs17436547	26221373	A	C	0.3753980	-0.0275108	0.0037937	1.5E-12
13	RNF6 *	rs3759468	26222606	C	T	0.4212420	0.0297152	0.0037222	9.2E-16
13	RNF6 *	rs3759469	26223183	G	C	0.4207540	0.0298672	0.0037262	7.3E-16
13	RNF6 *	rs3834504	26223618	TAA	T	0.3956180	-0.0276659	0.0037593	6.1E-13
13	RNF6 *	rs3834505	26224589	TA	T	0.3968510	-0.0281525	0.0037545	2.4E-13
13	RNF6 *	rs3759470	26224755	C	T	0.4286760	0.0299071	0.0036923	3.8E-16
13	RNF6 *	rs3848002	26225997	A	G	0.3958140	-0.0280767	0.0037573	2.6E-13
13	RNF6 *	rs10507353	26228798	A	G	0.3955590	-0.0278613	0.0037561	3.6E-13
13	RNF6 *	rs9553769	26230874	T	C	0.3967440	-0.0280917	0.0037557	2.4E-13
13	RNF6 *	rs9553770	26233049	A	G	0.3972140	-0.0279186	0.0037574	3.3E-13
13	RNF6 *	rs74884849	26234118	T	A	0.4260520	0.0289884	0.0037360	4.3E-15
13	RNF6 *	rs79340173	26234119	T	A	0.4187720	0.0300232	0.0037229	3.3E-16
13	RNF6 *	rs2010810	26234460	T	C	0.3970580	-0.0280668	0.0037589	2.7E-13
13	RNF6 *	rs1975261	26234666	C	G	0.3819080	-0.0263318	0.0037903	9.1E-12
13	RNF6 *	rs9551251	26237136	A	G	0.3966100	-0.0280695	0.0037608	2.6E-13
13	CDK8 *	rs573973	26241102	C	T	0.4258900	0.0302676	0.0037041	2.5E-16
13	CDK8 *	rs502264	26242372	C	T	0.4209610	0.0305514	0.0037160	1.1E-16
13	CDK8 *	rs555086	26242428	T	G	0.4201160	0.0301598	0.0037128	2.7E-16
13	CDK8 *	rs54434	26242797	G	C	0.4223700	0.0305427	0.0037244	1.5E-16
13	CDK8 *	rs624893	26242816	G	A	0.4215350	0.0303577	0.0037183	2.1E-16
13	CDK8 *	rs54433	26242819	C	T	0.4212680	0.0301736	0.0037182	3.1E-16
13	CDK8 *	rs623575	26243075	A	G	0.4250890	0.0302158	0.0037067	2.9E-16
13	CDK8 *	rs547632	26243246	T	C	0.4242140	0.0297288	0.0037291	9.7E-16
13	CDK8 *	rs532503	26243395	C	T	0.4191500	0.0297759	0.0037134	6.2E-16
13	CDK8 *	rs534195	26243542	G	T	0.4252930	0.0298723	0.0037041	5.8E-16
13	CDK8 *	rs610475	26243676	C	T	0.4201570	0.0299472	0.0037100	3.9E-16
13	CDK8 *	rs535880	26243705	G	T	0.4201420	0.0299331	0.0037099	4.0E-16
13	CDK8 *	rs7983171	26243898	A	G	0.4201430	0.0299259	0.0037099	4.1E-16
13	CDK8 *	rs7981748	26244180	A	G	0.4195470	0.0300523	0.0037136	3.2E-16
13	CDK8 *	rs34164436	26244202	AG	A	0.4195470	0.0300523	0.0037136	3.2E-16
13	CDK8 *	rs7988894	26244500	C	T	0.4201580	0.0299522	0.0037101	3.8E-16
13	CDK8 *	rs12874375	26244765	T	C	0.4170510	0.0296029	0.0037285	1.6E-15
13	CDK8 *	rs9507689	26244904	G	A	0.4201660	0.0300049	0.0037102	3.4E-16
13	CDK8 *	rs9581596	26245071	A	T	0.4201660	0.0300004	0.0037102	3.5E-16
13	CDK8 *	rs9507690	26245169	C	G	0.4201510	0.0300039	0.0037102	3.4E-16
13	CDK8 *	rs3981275	26245696	C	T	0.4209050	0.0301830	0.0037080	2.3E-16
13	CDK8 *	rs519084	26247027	A	T	0.4256780	0.0300575	0.0037041	3.8E-16
13	CDK8 *	rs576140	26248686	A	G	0.4250980	0.0297985	0.0037039	6.3E-16
13	CDK8 *	rs2497654	26249094	T	C	0.4201880	0.0298379	0.0037099	4.8E-16
13	CDK8 *	rs526961	26249356	A	T	0.4081000	0.0302969	0.0037696	4.1E-16
13	CDK8 *	rs628780	26249842	C	T	0.4153230	0.0300572	0.0037347	3.8E-16
13	CDK8 *	rs533314	26250022	T	C	0.4202030	0.0300584	0.0037099	2.9E-16
13	CDK8 *	rs626917	26250318	C	G	0.4199380	0.0297059	0.0037095	6.4E-16
13	CDK8 *	rs599700	26250407	G	T	0.4202050	0.0298968	0.0037095	4.3E-16
13	CDK8 *	rs677866	26252395	A	G	0.4205020	0.0298732	0.0037068	4.3E-16
13	CDK8	rs9512166	26257580	G	A	0.4621750	-0.0255750	0.0036446	2.6E-12
13	CDK8	rs9553777	26258209	G	A	0.3904260	-0.0272094	0.0037335	1.3E-12
13	CDK8	rs10871234	26261108	C	T	0.3901960	-0.0271813	0.0037279	1.1E-12
13	CDK8	rs1886253	26262023	G	A	0.3889150	-0.0270746	0.0037431	2.1E-12
13	CDK8	rs620267	26262643	A	G	0.4320820	0.0278318	0.0036620	2.5E-14
13	CDK8	rs682181	26266026	T	G	0.4324880	0.0277795	0.0036605	2.9E-14
13	CDK8	rs4770964	26266768	G	T	0.4695820	-0.0244624	0.0036483	2.6E-11
13	CDK8	rs4770965	26266928	A	G	0.4612170	-0.0256980	0.0036416	2.1E-12
13	CDK8	rs543474	26268752	C	T	0.4325020	0.0278838	0.0036606	2.3E-14
13	CDK8	rs576998	26273315	A	G	0.4378470	0.0281145	0.0036560	1.9E-14
13	CDK8	rs9553781	26276569	A	T	0.3897040	-0.0274234	0.0037304	8.0E-13
13	CDK8	rs11619482	26277877	G	A	0.3913260	-0.0271564	0.0037368	1.4E-12
13	CDK8	rs7992670	26279082	A	G	0.3893820	-0.0275381	0.0037270	6.1E-13
13	CDK8	rs676150	26279563	T	A	0.4331600	0.0281227	0.0036588	1.4E-14
13	CDK8	rs9551257	26281242	G	T	0.3900370	-0.0273504	0.0037277	8.4E-13
13	CDK8	rs3555802	26287999	G	A	0.3903010	-0.0274017	0.0037283	8.2E-13
13	CDK8	rs1175695	26289650	T	A	0.4325400	0.0279110	0.0036601	2.2E-14
13	CDK8	chr13:26291118_CAAA_C	26291118	C	CAAA	0.4295630	0.0276391	0.0036766	4.3E-14
13	CDK8	rs9551260	26293642	C	T	0.3888600	-0.0274628	0.0037360	8.4E-13
13	CDK8	rs9553783	26293813	G	A	0.3898250	-0.0278794	0.0037283	3.0E-13
13	CDK8	rs9553784	26294358	A	G	0.3898250	-0.0278794	0.0037283	3.0E-13
13	CDK8	rs1175684	26294696	T	C	0.4611540	-0.0258242	0.0036359	1.6E-12
13	CDK8	rs9553785	26297620	G	A	0.3902030	-0.0273503	0.0037261	8.1E-13
13	CDK8	rs608886	26302990	T	G	0.4325220	0.0278433	0.0036599	2.6E-14
13	CDK8	rs1175714	26306753	C	T	0.4612570	-0.0257100	0.0036357	1.9E-12
13	CDK8	rs566365	26309944	C	T	0.4331450	0.0279316	0.0036584	2.3E-14
13	CDK8	rs478752	26310125	A	C	0.4333340	0.0280744	0.0036575	1.6E-14
13	CDK8	rs9553786	26311283	T	C	0.3895170	-0.0276415	0.0037259	4.8E-13
13	CDK8	rs35170781	26311349	T	TCCC	0.4332790	0.0280810	0.0036576	1.6E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
13	CDK8	rs34937489	26312568	T	C	0.3899080	-0.0280365	0.0037270	2.1E-13
13	CDK8	rs7982229	26315904	A	C	0.3853480	-0.0279499	0.0037398	3.2E-13
13	CDK8	rs1175707	26321351	A	C	0.3907770	-0.0275374	0.0037266	4.2E-13
13	CDK8	rs1175723	26326867	C	T	0.4585960	-0.0262576	0.0036408	6.1E-13
13	CDK8	rs1175718	26329640	T	C	0.4591370	-0.0260872	0.0036394	8.5E-13
13	CDK8	rs1175716	26330316	C	A	0.4591340	-0.0259423	0.0036387	1.0E-12
13	CDK8	chr13:26330633_AT_A	26330633	A	AT	0.3980720	-0.0276293	0.0037643	8.9E-13
13	CDK8	rs56210064	26331754	A	G	0.4353010	0.0286142	0.0036596	4.2E-15
13	CDK8	rs9553792	26331951	G	T	0.3873640	-0.0278666	0.0037304	2.9E-13
13	CDK8	rs60425790	26334941	C	T	0.4589900	-0.0261812	0.0036385	6.8E-13
13	CDK8	rs17072235	26337062	AAC	A	0.4588950	-0.0262365	0.0036389	6.0E-13
13	CDK8	rs34466656	26338969	CTG	C	0.4589900	-0.0262148	0.0036388	6.3E-13
13	CDK8	rs71425157	26339754	A	T	0.4533580	0.0296920	0.0037064	1.9E-15
13	CDK8	rs4769496	26341273	G	C	0.3854200	-0.0275227	0.0037293	6.4E-13
13	CDK8	rs9553793	26344601	T	C	0.3853910	-0.0275542	0.0037291	5.9E-13
13	CDK8	rs2182849	26348160	A	G	0.4592450	-0.0263018	0.0036397	5.2E-13
13	CDK8	rs12865885	26361871	A	C	0.3825250	-0.0278913	0.0037515	2.7E-13
13	CDK8	rs7986682	26364146	C	T	0.4594360	-0.0257781	0.0036372	1.3E-12
13	CDK8	rs7325939	26366528	A	G	0.4591320	-0.0259311	0.0036352	9.2E-13
13	CDK8	rs7994844	26367351	C	T	0.4589410	-0.0258105	0.0036370	1.1E-12
13	CDK8	chr13:26367385_AT_A	26367385	A	AT	0.4349220	0.0288683	0.0036761	2.9E-15
13	CDK8	rs1541039	26372707	G	A	0.4591390	-0.0259207	0.0036353	9.3E-13
13	CDK8	rs9551265	26374707	A	G	0.3786520	-0.0275446	0.0037729	1.2E-12
13	CDK8	rs4770974	26375137	G	A	0.3708190	-0.0261264	0.0037603	9.1E-12
13	CDK8	rs17538850	26383580	A	G	0.4593420	-0.0257764	0.0036352	1.2E-12
13	CDK8	chr13:26384246_GT_G	26384246	G	GT	0.4273910	0.0283536	0.0037187	1.7E-14
13	CDK8	rs9551266	26384446	T	G	0.3850510	-0.0277302	0.0037288	4.1E-13
13	CDK8	rs7327769	26385456	T	G	0.4593650	-0.0258793	0.0036357	9.5E-13
13	CDK8	rs9553801	26385938	G	A	0.3855800	-0.0275625	0.0037261	5.0E-13
13	CDK8	rs9551267	26386998	C	G	0.3855850	-0.0275755	0.0037262	4.9E-13
13	CDK8	rs2420133	26390448	G	A	0.4594910	-0.0257366	0.0036361	1.3E-12
13	CDK8	rs1999020	26403252	A	G	0.4323190	0.0286757	0.0036862	5.4E-15
13	CDK8 *	rs718652	26406453	G	A	0.3823530	-0.0266344	0.0037650	4.3E-12
13	CDK8 *	rs9551269	26406930	T	C	0.3823540	-0.0266247	0.0037653	4.6E-12
13	CDK8 *	rs12431190	26408106	T	G	0.4340560	0.0289116	0.0037109	4.5E-15
13	CDK8 *	rs9553805	26409866	T	C	0.3818290	-0.0266661	0.0037741	3.9E-12
13	CDK8 *	rs17539697	26410057	T	C	0.3816670	-0.0267800	0.0037754	3.4E-12
13	CDK8 *	chr13:26414286_G_GA	26414286	G	GA	0.4433360	-0.0225907	0.0037269	2.9E-09
13	CDK8 *	rs7986383	26416937	T	C	0.4468580	-0.0220714	0.0037199	6.5E-09
13	CDK8 *	rs6491122	26422089	G	A	0.4466180	-0.0225665	0.0037202	2.6E-09
13	CDK8 *	rs9551271	26422917	A	G	0.4466360	-0.0222500	0.0037185	4.3E-09
13	CDK8 *	rs6491123	26424056	C	G	0.4449420	-0.0220115	0.0037131	5.5E-09
13	CDK8 *	rs12430282	26424359	G	A	0.4466280	-0.0222194	0.0037124	3.6E-09
13	CDK8 *	rs7993394	26425565	C	T	0.4459750	-0.0222142	0.0036906	2.9E-09
13	CDK8 *	rs793288	26426550	A	G	0.4458440	-0.0220860	0.0036888	3.3E-09
13	CDK8 *	rs512080	26426932	G	A	0.4457630	-0.0220706	0.0036878	3.4E-09
13	CDK8 *	rs1576129	26428046	A	T	0.4511160	-0.0219804	0.0036845	3.2E-09
13	CDK8 *	rs1576130	26428404	G	T	0.4453740	-0.0224002	0.0036879	2.0E-09
13	CDK8 *	rs1576131	26428632	A	G	0.4455060	-0.0219027	0.0036928	4.9E-09
13	CDK8 *	rs1576132	26428640	G	A	0.4453770	-0.0218532	0.0036932	5.1E-09
13	PDX1-AS1	rs9581925	27884732	G	A	0.2201050	-0.0322130	0.0044825	7.4E-14
13	PDX1-AS1	rs9581926	27885740	T	A	0.2236170	-0.0314844	0.0044263	1.1E-13
13	PDX1-AS1	rs61652270	27887589	T	C	0.3701000	-0.0326692	0.0038169	3.1E-18
13	PDX1-AS1	rs60004782	27887652	A	G	0.3700870	-0.0327023	0.0038164	2.8E-18
13	PDX1-AS1	rs9554188	27887995	A	G	0.3700980	-0.0329309	0.0038133	1.5E-18
13	PDX1-AS1	rs9581927	27888508	T	G	0.3698860	-0.0332075	0.0038075	6.2E-19
13	PDX1-AS1	rs6491237	27889429	A	G	0.4921730	-0.0394900	0.0036995	5.2E-28
13	PDX1-AS1	rs954750	27889801	C	T	0.4922570	-0.0396138	0.0036961	3.2E-28
13	PDX1-AS1	rs9581929	27890066	T	C	0.3685950	-0.0337584	0.0038010	1.5E-19
13	PDX1-AS1	rs11620076	27890302	C	T	0.2259960	-0.0326682	0.0043588	7.4E-15
13	PDX1-AS1	rs11149502	27890525	T	G	0.2260730	-0.0326863	0.0043569	6.8E-15
13	PDX1-AS1	rs12323283	27890741	C	T	0.2262300	-0.0324580	0.0043557	1.0E-14
13	PDX1-AS1	rs12323285	27890840	C	T	0.2262090	-0.0324685	0.0043536	9.6E-15
13	PDX1-AS1	rs12323307	27890901	C	T	0.2262700	-0.0325330	0.0043523	9.0E-15
13	PDX1-AS1	rs7985481	27891953	C	A	0.3710540	-0.0331202	0.0037780	5.0E-19
13	PDX1-AS1	rs12323015	27893270	C	T	0.2268200	-0.0329290	0.0043410	3.8E-15
13	PDX1-AS1	rs28513332	27893473	T	C	0.2265800	-0.0332502	0.0043426	2.4E-15
13	PDX1-AS1	rs9581931	27894085	G	A	0.3703540	-0.0336300	0.0037774	1.8E-19
13	PDX1-AS1	rs73169643	27894088	A	C	0.2261270	-0.0333423	0.0043473	2.3E-15
13	PDX1-AS1	rs73169644	27894128	G	T	0.2268570	-0.0330711	0.0043387	3.2E-15
13	PDX1-AS1	rs9579122	27895815	G	T	0.2275100	-0.0327400	0.0043290	4.7E-15
13	PDX1-AS1	rs4322512	27896228	C	A	0.2263030	-0.0331485	0.0043452	2.9E-15
13	PDX1-AS1	rs4304897	27896230	T	A	0.2263030	-0.0331485	0.0043452	2.9E-15
13	PDX1-AS1	rs4424773	27896407	G	C	0.3710620	-0.0334518	0.0037768	2.9E-19
13	PDX1-AS1	rs4465460	27896933	C	T	0.2268440	-0.0329528	0.0043404	4.1E-15
13	PDX1-AS1	chr13:27897008_TA_T	27897008	T	TA	0.4787950	0.0420659	0.0036769	2.3E-31
13	PDX1-AS1	rs9581934	27897053	C	T	0.2268280	-0.0329981	0.0043407	3.9E-15
13	PDX1-AS1	rs9554193	27897229	A	G	0.3694230	-0.0337456	0.0037851	1.7E-19
13	PDX1-AS1	rs73169653	27897418	C	T	0.2268070	-0.0330165	0.0043412	3.7E-15
13	PDX1-AS1	rs73169655	27897556	A	G	0.2268050	-0.0330304	0.0043413	3.7E-15
13	PDX1-AS1	rs9581935	27897903	A	G	0.2268030	-0.0330254	0.0043414	3.8E-15
13	PDX1-AS1	rs7995917	27898587	C	T	0.3704870	-0.0335076	0.0037757	2.4E-19
13	PDX1-AS1	rs9579123	27899917	A	G	0.2267710	-0.0330527	0.0043424	3.9E-15
13	PDX1-AS1	rs9551414	27900100	T	C	0.3697720	-0.0333351	0.0037829	4.1E-19
13	PDX1-AS1	rs58166834	27900338	A	T	0.4925980	-0.0395226	0.0036660	1.7E-28
13	PDX1-AS1	rs74241750	27900402	G	A	0.2263700	-0.0329331	0.0043479	4.9E-15
13	PDX1-AS1	rs74241751	27900408	G	C	0.2263700	-0.0329331	0.0043479	4.9E-15
13	PDX1-AS1	rs9581938	27900938	C	G	0.2267640	-0.0330639	0.0043429	3.7E-15
13	PDX1-AS1	rs7993114	27902140	G	A	0.3670350	-0.0352998	0.0037733	2.7E-21
13	PDX1-AS1	rs11616419	27902417	A	C	0.4829900	0.0433242	0.0036606	1.2E-33
13	PDX1-AS1	rs11618581	27902774	A	G	0.3670130	-0.0353147	0.0037730	2.6E-21
13	PDX1-AS1	rs9554197	27902841	T	C	0.3668490	-0.0351758	0.0037723	3.7E-21
13	PDX1-AS1	rs11618036	27902921	C	T	0.3660500	-0.0351918	0.0037842	4.5E-21
13	PDX1-AS1	rs11618832	27902974	A	G	0.3665200	-0.0355999	0.0037773	1.3E-21
13	PDX1-AS1	rs11616678	27902980	T	C	0.3665200	-0.0355999	0.0037773	1.3E-21
13	PDX1-AS1	rs11618052	27903012	C	T	0.3666950	-0.0354099	0.0037759	2.1E-21
13	PDX1-AS1	rs9579127	27903131	G	A	0.3670370	-0.0353677	0.0037732	2.2E-21
13	PDX1-AS1	rs7999100	27903264	A	C	0.3670400	-0.0353754	0.0037732	2.2E-21
13	PDX1-AS1	rs8000004	27903453	G	A	0.3670390	-0.0353736	0.0037733	2.2E-21
13	PDX1-AS1	rs17753933	27905357	C	T	0.2194620	-0.0370425	0.0044140	5.9E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
13	PDX1-AS1	rs7331951	27905517	C	T	0.4830980	0.0436384	0.0036593	3.4E-34
13	PDX1-AS1	rs7326283	27905548	T	C	0.4830950	0.0436542	0.0036593	3.2E-34
13	PDX1-AS1	rs17826863	27905667	C	T	0.2194310	-0.0369606	0.0044147	7.3E-18
13	PDX1-AS1	rs17826899	27905826	G	A	0.2194200	-0.0369429	0.0044150	7.6E-18
13	PDX1-AS1	rs9581939	27906156	T	C	0.2189610	-0.0367895	0.0044216	1.0E-17
13	PDX1-AS1	rs9581940	27906259	C	T	0.2194420	-0.0370414	0.0044158	6.6E-18
13	PDX1-AS1	rs149168187	27906993	C	CT	0.4814260	0.0438283	0.0036538	1.7E-34
13	PDX1-AS1	rs12429454	27907073	A	G	0.4787570	0.0434343	0.0036645	1.2E-33
13	PDX1-AS1	rs3086898	27907779	GTGTA	G	0.4859860	0.0443922	0.0036867	6.8E-35
13	PDX1-AS1	rs9579128	27907801	C	T	0.3671320	-0.0356695	0.0037831	1.2E-21
13	PDX1-AS1	rs56209434	27908320	A	G	0.4811940	0.0433620	0.0036467	5.6E-34
13	PDX1-AS1	rs11619319	27913462	G	A	0.4814300	0.0434468	0.0036411	3.6E-34
13	PDX1-AS1	rs55879744	27914875	GTAC	G	0.2510480	-0.0366142	0.0042685	7.8E-19
13	PDX1-AS1	rs4771189	27914991	C	A	0.4813130	0.0434822	0.0036421	3.1E-34
13	PDX1-AS1	rs2297316	27916074	A	G	0.3394300	-0.0326377	0.0038396	1.3E-17
13	PDX1-AS1	rs35369009	27916373	T	C	0.4803880	0.0433378	0.0036409	4.3E-34
13	PDX1-AS1	rs61944003	27916734	G	C	0.4803690	0.0433481	0.0036401	4.0E-34
13	PDX1-AS1	rs2293941	27917061	A	G	0.4803560	0.0433197	0.0036400	4.6E-34
13	PDX1-AS1	rs2293942	27917249	C	T	0.2532840	-0.0371049	0.0042475	2.0E-19
13	PDX1-AS1	rs61944005	27918876	T	G	0.4677790	0.0427487	0.0036487	8.0E-33
13	PDX1-AS1	rs3841228	27919351	TA	T	0.2629310	-0.0347772	0.0042047	2.1E-17
13	PDX1-AS1	rs3812861	27919352	T	A	0.4662140	0.0426532	0.0036566	1.4E-32
13	PDX1-AS1	rs137897924	27919682	G	AGAAAT	0.1708880	-0.0251133	0.0048776	4.5E-08
13	PDX1-AS1	rs7331478	27919720	G	T	0.4676260	0.0426388	0.0036475	1.1E-32
13	PDX1-AS1	rs9581943	27919860	A	G	0.3511910	-0.0307581	0.0038049	6.8E-16
13	PDX1-AS1	rs146021107	27920029	A	AG	0.4680770	0.0424472	0.0036489	2.4E-32
13	PDX1, PDX1-AS1	rs9512918	27920812	G	C	0.1794320	-0.0245565	0.0047367	4.8E-08
13	PDX1, PDX1-AS1	rs4430606	27921056	T	G	0.4676070	0.0425149	0.0036488	1.8E-32
13	PDX1, PDX1-AS1	rs1124607	27921083	C	A	0.2626180	-0.0346348	0.0042005	2.9E-17
13	PDX1	rs4002828	27921982	C	T	0.4676900	0.0424325	0.0036484	2.2E-32
13	PDX1	rs61944006	27922282	C	G	0.4676860	0.0424179	0.0036484	2.3E-32
13	PDX1	rs4415872	27923022	A	C	0.1794380	-0.0247098	0.0047365	4.0E-08
13	PDX1	rs4581569	27923484	T	C	0.1794470	-0.0246969	0.0047361	4.0E-08
13	PDX1	rs57247118	27923691	G	A	0.4676830	0.0423377	0.0036483	3.0E-32
13	PDX1	rs60353775	27924128	G	C	0.4674460	0.0425664	0.0036496	1.6E-32
13	PDX1	rs9805632	27924186	C	G	0.2624070	-0.0346868	0.0042043	2.8E-17
13	PDX1	rs139276646	27925446	C	CCCTCTT	0.4666250	0.0425181	0.0036533	2.1E-32
13	PDX1	rs7981781	27925825	A	G	0.4662350	0.0423496	0.0036453	2.2E-32
13	PDX1	rs9319402	27926043	A	G	0.2629270	-0.0348303	0.0042043	2.2E-17
13	PDX1 *	rs7982864	27926359	T	C	0.1821500	-0.0244694	0.0047010	3.7E-08
13	KL *	rs2067296	32979946	AAGAC	A	0.2200010	0.0475092	0.0044176	5.6E-28
13	KL *	rs576674	32980164	G	A	0.2181550	0.0478697	0.0043978	1.0E-28
13	KL *	rs488166	32980214	C	G	0.2176540	0.0484722	0.0044099	4.4E-29
13	KL *	rs488321	32980267	T	C	0.2168800	0.0481042	0.0044081	9.3E-29
13	KL *	rs75629141	32980290	T	A	0.2209430	0.0470788	0.0044271	1.3E-27
13	KL *	rs11842170	32980367	A	G	0.0873527	0.0415124	0.0064729	4.2E-11
13	KL *	rs2858980	32980449	G	A	0.2167500	0.0479613	0.0044090	1.5E-28
13	KL *	rs8002606	32980635	G	C	0.2167380	0.0478383	0.0044104	1.9E-28
13	KL *	rs533873	32981449	C	T	0.2946130	0.0357904	0.0039959	2.8E-20
13	KL *	rs56252704	32982090	A	G	0.2156600	0.0481373	0.0044310	1.6E-28
13	KL *	rs7983505	32983035	T	A	0.2160490	0.0485161	0.0044297	7.2E-29
13	KL *	rs556168	32983072	C	T	0.3527260	-0.0201878	0.0038380	1.7E-08
13	KL *	rs573013	32983117	T	C	0.3527120	-0.0201407	0.0038381	1.8E-08
13	KL *	rs580760	32983462	G	A	0.2936060	0.0356755	0.0040058	4.7E-20
13	KL *	rs57286125	32983506	C	G	0.2159190	0.0486850	0.0044318	4.8E-29
13	KL *	rs430883	32985168	T	C	0.4085410	-0.0201441	0.0037393	2.0E-08
13	KL *	rs389891	32985896	C	A	0.3482250	-0.0198086	0.0038363	4.3E-08
13	KL *	rs11839569	32986355	G	A	0.2153470	0.0488686	0.0044390	3.8E-29
13	KL *	rs7997912	32988367	C	T	0.2172700	0.0485236	0.0044294	6.4E-29
13	KL *	rs513320	32991014	C	A	0.0646179	0.0425279	0.0074336	6.6E-09
13	KL *	rs2094712	32991421	A	G	0.2370180	0.0281077	0.0043502	5.1E-11
13	KL *	rs7984515	32992027	G	A	0.1067240	0.0364419	0.0058790	2.9E-10
13	KL *	rs7984028	32992084	T	C	0.1047580	0.0355574	0.0059292	9.4E-10
13	KL *	chr13:32992298_T_TA	32992298	TA	T	0.1072960	0.0360858	0.0058730	5.0E-10
13	KL *	rs7324797	32992917	A	G	0.1067280	0.0362698	0.0058791	3.4E-10
13	KL *	rs17078327	32993389	A	G	0.1060910	0.0358673	0.0058971	6.3E-10
13	KL *	rs66609723	32993510	A	G	0.1067300	0.0362876	0.0058790	3.3E-10
13	KL *	rs4941731	32993922	A	G	0.1067330	0.0363864	0.0058797	3.1E-10
13	KL *	rs12428531	32994071	T	C	0.1067640	0.0363120	0.0058787	3.2E-10
13	KL *	rs73174981	32994738	C	T	0.1067560	0.0359790	0.0058779	4.7E-10
13	KL *	rs12583154	32995935	A	G	0.1067760	0.0358990	0.0058777	5.3E-10
13	KL *	rs56009467	32997100	T	A	0.1712100	0.0379022	0.0048312	1.5E-15
13	KL *	rs12429937	32997615	T	A	0.1712560	0.0377794	0.0048306	1.7E-15
13	KL *	rs34514215	32997931	AT	A	0.4470770	0.0246324	0.0036670	2.4E-11
13	KL *	rs12583607	32998289	T	G	0.1707350	0.0374835	0.0048355	2.8E-15
13	KL *	rs57562480	33000154	A	T	0.1713310	0.0378037	0.0048286	1.6E-15
13	KL *	rs380854	33000493	G	A	0.4464360	0.0250770	0.0036684	1.0E-11
13	KL *	rs391933	33001554	G	A	0.4453550	0.0249121	0.0036655	1.4E-11
13	KL *	rs551579	33001837	C	T	0.4300010	0.0245553	0.0037021	2.4E-11
13	KL *	rs493663	33003438	A	G	0.4299870	0.0237496	0.0036917	1.9E-10
13	KL *	rs450789	33004095	A	G	0.4301000	0.0239357	0.0036833	1.4E-10
13	KL *	rs447556	33004390	A	G	0.4301280	0.0239275	0.0036831	1.4E-10
13	KL *	rs35607689	33005277	G	GT	0.4301410	0.0239327	0.0036830	1.4E-10
13	KL *	rs379335	33005612	C	G	0.4453820	0.0252937	0.0036524	8.3E-12
13	KL *	rs371126	33006717	G	A	0.4455930	0.0253326	0.0036502	8.3E-12
13	KL *	rs564701	33007006	C	T	0.4455970	0.0253459	0.0036508	7.1E-12
13	KL *	rs211246	33007267	C	T	0.4455870	0.0253328	0.0036509	7.2E-12
13	KL *	rs211248	33008800	T	C	0.4299670	0.0235189	0.0036842	2.6E-10
13	KL *	rs211249	33009215	C	G	0.4299100	0.0236639	0.0036839	2.1E-10
13	KL *	rs211250	33009562	C	T	0.4331550	0.0231592	0.0036932	4.7E-10
13	KL *	rs211252	33010819	T	C	0.4297170	0.0236289	0.0036851	2.2E-10
14	FOXP3	rs10873398	89579726	A	G	0.1479160	-0.0277150	0.0051691	2.7E-08
14	FOXP3	rs11626777	89582590	C	T	0.1439100	-0.0281513	0.0052285	1.7E-08
14	FOXP3	rs35889227	89589124	T	G	0.1424700	-0.0285977	0.0052633	1.4E-08
14	SLC25A47 *	rs35617968	100321886	A	C	0.1531510	-0.0311333	0.0050487	8.4E-10
14	SLC25A47 *	rs4905947	100322236	A	G	0.1610720	-0.0296037	0.0049384	1.1E-09
14	SLC25A47 *	rs4900460	100322237	A	C	0.1607360	-0.0296609	0.0049436	1.1E-09
14	SLC25A47 *	rs4905948	100322303	G	A	0.1621450	-0.0296296	0.0049274	1.1E-09
14	SLC25A47 *	rs4905949	100322640	A	G	0.1488800	-0.0330813	0.0051484	1.2E-10
14	SLC25A47	rs35097172	100325789	T	C	0.1354740	-0.0329538	0.0053226	2.3E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
14	SLC25A47	rs1951519	100326145	C	A	0.2167990	-0.0262461	0.0044345	1.2E-09
14	SLC25A47	rs1535464	100327094	A	G	0.1434570	-0.0313361	0.0052114	7.2E-10
14	SLC25A47	rs732898	100327789	A	G	0.3921050	-0.0224902	0.0037344	4.4E-11
14	SLC25A47	rs11160580	100327977	T	C	0.4587740	-0.0233384	0.0036502	3.2E-12
14	SLC25A47	rs10144242	100328067	C	T	0.4586590	-0.0235478	0.0036543	2.3E-12
14	SLC25A47	rs8015259	100329001	C	G	0.2172320	-0.0272042	0.0044166	2.1E-10
14	SLC25A47	rs4905950	100329293	C	T	0.4642320	-0.0240768	0.0036527	1.1E-12
14	SLC25A47	rs10147903	100329326	G	A	0.4648630	-0.0240492	0.0036542	1.1E-12
14	SLC25A47	rs3736952	100330141	T	C	0.1432610	-0.0301455	0.0051943	2.2E-09
14	SLC25A47 *	rs7143025	100330863	A	T	0.2144510	-0.0268915	0.0044344	4.4E-10
14	SLC25A47 *	rs7143218	100330918	C	A	0.2144690	-0.0270216	0.0044342	3.7E-10
14	SLC25A47 *	rs35852289	100331675	G	A	0.1429100	-0.0304643	0.0052015	1.5E-09
14	SLC25A47 *	rs33952550	100331804	CCTCA	C	0.2168050	-0.0267279	0.0044158	4.4E-10
14	WARS *	rs12887559	100332442	T	C	0.1423950	-0.0312454	0.0052028	7.0E-10
14	WARS *	rs11160581	100333447	C	G	0.4722810	-0.0248028	0.0036663	2.6E-13
14	WARS *	rs3742384	100333766	T	C	0.1424270	-0.0311983	0.0052019	7.4E-10
14	WARS	rs10142340	100336148	T	C	0.2139900	-0.0271595	0.0044406	3.2E-10
14	WARS	rs11160582	100336536	T	C	0.2098160	-0.0269427	0.0044747	4.8E-10
14	WARS	rs2234530	100337027	A	G	0.1423970	-0.0310805	0.0052036	8.7E-10
14	WARS	rs2234528	100337318	C	A	0.1426500	-0.0311721	0.0052084	8.5E-10
14	WARS	rs11622361	100337405	G	C	0.1423970	-0.0310805	0.0052036	8.7E-10
14	WARS	rs7155068	100337978	T	C	0.2144290	-0.0273284	0.0044307	2.3E-10
14	WARS	rs7154151	100338207	C	T	0.2144290	-0.0273284	0.0044307	2.3E-10
14	WARS	rs11624738	100338949	C	A	0.2154770	-0.0272340	0.0044247	2.4E-10
14	WARS	rs11629457	100339246	T	C	0.2152920	-0.0266096	0.0044336	8.7E-10
14	WARS	rs4905952	100340799	G	A	0.2159030	-0.0271759	0.0044197	2.6E-10
14	WARS	rs35384251	100340936	T	C	0.1378840	-0.0315413	0.0053004	9.9E-10
14	WARS	rs11627197	100341107	A	G	0.1431980	-0.0308824	0.0052071	9.4E-10
14	WARS	rs1570305	100341818	G	A	0.1424560	-0.0312462	0.0052026	6.8E-10
14	WARS	rs1373	100342173	T	A	0.2156160	-0.0272888	0.0044218	2.1E-10
14	WARS	rs9453	100342508	G	A	0.2158770	-0.0272201	0.0044193	2.3E-10
14	WARS	rs34040257	100343762	T	C	0.1424560	-0.0312462	0.0052026	6.8E-10
14	WARS	rs11276770	100344059	CTTCCC'	G	0.2164810	-0.0272922	0.0044254	1.8E-10
14	WARS	rs4905953	100344089	G	A	0.2159800	-0.0271102	0.0044202	2.7E-10
14	WARS	rs75590582	100344547	G	A	0.2159070	-0.0273140	0.0044194	2.1E-10
14	WARS	rs149835073	100344766	C	T	0.2159070	-0.0272493	0.0044195	2.2E-10
14	WARS	rs10142580	100345405	G	C	0.2158790	-0.0272206	0.0044193	2.3E-10
14	WARS	chr14:100345660_AAAAT_A	100345660	AAAAT	A	0.2245820	-0.0266053	0.0044155	5.2E-10
14	WARS	rs72383545	100345677	T	TAA	0.1424560	-0.0312462	0.0052026	6.8E-10
14	WARS	rs1983770	100346069	A	G	0.2158640	-0.0272710	0.0044184	2.2E-10
14	WARS	rs941923	100346740	T	C	0.2158710	-0.0272653	0.0044185	2.2E-10
14	WARS	rs3073366	100348380	GGCA	G	0.2158920	-0.0272317	0.0044193	2.3E-10
14	WARS	rs7144866	100348809	A	G	0.1424430	-0.0312586	0.0052015	6.7E-10
14	WARS	rs56293834	100351949	T	C	0.1427680	-0.0311770	0.0052073	7.5E-10
14	WARS	rs143487325	100352002	A	AG	0.2163980	-0.0272765	0.0044330	2.3E-10
14	WARS	rs4905954	100352422	C	G	0.2158740	-0.0272769	0.0044183	2.2E-10
14	WARS	rs11626882	100353343	C	T	0.2158860	-0.0272607	0.0044183	2.2E-10
14	WARS	rs3783345	100354199	A	G	0.1428440	-0.0315953	0.0051999	4.7E-10
14	WARS	rs1009812	100354643	G	A	0.2159050	-0.0272681	0.0044178	2.1E-10
14	WARS	rs9324020	100354869	G	T	0.2159770	-0.0271280	0.0044171	2.5E-10
14	WARS	rs11623879	100355936	C	T	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs8008560	100357712	C	T	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs8009578	100358052	G	A	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs8009435	100358157	C	T	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs8009443	100358170	C	T	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs8009897	100358226	G	A	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs8010851	100358303	T	C	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs10438232	100359439	C	T	0.2159220	-0.0271674	0.0044167	2.4E-10
14	WARS	rs10438233	100359863	G	A	0.4743140	-0.0246231	0.0036685	4.1E-13
14	WARS	rs10438234	100359923	G	C	0.1425500	-0.0309394	0.0051973	9.3E-10
14	WARS	rs4900463	100360098	A	G	0.2159580	-0.0271220	0.0044159	2.5E-10
14	WARS	rs2234524	100360436	C	G	0.1425670	-0.0307954	0.0051970	1.1E-09
14	WARS	rs2146107	100361092	G	T	0.1425740	-0.0307705	0.0051971	1.1E-09
14	WARS	rs2146106	100361171	C	T	0.1426630	-0.0310444	0.0051964	8.1E-10
14	WARS	rs2400898	100362060	T	C	0.2159220	-0.0271563	0.0044167	2.4E-10
14	WARS	rs2400899	100362150	C	T	0.2159220	-0.0271563	0.0044167	2.4E-10
14	WARS	rs61990729	100362288	T	C	0.0980211	-0.0412664	0.0061670	3.7E-12
14	WARS	rs3783346	100362847	T	C	0.1425510	-0.0309278	0.0051973	9.4E-10
14	WARS	rs8018305	100363511	C	T	0.4746630	-0.0249903	0.0036663	2.1E-13
14	WARS	rs12888855	100364481	A	C	0.1426020	-0.0309801	0.0051965	8.6E-10
14	WARS	rs4541005	100365437	G	A	0.2155980	-0.0271162	0.0044227	2.4E-10
14	WARS	rs1998902	100365498	C	T	0.1431230	-0.0307331	0.0051955	1.1E-09
14	WARS	rs724392	100365915	C	T	0.4743110	-0.0249260	0.0036661	2.2E-13
14	WARS	rs2146105	100365945	C	G	0.1421760	-0.0307108	0.0052025	1.2E-09
14	WARS	rs724391	100366054	T	C	0.2159260	-0.0271626	0.0044166	2.4E-10
14	WARS	rs8022027	100368645	T	C	0.2170010	-0.0267704	0.0044106	3.6E-10
14	WARS	rs34966278	100368785	ACCC	A	0.2159440	-0.0271658	0.0044162	2.3E-10
14	WARS	rs1887198	100369641	T	C	0.2159590	-0.0271462	0.0044152	2.2E-10
14	WARS	rs3838956	100369908	AGCCTC	C	0.2161810	-0.0270236	0.0044164	2.7E-10
14	WARS	rs941931	100370016	C	T	0.2159480	-0.0271290	0.0044153	2.2E-10
14	WARS	rs35100722	100370072	C	A	0.2159480	-0.0271290	0.0044153	2.2E-10
14	WARS	rs4905956	100370646	A	G	0.2159210	-0.0272014	0.0044156	2.0E-10
14	WARS	rs4905957	100370893	C	T	0.2159130	-0.0272527	0.0044156	1.8E-10
14	WARS	rs8012938	100371045	C	G	0.2159210	-0.0272014	0.0044156	2.0E-10
14	WARS	chr14:100371447_CAAAAA_A	100371447	AAAAAA/	C	0.4674110	-0.0235242	0.0036974	4.5E-12
14	WARS	rs10149239	100371670	G	A	0.2159210	-0.0272014	0.0044156	2.0E-10
14	WARS	rs10149438	100371836	G	A	0.2159210	-0.0272014	0.0044156	2.0E-10
14	WARS	rs941929	100372791	G	C	0.2159210	-0.0272014	0.0044156	2.0E-10
14	WARS	rs3783347	100372924	T	G	0.1426980	-0.0307631	0.0051929	1.0E-09
14	WARS	rs3994912	100373953	C	T	0.2158720	-0.0273889	0.0044184	1.6E-10
14	WARS	rs941928	100374259	G	C	0.1426090	-0.0307763	0.0051954	1.0E-09
14	WARS	rs941927	100374476	T	C	0.2158620	-0.0274745	0.0044192	1.4E-10
14	WARS	rs941926	100374613	G	A	0.2158420	-0.0274404	0.0044198	1.5E-10
14	WARS	rs1957453	100374671	G	C	0.2158480	-0.0274479	0.0044198	1.5E-10
14	WARS	rs3835003	100374829	AT	A	0.2158550	-0.0275093	0.0044200	1.4E-10
14	WARS	rs7143006	100375363	T	A	0.1424730	-0.0305849	0.0051988	1.3E-09
14	WARS	rs2234518	100375722	A	G	0.2154510	-0.0277997	0.0044281	9.9E-11
14	WARS	rs17554326	100376040	G	A	0.1482350	-0.0321510	0.0051374	1.0E-10
14	WARS	rs2273804	100376300	G	C	0.2071220	-0.0259936	0.0044906	2.2E-09
14	WDR25	rs2273802	100376562	G	A	0.4746070	-0.0247349	0.0036766	3.6E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
14	WDR25	rs12891492	100377006	G	A	0.1413870	-0.0305954	0.0052291	1.4E-09
14	WDR25	chr14:100377467_A_ATT	100377467	ATT	A	0.1940390	-0.0254016	0.0046406	1.5E-08
14	WDR25	rs12897888	100378083	A	G	0.1411360	-0.0306791	0.0052401	1.4E-09
14	WDR25	rs12882934	100379120	A	C	0.2052510	-0.0264202	0.0045381	1.8E-09
14	WDR25	rs56062624	100380043	TTTTTC	T	0.4525460	-0.0264282	0.0037248	3.2E-14
14	WDR25	rs2273800	100381370	G	A	0.4550340	-0.0251650	0.0037025	3.0E-13
14	WDR25	rs3742387	100381593	G	A	0.4554410	-0.0251929	0.0037026	3.0E-13
14	WDR25	rs11624049	100386483	T	C	0.4812660	-0.0242509	0.0036792	3.4E-12
14	WDR25	rs4900464	100399524	C	T	0.4824380	-0.0254901	0.0036694	3.1E-13
14	WDR25	rs35414565	100405168	CT	C	0.4727300	-0.0241037	0.0036806	5.3E-12
14	WDR25	rs28581530	100405926	T	C	0.4803020	-0.0249039	0.0036495	6.0E-13
14	WDR25	rs10144321	100416068	A	G	0.4764560	-0.0237832	0.0036295	5.1E-12
14	WDR25	rs11626307	100475728	C	A	0.4761010	-0.0195386	0.0037159	1.3E-09
14	MIR4309 *	rs2277471	102558050	C	A	0.4636740	0.0189906	0.0036471	2.9E-08
14	MIR4309 *	rs11626063	102558369	G	C	0.4634400	0.0188957	0.0036493	3.5E-08
14	MIR4309 *	rs4906224	102558703	C	T	0.4640860	0.0187774	0.0036532	4.4E-08
14	MIR4309 *	rs7140280	102560654	G	A	0.4642530	0.0189141	0.0036483	3.4E-08
14	MIR4309 *	rs4906226	102561022	C	T	0.4644520	0.0187841	0.0036469	4.2E-08
14	MIR4309 *	rs6575922	102561452	A	G	0.4330930	0.0205250	0.0037185	1.1E-08
14	MIR4309 *	rs4906227	102562366	A	G	0.4657570	0.0192893	0.0036542	2.0E-08
14	MIR4309 *	rs4900543	102562687	T	C	0.4641400	0.0189974	0.0036463	2.9E-08
14	MIR4309 *	rs12891603	102565270	A	G	0.4642780	0.0189860	0.0036456	2.9E-08
14	MIR4309 *	rs7155171	102565508	C	T	0.4685780	0.0192865	0.0036568	1.6E-08
14	RCOR1 *	rs8009307	102567293	T	G	0.4643490	0.0189360	0.0036454	2.9E-08
14	RCOR1 *	rs6575925	102568170	G	A	0.4643490	0.0189349	0.0036454	2.9E-08
14	RCOR1 *	rs36047872	102568203	A	AAAG	0.4718340	0.0189489	0.0036571	2.8E-08
14	RCOR1 *	rs10138267	102569095	C	T	0.4643410	0.0188846	0.0036455	3.1E-08
14	RCOR1 *	chr14:102573472_C_CT	102573472	C	CT	0.4865650	0.0198081	0.0037000	1.5E-08
14	RCOR1 *	rs10151896	102573599	G	C	0.4643470	0.0188873	0.0036446	3.4E-08
14	RCOR1 *	rs28444760	102574811	A	G	0.4644160	0.0189412	0.0036448	3.1E-08
14	RCOR1 *	rs77689889	102582567	A	G	0.4632700	0.0189665	0.0036560	3.2E-08
14	RCOR1 *	rs8003309	102583806	C	G	0.4595550	0.0187556	0.0036638	4.8E-08
14	RCOR1 *	rs6575926	102583846	G	A	0.4629280	0.0188703	0.0036586	3.7E-08
14	RCOR1 *	rs1998419	102584060	C	G	0.4632020	0.0190905	0.0036623	2.9E-08
14	RCOR1 *	rs4900544	102584780	C	G	0.4629130	0.0188865	0.0036597	3.8E-08
14	RCOR1 *	rs4900545	102584795	C	T	0.4682770	0.0188179	0.0036654	3.1E-08
14	RCOR1 *	rs1815261	102589523	A	G	0.4631280	0.0196134	0.0036648	1.2E-08
14	RCOR1	rs12879103	102599808	G	T	0.4000140	0.0196122	0.0037387	4.8E-08
15	C15orf52 *	rs4143838	40330173	C	T	0.1136330	0.0340966	0.0057435	1.4E-08
15	C15orf52	rs58452154	40340167	G	T	0.1018460	0.0402657	0.0060724	2.9E-10
15	C15orf52	rs73397306	40340397	T	G	0.0921198	0.0414759	0.0063690	5.1E-10
15	C15orf52	rs77582559	40340447	T	C	0.0921211	0.0414778	0.0063690	5.1E-10
15	C15orf52 *	rs148790145	40341019	A	ACT	0.0918672	0.0421038	0.0063823	2.6E-10
15	DMXL2	rs12593979	51449382	T	C	0.4131700	-0.0218228	0.0037107	2.1E-09
15	DMXL2	rs4774590	51453080	A	G	0.4175850	-0.0222710	0.0037118	1.0E-09
15	DMXL2	rs11630743	51458412	T	C	0.4126170	-0.0213069	0.0037064	4.5E-09
15	DMXL2	rs11630842	51458455	A	G	0.4174270	-0.0219201	0.0037013	1.5E-09
15	DMXL2	rs7165887	51458649	A	G	0.4172290	-0.0219048	0.0037027	1.6E-09
15	DMXL2	rs141997431	51460572	ATATC	A	0.4310130	-0.0210422	0.0036986	8.2E-09
15	DMXL2	rs1031664	51462700	A	C	0.4227400	-0.0210436	0.0036864	5.8E-09
15	DMXL2	rs12441759	51462836	A	C	0.4212270	-0.0212628	0.0036863	4.3E-09
15	DMXL2	rs10220909	51470215	A	C	0.4140500	-0.0202654	0.0037016	2.5E-08
15	DMXL2	rs8042221	51482416	G	A	0.4257410	-0.0216787	0.0036765	1.8E-09
15	DMXL2	rs4775944	51483413	C	T	0.4257280	-0.0216659	0.0036764	1.8E-09
15	DMXL2	rs4775946	51483733	G	A	0.4257280	-0.0216659	0.0036764	1.8E-09
15	DMXL2	rs4774592	51486682	T	C	0.4206100	-0.0211935	0.0036793	4.3E-09
15	DMXL2	rs7171439	51489499	A	C	0.4201410	-0.0213352	0.0036788	3.7E-09
15	DMXL2	rs10851500	51491623	C	T	0.4205550	-0.0211434	0.0036782	4.6E-09
15	DMXL2	rs7173880	51493236	A	C	0.4212060	-0.0212609	0.0036889	4.4E-09
15	DMXL2	rs10467924	51495382	G	A	0.4239320	-0.0215108	0.0036859	2.8E-09
15	DMXL2	rs12102203	51499362	G	A	0.4256040	-0.0216629	0.0036794	1.9E-09
15	DMXL2	rs12592889	51502975	A	G	0.4249910	-0.0217795	0.0036749	1.6E-09
15	DMXL2	rs4144941	51504609	C	T	0.4258680	-0.0219928	0.0036742	9.9E-10
15	DMXL2	rs12101730	51508536	T	C	0.4212270	-0.0215678	0.0036782	2.0E-09
15	DMXL2	rs9806598	51511533	G	A	0.4259430	-0.0219528	0.0036738	1.0E-09
15	DMXL2	rs56259821	51523663	iAGGCAG	A	0.4158950	-0.0221418	0.0037294	1.7E-09
15	DMXL2	rs62014659	51526394	C	G	0.3591320	-0.0203987	0.0037912	3.8E-08
15	DMXL2	rs12101920	51528712	C	T	0.3591590	-0.0203526	0.0037895	4.1E-08
15	DMXL2	rs4359386	51533926	T	C	0.4266710	-0.0218061	0.0036725	1.5E-09
15	DMXL2	rs4462536	51534082	G	A	0.4270360	-0.0219670	0.0036722	1.1E-09
15	DMXL2	rs8031903	51545964	T	C	0.4208160	-0.0215566	0.0036760	2.5E-09
15	DMXL2	rs6493505	51552975	C	T	0.4209100	-0.0217145	0.0036761	2.0E-09
15	DMXL2	rs11070855	51558086	T	C	0.4208060	-0.0217031	0.0036743	2.0E-09
15	DMXL2	chr15:51560993_TA_T	51560993	T	TA	0.4208060	-0.0217031	0.0036743	2.0E-09
15	DMXL2	rs61623176	51561534	AG	A	0.4208060	-0.0217031	0.0036743	2.0E-09
15	DMXL2	rs11070856	51561620	T	C	0.4213370	-0.0217336	0.0036775	1.9E-09
15	DMXL2	rs7182977	51561933	G	C	0.4208060	-0.0217031	0.0036743	2.0E-09
15	DMXL2	rs7161973	51561966	C	T	0.4207090	-0.0217449	0.0036745	1.9E-09
15	DMXL2	rs28648597	51563869	A	T	0.4208060	-0.0217031	0.0036743	2.0E-09
15	DMXL2	rs60259473	51563993	G	GA	0.4208060	-0.0217031	0.0036743	2.0E-09
15	DMXL2	rs17609666	51565841	T	G	0.4206320	-0.0216519	0.0036745	2.1E-09
15	DMXL2	rs7170330	51567116	T	C	0.4198910	-0.0221580	0.0036788	1.1E-09
15	DMXL2	rs11635592	51567589	T	A	0.4208680	-0.0217732	0.0036745	1.7E-09
15	DMXL2	rs8036609	51569229	G	C	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs8036904	51569241	A	G	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs8037840	51569280	C	T	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs8036821	51569449	G	A	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs35020146	51570253	GA	G	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs4775951	51570903	C	T	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs12438491	51571375	A	G	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs7168546	51572125	T	C	0.4209470	-0.0217467	0.0036746	1.8E-09
15	DMXL2	rs12592653	51572871	G	A	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs8035135	51573137	A	C	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs8039255	51573228	T	C	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs8040648	51573379	A	T	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs8039835	51573667	G	A	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs8041197	51573680	C	T	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs8041514	51573857	C	T	0.4208250	-0.0216917	0.0036754	2.0E-09
15	DMXL2	chr15:51574437_CA_C	51574437	C	CA	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs4143721	51574584	G	A	0.4207690	-0.0217199	0.0036750	1.9E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	DMXL2	rs4143723	51574975	G	A	0.4209390	-0.0217589	0.0036746	1.8E-09
15	DMXL2	rs28393906	51575408	A	T	0.4205760	-0.0214727	0.0036753	2.9E-09
15	DMXL2	rs17609693	51575803	A	T	0.4205000	-0.0213494	0.0036757	3.4E-09
15	DMXL2	rs2414105	51576176	G	A	0.4205270	-0.0214279	0.0036750	3.0E-09
15	DMXL2	rs2414106	51576544	T	C	0.4212610	-0.0211257	0.0036772	5.0E-09
15	DMXL2	rs4775952	51576859	C	T	0.4205270	-0.0214266	0.0036750	3.1E-09
15	DMXL2	rs4143724	51578216	A	T	0.4205640	-0.0213886	0.0036747	3.3E-09
15	DMXL2	rs8038203	51578486	A	G	0.4199650	-0.0213393	0.0036788	3.5E-09
15	DMXL2	rs11634999	51579264	T	C	0.4205640	-0.0213941	0.0036747	3.2E-09
15	DMXL2	rs11635216	51579750	T	C	0.4205640	-0.0213941	0.0036747	3.2E-09
15	DMXL2	rs4775953	51580976	T	G	0.4206470	-0.0215103	0.0036745	2.7E-09
15	DMXL2	rs4775955	51581252	C	T	0.4206470	-0.0215103	0.0036745	2.7E-09
15	DMXL2	rs12442725	51582215	T	C	0.4209500	-0.0215910	0.0036746	2.3E-09
15	DMXL2	rs17609791	51582627	T	C	0.4209500	-0.0215910	0.0036746	2.3E-09
15	DMXL2	rs75683907	51582688	TATTA	T	0.4209500	-0.0215910	0.0036746	2.3E-09
15	DMXL2	rs28695624	51582731	C	A	0.4209500	-0.0215910	0.0036746	2.3E-09
15	DMXL2	rs28410165	51582822	A	C	0.4210320	-0.0217071	0.0036744	2.0E-09
15	DMXL2	rs4545756	51585593	G	A	0.4209530	-0.0215852	0.0036746	2.3E-09
15	DMXL2	rs17609812	51587063	A	G	0.4209530	-0.0215852	0.0036746	2.3E-09
15	DMXL2	rs9708186	51587346	G	A	0.4209530	-0.0215852	0.0036746	2.3E-09
15	DMXL2	rs7495962	51587815	A	T	0.4209530	-0.0215852	0.0036746	2.3E-09
15	DMXL2	rs1077361	51588722	A	T	0.4205670	-0.0213884	0.0036747	3.3E-09
15	DMXL2	rs1902592	51589783	T	C	0.4205670	-0.0213884	0.0036747	3.3E-09
15	DMXL2	rs1902593	51589883	T	C	0.4205670	-0.0213884	0.0036747	3.3E-09
15	DMXL2	rs882385	51590172	T	C	0.4205670	-0.0213884	0.0036747	3.3E-09
15	DMXL2	rs4775956	51590441	C	G	0.4194630	-0.0210985	0.0036775	4.7E-09
15	DMXL2	rs2899475	51590854	T	C	0.4209600	-0.0215700	0.0036747	2.4E-09
15	DMXL2	rs4438255	51591154	A	G	0.4209600	-0.0215700	0.0036747	2.4E-09
15	DMXL2	rs28866855	51592997	C	T	0.4202730	-0.0216790	0.0036764	2.1E-09
15	DMXL2	rs149605042	51593249	A	G	0.4198590	-0.0215809	0.0036815	2.4E-09
15	DMXL2	rs10438317	51594085	C	T	0.4209560	-0.0215667	0.0036747	2.4E-09
15	DMXL2	rs10438319	51594648	C	T	0.4118880	-0.0221127	0.0037060	1.1E-09
15	DMXL2	rs72623976	51594907	G	T	0.4209990	-0.0215085	0.0036746	2.7E-09
15	DMXL2	rs10438321	51595729	C	T	0.4206140	-0.0213116	0.0036747	3.7E-09
15	DMXL2	rs202140861	51595891	T	C	0.4206140	-0.0213116	0.0036747	3.7E-09
15	DMXL2	rs74903804	51596458	A	T	0.4206140	-0.0213116	0.0036747	3.7E-09
15	DMXL2	rs12050586	51596622	G	A	0.4206140	-0.0213116	0.0036747	3.7E-09
15	DMXL2	rs12050598	51596978	G	A	0.4208660	-0.0213532	0.0036753	3.4E-09
15	DMXL2	rs7177720	51598085	C	T	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs7170444	51598303	A	G	0.4211980	-0.0211972	0.0036757	4.2E-09
15	DMXL2	rs7170217	51598481	G	A	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs11070859	51598605	G	C	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs10775144	51598937	T	C	0.4202890	-0.0214036	0.0036770	3.4E-09
15	DMXL2	rs4775958	51599365	C	G	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs4775959	51599439	C	T	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs4775960	51599501	C	G	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs12442947	51599951	G	A	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs11070860	51600457	A	G	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs4775961	51600762	G	A	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs4774595	51600964	T	C	0.4206280	-0.0213242	0.0036746	3.6E-09
15	DMXL2	rs11636428	51601315	A	T	0.4198430	-0.0209924	0.0036784	6.3E-09
15	DMXL2	rs12372948	51602114	G	A	0.4205660	-0.0212541	0.0036743	4.1E-09
15	DMXL2	rs7174435	51602868	A	G	0.4237510	-0.0204985	0.0036674	1.4E-08
15	DMXL2	rs7176044	51603146	C	T	0.4251480	-0.0204859	0.0036666	1.3E-08
15	DMXL2	rs11634039	51603378	T	C	0.4237510	-0.0204985	0.0036674	1.4E-08
15	DMXL2	rs11634180	51603560	C	G	0.4237510	-0.0204985	0.0036674	1.4E-08
15	DMXL2	rs9944241	51605861	C	T	0.4118640	-0.0220354	0.0037367	1.7E-09
15	DMXL2	rs9944259	51606308	T	A	0.4205660	-0.0212668	0.0036744	4.0E-09
15	DMXL2	rs12442803	51606557	G	C	0.4237510	-0.0205126	0.0036675	1.4E-08
15	DMXL2	rs8042289	51607687	G	A	0.4237510	-0.0205126	0.0036675	1.4E-08
15	DMXL2	rs7183435	51607964	T	C	0.4236600	-0.0206256	0.0036679	1.1E-08
15	DMXL2	chr15:51608184_C_CA	51608184	CA	C	0.4224330	-0.0207533	0.0036733	9.6E-09
15	DMXL2	rs6493510	51608454	G	T	0.4238130	-0.0205828	0.0036678	1.2E-08
15	DMXL2	chr15:51608762_GA_G	51608762	G	GA	0.4235760	-0.0205444	0.0036687	1.4E-08
15	DMXL2	rs2414109	51608818	C	G	0.4235760	-0.0205444	0.0036687	1.4E-08
15	DMXL2	rs3078071	51609093	A	ATAAGT	0.4235360	-0.0204627	0.0036686	1.5E-08
15	DMXL2	rs2414111	51609160	T	C	0.4235890	-0.0204547	0.0036680	1.6E-08
15	DMXL2	rs35672248	51609940	AAC	A	0.4227190	-0.0204861	0.0037006	2.6E-08
15	DMXL2	rs11070862	51610030	A	G	0.4206260	-0.0212509	0.0036746	4.2E-09
15	DMXL2	rs7169753	51610640	C	T	0.4238230	-0.0204467	0.0036677	1.5E-08
15	DMXL2	rs7169786	51610686	C	T	0.4238230	-0.0204467	0.0036677	1.5E-08
15	DMXL2	rs2899476	51611677	T	C	0.4218160	-0.0201011	0.0036796	2.9E-08
15	DMXL2	rs2414113	51611699	T	C	0.4230070	-0.0203756	0.0036739	1.8E-08
15	DMXL2	rs2414114	51613584	G	T	0.4263710	-0.0204154	0.0036699	1.7E-08
15	DMXL2	rs2124876	51613965	C	T	0.4254970	-0.0204594	0.0036693	1.5E-08
15	DMXL2	rs4775966	51621591	G	A	0.4259450	-0.0206355	0.0036749	1.3E-08
15	DMXL2	rs10557164	51621836	CTG	C	0.4347790	-0.0213545	0.0036783	3.1E-09
15	DMXL2 *	rs2278988	51623037	C	A	0.4261980	-0.0205518	0.0036726	1.4E-08
15	DMXL2 *	rs2124879	51624636	C	T	0.4268960	-0.0208905	0.0036752	8.9E-09
15	VPS13C *	rs4775438	61828451	T	A	0.2104290	-0.0246982	0.0045386	3.4E-08
15	VPS13C *	rs4775440	61833440	T	G	0.2717470	-0.0295732	0.0041524	2.2E-13
15	VPS13C *	rs8026735	61833660	T	C	0.2931700	-0.0295086	0.0040687	6.6E-14
15	VPS13C *	chr15:61833724_TAA_T	61833724	T	TAA	0.2715260	-0.0294704	0.0041527	2.6E-13
15	VPS13C *	rs28755956	61834291	T	C	0.2679280	-0.0281839	0.0041726	2.6E-12
15	VPS13C *	rs9788653	61836902	C	A	0.1865940	-0.0299303	0.0047017	6.4E-11
15	VPS13C *	rs9788635	61841475	T	C	0.2304500	-0.0335196	0.0043165	2.2E-15
15	VPS13C *	rs2216999	61841532	A	T	0.4409330	0.0224245	0.0036979	1.7E-10
15	VPS13C *	rs17303831	61842133	C	T	0.1899520	-0.0302831	0.0046336	3.2E-11
15	VPS13C *	rs12909692	61843540	A	G	0.4382080	0.0220500	0.0037012	3.5E-10
15	VPS13C *	rs142337110	61844214	A	G	0.1883630	-0.0296653	0.0046519	8.0E-11
15	VPS13C *	rs12441791	61846388	G	A	0.1929270	-0.0282990	0.0046058	3.2E-10
15	VPS13C *	rs72747848	61847612	A	G	0.1902950	-0.0300399	0.0046327	4.5E-11
15	VPS13C *	rs12441436	61847794	A	T	0.1875280	-0.0308443	0.0046601	1.6E-11
15	VPS13C *	rs5813121	61847843	G	C	0.1875280	-0.0308443	0.0046601	1.6E-11
15	VPS13C *	rs71795512	61848509	G	GA	0.1903900	-0.0309451	0.0046489	1.0E-11
15	VPS13C *	rs72747849	61850860	C	T	0.2077470	-0.0270048	0.0044892	7.3E-10
15	VPS13C *	rs72747852	61851703	C	A	0.2062180	-0.0276215	0.0045029	3.8E-10
15	VPS13C *	rs72747853	61852172	T	C	0.2046190	-0.0279361	0.0045232	2.7E-10
15	VPS13C	rs2241492	61855008	A	T	0.2650090	-0.0313140	0.0041293	7.2E-15
15	VPS13C	chr15:61856531_TA_T	61856531	TA	T	0.4400910	0.0228921	0.0036985	5.6E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	VPS13C	rs17238110	61858165	G	A	0.2032370	-0.0284264	0.0045273	1.3E-10
15	VPS13C	rs72747855	61859314	A	G	0.2028960	-0.0285070	0.0045298	1.1E-10
15	VPS13C	rs72747856	61861121	A	C	0.2019700	-0.0281989	0.0045420	2.3E-10
15	VPS13C	rs1559673	61864315	C	A	0.2031210	-0.0279906	0.0045306	2.4E-10
15	VPS13C	rs11330878	61864877	G	GA	0.2031040	-0.0283841	0.0045281	1.4E-10
15	VPS13C	rs4775446	61865167	A	G	0.2031070	-0.0283870	0.0045279	1.4E-10
15	VPS13C	rs17303866	61865262	C	A	0.2032020	-0.0282710	0.0045280	1.6E-10
15	VPS13C	rs17303873	61865374	C	T	0.2027470	-0.0287042	0.0045340	1.0E-10
15	VPS13C	rs17238127	61865889	G	A	0.2019860	-0.0280229	0.0045431	3.1E-10
15	VPS13C	rs12591667	61868543	C	T	0.2031170	-0.0279830	0.0045296	2.6E-10
15	VPS13C	rs6494299	61874818	G	A	0.4507600	0.0222823	0.0036938	1.7E-10
15	VPS13C	rs12902092	61876093	C	T	0.4507630	0.0222535	0.0036936	1.8E-10
15	VPS13C	rs1364809	61880199	C	G	0.2038190	-0.0281253	0.0045222	2.0E-10
15	VPS13C	rs3809516	61880778	T	G	0.2034650	-0.0280436	0.0045247	2.3E-10
15	VPS13C	rs12442506	61882804	G	C	0.2033250	-0.0283757	0.0045249	1.4E-10
15	VPS13C	rs12442569	61882935	A	G	0.2032060	-0.0282872	0.0045263	1.6E-10
15	VPS13C	rs72747868	61885727	C	A	0.2038000	-0.0278121	0.0045246	3.2E-10
15	VPS13C	rs139641843	61887134	C	CAG	0.2029930	-0.0284090	0.0045278	1.5E-10
15	VPS13C	rs72747869	61888315	C	T	0.2034510	-0.0283395	0.0045253	1.5E-10
15	VPS13C	rs11071635	61889309	T	C	0.4452560	0.0228404	0.0037175	7.0E-11
15	VPS13C	rs72747870	61889999	T	C	0.2029660	-0.0282781	0.0045274	1.7E-10
15	VPS13C	rs11634516	61892713	G	T	0.4509640	0.0223267	0.0036924	1.5E-10
15	VPS13C	rs72747874	61894550	T	A	0.2027210	-0.0281442	0.0045305	2.3E-10
15	VPS13C	rs11071636	61896376	A	G	0.4412730	0.0227132	0.0036856	6.5E-11
15	VPS13C	rs186619770	61896766	C	T	0.2030030	-0.0282273	0.0045274	1.9E-10
15	VPS13C	rs4775448	61897735	A	T	0.4417010	0.0224164	0.0036837	1.3E-10
15	VPS13C	rs146164752	61897934	C	T	0.2030030	-0.0282273	0.0045274	1.9E-10
15	VPS13C	rs75917862	61899455	G	T	0.2029720	-0.0282943	0.0045274	1.7E-10
15	VPS13C	chr15:61903424_C_CA	61903424	CA	C	0.2030560	-0.0281858	0.0045269	2.0E-10
15	VPS13C	rs34516157	61904196	T	C	0.2029980	-0.0282111	0.0045274	1.9E-10
15	VPS13C	rs12441358	61907712	A	T	0.2028960	-0.0281716	0.0045283	2.0E-10
15	VPS13C	rs79855776	61910078	C	T	0.2035170	-0.0282957	0.0045226	1.5E-10
15	VPS13C	rs72747879	61910649	C	T	0.2035140	-0.0282692	0.0045226	1.6E-10
15	VPS13C	rs75685403	61912910	A	G	0.2033860	-0.0283930	0.0045234	1.3E-10
15	VPS13C	rs77838058	61913626	A	AGTTCTC	0.2010930	-0.0279122	0.0045493	3.2E-10
15	VPS13C	rs143487448	61914717	T	C	0.1809770	-0.0263948	0.0047628	1.1E-08
15	VPS13C	rs199649081	61914879	T	A	0.1986430	-0.0267275	0.0045820	2.8E-09
15	VPS13C	rs4541010	61915420	C	T	0.4440700	0.0227114	0.0036808	6.2E-11
15	VPS13C	rs7177538	61916389	C	T	0.2033420	-0.0281641	0.0045248	1.9E-10
15	VPS13C	rs4775452	61918376	C	T	0.2031170	-0.0283506	0.0045254	1.5E-10
15	VPS13C	rs4774426	61918744	T	G	0.2033410	-0.0284412	0.0045255	1.2E-10
15	VPS13C	rs963023	61919191	C	T	0.2034710	-0.0285263	0.0045235	1.0E-10
15	VPS13C	rs74347726	61919806	G	A	0.2034710	-0.0285263	0.0045235	1.0E-10
15	VPS13C	rs17238189	61920582	C	T	0.2034730	-0.0285405	0.0045236	1.0E-10
15	VPS13C	rs9788739	61926673	T	C	0.1970950	-0.0275020	0.0045793	8.6E-10
15	VPS13C	rs72747895	61929480	C	T	0.2034340	-0.0282861	0.0045203	1.6E-10
15	VPS13C	rs72747896	61930348	G	C	0.1976300	-0.0276421	0.0045708	7.6E-10
15	VPS13C	rs9788670	61931074	C	T	0.4564950	0.0209394	0.0036777	1.5E-09
15	VPS13C	rs12439027	61931499	G	C	0.1976530	-0.0271008	0.0045688	1.6E-09
15	VPS13C	rs2113935	61931884	C	T	0.1986720	-0.0272013	0.0045606	1.4E-09
15	VPS13C	rs8030161	61934489	C	T	0.1989150	-0.0273485	0.0045593	1.1E-09
15	VPS13C	rs17303968	61935087	T	A	0.4506930	0.0213838	0.0036672	5.6E-10
15	VPS13C	rs17238210	61935196	G	C	0.1991510	-0.0274372	0.0045600	8.8E-10
15	VPS13C	rs12232347	61935502	T	C	0.1973530	-0.0271742	0.0045724	1.5E-09
15	VPS13C	rs10519144	61936109	T	G	0.1977180	-0.0274802	0.0045686	9.0E-10
15	VPS13C	rs11071641	61936497	C	G	0.4467450	0.0209185	0.0036725	1.3E-09
15	VPS13C	rs35262268	61938266	T	TG	0.4691060	0.0200159	0.0037016	1.3E-08
15	VPS13C	rs12594396	61940106	T	G	0.1971200	-0.0275542	0.0045744	8.6E-10
15	VPS13C	rs7172838	61940597	C	T	0.4498820	0.0207969	0.0036672	1.8E-09
15	VPS13C	rs8038328	61941240	C	T	0.4465600	0.0207303	0.0036792	3.0E-09
15	VPS13C	rs72747901	61943255	A	C	0.1972790	-0.0270887	0.0045728	1.7E-09
15	VPS13C	rs72749703	61944649	A	G	0.1978660	-0.0270858	0.0045669	1.6E-09
15	VPS13C	rs2113932	61946032	A	G	0.4481390	0.0213734	0.0036658	6.4E-10
15	VPS13C	rs2113933	61946149	T	C	0.4498250	0.0215350	0.0036648	4.7E-10
15	VPS13C	rs8028217	61946585	A	T	0.4484210	0.0216072	0.0036739	6.2E-10
15	VPS13C	rs6494300	61947602	C	A	0.4500080	0.0211580	0.0036637	9.6E-10
15	VPS13C	rs1965048	61948404	A	G	0.4476800	0.0209454	0.0036671	1.4E-09
15	VPS13C	rs4581655	61949987	C	T	0.4500740	0.0212722	0.0036625	7.2E-10
15	VPS13C	rs17238252	61952082	G	C	0.4503500	0.0205992	0.0036649	1.9E-09
15	VPS13C	rs4620905	61953962	C	T	0.4504560	0.0210191	0.0036608	1.0E-09
15	VPS13C	rs3784635	61962790	C	T	0.2052320	-0.0280791	0.0045017	1.5E-10
15	VPS13C	rs2042610	61988718	C	G	0.4422800	0.0227804	0.0036828	6.5E-11
15	VPS13C	rs8035049	61995679	G	A	0.4401640	0.0218943	0.0036787	3.5E-10
15	VPS13C	rs12443311	61996498	A	C	0.4389940	0.0222268	0.0036831	2.1E-10
15	VPS13C	rs11071647	61998288	C	T	0.4498970	0.0208162	0.0037022	4.0E-09
15	VPS13C	rs72749742	61998493	A	T	0.2014290	-0.0294772	0.0045417	4.6E-11
15	VPS13C	rs11071648	61999679	C	T	0.4410670	0.0222281	0.0036819	2.1E-10
15	VPS13C	rs72749744	61999725	A	G	0.2008980	-0.0294825	0.0045472	5.2E-11
15	VPS13C	rs28763421	62002835	C	T	0.4410610	0.0221977	0.0036824	2.2E-10
15	VPS13C	rs187432044	62003285	G	T	0.2025340	-0.0297615	0.0045274	2.4E-11
15	VPS13C	rs185160237	62006519	G	A	0.2010490	-0.0297361	0.0045435	2.3E-11
15	VPS13C	rs9635356	62007404	G	T	0.2035230	-0.0295903	0.0045181	3.0E-11
15	VPS13C	rs11629528	62014256	A	G	0.4422350	0.0227676	0.0036817	6.3E-11
15	VPS13C	rs375442829	62017416	A	T	0.2015770	-0.0296708	0.0045373	2.9E-11
15	VPS13C	rs28798715	62017510	A	C	0.3059470	-0.0264466	0.0039615	1.5E-12
15	VPS13C	rs12440748	62021298	T	A	0.2016260	-0.0295295	0.0045367	3.5E-11
15	VPS13C	rs12595158	62023836	T	C	0.2025680	-0.0296290	0.0045220	2.9E-11
15	VPS13C	rs35592904	62025948	G	T	0.2039030	-0.0291916	0.0045158	4.9E-11
15	VPS13C	rs72749754	62027233	C	G	0.2063600	-0.0294620	0.0045021	2.4E-11
15	VPS13C	rs12917535	62033319	A	T	0.4416980	0.0226469	0.0036819	1.0E-10
15	VPS13C	rs12439366	62035467	C	T	0.2024570	-0.0293229	0.0045271	5.1E-11
15	VPS13C	rs200931598	62037414	A	AAT	0.2022160	-0.0291956	0.0045294	6.0E-11
15	VPS13C	rs71125963	62037708	T	TA	0.4219860	0.0204293	0.0037054	5.3E-09
15	VPS13C	rs76592481	62038207	T	A	0.2015520	-0.0293428	0.0045385	5.4E-11
15	VPS13C	rs8023668	62042506	T	A	0.4448120	0.0219803	0.0036883	2.6E-10
15	VPS13C	rs149869681	62043564	T	C	0.1960480	-0.0294990	0.0045965	6.2E-11
15	VPS13C	rs35057371	62051133	C	T	0.2008760	-0.0299177	0.0045423	1.6E-11
15	VPS13C	rs10519153	62057318	T	A	0.4442500	0.0226473	0.0036888	8.8E-11
15	C2CD4A *	rs12440611	62063982	T	C	0.1983910	-0.0298446	0.0045798	2.2E-11
15	C2CD4A	rs4775456	62069996	A	G	0.1976610	-0.0306038	0.0045927	8.4E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	C2CD4A *	rs72749772	62074814	C	T	0.1975980	-0.0309842	0.0045982	5.7E-12
15	C2CD4A *	rs9989354	62077462	A	G	0.4407500	0.0224284	0.0037028	1.1E-10
15	C2CD4A *	rs10519154	62082327	T	C	0.1965210	-0.0307915	0.0046220	5.9E-12
15	C2CD4A *	rs144047837	62084197	T	C	0.1943040	-0.0312170	0.0046548	4.6E-12
15	C2CD4A *	rs7163194	62090576	A	G	0.0803456	-0.0466161	0.0067872	6.9E-13
15	C2CD4A *	rs7164482	62090684	G	T	0.0825356	-0.0467836	0.0066701	2.5E-13
15	C2CD4A *	rs4502156	62090956	C	T	0.4804110	-0.0334142	0.0036357	8.4E-22
15	C2CD4A *	rs12907540	62091922	A	G	0.1572560	-0.0463825	0.0050101	1.3E-20
15	C2CD4A *	rs12907605	62092143	T	C	0.0829325	-0.0458558	0.0066664	4.4E-12
15	C2CD4A *	rs17304080	62094131	T	G	0.1594450	-0.0459787	0.0049708	1.6E-20
15	C2CD4A *	rs17238329	62095155	A	T	0.1593320	-0.0457546	0.0049733	2.6E-20
15	C2CD4A *	rs28690513	62095247	G	A	0.1593390	-0.0457295	0.0049733	2.7E-20
15	C2CD4A *	rs71411478	62095339	C	T	0.1593400	-0.0457064	0.0049732	2.8E-20
15	C2CD4A *	rs4775460	62095392	G	A	0.1593370	-0.0457527	0.0049733	2.6E-20
15	C2CD4A *	rs4775461	62095652	G	A	0.1593370	-0.0457527	0.0049733	2.6E-20
15	C2CD4A *	rs4775462	62095859	G	A	0.0801312	-0.0498115	0.0067224	3.2E-14
15	C2CD4A *	rs8033623	62095888	C	G	0.0801307	-0.0498120	0.0067224	3.2E-14
15	C2CD4A *	rs19905554	62096073	T	TC	0.4761700	-0.0353111	0.0036696	5.4E-24
15	C2CD4A *	rs4774428	62096074	T	C	0.4634120	-0.0363501	0.0037206	4.9E-25
15	C2CD4A *	rs1881415	62096331	C	T	0.4732020	-0.0356390	0.0036573	1.5E-24
15	C2CD4A *	rs4775463	62096585	A	G	0.1597250	-0.0456833	0.0049727	3.0E-20
15	C2CD4A *	chr15:62096613_AT_A	62096613	A	AT	0.2299710	-0.0461386	0.0043874	1.8E-26
15	C2CD4A *	rs4775464	62096905	A	G	0.1593540	-0.0457166	0.0049736	2.9E-20
15	C2CD4A *	rs17238342	62097334	A	G	0.1594040	-0.0458790	0.0049730	2.1E-20
15	C2CD4A *	rs76744825	62097500	C	G	0.0800532	-0.0501545	0.0067219	1.8E-14
15	C2CD4A *	rs8025500	62097852	A	T	0.1593720	-0.0459457	0.0049736	1.9E-20
15	C2CD4A *	rs8024531	62098057	T	A	0.1593710	-0.0459220	0.0049737	2.0E-20
15	C2CD4A *	rs17238349	62098354	G	A	0.1593780	-0.0458990	0.0049737	2.1E-20
15	C2CD4A *	rs67818839	62098985	A	AT	0.3387740	-0.0522201	0.0038456	4.2E-44
15	C2CD4A *	rs28578604	62099222	T	C	0.2584030	-0.0423237	0.0041660	1.9E-25
15	C2CD4A *	rs7163757	62099409	T	C	0.3387180	-0.0522812	0.0038454	3.6E-44
15	C2CD4A *	rs7164359	62099704	G	C	0.2584200	-0.0423332	0.0041656	1.8E-25
15	C2CD4A *	rs3985685	62099982	C	G	0.0792067	-0.0502049	0.0067492	2.6E-14
15	C2CD4A *	rs4613049	62100868	G	A	0.0802656	-0.0498831	0.0067057	2.6E-14
15	C2CD4A *	rs8037894	62102065	C	G	0.3410780	-0.0517322	0.0038402	2.1E-43
15	C2CD4A *	rs8038040	62102140	A	G	0.3410760	-0.0517346	0.0038402	2.1E-43
15	C2CD4A *	rs8037796	62102186	T	C	0.2604850	-0.0416960	0.0041536	8.2E-25
15	C2CD4A *	rs6494306	62102341	A	G	0.2605040	-0.0416553	0.0041534	9.2E-25
15	C2CD4A *	rs6494307	62102491	G	C	0.3404680	-0.0517884	0.0038425	1.9E-43
15	C2CD4A *	rs7161785	62103025	C	G	0.3415230	-0.0517504	0.0038397	2.0E-43
15	C2CD4A *	rs10851708	62103919	A	G	0.2604360	-0.0418312	0.0041531	4.8E-25
15	C2CD4A *	rs7167878	62103990	A	C	0.3403130	-0.0518015	0.0038429	1.7E-43
15	C2CD4A *	rs7167881	62103999	T	C	0.0792418	-0.0498626	0.0067425	3.9E-14
15	C2CD4A *	rs7167932	62104079	T	C	0.3402800	-0.0518873	0.0038419	1.2E-43
15	C2CD4A *	rs7172432	62104190	G	A	0.3488650	-0.0521285	0.0038160	2.2E-44
15	C2CD4A *	rs7173964	62104743	A	G	0.3476060	-0.0521106	0.0038202	2.3E-44
15	C2CD4A *	rs4775466	62104919	T	C	0.3476230	-0.0520506	0.0038202	3.2E-44
15	C2CD4A *	rs11071652	62104987	C	G	0.2680370	-0.0419138	0.0041145	1.9E-25
15	C2CD4A *	rs1370176	62105035	A	G	0.2678950	-0.0418773	0.0041131	1.9E-25
15	C2CD4A *	rs4775467	62105199	A	G	0.3478170	-0.0521506	0.0038227	2.5E-44
15	C2CD4A *	rs7180689	62105437	A	T	0.2397360	-0.0531437	0.0042670	3.0E-36
15	C2CD4A *	rs7179885	62105538	A	G	0.1601420	-0.0451305	0.0049697	9.8E-20
15	C2CD4A *	rs10083587	62106334	T	C	0.3403960	-0.0517800	0.0038471	2.0E-43
15	C2CD4A *	rs11856307	62106894	C	A	0.3547290	-0.0518866	0.0038233	5.5E-44
15	C2CD4A *	rs8030016	62107195	T	C	0.0792256	-0.0498400	0.0067415	3.9E-14
15	C2CD4A *	rs8030240	62107365	T	C	0.1992560	-0.0491381	0.0045677	1.5E-27
15	C2CD4A *	rs16944723	62108848	C	G	0.0792155	-0.0498652	0.0067423	4.0E-14
15	C2CD4A *	rs2083013	62109283	T	C	0.0771037	-0.0498851	0.0068327	9.7E-14
15	C2CD4A *	rs4775468	62109727	T	C	0.1180500	-0.0407936	0.0056489	4.5E-13
15	C2CD4A *	rs1370173	62111546	G	A	0.1189240	-0.0412829	0.0056236	2.3E-13
15	C2CD4A *	rs10583788	62112058	C	CTCTTT	0.0792816	-0.0496355	0.0067373	4.9E-14
15	C2CD4A *	rs1436955	62112183	T	C	0.1986370	-0.0499523	0.0045631	1.6E-28
15	C2CD4A *	rs1436954	62112281	T	C	0.1981450	-0.0498645	0.0045686	2.3E-28
15	C2CD4A *	rs17205498	62113056	A	G	0.0792257	-0.0497045	0.0067396	4.8E-14
15	C2CD4A *	rs12912130	62113371	C	T	0.1186430	-0.0407302	0.0056315	4.3E-13
15	C2CD4A *	rs12911635	62113809	T	C	0.1186180	-0.0407586	0.0056318	4.0E-13
15	C2CD4A *	rs68086954	62114103	A	ATAG	0.1185980	-0.0407146	0.0056327	4.2E-13
15	C2CD4A *	rs12916547	62114302	C	G	0.1185970	-0.0407075	0.0056327	4.2E-13
15	C2CD4A *	rs12917111	62114821	T	C	0.1185990	-0.0406841	0.0056326	4.4E-13
15	C2CD4A *	rs2414760	62114844	C	G	0.0791720	-0.0493286	0.0067429	7.6E-14
15	C2CD4A *	rs2141376	62115039	C	T	0.0791720	-0.0493110	0.0067429	7.8E-14
15	C2CD4A *	rs11071653	62116043	G	C	0.0792474	-0.0491215	0.0067407	9.4E-14
15	C2CD4A *	chr15:62116247_AT_A	62116247	A	AT	0.1268000	-0.0386274	0.0055965	2.8E-12
15	C2CD4A *	rs112388503	62116279	T	G	0.0770545	-0.0451444	0.0068576	1.6E-11
15	C2CD4A *	rs62008555	62116344	G	A	0.3097650	-0.0468644	0.0039466	3.2E-34
15	C2CD4A *	rs8032416	62116871	C	G	0.3079250	-0.0471768	0.0039520	1.4E-34
15	C2CD4A *	rs10851709	62117129	A	G	0.0785352	-0.0496707	0.0067748	6.8E-14
15	C2CD4B *	rs17304087	62118985	G	A	0.1205570	-0.0402335	0.0055886	6.2E-13
15	C2CD4B *	rs12908362	62119527	C	T	0.1199840	-0.0405692	0.0056014	3.6E-13
15	C2CD4B *	rs58728679	62119725	G	GT	0.3077930	-0.0472114	0.0039482	1.1E-34
15	C2CD4B *	rs920179	62121140	G	A	0.1236840	-0.0383201	0.0055290	3.9E-12
15	C2CD4B *	rs920178	62121497	A	G	0.3078630	-0.0471181	0.0039463	1.4E-34
15	C2CD4B *	rs920177	62121543	G	A	0.2006300	-0.0485384	0.0045461	2.4E-27
15	C2CD4B *	rs1436953	62121815	T	C	0.3110040	-0.0461879	0.0039323	1.3E-33
15	C2CD4B *	rs4474658	62123230	C	T	0.3093520	-0.0468780	0.0039409	3.2E-34
15	C2CD4B *	rs6494309	62123529	A	T	0.3092060	-0.0470238	0.0039425	2.1E-34
15	C2CD4B *	rs6494310	62123537	A	G	0.3077810	-0.0471854	0.0039458	1.2E-34
15	C2CD4B *	rs17271493	62124760	A	C	0.0966482	-0.0413787	0.0062088	2.5E-11
15	C2CD4B *	rs17205526	62124935	A	T	0.3153190	-0.0457189	0.0039408	4.7E-33
15	C2CD4B *	rs111423330	62126611	C	T	0.0725570	-0.0505715	0.0071045	2.5E-13
15	C2CD4B *	rs112545984	62126618	C	T	0.0728705	-0.0505998	0.0070966	2.6E-13
15	C2CD4B *	rs143065261	62126625	C	T	0.0730792	-0.0499607	0.0070919	4.4E-13
15	C2CD4B *	rs139430286	62126626	A	G	0.0727260	-0.0508223	0.0071012	2.0E-13
15	C2CD4B *	rs111605622	62126636	G	A	0.0732480	-0.0491647	0.0070790	9.7E-13
15	C2CD4B *	rs2178207	62128606	G	C	0.0565347	-0.0552372	0.0079102	7.6E-13
15	C2CD4B *	rs79975177	62130316	G	C	0.0552372	-0.0571257	0.0079935	2.5E-13
15	C2CD4B *	rs78800152	62130776	G	C	0.0566102	-0.0546975	0.0079038	1.2E-12
15	C2CD4B *	rs76011059	62131684	C	T	0.0566749	-0.0552617	0.0079052	7.7E-13
15	C2CD4B *	rs4775471	62132450	T	C	0.0550535	-0.0572224	0.0080067	2.6E-13
15	C2CD4B *	rs6494311	62135165	T	C	0.2017410	-0.0288492	0.0045564	1.0E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	AAF	BETA	SE	P
15	C2CD4B *	rs7177332	62136596	A	G	0.2017070	-0.0291531	0.0045575	6.9E-11
15	C2CD4B *	rs62009613	62138545	C	A	0.0534144	-0.0490258	0.0081599	4.8E-10
15	C2CD4B *	rs74770198	62139169	G	C	0.0503961	-0.0518069	0.0084104	2.2E-10
15	C2CD4B *	rs144996318	62139569	T	C	0.0509117	-0.0501327	0.0083807	7.0E-10
15	PEAK1 *	rs12901739	77103149	T	C	0.3421730	0.0257235	0.0038702	1.6E-11
15	PEAK1 *	rs11853287	77107029	G	A	0.3459040	0.0251281	0.0038595	3.0E-11
15	PEAK1 *	rs12904088	77107055	G	C	0.3445240	0.0248450	0.0038642	5.2E-11
15	PEAK1 *	rs3743478	77108046	C	T	0.3447490	0.0249962	0.0038465	3.4E-11
15	PEAK1	rs1823100	77110402	T	C	0.3441760	0.0249967	0.0038447	3.2E-11
15	PEAK1	rs4886850	77111818	C	G	0.3443650	0.0253329	0.0038435	1.8E-11
15	PEAK1	rs3743479	77114054	T	C	0.3435410	0.0249853	0.0038468	3.5E-11
15	PEAK1	rs1446312	77119847	C	G	0.3467890	0.0253219	0.0038252	1.8E-11
15	PEAK1	rs11072643	77123166	T	A	0.3466950	0.0251694	0.0038252	2.5E-11
15	PEAK1	rs35958775	77140307	CTAA	C	0.3491760	0.0249111	0.0038190	3.5E-11
15	PEAK1	rs8028571	77152115	C	T	0.3470250	0.0252004	0.0038215	2.3E-11
15	PEAK1	rs4886511	77156496	C	T	0.3456110	0.0250389	0.0038349	3.7E-11
15	PEAK1	rs35772575	77162612	CA	C	0.3461690	0.0251030	0.0038257	3.0E-11
15	PEAK1	rs4243045	77163572	C	A	0.3470720	0.0251585	0.0038214	2.5E-11
15	PEAK1	rs11854193	77165794	A	C	0.3465050	0.0254137	0.0038218	1.7E-11
15	PEAK1	rs1867779	77193666	T	C	0.3469950	0.0252064	0.0038218	2.4E-11
15	PEAK1	rs12443386	77199047	C	T	0.3469860	0.0252467	0.0038217	2.2E-11
15	PEAK1	rs12907847	77200832	T	C	0.3458360	0.0251774	0.0038280	2.7E-11
15	PEAK1	rs12908262	77200914	A	G	0.3467870	0.0254646	0.0038218	1.4E-11
15	PEAK1	rs7163503	77201163	A	C	0.3461540	0.0255730	0.0038265	1.3E-11
15	PEAK1	rs12914128	77201533	C	T	0.3467870	0.0254646	0.0038218	1.4E-11
15	PEAK1	rs12900433	77202686	C	T	0.3445780	0.0252218	0.0038336	2.5E-11
15	PEAK1	rs12916731	77214679	T	C	0.3472090	0.0254802	0.0038214	1.5E-11
15	PEAK1	chr15:77215906_TTTTATA_T	77215906	T	TTTTATA	0.3465730	0.0253734	0.0038238	1.8E-11
15	PEAK1	rs4886856	77218243	G	A	0.3467860	0.0253376	0.0038215	1.7E-11
15	PEAK1	rs11853460	77222977	T	C	0.3461740	0.0250017	0.0038268	3.4E-11
15	PEAK1	rs11630689	77227752	T	C	0.3468680	0.0254719	0.0038214	1.4E-11
15	PEAK1	chr15:77230205_CT_C	77230205	C	CT	0.3396960	0.0259804	0.0038836	1.3E-11
15	PEAK1	rs4414462	77230232	C	A	0.3465440	0.0254697	0.0038235	1.4E-11
15	PEAK1	rs1125617	77240369	G	A	0.3461220	0.0254221	0.0038300	1.8E-11
15	PEAK1	rs11632941	77241546	G	A	0.3472200	0.0252842	0.0038215	1.9E-11
15	PEAK1	rs11639314	77247760	C	T	0.3257260	0.0234242	0.0038814	5.2E-10
15	PEAK1	rs12913233	77250955	T	C	0.3469330	0.0257411	0.0038210	8.2E-12
15	PEAK1	rs12909924	77259103	G	T	0.3465600	0.0257608	0.0038230	7.8E-12
15	PEAK1	rs5813861	77277617	GAATT	G	0.3479700	0.0251704	0.0038321	2.4E-11
15	PEAK1	rs2175941	77292156	C	T	0.3467210	0.0257988	0.0038235	7.6E-12
15	PEAK1	rs11858641	77293478	T	C	0.3468160	0.0256352	0.0038227	1.0E-11
15	PEAK1	rs34504274	77294833	GT	G	0.3468210	0.0256691	0.0038226	9.3E-12
15	PEAK1	chr15:77298155_GA_G	77298155	G	GA	0.3467940	0.0256918	0.0038223	8.7E-12
15	PEAK1	rs62008452	77298665	G	A	0.3467970	0.0256863	0.0038223	8.8E-12
15	PEAK1	rs6495237	77299193	T	G	0.3257570	0.0239710	0.0038851	2.1E-10
15	PEAK1	rs8037426	77299435	T	A	0.3267790	0.0244601	0.0038938	1.1E-10
15	PEAK1	rs11857294	77304383	T	C	0.3467670	0.0256547	0.0038223	9.2E-12
15	PEAK1	rs28524916	77306660	T	A	0.3468680	0.0254261	0.0038269	1.4E-11
15	PEAK1	rs28584877	77306661	C	A	0.3468680	0.0254261	0.0038269	1.4E-11
15	PEAK1	rs11636554	77316405	A	G	0.3469830	0.0258952	0.0038223	6.0E-12
15	PEAK1	rs12594505	77316615	C	G	0.4249660	0.0262724	0.0036836	4.0E-13
15	PEAK1	rs11632966	77329463	C	A	0.3474430	0.0258901	0.0038239	5.9E-12
15	PEAK1	rs1493700	77336718	C	T	0.3471160	0.0258244	0.0038212	6.5E-12
15	PEAK1	chr15:77342156_TAA_T	77342156	T	TAA	0.3146740	0.0249074	0.0039702	9.9E-11
15	PEAK1	rs7167794	77343533	C	T	0.3434490	0.0243085	0.0038561	1.3E-10
15	PEAK1	rs1191196	77354162	C	T	0.3471900	0.0258573	0.0038211	5.9E-12
15	PEAK1	rs12905951	77357089	A	G	0.3457720	0.0251884	0.0038272	2.5E-11
15	PEAK1	rs4886862	77360026	C	T	0.3471580	0.0258039	0.0038215	6.7E-12
15	PEAK1	rs8030074	77361890	T	C	0.3449290	0.0259777	0.0038342	5.0E-12
15	PEAK1	rs1473922	77364456	T	G	0.3471080	0.0258472	0.0038213	6.4E-12
15	PEAK1	rs1565757	77365340	T	C	0.3471690	0.0259054	0.0038233	5.8E-12
15	PEAK1	chr15:77371508_TACCACC_T	77371508	T	TACCACC	0.3466820	0.0258748	0.0038240	6.1E-12
15	PEAK1	rs12910480	77371870	C	G	0.3471480	0.0258571	0.0038209	5.8E-12
15	PEAK1	rs1389436	77373506	T	G	0.3471480	0.0258571	0.0038209	5.8E-12
15	PEAK1	rs12914345	77378059	C	A	0.3474050	0.0259121	0.0038204	5.6E-12
15	PEAK1	rs7175674	77378568	T	C	0.3471430	0.0258532	0.0038209	5.8E-12
15	PEAK1	rs7176302	77378874	G	C	0.3471430	0.0258532	0.0038209	5.8E-12
15	PEAK1	rs12594346	77379624	A	T	0.4252130	0.0261450	0.0036829	4.2E-13
15	PEAK1	rs16968809	77379776	C	T	0.4251310	0.0262460	0.0036823	3.4E-13
15	PEAK1	rs7166927	77381117	T	C	0.3473040	0.0257724	0.0038190	6.1E-12
15	PEAK1	rs10152181	77386004	G	A	0.3473080	0.0257674	0.0038190	6.2E-12
15	PEAK1	rs8037561	77388120	G	A	0.3473080	0.0257674	0.0038190	6.2E-12
15	PEAK1	rs12906708	77389102	G	A	0.3441320	0.0257810	0.0038433	9.5E-12
15	PEAK1	rs1602925	77393515	C	T	0.3472760	0.0256796	0.0038191	7.3E-12
15	PEAK1	rs4886515	77394544	A	G	0.3473150	0.0257649	0.0038190	6.2E-12
15	PEAK1	rs12911371	77396708	T	C	0.3473050	0.0257507	0.0038190	6.4E-12
15	PEAK1	rs12912050	77397081	T	C	0.3473050	0.0257507	0.0038190	6.4E-12
15	PEAK1	rs11072653	77401592	T	C	0.3473060	0.0257554	0.0038190	6.3E-12
15	PEAK1	rs4886866	77403824	T	A	0.3473010	0.0258901	0.0038188	4.8E-12
15	PEAK1	rs11852471	77407243	A	G	0.3473500	0.0258954	0.0038195	4.4E-12
15	PEAK1	rs62007299	77419377	A	G	0.3481540	0.0257086	0.0038202	8.0E-12
15	HMG20A	rs34591043	77421244	G	A	0.3504640	0.0257175	0.0038166	6.5E-12
15	HMG20A	rs8024485	77426026	A	C	0.3483260	0.0261024	0.0038161	2.8E-12
15	HMG20A	rs12904938	77428883	G	A	0.3479040	0.0260058	0.0038186	3.3E-12
15	HMG20A	rs1565756	77449298	A	G	0.3506340	0.0257267	0.0038203	4.4E-12
15	HMG20A	rs7178572	77454848	G	A	0.3487120	0.0261335	0.0038134	2.6E-12
15	HMG20A	rs11633054	77454934	G	A	0.3485840	0.0262112	0.0038136	2.1E-12
15	HMG20A	rs2055901	77466953	A	G	0.3485690	0.0262394	0.0038138	2.0E-12
15	HMG20A	rs8034133	77471370	G	C	0.3485850	0.0262618	0.0038137	1.9E-12
15	HMG20A	rs6495240	77474214	C	T	0.3487460	0.0263148	0.0038141	1.8E-12
15	HMG20A	rs12324627	77475197	G	A	0.3487070	0.0262997	0.0038144	1.8E-12
15	HMG20A	rs12591335	77482552	A	G	0.4267090	0.0272815	0.0036895	3.4E-14
15	HMG20A	rs952471	77484156	G	C	0.3487090	0.0262934	0.0038144	1.8E-12
15	HMG20A	rs952472	77484220	C	A	0.3487090	0.0262934	0.0038144	1.8E-12
15	HMG20A *	rs965480	77489584	G	A	0.3598650	0.0247897	0.0037969	1.9E-11
15	HMG20A *	rs12910361	77489993	G	A	0.3599890	0.0247559	0.0037979	2.0E-11
15	HMG20A *	rs1022172	77501017	G	A	0.3483810	0.0265480	0.0038156	1.2E-12
15	HMG20A *	rs4886869	77507315	G	A	0.3474950	0.0261906	0.0038450	5.3E-12
15	HMG20A *	rs11857450	77510449	C	G	0.3499380	0.0262160	0.0038453	5.2E-12
15	HMG20A *	rs59153558	77514428	G	A	0.3500330	0.0264013	0.0038441	3.3E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	HMG20A *	chr15:77518009_TA_T	77518009	T	TA	0.3484160	0.0259817	0.0038571	7.4E-12
15	HMG20A *	rs12907222	77520570	T	A	0.3453550	0.0264286	0.0038722	3.5E-12
15	HMG20A *	rs62009066	77520612	C	G	0.3384160	0.0253261	0.0039055	4.0E-11
15	HMG20A *	chr15:77523959_C_CA	77523959	CA	C	0.3460750	0.0253414	0.0038667	3.2E-11
15	HMG20A *	rs1005752	77525786	A	C	0.3463480	0.0257341	0.0038554	1.1E-11
15	HMG20A *	rs12901503	77526714	G	A	0.3459710	0.0255191	0.0038613	1.7E-11
15	HMG20A *	rs907388	77536326	A	G	0.3631090	0.0240625	0.0037910	5.2E-11
15	HMG20A *	rs907385	77536627	T	C	0.3418390	0.0259207	0.0039122	7.2E-12
15	HMG20A *	rs4886873	77536834	A	G	0.4340940	0.0251597	0.0037171	2.1E-12
15	HMG20A *	rs869301	77538291	C	T	0.3857940	0.0246317	0.0037813	3.4E-11
15	HMG20A *	rs2867306	77539603	A	T	0.3336830	0.0220065	0.0038567	2.7E-09
15	HMG20A *	rs781071117	77539605	G	GCC	0.3319560	0.0215880	0.0038708	5.5E-09
15	HMG20A *	rs745599922	77539608	AGC	A	0.3319560	0.0215880	0.0038708	5.5E-09
15	HMG20A *	rs147160840	77539611	G	A	0.3209160	0.0215968	0.0039221	1.1E-08
15	HMG20A *	rs7170877	77539677	G	C	0.3629910	0.0234644	0.0037848	1.4E-10
15	HMG20A *	rs11318365	77539802	T	TG	0.3344070	0.0224575	0.0038484	1.1E-09
15	HMG20A *	rs7171448	77539974	G	C	0.3340750	0.0223066	0.0038485	1.5E-09
15	HMG20A *	rs7172144	77540182	A	G	0.3340010	0.0223426	0.0038483	1.5E-09
15	HMG20A *	rs7177055	77540420	A	G	0.3344060	0.0222630	0.0038458	1.7E-09
15	HMG20A *	rs34517105	77541376	T	TG	0.3505690	0.0218116	0.0038470	1.6E-09
15	HMG20A *	rs62009090	77544713	G	T	0.3920880	0.0198225	0.0037637	9.1E-09
15	HMG20A *	rs4886875	77546077	C	T	0.3917740	0.0197988	0.0037639	9.1E-09
15	HMG20A *	rs4886876	77546149	T	C	0.3917740	0.0197988	0.0037639	9.1E-09
15	HMG20A *	rs4886877	77546193	G	C	0.3917780	0.0197916	0.0037639	9.2E-09
15	HMG20A *	chr15:77546950_G_GA	77546950	GA	G	0.3905540	0.0204265	0.0037776	4.5E-09
15	HMG20A *	rs11857419	77547419	C	T	0.3924890	0.0197339	0.0037660	1.1E-08
15	HMG20A *	rs11854328	77547787	G	A	0.3917820	0.0197014	0.0037634	1.1E-08
15	LINGO1 *	rs12907746	77550984	G	A	0.3902920	0.0192645	0.0037568	3.1E-08
15	LINGO1 *	rs7162637	77551023	G	A	0.4165710	0.0193400	0.0037401	2.1E-08
15	LINGO1 *	rs907369	77551218	G	A	0.3896780	0.0191331	0.0037580	4.2E-08
15	LINGO1 *	rs12900004	77552562	C	T	0.3910460	0.0190482	0.0037494	4.0E-08
15	LINGO1 *	rs12901130	77556464	T	C	0.3913650	0.0194513	0.0037387	2.1E-08
15	LINGO1 *	rs939490	77575340	A	G	0.4086530	-0.0214225	0.0037070	1.2E-09
15	HDDC3, UNC45A	rs1052532	90931006	T	C	0.4153430	-0.0198320	0.0037503	4.4E-08
15	HDDC3, UNC45A	rs1052535	90931508	G	C	0.4129570	-0.0198731	0.0037405	4.3E-08
15	RCCD1	rs1105292	90959125	C	T	0.4963680	0.0206195	0.0036493	7.5E-09
15	RCCD1	rs1105291	90959153	T	C	0.4905640	0.0213488	0.0036389	2.0E-09
15	RCCD1	rs8038661	90959619	A	G	0.4893920	0.0214553	0.0036521	2.0E-09
15	RCCD1	rs3743451	90960951	A	G	0.4778000	-0.0195370	0.0036380	2.9E-08
15	RCCD1	rs7166130	90962486	T	A	0.4995510	-0.0196818	0.0036322	1.9E-08
15	RCCD1	rs79548680	90962549	C	G	0.4970190	0.0207810	0.0036335	3.6E-09
15	RCCD1 *	rs5814452	90963177	C	CT	0.4758250	-0.0192805	0.0036444	3.2E-08
15	RCCD1 *	rs8028409	90963192	T	A	0.4965300	0.0211444	0.0036371	2.0E-09
15	RCCD1 *	rs8037137	90963407	C	T	0.4975490	0.0216588	0.0036498	9.4E-10
15	RCCD1 *	rs112770790	90964265	G	A	0.4860040	-0.0200986	0.0036648	1.2E-08
15	PRC1 *	rs59881828	90965115	C	CA	0.4992640	0.0211200	0.0036601	3.1E-09
15	PRC1 *	rs56665089	90965349	AG	A	0.4853360	-0.0217446	0.0036705	9.4E-10
15	PRC1, PRC1-AS1	rs2290203	90968837	A	G	0.4974250	0.0222898	0.0036288	3.5E-10
15	PRC1, PRC1-AS1	rs2290202	90969037	T	G	0.4994770	0.0229187	0.0036366	1.5E-10
15	PRC1, PRC1-AS1	rs2890156	90969927	T	A	0.4992840	-0.0232210	0.0036370	8.7E-11
15	PRC1, PRC1-AS1	rs4517768	90970805	T	C	0.4755500	-0.0214109	0.0036456	1.7E-09
15	PRC1, PRC1-AS1	rs59278520	90971477	G	A	0.4819250	-0.0223834	0.0036392	2.8E-10
15	PRC1, PRC1-AS1	rs11852999	90971530	T	C	0.4773330	-0.0213255	0.0036374	1.7E-09
15	PRC1, PRC1-AS1	rs17636091	90974249	A	G	0.4744150	-0.0206520	0.0036395	5.1E-09
15	PRC1, PRC1-AS1	rs8035844	90976412	C	T	0.4974560	-0.0235190	0.0037141	1.2E-10
15	PRC1, PRC1-AS1	rs8036430	90976430	A	C	0.4957150	-0.0225380	0.0037175	7.2E-10
15	PRC1, PRC1-AS1	rs12595025	90976901	T	C	0.4984460	0.0233361	0.0036321	7.6E-11
15	PRC1, PRC1-AS1	rs12594925	90977057	A	G	0.4974160	0.0241807	0.0036456	2.0E-11
15	PRC1, PRC1-AS1	rs12595052	90977078	C	T	0.4794270	-0.0225698	0.0036488	2.4E-10
15	PRC1, PRC1-AS1	rs60640465	90977892	T	G	0.4739140	-0.0213754	0.0036649	2.6E-09
15	PRC1, PRC1-AS1	rs8032722	90978840	T	C	0.4787440	-0.0213479	0.0036433	1.8E-09
15	PRC1, PRC1-AS1	rs8026714	90979023	A	G	0.4992610	0.0230987	0.0036267	9.9E-11
15	PRC1, PRC1-AS1	rs6496742	90979806	C	T	0.4799940	-0.0218576	0.0036326	5.9E-10
15	PRC1, PRC1-AS1	rs1867226	90980483	C	G	0.4804650	-0.0222267	0.0036373	3.2E-10
15	PRC1, PRC1-AS1	rs2301826	90981967	T	C	0.4960370	0.0230349	0.0036295	1.4E-10
15	PRC1, PRC1-AS1	rs7180016	90983045	G	A	0.4808320	-0.0225029	0.0036322	2.4E-10
15	PRC1, PRC1-AS1	rs2285937	90983922	A	G	0.4766190	-0.0219580	0.0036407	6.4E-10
15	PRC1, PRC1-AS1	rs8031684	90984221	T	A	0.4796000	-0.0224590	0.0036345	2.8E-10
15	PRC1, PRC1-AS1	rs2301825	90984840	G	C	0.4982560	0.0229729	0.0036277	1.4E-10
15	PRC1, PRC1-AS1	chr15:90985564_CT_C	90985564	CT	C	0.4889940	-0.0217514	0.0036998	2.4E-09
15	PRC1, PRC1-AS1	rs15033865	90985645	A	G	0.4988620	0.0233726	0.0036329	8.4E-11
15	PRC1, PRC1-AS1	rs8036115	90985731	G	A	0.4788750	-0.0225951	0.0036374	2.5E-10
15	PRC1, PRC1-AS1	rs8042518	90985892	T	C	0.4790020	-0.0227374	0.0036374	2.0E-10
15	PRC1, PRC1-AS1	rs60290423	90986222	C	T	0.4989080	0.0226389	0.0036273	2.5E-10
15	PRC1, PRC1-AS1	rs149790373	90986694	TTTATTT	T	0.4816570	-0.0221151	0.0036461	6.8E-10
15	PRC1, PRC1-AS1	chr15:90986893_G_GA	90986893	G	GA	0.4907980	-0.0213215	0.0036971	8.5E-09
15	PRC1, PRC1-AS1	rs11853073	90986928	T	C	0.4788810	-0.0221134	0.0036314	5.3E-10
15	PRC1, PRC1-AS1	rs8026781	90987445	G	A	0.4799260	-0.0223852	0.0036323	3.6E-10
15	PRC1, PRC1-AS1	rs8028856	90987590	A	G	0.4790870	-0.0221057	0.0036325	5.2E-10
15	PRC1, PRC1-AS1	rs3803563	90988122	C	A	0.4804330	-0.0222056	0.0036323	4.4E-10
15	PRC1, PRC1-AS1	rs17692742	90988568	G	C	0.4755890	-0.0212966	0.0036338	2.3E-09
15	PRC1	rs12594752	90988765	T	C	0.4980990	0.0231962	0.0036273	1.1E-10
15	PRC1	rs6496745	90989400	C	T	0.4827200	-0.0220688	0.0036515	6.8E-10
15	PRC1	rs6496746	90989639	C	A	0.4805310	-0.0225067	0.0036362	2.9E-10
15	PRC1	rs8025699	90990586	A	G	0.4803010	-0.0222116	0.0036357	4.3E-10
15	PRC1	rs112553294	90991064	A	G	0.4797440	-0.0217907	0.0036359	8.2E-10
15	PRC1	rs72630488	90991143	T	C	0.4762970	-0.0209967	0.0036374	3.2E-09
15	PRC1	rs76119208	90992099	T	G	0.4973810	0.0232452	0.0036284	8.8E-11
15	PRC1	chr15:90992708_GT_G	90992708	GT	G	0.4795410	-0.0222689	0.0036400	4.2E-10
15	PRC1	rs73502775	90992995	G	A	0.4818430	-0.0223544	0.0036463	4.1E-10
15	PRC1	rs72630489	90994176	A	G	0.4743440	-0.0207002	0.0036440	5.7E-09
15	PRC1 *	rs78029804	90995690	C	T	0.4971980	-0.0233317	0.0036359	1.1E-10
15	PRC1 *	rs11386525	90995819	AT	A	0.4750320	-0.0212539	0.0036675	3.9E-09
15	VPS33B *	rs8042416	90996783	G	A	0.4713980	-0.0213843	0.0036423	2.6E-09
15	VPS33B *	rs4932184	90997634	G	T	0.4715000	-0.0214485	0.0036420	2.2E-09
15	VPS33B	rs876874	90998505	T	A	0.4709980	-0.0217156	0.0036388	1.5E-09
15	VPS33B	rs3743449	90999107	T	C	0.4699140	-0.0214747	0.0036374	1.9E-09
15	VPS33B	rs75453156	90999251	G	GT	0.4694900	-0.0216833	0.0036406	1.2E-09
15	VPS33B	rs35582587	91000051	C	CTG	0.4702970	-0.0217267	0.0036414	1.3E-09
15	VPS33B	rs72759321	91001187	G	A	0.4680950	-0.0210968	0.0036505	4.5E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	VPS33B	rs12439887	91001601	T	C	0.4710180	-0.0218367	0.0036385	1.0E-09
15	VPS33B	rs111073965	91001615	T	C	0.4709360	-0.0218758	0.0036381	9.4E-10
15	VPS33B	rs3743448	91001881	T	C	0.4705040	-0.0221401	0.0036424	6.4E-10
15	VPS33B	rs3784776	91002674	T	A	0.4704440	-0.0219910	0.0036462	7.7E-10
15	VPS33B	rs7170130	91003525	T	C	0.4690690	-0.0212056	0.0036503	2.9E-09
15	VPS33B	rs3826033	91005371	G	A	0.4981080	-0.0240408	0.0036334	2.6E-11
15	VPS33B	rs59910084	91006281	T	'AGCCTG'	0.4637180	-0.0209536	0.0036811	5.0E-09
15	VPS33B	rs3826032	91006592	C	G	0.4687750	-0.0210649	0.0036468	3.2E-09
15	VPS33B	rs3743447	91007723	G	C	0.4729430	-0.0226641	0.0036377	2.2E-10
15	VPS33B	rs12439788	91008484	G	C	0.4640650	-0.0223027	0.0036526	5.0E-10
15	VPS33B	rs79253100	91008646	C	T	0.4978100	-0.0237652	0.0036315	5.3E-11
15	VPS33B	rs57486507	91010382	T	C	0.4386140	-0.0222776	0.0036824	3.7E-10
15	VPS33B	rs56838761	91010724	C	T	0.4388960	-0.0220758	0.0036844	5.4E-10
15	VPS33B	rs1972926	91013956	C	T	0.4443140	-0.0224997	0.0036771	2.6E-10
15	VPS33B	rs7183740	91015227	G	A	0.4685700	-0.0218003	0.0036601	9.9E-10
15	VPS33B	rs12438273	91015340	T	A	0.4436860	-0.0205816	0.0036661	5.1E-09
15	VPS33B	rs873130	91016848	C	T	0.4442080	-0.0202461	0.0036539	9.0E-09
15	VPS33B	rs11857433	91017137	G	T	0.4476580	-0.0215878	0.0036512	1.1E-09
15	VPS33B	rs3743445	91017952	C	T	0.4679940	-0.0216812	0.0036384	1.4E-09
15	VPS33B	rs12161921	91018356	C	T	0.4477580	-0.0212160	0.0036492	2.2E-09
15	VPS33B	rs1108351	91019707	C	A	0.4480100	-0.0213273	0.0036503	1.8E-09
15	VPS33B	rs68102919	91021223	T	C	0.4434610	-0.0197392	0.0036614	2.4E-08
15	VPS33B	rs28478359	91021526	C	T	0.4508470	-0.0218072	0.0036810	9.9E-10
16	ITFG3	rs2858010	239695	T	C	0.4021700	0.0203816	0.0037292	4.5E-08
16	ITFG3	rs9788833	242773	T	C	0.4032770	0.0213386	0.0037139	1.1E-08
16	ITFG3	rs7189020	254804	A	T	0.3667710	0.0209764	0.0037738	3.7E-08
16	FTO	rs55872725	53775211	T	C	0.1219690	0.0312711	0.0055426	1.3E-08
16	FTO	rs7187250	53776634	A	C	0.1218660	0.0310534	0.0055469	1.7E-08
16	FTO	rs7193144	53776774	C	T	0.1234310	0.0308231	0.0055162	2.1E-08
16	FTO	rs62033399	53777031	T	C	0.1220830	0.0308736	0.0055432	2.0E-08
16	FTO	rs62033400	53777876	G	A	0.1227870	0.0306582	0.0055275	2.3E-08
16	FTO	rs8063057	53778521	C	T	0.1228860	0.0306317	0.0055258	2.3E-08
16	FTO	rs17817449	53779455	G	T	0.1224540	0.0307211	0.0055330	2.2E-08
16	FTO	rs8043757	53779538	T	A	0.1224610	0.0306672	0.0055329	2.5E-08
16	FTO	rs9972653	53780451	T	G	0.1228140	0.0307070	0.0055263	2.2E-08
16	FTO	rs17817497	53781523	C	T	0.1226920	0.0306453	0.0055292	2.2E-08
16	FTO	rs8050136	53782363	A	C	0.1223010	0.0310375	0.0055368	1.5E-08
16	FTO	rs8051591	53782840	G	A	0.1225180	0.0308285	0.0055321	1.8E-08
16	FTO	rs9935401	53782926	A	G	0.1224900	0.0307507	0.0055327	2.0E-08
16	FTO	rs3751812	53784548	T	G	0.1223720	0.0305025	0.0055355	2.6E-08
16	FTO	rs3751814	53784812	A	G	0.1225540	0.0307899	0.0055315	1.9E-08
16	FTO	rs56313538	53784922	G	A	0.1228330	0.0309234	0.0055343	1.9E-08
16	FTO	rs9936385	53785257	C	T	0.1225480	0.0306705	0.0055315	2.2E-08
16	FTO	rs9923233	53785286	C	G	0.1224450	0.0309104	0.0055344	1.7E-08
16	FTO	rs9923312	53785455	A	G	0.1226550	0.0306540	0.0055304	2.3E-08
16	FTO	rs11075989	53785965	T	C	0.1225470	0.0306000	0.0055315	2.4E-08
16	FTO	rs11075990	53785981	G	A	0.1227930	0.0306266	0.0055283	2.3E-08
16	FTO	rs11075991	53786025	T	A	0.1225680	0.0307389	0.0055312	2.1E-08
16	FTO	rs11075992	53786154	C	T	0.1225440	0.0306734	0.0055314	2.2E-08
16	FTO	rs9926289	53786591	A	G	0.1225860	0.0305311	0.0055308	2.5E-08
16	FTO	rs9939609	53786615	A	T	0.1225580	0.0306186	0.0055312	2.4E-08
16	FTO	rs9927317	53787084	G	C	0.1132920	0.0322414	0.0057731	2.0E-08
16	FTO	rs17817712	53787213	G	A	0.1223690	0.0307160	0.0055355	2.1E-08
16	FTO	rs7206410	53787385	C	T	0.1225410	0.0306777	0.0055315	2.2E-08
16	FTO	rs7202116	53787703	G	A	0.1225750	0.0308107	0.0055292	1.9E-08
16	FTO	rs7202296	53787778	G	A	0.1225540	0.0306817	0.0055314	2.2E-08
16	FTO	rs66908032	53788230	A	C	0.1226830	0.0313624	0.0055329	1.1E-08
16	FTO	chr16:53788257_AT_A	53788257	A	AT	0.1223440	0.0305785	0.0055371	2.4E-08
16	FTO	rs72803697	53788271	T	C	0.1225480	0.0306362	0.0055316	2.3E-08
16	FTO	rs62033403	53788325	G	A	0.1225370	0.0307270	0.0055316	2.0E-08
16	FTO	rs62033404	53788327	G	A	0.1225330	0.0307028	0.0055316	2.1E-08
16	FTO	rs62033405	53788475	T	C	0.1223670	0.0307719	0.0055354	2.0E-08
16	FTO	rs7206122	53788528	A	G	0.1225300	0.0307311	0.0055319	2.0E-08
16	FTO	rs7190396	53788590	G	T	0.1192900	0.0315915	0.0056309	1.9E-08
16	FTO	rs7185735	53788739	G	A	0.1225260	0.0305032	0.0055287	2.7E-08
16	FTO	rs7994966	53789815	C	T	0.1140820	0.0313625	0.0057553	3.9E-08
16	FTO	rs56137030	53791993	A	G	0.1226430	0.0307340	0.0055311	2.0E-08
16	FTO	rs10468280	53793567	G	A	0.1228550	0.0313359	0.0055265	1.1E-08
16	FTO	rs62033408	53794050	G	A	0.1226870	0.0314370	0.0055285	9.4E-09
16	FTO	rs17817964	53794154	T	C	0.1394640	0.0303179	0.0052360	5.0E-09
17	SLC16A13	rs76070643	7038306	T	C	0.1001290	0.0337376	0.0060406	1.8E-08
17	SLC16A13	rs78972129	7039011	A	G	0.1001370	0.0337162	0.0060404	1.8E-08
17	SLC16A13	rs4630597	7039227	C	T	0.1001360	0.0337129	0.0060404	1.8E-08
17	SLC16A13 *	rs58223766	7040410	T	C	0.1001520	0.0336864	0.0060406	1.9E-08
17	SLC16A13 *	rs17203120	7040670	G	T	0.1001640	0.0337235	0.0060396	1.8E-08
17	SLC16A13 *	rs75075014	7040770	A	G	0.1001590	0.0336978	0.0060396	1.9E-08
17	SLC16A11 *	rs145952323	7041030	C	G	0.0998634	0.0339026	0.0060481	1.6E-08
17	SLC16A11	rs75493593	7041768	T	G	0.1002370	0.0338443	0.0060349	1.7E-08
17	SLC16A11	rs75418188	7042164	T	C	0.1002820	0.0335619	0.0060318	2.2E-08
17	SLC16A11	rs13342232	7042621	G	A	0.1002030	0.0338104	0.0060339	1.8E-08
17	SLC16A11	rs13342692	7042968	C	T	0.1002160	0.0336202	0.0060336	2.1E-08
17	SLC16A11	rs117767867	7043011	T	C	0.1002140	0.0336037	0.0060337	2.2E-08
17	SLC16A11	rs2292351	7043602	G	C	0.0994344	0.0337937	0.0060623	2.6E-08
17	SLC16A11 *	rs77086571	7044074	C	G	0.0990743	0.0340673	0.0060832	2.0E-08
17	SLC16A11 *	rs74577409	7044134	G	C	0.0989503	0.0339177	0.0060862	2.3E-08
17	SLC16A11 *	rs35489850	7049784	C	T	0.1042570	0.0342691	0.0059859	1.2E-08
17	SMCR9 *	rs8076224	17434247	A	T	0.4426040	-0.0205277	0.0036649	5.2E-09
17	SMCR9 *	rs7219123	17434525	C	G	0.4421540	-0.0203481	0.0036653	7.1E-09
17	SMCR9 *	rs11654613	17436203	G	C	0.4475930	-0.0204474	0.0036638	5.4E-09
17	SMCR9 *	rs8073398	17437198	C	T	0.4476750	-0.0203598	0.0036721	6.9E-09
17	TUBD1 *	rs1292043	59856808	G	A	0.3845130	0.0199917	0.0037541	4.8E-08
17	TUBD1	rs201574199	59873259	TG	T	0.3775620	0.0201062	0.0037545	4.5E-08
17	TUBD1	rs1292057	59880763	T	C	0.3937620	0.0211155	0.0037263	6.5E-09
17	TUBD1	rs111282327	59889907	C	T	0.3787680	0.0202156	0.0037641	4.4E-08
17	RPS6KB1	rs7224366	59906904	T	G	0.3779520	0.0199385	0.0037553	4.7E-08
17	PRKARIA, WIP1	rs8072180	68437040	A	G	0.4256890	0.0247552	0.0037597	1.3E-10
17	PRKARIA, WIP1	rs8072338	68437158	A	T	0.4214490	0.0247578	0.0037457	1.0E-10
17	PRKARIA, WIP1	rs2909207	68443464	T	C	0.4217730	0.0248433	0.0037330	7.3E-11
17	PRKARIA, WIP1	rs2952296	68449328	G	C	0.4771670	0.0293151	0.0036548	9.8E-15
17	PRKARIA, WIP1	rs2909209	68449995	G	A	0.4768040	0.0293489	0.0036532	8.7E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	PRKARIA, WIPI1	rs2302783	68450932	T	C	0.4755780	0.0290648	0.0036520	1.5E-14
17	PRKARIA, WIPI1	rs2952295	68451280	A	T	0.4753280	0.0288480	0.0036524	2.5E-14
17	PRKARIA, WIPI1	rs1808335	68452349	A	G	0.4694510	0.0284185	0.0036604	7.3E-14
17	PRKARIA, WIPI1	rs883541	68452981	G	A	0.4752350	0.0290065	0.0036514	1.6E-14
17	PRKARIA, WIPI1	rs3896656	68454885	A	G	0.4764080	0.0289472	0.0036576	2.3E-14
17	PRKARIA, WIPI1	rs2952294	68455567	A	G	0.4754970	0.0289225	0.0036537	1.8E-14
17	PRKARIA, WIPI1	rs71378928	68457164	C	G	0.4797010	0.0283141	0.0036632	6.2E-14
17	PRKARIA	rs2909211	68461517	C	T	0.4794910	0.0280125	0.0036645	1.4E-13
17	PRKARIA	rs2909213	68464174	A	G	0.4794360	0.0278713	0.0036713	2.1E-13
17	PRKARIA	rs2952290	68467242	G	A	0.4855390	0.0269240	0.0037061	1.6E-12
17	PRKARIA	rs2909216	68467820	C	G	0.4855520	0.0268746	0.0037077	1.7E-12
17	PRKARIA	rs2909217	68467844	C	T	0.4855510	0.0268494	0.0037077	1.8E-12
17	PRKARIA	rs2952289	68468273	C	T	0.4856060	0.0267679	0.0037086	2.1E-12
17	PRKARIA	rs2909218	68468405	C	T	0.4856090	0.0266894	0.0037088	2.3E-12
17	PRKARIA	rs4968898	68509715	T	G	0.4927780	-0.0227468	0.0037126	2.8E-09
17	MAP2K6	rs3815035	69536247	G	A	0.2692160	-0.0236744	0.0041618	2.9E-09
17	MAP2K6	chr17:69537087_A_AAAAC	69537087	AAAAC	A	0.2919740	-0.0256959	0.0040097	1.6E-11
17	MAP2K6	rs16974184	69537118	C	T	0.2919740	-0.0256959	0.0040097	1.6E-11
17	MAP2K6	rs12603427	69538096	C	G	0.2666570	-0.0241969	0.0041568	9.5E-10
17	MAP2K6	rs12603937	69538746	T	G	0.2665640	-0.0244096	0.0041577	7.0E-10
17	MAP2K6	rs12600415	69539552	T	C	0.2666760	-0.0242902	0.0041563	8.4E-10
17	MAP2K6	rs12600726	69539982	C	G	0.2860980	-0.0258763	0.0040382	1.7E-11
17	MAP2K6	chr17:69542199_CA_C	69542199	C	CA	0.2672050	-0.0245863	0.0041600	5.6E-10
17	MAP2K6 *	rs2072073	69542829	G	C	0.2706060	-0.0239182	0.0041534	1.3E-09
17	MAP2K6 *	rs2072074	69543087	C	G	0.2666640	-0.0242753	0.0041560	8.6E-10
17	MAP2K6 *	rs2072075	69543430	T	C	0.2706130	-0.0239497	0.0041533	1.3E-09
17	MAP2K6 *	rs11650716	69545194	G	C	0.2901100	-0.0255696	0.0040378	2.7E-11
17	MAP2K6 *	chr17:69546848_CT_C	69546848	C	CT	0.2892100	-0.0249099	0.0040719	1.6E-10
17	MAP2K6 *	rs17823190	69546972	C	G	0.2892070	-0.0260451	0.0040159	7.9E-12
17	MAP2K6 *	rs200120981	69547071	TG	T	0.2792630	-0.0262595	0.0040957	2.0E-11
17	MAP2K6 *	rs73371387	69547075	G	T	0.2883990	-0.0259371	0.0040235	1.1E-11
17	MAP2K6 *	rs17223504	69547171	A	G	0.2892290	-0.0260186	0.0040157	8.3E-12
17	MAP2K6 *	rs11867261	69547394	A	T	0.2892290	-0.0260186	0.0040157	8.3E-12
17	MAP2K6 *	rs78679262	69547473	T	A	0.2891850	-0.0260198	0.0040161	8.0E-12
17	MAP2K6 *	rs17823202	69548123	A	G	0.2693560	-0.0246703	0.0041356	3.1E-10
17	MAP2K6 *	rs11654541	69548402	T	G	0.2892290	-0.0260186	0.0040157	8.3E-12
17	MAP2K6 *	rs78810797	69548432	A	AT	0.2892290	-0.0260186	0.0040157	8.3E-12
17	MAP2K6 *	rs10512573	69548838	A	G	0.2892290	-0.0260186	0.0040157	8.3E-12
17	MAP2K6 *	rs11868542	69548969	C	T	0.2893860	-0.0260431	0.0040162	7.1E-12
17	MAP2K6 *	rs60833993	69549210	A	G	0.2889470	-0.0260656	0.0040183	8.3E-12
17	MAP2K6 *	rs17223089	69549454	G	A	0.2893080	-0.0259891	0.0040148	8.3E-12
17	MAP2K6 *	rs17223095	69549503	T	G	0.2892290	-0.0260186	0.0040157	8.3E-12
17	MAP2K6 *	rs8072325	69549955	T	G	0.2887520	-0.0262106	0.0040185	6.5E-12
17	MAP2K6 *	rs990231	69550136	T	C	0.2892240	-0.0260004	0.0040156	8.5E-12
17	MAP2K6 *	rs990232	69550227	A	G	0.2892390	-0.0259874	0.0040158	8.7E-12
17	MAP2K6 *	rs7216405	69550555	A	G	0.2892240	-0.0260004	0.0040156	8.5E-12
17	MAP2K6 *	rs17823238	69550945	C	G	0.2892200	-0.0259887	0.0040156	8.7E-12
17	MAP2K6 *	rs7219156	69552339	G	A	0.2893170	-0.0260585	0.0040162	7.6E-12
17	MAP2K6 *	rs2285601	69552981	A	T	0.2868640	-0.0257808	0.0040766	3.2E-11
17	MAP2K6 *	rs2285600	69553320	A	G	0.2866560	-0.0258231	0.0040893	3.7E-11
17	MAP2K6 *	rs12601271	69554374	C	T	0.3009830	-0.0267518	0.0040613	9.1E-12
17	MAP2K6 *	rs11868800	69559125	T	C	0.3758350	-0.0209379	0.0038317	1.2E-08
17	MAP2K6 *	rs9916229	69560001	A	C	0.3845430	-0.0207053	0.0038157	1.5E-08
17	MAP2K6 *	rs756942	69560817	T	C	0.3754360	-0.0210088	0.0038294	1.1E-08
17	MAP2K6 *	rs8081578	69562142	C	A	0.3778790	-0.0203937	0.0038260	3.2E-08
17	MAP2K6 *	rs8082194	69562524	G	A	0.3778850	-0.0203648	0.0038260	3.4E-08
17	MAP2K6 *	rs79275738	69564667	A	G	0.3049950	-0.0275889	0.0040337	1.9E-12
17	MAP2K6 *	rs75584695	69564628	C	T	0.3050930	-0.0277958	0.0040311	1.2E-12
17	MAP2K6 *	rs7501457	69566558	G	A	0.3364340	-0.0249024	0.0039215	8.3E-11
17	MAP2K6 *	rs8068044	69570499	C	T	0.3377800	-0.0246488	0.0039120	1.2E-10
17	MAP2K6 *	rs16974205	69573554	A	G	0.3072880	-0.0277347	0.0039913	1.2E-12
17	MAP2K6 *	rs12941110	69575232	G	A	0.3399070	-0.0243904	0.0038808	1.6E-10
17	MAP2K6 *	rs58601248	69576297	T	A	0.3093860	-0.0275407	0.0039608	1.4E-12
17	MAP2K6 *	rs13341168	69577986	C	T	0.3097050	-0.0263013	0.0039380	1.3E-11
17	MAP2K6 *	rs7225826	69578580	C	T	0.3274400	-0.0241478	0.0038828	3.6E-10
17	MAP2K6 *	rs9906147	69579532	G	T	0.3097250	-0.0263102	0.0039378	1.3E-11
17	MAP2K6 *	rs16966912	69580280	C	G	0.3095500	-0.0263087	0.0039394	1.4E-11
17	MAP2K6 *	rs16966913	69580339	T	C	0.3097270	-0.0263160	0.0039377	1.3E-11
17	MAP2K6 *	rs8182335	69581104	C	T	0.3269900	-0.0243470	0.0038829	2.4E-10
17	MAP2K6 *	rs75359828	69581388	C	G	0.3097090	-0.0262876	0.0039378	1.3E-11
17	MAP2K6 *	rs16974218	69581896	C	A	0.3099270	-0.0266004	0.0039365	8.0E-12
17	MAP2K6 *	rs12453895	69582568	T	C	0.3345770	-0.0243494	0.0038603	1.9E-10
17	MAP2K6 *	rs75456534	69582573	CAT	C	0.3097120	-0.0262653	0.0039383	1.4E-11
17	MAP2K6 *	rs78049753	69582705	C	T	0.3096770	-0.0261942	0.0039381	1.6E-11
17	MAP2K6 *	rs16974219	69582967	C	T	0.3096770	-0.0261942	0.0039381	1.6E-11
17	MAP2K6 *	rs7209518	69584034	C	A	0.3268430	-0.0244591	0.0038844	2.0E-10
17	MAP2K6 *	rs6501331	69584608	T	C	0.3095970	-0.0263147	0.0039400	1.3E-11
17	MAP2K6 *	rs6501332	69584841	A	G	0.3095720	-0.0263718	0.0039403	1.2E-11
17	MAP2K6 *	rs8076261	69584956	C	T	0.3095770	-0.0263521	0.0039409	1.3E-11
17	MAP2K6 *	rs9911185	69585306	C	T	0.3095690	-0.0262955	0.0039416	1.4E-11
17	MAP2K6 *	rs9911351	69585980	T	C	0.3095770	-0.0263056	0.0039425	1.4E-11
17	MAP2K6 *	rs12051859	69586293	G	A	0.3269100	-0.0243550	0.0038880	2.3E-10
17	MAP2K6 *	rs57196051	69586677	TGAAAG	T	0.3344370	-0.0246418	0.0038703	1.1E-10
17	MAP2K6 *	rs58343496	69587127	G	C	0.3093390	-0.0264477	0.0039532	1.1E-11
17	MAP2K6 *	rs8081311	69587151	G	T	0.3266290	-0.0246358	0.0038976	1.4E-10
17	MAP2K6 *	rs79326607	69588575	A	G	0.3090210	-0.0262547	0.0039608	1.4E-11
17	MAP2K6 *	rs8070514	69588581	G	A	0.3091520	-0.0263511	0.0039594	1.3E-11
17	MAP2K6 *	rs9913592	69590091	G	A	0.3262760	-0.0243562	0.0039068	2.3E-10
17	MAP2K6 *	rs6501333	69590732	G	A	0.3262360	-0.0244001	0.0039080	2.2E-10
17	MAP2K6 *	rs78711874	69592368	A	G	0.3085740	-0.0267248	0.0039694	7.9E-12
17	MAP2K6 *	chr17:69592795 CCTTT_C	69592795	CCTTT	C	0.3227670	-0.0237510	0.0039401	9.0E-10
17	MAP2K6 *	rs79053215	69592990	A	C	0.3061760	-0.0261848	0.0039833	2.5E-11
17	MAP2K6 *	rs2365766	69593009	C	T	0.3237200	-0.0239920	0.0039230	5.3E-10
17	LOC101928122	rs6501335	69594962	G	A	0.3285600	-0.0236969	0.0039181	8.2E-10
17	LOC101928122	rs16974223	69594972	A	G	0.3108770	-0.0256948	0.0039757	5.0E-11
17	LOC101928122	rs7207537	69595587	T	C	0.3285240	-0.0236272	0.0039190	9.3E-10
17	LOC101928122	rs2365767	69596278	G	A	0.3107940	-0.0257447	0.0039769	4.8E-11
17	LOC101928122	rs7207924	69596299	C	T	0.3265590	-0.0232043	0.0039274	1.7E-09
17	LOC101928122	rs74786272	69596773	C	T	0.3107720	-0.0256651	0.0039771	5.5E-11
17	LOC101928122	rs79489128	69597010	G	A	0.3107620	-0.0257086	0.0039772	5.2E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	LOC101928122	rs59547750	69598506	A	T	0.3107660	-0.0256808	0.0039774	5.6E-11
17	LOC101928122	rs9889995	69599172	A	C	0.3283940	-0.0236496	0.0039197	9.4E-10
17	LOC101928122	rs11307812	69601505	AG	A	0.3292080	-0.0235007	0.0039226	1.2E-09
17	LOC101928122	rs7216313	69601500	C	T	0.3354230	-0.0236508	0.0038995	7.3E-10
17	LOC101928122	rs6501339	69602017	G	T	0.3283070	-0.0239102	0.0039210	6.3E-10
17	LOC101928122	rs75505328	69602124	C	T	0.3102880	-0.0262486	0.0039821	2.3E-11
17	LOC101928122	rs9899582	69602427	C	T	0.3282390	-0.0238498	0.0039216	6.8E-10
17	LOC101928122	rs533731481	69604233	AG	A	0.3106830	-0.0257466	0.0039790	5.0E-11
17	LOC101928122	rs5821721	69605210	A	AC	0.3283200	-0.0237996	0.0039216	7.5E-10
17	LOC101928122	rs7213230	69606380	G	A	0.3251120	-0.0235545	0.0039360	1.1E-09
17	LOC101928122	rs9897105	69608091	T	C	0.3280970	-0.0237936	0.0039273	7.6E-10
17	LOC101928122	rs2074112	69608527	G	C	0.3114240	-0.0252243	0.0039916	1.3E-10
17	LOC101928122	rs728205	69610711	G	A	0.3506180	-0.0216729	0.0038893	3.2E-08
17	LOC101928122	rs2716190	69610852	C	T	0.3440910	-0.0225194	0.0038915	4.8E-09
17	LOC101928122	rs117677125	69611205	G	C	0.2982850	-0.0250813	0.0040092	1.9E-10
17	LOC101928122	rs2013118	69611361	C	T	0.3184660	-0.0223209	0.0039545	1.4E-08
17	LOC101928122	rs2947867	69611544	C	G	0.3352400	-0.0220192	0.0038974	1.2E-08
17	LOC101928122	rs8067400	69611843	A	G	0.3342970	-0.0224912	0.0039009	6.4E-09
17	LOC101928122	chr17:69611907_G_GT	69611907	G	GT	0.3344690	-0.0225300	0.0038873	5.3E-09
17	LOC101928122	chr17:69611941_T_TA	69611941	T	TA	0.3264220	-0.0226747	0.0039186	4.3E-09
17	LOC101928122	rs59483743	69611942	T	A	0.3337000	-0.0224877	0.0038914	5.8E-09
17	LOC101928122	rs77936068	69613689	T	C	0.3344980	-0.0223817	0.0038851	6.8E-09
17	LOC101928122	rs76566825	69613741	T	C	0.3344950	-0.0223952	0.0038851	6.6E-09
17	LOC101928122	rs77945711	69614340	G	A	0.3353780	-0.0225574	0.0038852	5.7E-09
17	LOC101928122	rs181341148	69614622	T	G	0.3345350	-0.0224572	0.0038840	6.0E-09
17	LOC101928122	rs28848882	69614781	A	G	0.3350590	-0.0221450	0.0038842	9.7E-09
17	LOC101928122	rs12950371	69616822	T	G	0.3345780	-0.0224444	0.0038819	6.1E-09
17	LOC101928122	rs12942023	69616976	C	A	0.3345860	-0.0225017	0.0038816	5.6E-09
17	LOC101928122	rs12940007	69616996	G	A	0.3345860	-0.0225017	0.0038816	5.6E-09
17	LOC101928122	rs9915726	69617397	T	C	0.3346050	-0.0224452	0.0038812	6.2E-09
17	LOC101928122	rs9916377	69617615	T	C	0.3428130	-0.0230792	0.0038945	2.9E-09
17	LOC101928122	rs9916153	69617729	A	T	0.3342290	-0.0226049	0.0038830	5.2E-09
17	LOC101928122	rs8078469	69617789	G	A	0.3346680	-0.0224264	0.0038811	6.2E-09
17	LOC101928122	rs137952303	69617792	T	C	0.3019130	-0.0255405	0.0039857	7.7E-11
17	LOC101928122	rs10634506	69617820	A	AGT	0.3346300	-0.0223514	0.0038807	7.0E-09
17	LOC101928122	rs143370267	69617938	A	G	0.3019240	-0.0255652	0.0039855	7.4E-11
17	LOC101928122	rs2716189	69617949	A	C	0.3346360	-0.0223513	0.0038806	7.1E-09
17	LOC101928122	rs2716188	69618028	A	G	0.3385630	-0.0213842	0.0038950	4.4E-08
17	LOC101928122	rs2716187	69618037	G	A	0.3381970	-0.0216243	0.0038930	3.0E-08
17	LOC101928122	rs2716186	69618078	T	C	0.3346460	-0.0223663	0.0038802	6.8E-09
17	LOC101928122	rs2716184	69618435	A	G	0.3346530	-0.0223726	0.0038797	6.8E-09
17	LOC101928122	rs2716183	69618564	A	G	0.3529340	-0.0231055	0.0038766	2.7E-09
17	LOC101928122	rs2716182	69618683	C	T	0.3346290	-0.0224738	0.0038793	5.8E-09
17	LOC101928122	rs11473815	69618709	T	TTC	0.3348070	-0.0224473	0.0038804	6.5E-09
17	LOC101928122	rs2716181	69618847	A	G	0.3346030	-0.0222658	0.0038783	8.2E-09
17	LOC101928122	rs2716180	69619363	G	A	0.3346320	-0.0222832	0.0038773	7.9E-09
17	LOC101928122	rs2158039	69619523	C	T	0.3346600	-0.0222711	0.0038769	8.1E-09
17	LOC101928122	rs2716177	69620064	G	A	0.3346920	-0.0223251	0.0038756	7.1E-09
17	LOC101928122	chr17:69620326_CA_C	69620326	C	CA	0.3356820	-0.0223009	0.0038888	8.0E-09
17	LOC101928122	rs2521691	69621098	C	T	0.3351060	-0.0223166	0.0038741	6.7E-09
17	LOC101928122	rs2716176	69621346	A	G	0.3346540	-0.0223047	0.0038725	6.6E-09
17	LOC101928122	rs2716175	69621877	G	A	0.3346040	-0.0220024	0.0038728	1.0E-08
17	LOC101928122	rs2716174	69621878	C	G	0.3346220	-0.0219841	0.0038727	1.0E-08
17	LOC101928122	rs71147173	69622307	TTAA	T	0.3355960	-0.0215294	0.0038555	1.5E-08
17	LOC101928122	rs2716170	69622509	G	T	0.3354600	-0.0216819	0.0038544	1.2E-08
17	LOC101928122	rs2716168	69622657	A	G	0.3355150	-0.0216627	0.0038544	1.2E-08
17	LOC101928122	rs2252056	69623368	T	C	0.3041590	-0.0241220	0.0039590	4.3E-10
17	LOC101928122	rs2947866	69625599	G	T	0.3339850	-0.0231358	0.0039314	2.8E-09
17	LOC101928122	rs2947865	69625683	A	G	0.3335100	-0.0227497	0.0039353	5.3E-09
18	ZNF516	rs689952	76483815	G	C	0.2338300	0.0254401	0.0043888	1.6E-08
18	ZNF516	chr18:76485868_T_TAA	76485868	TAA	T	0.2244830	0.0256378	0.0044275	2.7E-08
18	ZNF516	rs75307678	76486913	A	C	0.2238760	0.0254473	0.0044394	4.1E-08
18	ZNF516	rs77998951	76487020	T	C	0.2236990	0.0254335	0.0044398	4.2E-08
19	SYT5	rs2301278	55179056	A	G	0.1926500	-0.0261676	0.0046672	2.1E-08
19	PTPRH	rs17458	55181647	T	C	0.2105410	-0.0253919	0.0044825	1.1E-08
19	PTPRH	rs2288420	55181755	C	T	0.2105680	-0.0252719	0.0044819	1.3E-08
19	PTPRH	rs3760870	55182833	C	G	0.2101220	-0.0249334	0.0044894	1.9E-08
19	PTPRH	rs58017412	55184466	A	G	0.2104050	-0.0248051	0.0044881	2.5E-08
20	FOXA2 *	rs145531522	22512537	T	C	0.0171462	-0.0867332	0.0140261	1.1E-10
20	FOXA2 *	rs73902817	22513422	T	C	0.0368750	-0.0493675	0.0096355	2.4E-08
20	FOXA2 *	rs79439711	22514367	T	G	0.0368847	-0.0496838	0.0096243	2.0E-08
20	FOXA2 *	rs78793553	22514661	G	A	0.0369948	-0.0499518	0.0096215	1.7E-08
20	FOXA2 *	rs116680020	22524159	T	C	0.0369094	-0.0496356	0.0096264	2.1E-08
20	FOXA2 *	rs117888786	22526829	T	C	0.0942078	-0.0746347	0.0063416	4.6E-33
20	FOXA2 *	rs201322128	22528289	G	T	0.0226171	-0.0622355	0.0123366	3.1E-08
20	FOXA2 *	rs6113693	22528352	C	T	0.0606579	-0.0388970	0.0076053	3.3E-08
20	FOXA2 *	rs6113694	22528354	T	C	0.0606579	-0.0388970	0.0076053	3.3E-08
20	FOXA2 *	rs115740517	22529692	G	T	0.0370909	-0.0485970	0.0096058	4.1E-08
20	FOXA2 *	rs79474117	22529802	T	C	0.0399687	-0.0498135	0.0092904	5.6E-09
20	FOXA2 *	rs117155701	22531189	G	C	0.0362122	-0.0495168	0.0097213	3.4E-08
20	FOXA2 *	rs6048172	22535546	C	T	0.1580320	-0.0677289	0.0049808	1.5E-44
20	FOXA2 *	rs6036141	22536091	T	C	0.1592590	-0.0673506	0.0049612	2.2E-44
20	FOXA2 *	rs6036142	22536117	A	G	0.1594750	-0.0673551	0.0049575	1.7E-44
20	FOXA2 *	rs73902875	22536674	G	A	0.1578920	-0.0676152	0.0049797	3.0E-44
20	FOXA2 *	rs952690	22537885	A	C	0.1903920	-0.0530979	0.0046346	7.8E-32
20	FOXA2 *	rs13040491	22538726	C	T	0.1908260	-0.0532054	0.0046307	5.7E-32
20	FOXA2 *	rs80146373	22539018	A	G	0.1586600	-0.0666229	0.0049952	9.5E-43
20	FOXA2 *	rs6113698	22539504	T	G	0.2096850	-0.0513271	0.0044965	1.5E-31
20	FOXA2 *	chr20:22539609_GA_G	22539609	G	GA	0.1597650	-0.0671920	0.0049906	7.2E-44
20	FOXA2 *	rs79806472	22540023	T	C	0.1562020	-0.0682757	0.0050158	1.6E-44
20	FOXA2 *	rs73902879	22540048	A	G	0.1554440	-0.0684663	0.0050305	1.4E-44
20	FOXA2 *	rs61520093	22540218	A	C	0.1562520	-0.0684299	0.0050165	1.2E-44
20	FOXA2 *	rs77411603	22540411	T	A	0.0578819	-0.0639986	0.0078405	7.9E-17
20	FOXA2 *	rs59061776	22540427	T	C	0.1561230	-0.0682307	0.0050188	2.2E-44
20	FOXA2 *	rs4815126	22540431	A	C	0.1897950	-0.0539685	0.0046537	2.0E-32
20	FOXA2 *	rs6082742	22541698	A	T	0.1896630	-0.0540788	0.0046574	1.9E-32
20	FOXA2 *	rs5029909	22543443	T	C	0.1530730	-0.0709726	0.0050777	3.5E-46
20	FOXA2 *	rs4519600	22543693	T	A	0.1530650	-0.0708671	0.0050779	4.6E-46
20	FOXA2 *	rs6036143	22543864	A	C	0.1530650	-0.0708682	0.0050779	4.6E-46
20	FOXA2 *	rs6082743	22545748	G	A	0.1878500	-0.0562835	0.0046914	5.3E-34

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	FOXA2 *	chr20:22546024_TA_T	22546024	TA	T	0.1872600	-0.0551505	0.0047076	2.2E-32
20	FOXA2 *	rs6048179	22546398	T	A	0.1530020	-0.0709321	0.0050801	4.1E-46
20	FOXA2 *	rs6048180	22547179	T	G	0.1133300	-0.0696527	0.0058112	1.0E-34
20	FOXA2 *	rs2021680	22548114	T	C	0.1907310	-0.0565562	0.0046760	1.1E-34
20	FOXA2 *	rs2021681	22548121	G	T	0.1907280	-0.0564220	0.0046760	1.6E-34
20	FOXA2 *	rs1203867	22550503	T	C	0.1906470	-0.0567309	0.0046784	7.0E-35
20	FOXA2 *	rs6036144	22551014	T	C	0.1547470	-0.0720304	0.0050732	9.5E-48
20	FOXA2 *	rs1203868	22551374	A	T	0.1902990	-0.0567098	0.0046838	1.1E-34
20	FOXA2 *	rs6036145	22553398	A	G	0.1565240	-0.0773124	0.0050734	8.0E-55
20	FOXA2 *	rs945982	22553503	G	A	0.1880510	-0.0626143	0.0047101	6.5E-42
20	FOXA2 *	rs113895954	22554058	A	G	0.1520140	-0.0786981	0.0051107	3.5E-56
20	FOXA2 *	rs6036146	22554983	G	T	0.1520480	-0.0787694	0.0051099	2.8E-56
20	FOXA2 *	rs1203871	22555042	A	G	0.1881950	-0.0625158	0.0047078	7.5E-42
20	FOXA2 *	rs6048183	22556674	G	A	0.1520580	-0.0786665	0.0051097	3.9E-56
20	FOXA2 *	rs6048184	22557227	A	G	0.1528000	-0.0795759	0.0050977	1.3E-57
20	FOXA2 *	rs1203873	22557295	C	T	0.1889170	-0.0631984	0.0046995	7.8E-43
20	FOXA2 *	rs6048186	22557624	C	T	0.1527930	-0.0795950	0.0050976	1.3E-57
20	FOXA2 *	chr20:22557930_G_GGGGTCCTCCCAAGTC	22557930	TCCCCA	G	0.1472680	-0.0817790	0.0051967	1.3E-58
20	FOXA2 *	rs150149692	22559095	A	C	0.0109757	-0.0936686	0.0174494	2.1E-08
20	FOXA2 *	rs1203874	22559354	T	C	0.2384680	-0.0528787	0.0043006	9.4E-36
20	FOXA2 *	rs1203875	22559683	A	T	0.2175360	-0.0557165	0.0044158	1.3E-37
20	FOXA2 *	rs1203876	22560277	C	A	0.2165230	-0.0562500	0.0044191	3.6E-38
20	FOXA2 *	chr20:22560456_G_GA	22560456	GA	G	0.2157330	-0.0562564	0.0044283	4.9E-38
20	LINC00261	rs1203877	22560838	G	C	0.2164780	-0.0558643	0.0044192	1.2E-37
20	LINC00261	rs1203879	22561178	C	T	0.2164730	-0.0558212	0.0044190	1.3E-37
20	LINC00261	rs6048191	22561282	G	A	0.1798090	-0.0682717	0.0047367	9.4E-49
20	LINC00261	rs1203880	22561385	C	A	0.2164720	-0.0558070	0.0044190	1.4E-37
20	LINC00261	rs6048192	22561479	A	G	0.1797160	-0.0683487	0.0047377	8.1E-49
20	LINC00261	rs1203881	22561883	C	T	0.2164330	-0.0558013	0.0044200	1.5E-37
20	LINC00261	chr20:22561914_C_CAAGA	22561914	CAAGA	C	0.2164310	-0.0557875	0.0044200	1.6E-37
20	LINC00261	rs4815127	22562396	A	C	0.1795550	-0.0687749	0.0047373	2.3E-49
20	LINC00261	rs1203883	22563008	C	T	0.2161890	-0.0559527	0.0044168	9.8E-38
20	LINC00261	rs1203884	22563062	G	A	0.2158480	-0.0565073	0.0044199	2.1E-38
20	LINC00261	rs1203886	22563877	T	C	0.2161890	-0.0559527	0.0044168	9.8E-38
20	LINC00261	rs2471	22564111	C	T	0.2163560	-0.0560056	0.0044157	8.7E-38
20	LINC00261	rs6048196	22565548	A	G	0.1778090	-0.0682137	0.0047555	3.6E-48
20	LINC00261	rs1203889	22566283	C	T	0.1897980	-0.0661016	0.0046616	5.8E-47
20	LINC00261	rs2277762	22567645	T	C	0.1759220	-0.0701141	0.0047839	1.9E-50
20	LINC00261	rs2277763	22567656	T	C	0.1759200	-0.0701021	0.0047838	2.0E-50
20	LINC00261	rs1203892	22567882	G	A	0.1930140	-0.0650059	0.0046455	3.0E-46
20	LINC00261	rs932560	22568060	G	C	0.1861880	-0.0622387	0.0047290	3.2E-41
20	LINC00261	rs11087387	22568541	C	T	0.1542340	-0.0802363	0.0050690	5.2E-59
20	LINC00261	rs1203894	22568731	C	T	0.1919830	-0.0650205	0.0046603	6.6E-46
20	LINC00261	rs11087388	22568799	A	C	0.1542830	-0.0802876	0.0050694	4.3E-59
20	LINC00261	rs6048197	22569319	A	G	0.1542710	-0.0803149	0.0050721	4.5E-59
20	LINC00261	rs1203895	22569788	C	T	0.1926760	-0.0649329	0.0046597	5.4E-46
20	LINC00261	rs6048199	22569807	C	T	0.1542640	-0.0802374	0.0050727	6.1E-59
20	LINC00261	rs6048200	22569896	C	T	0.1543000	-0.0802949	0.0050728	5.2E-59
20	LINC00261	rs73300990	22570221	A	G	0.1535850	-0.0803544	0.0050856	6.7E-59
20	LINC00261	rs1203896	22570456	G	A	0.1686760	-0.0759356	0.0048853	1.3E-56
20	LINC00261	rs73300991	22570688	T	C	0.1311650	-0.0966196	0.0053999	6.9E-75
20	LINC00261	rs73300993	22570865	A	G	0.1311600	-0.0966623	0.0054000	6.0E-75
20	LINC00261	rs6048202	22571368	A	G	0.1312000	-0.0966552	0.0054000	6.0E-75
20	LINC00261	rs1203898	22572502	C	T	0.1695330	-0.0784635	0.0048780	5.2E-61
20	LINC00261	rs1203899	22572658	T	C	0.1693550	-0.0783607	0.0048777	7.2E-61
20	LINC00261	rs14803607	22572923	C	CTT	0.1333740	-0.1000210	0.0053609	6.1E-82
20	LINC00261	rs11477526	22574444	A	AT	0.1334260	-0.1001800	0.0053582	3.1E-82
20	LINC00261	rs6036152	22575955	C	A	0.1419080	-0.1008960	0.0052027	1.2E-88
20	LINC00261	rs6113722	22576461	A	G	0.1417220	-0.1012260	0.0052047	4.1E-89
20	LINC00261	rs77509977	22578009	T	C	0.0416930	-0.0776027	0.0091095	1.6E-19
20	LINC00261	rs1203902	22578486	C	T	0.1989510	-0.0752255	0.0046097	1.1E-62
20	FOXA2 *	chr20:22578744_C_CAAA	22578744	CAAA	C	0.1699440	-0.0822090	0.0048811	1.0E-66
20	FOXA2 *	rs6048205	22578963	G	A	0.1422680	-0.0995178	0.0051940	6.3E-87
20	FOXA2 *	rs117611011	22579071	A	C	0.0179741	-0.0837159	0.0137991	4.7E-10
20	FOXA2 *	rs1203905	22580051	G	A	0.1765620	-0.0806933	0.0047898	3.5E-67
20	FOXA2 *	rs72470563	22580294	A	T	0.1409940	-0.1010200	0.0052356	3.0E-88
20	FOXA2 *	rs1203907	22580333	C	T	0.1770590	-0.0806085	0.0047875	3.3E-67
20	FOXA2 *	rs6048206	22580744	C	T	0.1409440	-0.1013060	0.0052370	1.3E-88
20	FOXA2	rs112021763	22581333	CT	C	0.1769540	-0.0797627	0.0047973	6.9E-66
20	FOXA2	rs1974	22581673	A	G	0.1371540	-0.1046500	0.0053109	5.9E-92
20	FOXA2	rs3833331	22581688	AG	A	0.1371060	-0.1047870	0.0053118	3.6E-92
20	FOXA2	rs1055080	22581800	A	G	0.1772540	-0.0799723	0.0047927	6.0E-66
20	FOXA2	rs1203910	22582387	C	T	0.1811150	-0.0782384	0.0047555	2.7E-64
20	FOXA2	rs1800847	22582933	A	G	0.1360280	-0.1031260	0.0053332	7.3E-89
20	FOXA2 *	rs2277764	22585486	C	T	0.1363370	-0.1027890	0.0053259	1.4E-88
20	FOXA2 *	rs1337918	22586970	A	C	0.1384570	-0.1014530	0.0052713	5.1E-88
20	FOXA2 *	rs1209523	22587304	T	C	0.1810090	-0.0773674	0.0047199	4.9E-64
20	LOC101929685	rs1337919	22587957	T	G	0.1377150	-0.1016810	0.0052828	8.5E-88
20	LOC101929685	rs6048209	22590445	G	A	0.1392310	-0.1010650	0.0052587	1.9E-87
20	LOC101929685	rs1337920	22590566	T	A	0.1814410	-0.0773857	0.0047177	4.8E-64
20	LOC101929685	rs1337921	22590570	G	T	0.1814410	-0.0773857	0.0047177	4.8E-64
20	LOC101929685	rs1203915	22591866	C	T	0.1800560	-0.0777346	0.0047287	2.7E-64
20	LOC101929685	rs8123991	22592696	T	C	0.1378420	-0.1016690	0.0052777	8.2E-88
20	LOC101929685	rs6048211	22593298	A	C	0.1374450	-0.1021110	0.0052921	3.6E-88
20	LOC101929685	rs200638849	22595154	G	T	0.1345620	-0.0990704	0.0053591	2.0E-81
20	LOC101929685	rs1203916	22595643	C	G	0.1796800	-0.0782803	0.0047658	9.9E-65
20	LOC101929685	rs1203917	22595877	C	T	0.1775310	-0.0783491	0.0047826	5.6E-64
20	LOC101929685	rs7266093	22596998	G	A	0.1370070	-0.1005280	0.0052907	9.7E-86
20	LOC101929685	rs910958	22597366	A	G	0.1775490	-0.0783479	0.0047833	5.5E-64
20	LOC101929685	rs910959	22597373	C	T	0.1369410	-0.1005040	0.0052902	1.0E-85
20	LOC101929685	rs6036157	22597777	A	G	0.1369440	-0.1005080	0.0052902	1.0E-85
20	LOC101929685	rs1203918	22598869	G	A	0.1770940	-0.0784145	0.0047875	8.0E-64
20	LOC101929685	rs2003076	22598907	A	G	0.1365620	-0.1006920	0.0052954	1.1E-85
20	LOC101929685	rs17754033	22600175	T	C	0.0354453	-0.0813881	0.0098455	7.1E-19
20	LOC101929685	rs16984154	22600263	A	G	0.1365090	-0.1008610	0.0052959	6.3E-86
20	LOC101929685	rs6036158	22600422	C	T	0.1366190	-0.1007030	0.0052942	1.1E-85
20	LOC101929685	rs6048216	22600630	C	T	0.1371830	-0.1001910	0.0052913	6.4E-85
20	LOC101929685	rs1203919	22602316	T	G	0.1740250	-0.0785739	0.0048368	6.0E-63
20	LOC101929685	rs1203920	22604789	G	A	0.1138050	-0.0794407	0.0057307	1.4E-45
20	LOC101929685	rs1203921	22604846	T	G	0.1547470	-0.0821834	0.0050258	3.6E-64

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	LOC101929685	rs1203922	22605062	G	T	0.1568380	-0.0826498	0.0049897	1.0E-65
20	LOC101929685	rs1203923	22605190	T	G	0.1568300	-0.0826663	0.0049897	9.7E-66
20	LOC101929685	rs117769019	22605243	A	G	0.0128396	-0.1041910	0.0161148	2.1E-11
20	LOC101929685	rs11480708	22605448	C	CT	0.1568380	-0.0826498	0.0049897	1.0E-65
20	LOC101929685	rs1203924	22605670	G	A	0.1570370	-0.0827740	0.0049866	6.3E-66
20	LOC101929685	rs16984166	22605730	T	C	0.0428936	-0.0720424	0.0089841	1.5E-17
20	LOC101929685	rs11474135	22605991	C	CAA	0.1570340	-0.0827932	0.0049866	5.8E-66
20	LOC101929685	rs11087391	22606202	GC	G	0.1570340	-0.0827932	0.0049866	5.8E-66
20	LOC101929685	rs59654629	22606384	T	A	0.0429675	-0.0720977	0.0089745	1.4E-17
20	LOC101929685	rs1007458	22607038	G	A	0.1575420	-0.0819586	0.0049778	6.2E-65
20	LOC101929685	rs995734	22607370	G	T	0.1570390	-0.0827629	0.0049868	6.8E-66
20	FOXA2 *	rs1203925	22608135	G	A	0.1570320	-0.0827425	0.0049869	7.4E-66
20	FOXA2 *	rs1203926	22608279	A	T	0.1583880	-0.0818742	0.0049817	8.5E-65
20	FOXA2 *	rs1007202	22608882	T	G	0.1567730	-0.0825708	0.0049914	1.6E-65
20	FOXA2 *	rs1203927	22608927	G	A	0.1140540	-0.0788163	0.0057296	4.7E-45
20	FOXA2 *	rs1203928	22609245	G	A	0.1569810	-0.0828218	0.0049879	6.2E-66
20	FOXA2 *	rs1203929	22609266	C	G	0.1569810	-0.0828218	0.0049879	6.2E-66
20	FOXA2 *	rs2424435	22609912	C	T	0.1570180	-0.0826256	0.0049888	1.1E-65
20	FOXA2 *	rs2424436	22609914	G	T	0.1570180	-0.0826256	0.0049888	1.1E-65
20	FOXA2 *	rs1203930	22610197	A	G	0.1588220	-0.0815717	0.0049736	1.6E-64
20	FOXA2 *	rs1203931	22610325	A	G	0.1568570	-0.0827836	0.0049906	7.1E-66
20	FOXA2 *	chr20:22610445_ATT_T_A	22610445	ATT	A	0.1612290	-0.0822315	0.0049744	2.3E-65
20	FOXA2 *	rs1203932	22610530	T	G	0.1568450	-0.0827901	0.0049910	7.0E-66
20	FOXA2 *	rs1203933	22610551	T	C	0.1568450	-0.0827901	0.0049910	7.0E-66
20	FOXA2 *	rs1203934	22611326	A	C	0.1568180	-0.0827449	0.0049924	8.5E-66
20	FOXA2 *	rs1203935	22611348	G	A	0.1136570	-0.0795342	0.0057351	1.2E-45
20	FOXA2 *	rs1203936	22611792	G	T	0.1568320	-0.0827201	0.0049922	8.7E-66
20	FOXA2 *	rs73900508	22612023	T	G	0.0427078	-0.0716310	0.0090015	2.6E-17
20	FOXA2 *	rs73900510	22612150	A	G	0.0427078	-0.0716310	0.0090015	2.6E-17
20	FOXA2 *	rs12479757	22612556	T	C	0.1133650	-0.0791557	0.0057499	3.5E-45
20	FOXA2 *	rs1203937	22612728	T	C	0.1567170	-0.0827846	0.0049944	8.4E-66
20	FOXA2 *	rs1203938	22614320	G	A	0.1569290	-0.0830954	0.0049933	2.6E-66
20	FOXA2 *	rs1203939	22614618	A	G	0.1568630	-0.0832012	0.0049947	1.9E-66
20	FOXA2 *	rs1203940	22615005	T	C	0.1568150	-0.0830614	0.0049955	2.8E-66
20	FOXA2 *	rs61186493	22615369	TG	T	0.1567200	-0.0829448	0.0049983	6.0E-66
20	FOXA2 *	rs1203941	22615951	T	C	0.1564780	-0.0831487	0.0050023	4.3E-66
20	FOXA2 *	rs1203942	22615997	C	G	0.1564730	-0.0831246	0.0050024	4.7E-66
20	FOXA2 *	rs1203943	22616187	T	C	0.1564580	-0.0830169	0.0050029	7.0E-66
20	FOXA2 *	rs16984204	22616207	A	C	0.0424986	-0.0717723	0.0090231	2.4E-17
20	FOXA2 *	rs1203944	22616241	T	C	0.1564510	-0.0830001	0.0050030	7.4E-66
20	FOXA2 *	rs1203945	22616255	G	T	0.1564490	-0.0829927	0.0050030	7.7E-66
20	FOXA2 *	rs16984209	22616565	G	A	0.0424921	-0.0718538	0.0090238	2.3E-17
20	FOXA2 *	rs1572579	22616977	G	A	0.1694460	0.0280301	0.0048352	6.0E-09
20	FOXA2 *	rs186119011	22617137	T	C	0.0224530	-0.0863371	0.0123580	5.7E-13
20	FOXA2 *	rs7265984	22617693	G	T	0.0424915	-0.0718541	0.0090238	2.3E-17
20	FOXA2 *	rs5840968	22617806	G	GA	0.1564180	-0.0830152	0.0050035	7.2E-66
20	FOXA2 *	rs16984212	22618967	A	G	0.0424909	-0.0714941	0.0090238	3.2E-17
20	FOXA2 *	rs10485632	22619048	C	G	0.0424876	-0.0713437	0.0090241	3.6E-17
20	FOXA2 *	rs1203946	22620340	A	C	0.1563450	-0.0831942	0.0050050	4.1E-66
20	FOXA2 *	chr20:22621385_GA_G	22621385	GA	G	0.1563660	-0.0831347	0.0050057	5.3E-66
20	FOXA2 *	rs1203947	22621725	C	T	0.1563190	-0.0830599	0.0050055	7.0E-66
20	FOXA2 *	rs17754147	22622527	T	C	0.0423978	-0.0718579	0.0090331	2.3E-17
20	FOXA2 *	rs73900511	22622949	G	C	0.0424620	-0.0714312	0.0090268	3.4E-17
20	FOXA2 *	rs1203948	22624134	G	A	0.1579040	-0.0827221	0.0049854	8.1E-66
20	FOXA2 *	rs1203949	22625059	T	C	0.1578950	-0.0827100	0.0049855	8.5E-66
20	FOXA2 *	rs12624528	22625133	T	C	0.0440403	-0.0697753	0.0088690	6.6E-17
20	FOXA2 *	rs3920804	22625864	C	A	0.0440403	-0.0697753	0.0088690	6.6E-17
20	FOXA2 *	rs1933205	22626157	T	G	0.0440403	-0.0697753	0.0088690	6.6E-17
20	FOXA2 *	rs79781233	22626355	C	T	0.0439976	-0.0702276	0.0088731	4.2E-17
20	FOXA2 *	rs73900515	22626464	G	A	0.0440389	-0.0697493	0.0088693	7.2E-17
20	FOXA2 *	rs76136002	22626894	A	T	0.0437844	-0.0703230	0.0088940	4.9E-17
20	FOXA2 *	chr20:22627155_A_AAAAC	22627155	AAAAC	A	0.0440357	-0.0698273	0.0088696	6.8E-17
20	FOXA2 *	rs1157319	22627685	T	C	0.0440305	-0.0698984	0.0088699	6.4E-17
20	FOXA2 *	rs1146365	22628040	A	G	0.1133670	-0.0795813	0.0057479	1.6E-45
20	FOXA2 *	rs73900516	22628349	G	C	0.0440204	-0.0699538	0.0088708	6.1E-17
20	FOXA2 *	rs6106535	22628411	G	A	0.0440139	-0.0698010	0.0088715	6.9E-17
20	FOXA2 *	rs1203950	22628463	A	G	0.1133510	-0.0794357	0.0057485	2.3E-45
20	FOXA2 *	rs7270376	22628965	A	G	0.0440139	-0.0697807	0.0088715	7.0E-17
20	FOXA2 *	rs7270463	22629153	T	G	0.0412149	-0.0647590	0.0091498	4.8E-14
20	FOXA2 *	rs1415812	22629202	A	T	0.0412384	-0.0648280	0.0091474	4.4E-14
20	FOXA2 *	rs150370430	22629684	A	G	0.0126986	-0.1046540	0.0162059	2.0E-11
20	FOXA2 *	rs11907070	22630166	C	T	0.0413026	-0.0646735	0.0091431	4.6E-14
20	FOXA2 *	rs16984243	22630501	A	G	0.0412372	-0.0648403	0.0091474	4.3E-14
20	FOXA2 *	rs73900517	22630685	T	C	0.0412137	-0.0647713	0.0091498	4.7E-14
20	FOXA2 *	rs1890205	22631061	C	T	0.0412372	-0.0648403	0.0091474	4.3E-14
20	FOXA2 *	rs75135122	22632250	A	G	0.0409745	-0.0650524	0.0091768	3.9E-14
20	FOXA2 *	rs73900518	22632580	G	A	0.0409776	-0.0648775	0.0091757	4.5E-14
20	FOXA2 *	rs183884743	22632744	C	T	0.0124689	-0.1073600	0.0163512	1.0E-11
20	FOXA2 *	rs1203952	22633494	G	A	0.1911420	-0.0707693	0.0046856	3.2E-55
20	FOXA2 *	rs12625453	22633748	T	C	0.0411819	-0.0645313	0.0091469	5.3E-14
20	FOXA2 *	rs12624618	22633767	C	T	0.0411852	-0.0645159	0.0091465	5.4E-14
20	FOXA2 *	rs60021982	22634921	G	A	0.0421118	-0.0646622	0.0090516	2.4E-14
20	FOXA2 *	rs1203953	22635505	T	C	0.1552200	-0.0798991	0.0050136	5.9E-61
20	FOXA2 *	chr20:22636454_G_GA	22636454	GA	G	0.0420859	-0.0644964	0.0090535	2.9E-14
20	FOXA2 *	rs73900521	22637611	G	T	0.0420859	-0.0644964	0.0090535	2.9E-14
20	FOXA2 *	rs200659255	22638162	G	GT	0.0311477	-0.0624461	0.0105766	2.6E-10
20	FOXA2 *	rs56225606	22638328	T	C	0.0415813	-0.0662508	0.0091084	7.8E-15
20	FOXA2 *	rs6137704	22639060	A	T	0.1551760	-0.0798402	0.0050150	8.5E-61
20	FOXA2 *	rs2424439	22639402	G	A	0.1551760	-0.0798402	0.0050150	8.5E-61
20	FOXA2 *	rs55773617	22639529	T	C	0.0420910	-0.0643446	0.0090528	3.3E-14
20	FOXA2 *	rs73900522	22640075	A	G	0.0420910	-0.0643446	0.0090528	3.3E-14
20	FOXA2 *	rs73900523	22640088	C	T	0.0420910	-0.0643446	0.0090528	3.3E-14
20	FOXA2 *	rs34695810	22640674	C	CT	0.0416670	-0.0648761	0.0090964	4.0E-14
20	FOXA2 *	rs16984250	22641001	T	C	0.0416670	-0.0648761	0.0090964	4.0E-14
20	FOXA2 *	rs6137706	22642445	C	G	0.0444716	-0.0630332	0.0088227	2.4E-14
20	FOXA2 *	rs2208168	22642628	C	T	0.1574790	-0.0756161	0.0049908	3.7E-55
20	FOXA2 *	rs6137707	22643073	G	A	0.0444491	-0.0628789	0.0088248	2.9E-14
20	FOXA2 *	rs2424440	22643338	C	T	0.1574680	-0.0756447	0.0049909	3.4E-55
20	FOXA2 *	rs2208169	22643647	T	C	0.1127760	-0.0738986	0.0057614	3.7E-39
20	FOXA2 *	rs6137708	22643935	C	T	0.0444491	-0.0628789	0.0088248	2.9E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	FOXA2 *	rs2424442	22644151	C	T	0.1574050	-0.0754760	0.0049921	5.6E-55
20	FOXA2 *	rs6082762	22644378	A	T	0.1574070	-0.0754201	0.0049925	6.5E-55
20	FOXA2 *	rs78703248	22644389	G	A	0.0444508	-0.0628130	0.0088259	3.2E-14
20	FOXA2 *	rs2424443	22644497	G	A	0.1574820	-0.0750168	0.0049911	2.1E-54
20	FOXA2 *	rs6075931	22644757	C	A	0.1625090	-0.0725308	0.0049433	5.7E-52
20	FOXA2 *	rs6137709	22645601	G	A	0.0443312	-0.0637007	0.0088380	1.5E-14
20	FOXA2 *	rs6137710	22646320	T	G	0.0435950	-0.0659518	0.0089119	4.9E-15
20	FOXA2 *	rs910960	22647249	G	C	0.1136460	-0.0741993	0.0057409	7.5E-40
20	FOXA2 *	rs1884742	22647875	G	A	0.2051600	-0.0581444	0.0045479	9.4E-40
20	FOXA2 *	rs6132534	22648006	A	G	0.0514277	-0.0515357	0.0082506	4.0E-11
20	FOXA2 *	rs117543213	22648249	A	G	0.1095870	-0.0701908	0.0058539	6.9E-35
20	FOXA2 *	rs6137712	22648298	C	T	0.1133380	-0.0735322	0.0057484	4.3E-39
20	FOXA2 *	rs2424444	22648681	C	T	0.1136880	-0.0741325	0.0057375	7.6E-40
20	FOXA2 *	chr20:22649863_C_CT	22649863	C	CT	0.1170800	-0.0704752	0.0057118	2.0E-36
20	FOXA2 *	rs8118625	22649878	C	A	0.1138900	-0.0735314	0.0057282	1.9E-39
20	FOXA2 *	rs75851221	22650420	G	C	0.0518530	-0.0513835	0.0082165	3.2E-11
20	FOXA2 *	rs2224316	22651202	T	C	0.1138940	-0.0736175	0.0057278	1.5E-39
20	FOXA2 *	rs6082765	22651338	T	C	0.1139120	-0.0737076	0.0057280	1.3E-39
20	FOXA2 *	rs2180553	22651781	C	T	0.1660110	-0.0714299	0.0048827	1.2E-51
20	FOXA2 *	rs10534088	22651939	GCCAGC	G	0.1659960	-0.0709754	0.0048837	5.3E-51
20	FOXA2 *	rs747911	22652293	T	C	0.1140470	-0.0739549	0.0057238	6.2E-40
20	FOXA2 *	rs747912	22652422	T	C	0.1679270	-0.0710591	0.0048590	1.4E-51
20	FOXA2 *	rs910956	22652517	A	G	0.1137240	-0.0735789	0.0057305	1.9E-39
20	FOXA2 *	rs754855	22653005	T	C	0.1129820	-0.0730949	0.0057592	1.3E-38
20	FOXA2 *	rs910957	22653216	C	G	0.1129590	-0.0728167	0.0057658	2.4E-38
20	FOXA2 *	chr20:22654266_T_TAC	22654266	T	TAC	0.1158220	-0.0698806	0.0056985	4.3E-36
20	FOXA2 *	rs113275570	22654306	C	CAGAT	0.1156440	-0.0695870	0.0057012	8.2E-36
20	FOXA2 *	rs4815129	22654716	G	C	0.1156380	-0.0696724	0.0057014	6.9E-36
20	FOXA2 *	rs4815130	22655214	G	A	0.1157860	-0.0696004	0.0056993	7.4E-36
20	FOXA2 *	rs2424445	22655924	A	G	0.1599830	-0.0648144	0.0049573	2.0E-41
20	FOXA2 *	rs2424446	22656118	A	G	0.1157040	-0.0699240	0.0056999	3.9E-36
20	FOXA2 *	rs2424447	22656380	T	C	0.1599880	-0.0648217	0.0049572	2.0E-41
20	FOXA2 *	rs2424448	22656474	C	T	0.1599880	-0.0648217	0.0049572	2.0E-41
20	FOXA2 *	rs2424449	22656665	A	G	0.1605160	-0.0650197	0.0049530	9.8E-42
20	FOXA2 *	rs2424450	22657348	C	A	0.1157960	-0.0697277	0.0056964	5.5E-36
20	FOXA2 *	rs6082767	22658341	T	A	0.1670130	-0.0681504	0.0048643	2.0E-47
20	FOXA2 *	rs4815131	22658994	T	C	0.1226340	-0.0736141	0.0055511	4.3E-42
20	FOXA2 *	rs975525	22659774	G	A	0.1226670	-0.0736197	0.0055503	4.0E-42
20	FOXA2 *	rs2145058	22660132	T	C	0.1227220	-0.0737238	0.0055499	2.8E-42
20	FOXA2 *	rs4815132	22661195	T	C	0.1258970	-0.0721852	0.0055005	3.0E-41
20	FOXA2 *	rs4815133	22661325	C	A	0.1676270	-0.0678963	0.0048537	2.5E-47
20	FOXA2 *	rs2424451	22662187	A	G	0.1638950	-0.0692359	0.0049308	1.5E-47
20	FOXA2 *	rs2424454	22662292	G	A	0.1264950	-0.0733452	0.0055497	1.8E-41
20	FOXA2 *	rs6036168	22662688	G	A	0.1229980	-0.0738445	0.0055373	1.5E-42
20	FOXA2 *	rs2424456	22663024	C	A	0.1230050	-0.0738608	0.0055369	1.5E-42
20	FOXA2 *	rs4815134	22663923	C	T	0.1229990	-0.0738777	0.0055368	1.4E-42
20	FOXA2 *	rs4815135	22663951	C	G	0.1229990	-0.0738777	0.0055368	1.4E-42
20	FOXA2 *	rs55803110	22664344	C	T	0.1234570	-0.0739112	0.0055271	1.4E-42
20	FOXA2 *	rs2424457	22664411	C	T	0.1236460	-0.0739030	0.0055231	1.2E-42
20	FOXA2 *	rs2424458	22664505	C	T	0.1236490	-0.0738789	0.0055231	1.3E-42
20	FOXA2 *	rs2145059	22664889	C	T	0.1230340	-0.0741022	0.0055342	1.0E-42
20	FOXA2 *	rs2145060	22664994	T	A	0.1230340	-0.0741022	0.0055342	1.0E-42
20	FOXA2 *	rs2145061	22665097	A	G	0.1230340	-0.0741022	0.0055342	1.0E-42
20	FOXA2 *	rs6036169	22665239	G	A	0.1230880	-0.0739345	0.0055326	1.6E-42
20	FOXA2 *	rs35336166	22666799	TC	T	0.1228630	-0.0738262	0.0055376	2.0E-42
20	FOXA2 *	rs6036170	22666949	T	C	0.1228630	-0.0738262	0.0055376	2.0E-42
20	FOXA2 *	rs6113758	22667010	C	T	0.1228630	-0.0738262	0.0055376	2.0E-42
20	FOXA2 *	rs2424459	22667434	C	A	0.1228630	-0.0738270	0.0055376	2.0E-42
20	FOXA2 *	rs1543443	22667935	G	A	0.1660790	-0.0683268	0.0048684	1.2E-47
20	FOXA2 *	rs11087394	22669346	TC	T	0.1228590	-0.0738660	0.0055377	1.8E-42
20	FOXA2 *	rs6082774	22669410	G	A	0.1228590	-0.0738660	0.0055377	1.8E-42
20	FOXA2 *	rs6048241	22669505	T	C	0.1661110	-0.0683886	0.0048676	1.0E-47
20	FOXA2 *	rs6137721	22670000	G	A	0.1228590	-0.0738660	0.0055377	1.8E-42
20	FOXA2 *	rs6036172	22670551	A	G	0.1661090	-0.0684094	0.0048677	9.5E-48
20	FOXA2 *	rs7273357	22671324	T	C	0.1228590	-0.0738660	0.0055377	1.8E-42
20	FOXA2 *	rs117923305	22671520	C	A	0.0315498	-0.0861585	0.0104382	1.5E-16
20	FOXA2 *	rs6082777	22672079	A	G	0.1661980	-0.0681573	0.0048682	2.3E-47
20	FOXA2 *	rs10708423	22672870	T	TG	0.1219090	-0.0731585	0.0055592	2.5E-41
20	FOXA2 *	rs6113762	22672946	C	T	0.1661220	-0.0683802	0.0048706	1.2E-47
20	FOXA2 *	rs6132536	22673262	T	C	0.1226580	-0.0738006	0.0055419	2.4E-42
20	FOXA2 *	rs6075933	22673421	A	T	0.1662530	-0.0685398	0.0048721	9.2E-48
20	FOXA2 *	rs6082778	22673436	T	C	0.1230700	-0.0735956	0.0055350	3.3E-42
20	FOXA2 *	rs6075934	22673477	G	T	0.1660100	-0.0686764	0.0048732	6.4E-48
20	FOXA2 *	rs73304706	22673756	A	G	0.1659510	-0.0686146	0.0048746	9.4E-48
20	FOXA2 *	rs73304707	22673921	A	C	0.1228460	-0.0739637	0.0055382	1.5E-42
20	FOXA2 *	rs6048245	22674559	A	C	0.1228160	-0.0739964	0.0055394	1.4E-42
20	FOXA2 *	rs6082779	22675057	T	C	0.1227280	-0.0738171	0.0055423	2.3E-42
20	FOXA2 *	rs6132537	22675285	C	T	0.1226190	-0.0737012	0.0055475	4.0E-42
20	FOXA2 *	rs4499503	22675323	G	A	0.1740810	-0.0656726	0.0048118	3.1E-45
20	FOXA2 *	rs6036173	22676008	C	A	0.1283130	-0.0663873	0.0054674	1.3E-35
20	FOXA2 *	rs76495668	22677300	A	G	0.0723733	-0.0577380	0.0070952	5.4E-17
20	FOXA2 *	rs6048247	22677335	C	A	0.0517466	-0.0871478	0.0082452	8.6E-27
20	FOXA2 *	rs2209796	22678812	G	A	0.0518316	-0.0866434	0.0082391	1.7E-26
20	FOXA2 *	rs6048249	22679473	G	C	0.0982597	-0.0684260	0.0061420	1.7E-30
20	FOXA2 *	rs6082784	22679757	T	C	0.0519060	-0.0866664	0.0082322	1.3E-26
20	FOXA2 *	chr20:22680998_A_AT	22680998	AT	A	0.0572090	-0.0762931	0.0079716	8.9E-22
20	FOXA2 *	rs11471376	22681678	T	TTTAC	0.0519276	-0.0867471	0.0082308	1.2E-26
20	FOXA2 *	rs6036175	22682100	C	A	0.0519254	-0.0867782	0.0082308	1.1E-26
20	FOXA2 *	rs1571249	22682719	T	C	0.0518245	-0.0865747	0.0082385	1.7E-26
20	FOXA2 *	rs6082789	22686250	T	C	0.0204948	-0.0719997	0.0128573	2.5E-09
20	FOXA2 *	rs6082790	22686824	A	G	0.0205494	-0.0726340	0.0128404	1.8E-09
20	FOXA2 *	rs6048253	22686883	C	T	0.1101000	-0.0609160	0.0058426	2.4E-27
20	FOXA2 *	rs6048254	22686961	C	T	0.0206386	-0.0724396	0.0128142	1.7E-09
20	FOXA2 *	rs139828317	22687310	C	T	0.0131911	-0.1040690	0.0159229	9.5E-12
20	FOXA2 *	rs6036176	22687667	G	T	0.0207361	-0.0734105	0.0127830	9.7E-10
20	FOXA2 *	rs1571251	22688144	A	G	0.0207890	-0.0746598	0.0127653	5.0E-10
20	FOXA2 *	rs1571252	22688299	T	C	0.0208084	-0.0744662	0.0127633	5.7E-10
20	FOXA2 *	rs6137726	22691782	A	C	0.0950793	-0.0519620	0.0061868	2.7E-18
20	FOXA2 *	rs6137727	22691914	A	G	0.0957606	-0.0516475	0.0061787	5.6E-18
20	FOXA2 *	rs6048268	22696980	A	C	0.1436700	-0.0387050	0.0052963	6.8E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	FOXA2 *	rs6048269	22696983	T	A	0.1436700	-0.0387050	0.0052963	6.8E-14
20	FOXA2 *	rs79057176	22701419	T	C	0.0645654	-0.0477224	0.0074258	3.5E-11
20	FOXA2 *	rs79950914	22707433	A	G	0.0648664	-0.0484894	0.0073815	1.1E-11
20	FOXA2 *	rs6106546	22707782	A	T	0.0653830	-0.0485618	0.0073503	1.1E-11
20	FOXA2 *	rs75240300	22711602	C	T	0.0655631	-0.0482193	0.0073357	1.4E-11
20	FOXA2 *	rs79064604	22718335	A	G	0.0653084	-0.0469923	0.0073505	4.8E-11
20	FOXA2 *	rs17816623	22718578	A	G	0.0653412	-0.0473093	0.0073521	3.6E-11
20	FOXA2 *	rs73900543	22722444	G	C	0.0737369	-0.0386899	0.0069471	9.2E-09
20	FOXA2 *	rs73900546	22725654	C	T	0.0735203	-0.0402573	0.0069579	2.5E-09
20	FOXA2 *	rs55844003	22727786	C	T	0.0729484	-0.0408692	0.0069887	2.2E-09
20	NFATC2	rs6067810	51527262	T	C	0.3197190	0.0217297	0.0039049	2.9E-08
20	NFATC2	chr20:51529358_GT_G	51529358	G	GT	0.3381680	0.0235824	0.0038947	1.7E-09
20	NFATC2	rs6063665	51530346	A	T	0.3427480	0.0235130	0.0038600	1.5E-09
20	NFATC2	rs8119787	51530532	G	A	0.3418080	0.0238344	0.0038631	8.1E-10
20	EEF1A2 *	rs1619876	63506002	A	G	0.2440280	-0.0234125	0.0042464	4.7E-08

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error

This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.

The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 8. Summary of top variants exhibiting genome-wide significance for the TG:HDL-C ratio, a marker of insulin resistance, identified within the Taiwan Biobank.

CHR	Rank	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	6	GCKR	rs1260326	27508073	T	C	0.4922090	0.1477180	0.0061040	7.4E-140
2	16	C2orf16	rs1919127	27578626	C	T	0.4715930	0.1077410	0.0061122	6.3E-73
2	15	ZNF512	rs12989678	27598615	T	C	0.4718700	0.1095830	0.0061315	1.1E-74
7	20	BCL7B	rs7793710	73557201	G	C	0.0951728	-0.1644970	0.0104182	3.6E-62
7	19	TBL2	rs13246490	73578020	T	C	0.0951782	-0.1652430	0.0104213	1.4E-62
7	14	MLXIPL	rs3812316	73606007	G	C	0.0862707	-0.1948320	0.0108875	4.3E-78
8	5	LPL	rs12679834	19962922	C	T	0.1031270	-0.2691430	0.0100265	6.3E-171
8	8	SLC18A1 *	rs9644568	20071071	A	G	0.1125720	-0.2001920	0.0096479	1.8E-106
11	3	BUD13	rs74368849	116751583	A	G	0.0667423	0.5454510	0.0122799	2.8E-446
11	2	ZPR1	rs3741297	116786951	T	C	0.0651757	0.6149740	0.0123280	2.9E-559
11	1	APOA5	rs651821	116791863	C	T	0.2709740	0.4536030	0.0068455	2.3E-979
11	4	APOA4	rs5104	116821618	C	T	0.3197880	0.1908020	0.0065521	1.6E-191
11	11	APOC3	rs5128	116832924	G	C	0.2906650	0.1409010	0.0066936	1.6E-100
11	12	APOA1 *	rs10750098	116834852	G	T	0.2901420	0.1402320	0.0067152	8.9E-99
11	17	SIK3	rs199986368	117031627	C	T	0.0152296	0.4418270	0.0249106	3.4E-71
11	18	PAFAH1B2	rs117592676	117146994	T	C	0.0193645	0.3813050	0.0221405	3.8E-68
19	13	NECTIN2	rs283811	44885243	G	A	0.1685240	0.1656780	0.0081834	5.7E-97
19	9	TOMM40	rs10119	44903416	A	G	0.0869311	0.2272840	0.0108798	1E-103
19	7	APOE	rs429358	44908684	C	T	0.0864235	0.2363640	0.0108879	7.9E-112
19	10	APOC1	rs5117	44915533	C	T	0.1686800	0.1707800	0.0082021	2.2E-101

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error

This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.

The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 9. Summary of top variants exhibiting genome-wide significance for the glucose levels, identified within the Taiwan Biobank.

CHR	Rank	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	15	GCKR	rs1260326	27508073	T	C	0.4935410	-0.0586768	0.0036201	6.8E-60
2	7	SIX3 *	rs12712928	44964941	C	G	0.4332780	0.0880344	0.0036880	1.4E-126
2	11	NOSTRIN	rs143166986	168862756	C	CTTCTTTAT	0.4154620	0.0737082	0.0037045	1.2E-90
2	8	SPC25	rs493816	168881727	C	T	0.4407320	0.0788304	0.0037154	2.2E-102
2	1	G6PC2	rs2232326	168907981	C	T	0.0403894	-0.3005850	0.0092633	1.9E-235
2	2	ABCB11	rs139014876	168950218	A	G	0.0372648	-0.2967150	0.0096923	1.8E-209
6	20	CDKAL1	rs34499031	20676183	TAA	T	0.3447450	0.0555282	0.0038268	3.0E-51
7	16	AGMO *	rs6947830	15025359	G	A	0.3108010	-0.0628506	0.0039218	5.2E-59
7	18	POLD2	rs3087370	44122210	G	A	0.2344250	-0.0679338	0.0043335	2.5E-57
7	17	MYL7	rs741033	44140166	G	C	0.2546860	-0.0675905	0.0042724	3.9E-58
7	3	GCK	rs2908289	44184343	A	G	0.1967390	0.1224130	0.0045672	2.9E-161
7	4	YKT6	rs2971667	44205461	C	T	0.1978460	0.1212520	0.0045591	8.1E-159
7	6	CAMK2B	rs732360	44222379	A	G	0.1974650	0.1154090	0.0046175	3.6E-140
8	9	SLC30A8	rs13266634	117172544	T	C	0.4600100	-0.0748002	0.0036452	4.3E-95
9	19	KANK1	rs16922302	672920	C	G	0.2698010	0.0593839	0.0041094	2.6E-51
9	14	CDKN2B *	rs10811661	22134095	C	T	0.4151890	-0.0638352	0.0036943	5.1E-68
11	5	MTNR1B	rs10830963	92975544	G	C	0.4333730	0.0924650	0.0036648	5.5E-144
20	12	LINC00261	rs6113722	22576461	A	G	0.1417220	-0.1012260	0.0052047	4.1E-89
20	10	FOXA2	rs3833331	22581688	AG	A	0.1371060	-0.1047870	0.0053118	3.6E-92
20	13	LOC101929685	rs6048211	22593298	A	C	0.1374450	-0.1021110	0.0052921	3.6E-88

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error
This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.
The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 10. Summary of genome-wide significance for variants associated with insulin-related traits in previous studies.

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
1	<i>MTOR - UBIAD1</i>	rs2295080	11,322,628	T	G	0.0394	[0.026-0.053] unit decrease	0.00000001	37291194
1	<i>ARID1A</i>	rs114165349	27,021,913	C	G	0.138022	0.00851415	1.61E-39	38200128
1	<i>NR0B2</i>	rs11581460	27,242,009	G	A	0.0200011	0.00261802	5.68E-10	38200128
1	<i>PABPC4-AS1</i>	rs3768321	40,035,928	T	G	0.0480953	0.00320619	4.38E-34	38200128
1	<i>MYCL</i>	rs61781290	40,393,160	G	A	0.0221266	0.00288512	4.88E-10	38200128
1	<i>CDKN2C</i>	rs72904737	51,351,846	G	A	0.034614	0.00451929	5.14E-10	38200128
1	<i>SSBP3</i>	rs213494	54,877,103	T	C	0.0179418	0.00266691	4.79E-08	38200128
1	<i>ANGPTL3</i>	rs10889333	62,957,030	G	A	0.0658915	0.00267004	3.37E-89	38200128
1	<i>PTGER3</i>	rs650194	71,414,863	A	G	0.0192074	0.00269257	7.11E-09	38200128
1	<i>NEGR1</i>	rs2613505	72,835,410	T	C	0.0218899	0.00320724	3.06E-08	38200128
1	<i>ELTD1</i>	rs1857095	80,246,020	T	C	0.08	0.12	7.90E-09	27416945
1	<i>CCDC18</i>	rs1365297	93,858,292	A	G	0.034367	0.00328643	2.15E-17	38200128
1	<i>DPYD</i>	rs1938566	98,478,981	C	T	0.0248702	0.00342705	3.9E-09	38200128
1	<i>CELSR2</i>	rs646776	109,818,530	T	C	0.0306472	0.00306179	4.58E-16	38200128
1	<i>CSF1</i>	rs333947	110,470,764	A	G	0.0315368	0.00356226	6.79E-13	38200128
1	<i>BOLA1</i>	rs1044808	149,871,905	G	C	0.0431286	0.00464337	4.82E-14	38200128
1	<i>CTSS</i>	rs6677420	150,946,490	A	G	0.0207841	0.00266617	2.52E-10	38200128
1	<i>UBAP2L</i>	rs2282227	154,243,097	G	A	0.0246886	0.00279484	7.62E-13	38200128
1	<i>DNM3</i>	rs2227198	172,360,164	A	G	0.0196965	0.00257	5.01E-10	38200128
1	<i>C1orf220</i>	rs6700266	178,508,930	G	A	0.0206853	0.00268859	4.29E-10	38200128
1	<i>OPTC</i>	rs36043408	203,511,492	G	A	0.0188793	0.00254854	1.84E-09	38200128
1	<i>CNTN2</i>	rs3903399	205,041,542	C	T	0.0239229	0.00311982	4.91E-10	38200128
1	<i>LYPLAL1</i>	rs6674544	219,628,973	A	G	0.018	0.002	6.97E-21	34059833
1	<i>LYPLAL1</i>	rs2820436	219,640,680	C	A	0.0153	0.003	4.40E-09	22885924
1	<i>LYPLAL1-AS1</i>	rs1538742	219,668,252	A	C	0.0278115	0.00258198	2.33E-18	38200128
1	<i>LYPLAL1</i>	rs2785980	219,700,519	T	C	0.017	0.004	2.00E-08	22581228
1	<i>LYPLAL1</i>	rs4846565	219,722,104	G	A	0.0132	0.002	1.80E-09	22885924
1	<i>LYPLAL1-AS1</i>	rs6678052	219,755,057	G	A	0.0230707	0.00294198	1.98E-10	38200128
1	<i>MTARC1</i>	rs2642438	220,970,028	A	G	0.0274332	0.00278243	1.24E-15	38200128
1	<i>LINC01352</i>	rs61830291	221,001,142	C	A	0.0299533	0.00433367	2.04E-08	38200128
1	<i>WNT9A</i>	rs68160490	228,078,132	G	A	0.0198132	0.00264393	1.2E-09	38200128
1	<i>GALNT2</i>	rs6684677	230,206,963	C	T	0.0250347	0.00311266	6.75E-11	38200128
1	<i>GALNT2</i>	rs10779835	230,299,949	T	C	0.084208	0.00261652	2.51E-150	38200128
1	<i>GALNT2</i>	rs632557	230,398,102	A	G	0.0911647	0.00640068	6.79E-31	38200128
1	<i>GALNT2</i>	rs2273967	230,415,293	C	T	0.0256008	0.00293879	1.56E-12	38200128
2	<i>TMEM18</i>	rs5017305	630,902	A	T	0.014	0.003	1.07E-08	34059833
2	<i>COLEC11</i>	rs3820897	3,642,361	C	T	0.0345696	0.00334351	4.88E-17	38200128
2	<i>APOB</i>	rs676210	21,231,524	G	A	0.106411	0.00315015	2.11E-165	38200128
2	<i>ASXL2</i>	rs34820121	26,098,259	C	A	0.0199492	0.00269358	1.86E-09	38200128
2	<i>KCNK3</i>	rs935168	26,914,787	A	G	0.0182814	0.00268182	3.18E-08	38200128
2	<i>DPYSL5</i>	rs61007968	27,177,428	C	G	0.011	0.003	2.63E-06	34059833
2	<i>GCKR</i>	rs6714780	27,189,063	A	G	0.0771431	0.00572893	8.63E-28	38200128
2	<i>GCKR</i>	rs115961201	27,704,896	G	A	0.0853067	0.00684541	4.89E-24	38200128
2	<i>GCKR</i>	rs1260326	27,730,940	T	C	-0.023	0.002	8.42E-38	34059833
2	<i>GCKR</i>	rs1260326	27,730,940	T	C	0.107618	0.00260329	1.11E-246	38200128
2	<i>GCKR</i>	rs62131877	27,740,328	C	T	0.076273	0.00578796	1.1E-26	38200128
2	<i>GCKR</i>	rs780094	27,741,237	C	T	0.035	0.004	3.00E-24	20081858
2	<i>STRN</i>	rs3770781	37,078,839	A	G	0.0178168	0.00257503	1.97E-08	38200128
2	<i>LHCGR</i>	rs17326656	48,962,291	T	G	0.0275696	0.00299784	8.5E-14	38200128
2	<i>CEP68</i>	rs2723065	65,279,414	A	G	0.0273314	0.00262887	3.28E-17	38200128
2	<i>CEP68</i>	rs2252867	65,296,280	T	C	0.007	0.002	1.46E-05	34059833
2	<i>BCL2L1</i>	rs6708784	111,927,379	A	G	0.0182037	0.00255468	7.39E-09	38200128
2	<i>LINC01101</i>	rs954244	121,309,231	G	C	0.0228021	0.00292135	2.4E-10	38200128
2	<i>LINC01101</i>	rs11688682	121,347,612	G	C	0.0216681	0.00296417	3E-09	38200128
2	<i>TMEM163</i>	rs60802178	135,268,836	G	A	0.0255716	0.00343656	1.56E-09	38200128
2	<i>YSK4</i>	rs1530559	135,755,629	A	G	0.0145	0.003	3.40E-08	22885924
2	<i>LINC01911</i>	rs77164426	147,514,456	G	A	29.65	[NR]	5E-09	30327367
2	<i>ACVR1C</i>	rs12694933	158,525,226	T	C	0.027102	0.0039218	2.05E-08	38200128
2	<i>GRB14</i>	rs62173875	165,462,543	C	T	0.0197975	0.00258416	5.09E-10	38200128
2	<i>COBLL1</i>	rs6713419	165,508,300	T	C	0.019	0.002	1.44E-24	34059833
2	<i>GRB14</i>	rs10195252	165,513,091	T	C	0.0174	0.002	1.30E-16	22885924
2	<i>COBLL1</i>	rs75265117	165,518,799	C	G	0.028	0.003	1.54E-24	34059833
2	<i>COBLL1</i>	rs1128249	165,528,624	T	G	-0.02	0.002	7.71E-28	34059833
2	<i>COBLL1</i>	rs13389219	165,528,876	T	C	-0.02	0.002	5.84E-28	34059833
2	<i>GRB14</i>	rs13389219	165,528,876	C	T	0.0544298	0.00260495	1.78E-64	38200128
2	<i>GRB14,COBLL1</i>	rs7607980	165,551,201	T	C	0.039	0.004	4.30E-20	22581228
2	<i>COBLL1</i>	rs12692738	165,558,252	T	C	0.05806	[0.044-0.072] unit decrease	2E-15	37291194
2	<i>COBLL1</i>	rs355849	165,625,830	T	C	0.0510286	0.00405324	1.69E-24	38200128
2	<i>ERICH2</i>	rs4668313	171,631,225	A	G	0.0189784	0.0026459	5.88E-09	38200128
2	<i>CYP27A1</i>	rs148358468	219,590,348	A	G	0.0568267	0.00586984	3.98E-15	38200128
2	<i>CYP27A1</i>	rs691066	219,678,421	C	T	0.0223346	0.00272436	2.89E-11	38200128
2	<i>GLB1L</i>	rs61733623	220,101,974	G	A	rs61781316	0.00965685	5.2E-11	38200128
2	<i>NYAP2</i>	rs13422522	227,011,320	C	G	-0.06	0.01	8.90E-11	27416945
2	<i>IRS1</i>	rs2943634	227,068,080	C	A	0.025	0.004	2.50E-14	22581228
2	<i>IRS1</i>	rs2943645	227,099,180	T	C	0.0193	0.002	2.30E-19	22885924
2	<i>LOC646736</i>	rs2943645	227,099,180	T	C	0.0565537	0.0026615	1.29E-66	38200128
2	<i>LOC646736</i>	rs2943646	227,099,534	A	G	-0.025	0.002	8.47E-39	34059833
2	<i>LOC646736</i>	rs2972145	227,101,309	T	C	-0.025	0.002	6.08E-38	34059833
2	<i>NYAP2 - MIR5702</i>	rs2972144	227,101,411	A	C	0.06398	[0.051-0.077] unit increase	2E-22	37291194
2	<i>IRS1</i>	rs2972143	227,116,365	G	A	0.0142	0.003	3.20E-08	22885924
2	<i>IRS1</i>	rs17508368	227,651,446	T	C	0.019	0.004	2.12E-06	34059833
2	<i>PID1</i>	rs7596814	230,128,204	G	T	0.019079	0.00280031	3.23E-08	38200128
2	<i>HDLBP</i>	rs59104589	242,237,902	C	T	0.0203313	0.00265168	4.92E-10	38200128
3	<i>ITPR1</i>	rs9812100	4,763,301	G	A	0.0173925	0.00255379	3.27E-08	38200128
3	<i>SYN2</i>	rs308971	12,116,620	A	G	-0.022	0.003	3.91E-13	34059833

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
3	PPARG	rs11712037	12,344,730	C	G	0.028	0.003	2.10E-21	34059833
3	PPARG	rs12485478	12,351,223	G	A	0.0628043	0.00794243	1.4E-10	38200128
3	PPARG	rs35000407	12,351,521	T	G	0.026	0.003	1.50E-21	34059833
3	PPARG	rs2067819	12,359,049	G	A	0.0347225	0.00310197	1.06E-19	38200128
3	PPARG	rs11128603	12,385,828	A	G	0.06367	[0.046-0.081] unit decrease	5E-13	37291194
3	PPARG	rs17036328	12,390,484	T	C	0.0212	0.003	3.60E-12	22885924
3	PPARG	rs3103310	12,473,045	G	A	0.0262696	0.00302865	1.95E-12	38200128
3	BTDR	rs13097947	15,846,011	T	C	0.021207	0.00271413	2.3E-10	38200128
3	TRAP	rs9819511	49,884,261	T	C	0.014	0.002	2.26E-08	34059833
3	MST1R	rs11130227	49,993,319	G	A	0.0188406	0.0026065	4.48E-09	38200128
3	STAB1	rs57172722	52,391,182	G	C	0.0375819	0.00558247	4.69E-08	38200128
3	NISCH	rs6800707	52,516,293	G	C	0.0434857	0.00325265	2.03E-27	38200128
3	ITIH3	rs17331151	52,844,534	T	C	-0.016	0.003	1.52E-08	34059833
3	EIF4E3,FOXP1	rs830620	71,679,148	C	T	0.01875897	0.00258091	3.69E-09	38200128
3	ADCY5	rs11708067	123,065,778	A	G	-0.014	0.002	1.30E-09	34059833
3	TPRA1	rs79983121	127,306,462	T	C	0.0234998	0.00318749	2.2E-09	38200128
3	PCCB	rs684773	135,956,305	C	A	0.0433159	0.0030067	1.44E-31	38200128
3	PAQR9	rs12638256	142,655,290	A	G	0.0174842	0.00256115	3.04E-08	38200128
3	LINC01214	rs62271373	150,066,540	A	T	0.026	0.005	1.60E-08	34059833
3	LINC01214,TSC22D2	rs62271373	150,066,540	A	T	0.0669914	0.00546369	2.55E-23	38200128
3	LINC00880	rs9817452	156,795,414	G	T	0.0269754	0.00262829	8.22E-17	38200128
3	SLC2A2	rs5402	170,727,739	A	T	0.0270032	0.00392356	2.34E-08	38200128
3	LINC02068	rs79287178	172,294,500	A	G	0.0647525	0.00769167	8.43E-12	38200128
3	BCL6	rs7631606	187,628,006	T	G	0.0210464	0.00290824	4.3E-09	38200128
3	UBXN7-AS1	rs13094241	196,190,893	T	G	0.0205999	0.00286045	5.11E-09	38200128
4	DGKQ, IDUA	rs13101828	965,720	A	G	0.0181539	0.00256066	8.78E-09	38200128
4	HGFAC	rs13108218	3,443,931	A	G	0.0278127	0.00263906	1.21E-17	38200128
4	DOK7	rs731450	3,490,328	T	C	0.0245397	0.0026997	1.63E-13	38200128
4	CYTL1	rs4450871	4,990,298	A	G	0.019929	0.00255946	2.65E-10	38200128
4	LCORL	rs71603401	18,034,463	G	A	0.0376217	0.00374037	3.31E-16	38200128
4	RBPJ	rs73243877	26,047,616	G	A	0.0442274	0.00340472	5.62E-26	38200128
4	UBE2K	rs1055582	39,700,173	C	T	0.0196344	0.00254957	4.13E-10	38200128
4	KIT	rs2159935	55,521,017	G	A	0.0226027	0.0025458	5.84E-13	38200128
4	SHROOM3	rs7675258	77,413,179	A	G	0.0189195	0.00255136	1.78E-09	38200128
4	AFF1	rs3775228	87,985,166	T	C	0.0456982	0.00260878	7.52E-46	38200128
4	AFF1	rs447990	88,033,352	G	T	0.02310764	0.00261764	7.89E-13	38200128
4	FAM13A	rs10011342	89,672,077	A	G	0.0247207	0.00331979	1.52E-09	38200128
4	FAM13A	rs2276936	89,726,283	A	C	-0.012	0.002	4.25E-11	34059833
4	FAM13A	rs3775380	89,739,808	A	G	-0.012	0.002	1.48E-11	34059833
4	FAM13A	rs3822072	89,741,269	A	G	0.0116	0.002	1.80E-08	22885924
4	FAM13A	rs4425336	89,753,225	A	G	0.0208542	0.00309845	4.73E-08	38200128
4	ADH4	rs6848050	100,053,733	C	T	0.0209222	0.00277039	8.9E-10	38200128
4	SLC39A8	rs13107325	103,188,709	T	C	0.0702962	0.00484448	5.3E-32	38200128
4	TET2	rs974801	106,071,064	G	A	0.0139	0.002	3.30E-11	22885924
4	TET2	rs9884482	106,081,636	T	C	-0.013	0.002	2.88E-11	34059833
4	TET2	rs9884482	106,081,636	C	T	0.0165	0.002	1.40E-11	22885924
4	TET2; TET2-AS1	rs10010325	106,106,353	A	C	0.012	0.002	4.05E-11	34059833
4	MCUB	rs78025076	110,569,620	T	C	0.0764923	0.00901604	5.81E-12	38200128
4	HHIP-AS1	rs7654571	145,321,006	A	G	0.012	0.002	7.77E-08	34059833
4	HHIP	rs11727676	145,659,064	T	C	-0.02	0.004	2.90E-08	34059833
4	PDGFC	rs6855363	157,670,537	T	C	0.013	0.002	4.04E-08	34059833
4	PDGFC	rs1816164	157,696,636	C	T	0.0214634	0.003048	1.1E-08	38200128
4	PDGFC	rs4691380	157,720,124	C	T	0.021	0.004	5.30E-09	22581228
4	PDGFC	rs6822892	157,734,675	A	G	0.0138	0.002	2.60E-10	22885924
5	ARL15	rs4865796	53,272,664	A	G	0.017	0.002	7.33E-17	34059833
5	ARL15	rs4865796	53,272,664	A	G	0.0154	0.002	2.20E-12	22885924
5	ARL15	rs80138475	53,304,991	T	C	0.0303003	0.0040373	1.13E-09	38200128
5	LOC101928448	rs459193	55,806,751	A	G	-0.018	0.002	1.12E-18	34059833
5	ANKRD55-MAP3K1	rs459193	55,806,751	G	A	0.0147	0.002	1.20E-10	22885924
5	RPL26P19 - C5orf67	rs459193	55,806,751	A	G	0.041777	[0.028-0.055] unit increase	7E-10	37291194
5	C5orf67	rs392794	55,808,342	T	C	0.0475555	0.00292417	9.23E-40	38200128
5	LOC101928448	rs3936511	55,860,781	A	G	-0.019	0.003	2.81E-14	34059833
5	MIER3	rs9687846	55,861,894	A	G	0.0635395	0.00317363	2.4E-59	38200128
5	MAP3K1	rs252913	56,195,846	A	G	0.0179978	0.00267635	4.85E-08	38200128
5	PIK3R1	rs4976033	67,714,246	G	A	0.0231424	0.00262971	9.28E-13	38200128
5	JMY	rs10052346	78,472,599	G	T	0.0201385	0.00262536	4.84E-10	38200128
5	VCAN	rs115912456	82,815,158	A	G	0.0469414	0.00639659	2.61E-09	38200128
5	TNFAIP8	rs1045241	118,729,286	C	T	0.0300479	0.00287818	2.43E-17	38200128
5	FNIP1	rs664732	131,281,458	C	G	0.0479876	0.00651591	2.29E-09	38200128
5	HSPA4	rs72801474	132,444,128	G	A	0.0353571	0.00440658	7.48E-11	38200128
5	TIMD4	rs6882076	156,390,297	C	T	0.0271542	0.00264003	7.06E-17	38200128
5	LOC101927697	rs1023667	157,968,901	A	G	-0.01	0.002	5.70E-07	34059833
5	EBF1	rs1030472	157,994,544	G	A	0.0335843	0.00311769	2.31E-18	38200128
6	E2F3	rs4134963	20,486,798	C	T	0.0247133	0.00326148	7.82E-10	38200128
6	CDKAL1	rs7754840	20,661,250	G	A			3E-12	37116407
6	CDKAL1	rs7756992	20,679,709	G	A	-0.11	0.015	3.07E-13	24699409
6	HLA-C	rs2074493	31,239,776	C	A	0.0496279	0.00304462	6.18E-40	38200128
6	HLA-B	rs2394987	31,327,217	A	C	0.0476286	0.00404853	1.35E-21	38200128
6	MICB	rs3093999	31,484,550	A	T	-0.014	0.003	1.31E-07	34059833
6	HLA-DQA1	rs11751024	32,586,236	A	C	0.0365969	0.00260322	3.84E-30	38200128
6	HLA-DQB1	rs114786106	32,596,878	G	A	0.0989186	0.00655355	1.73E-34	38200128
6	HMGAI	rs114760566	34,192,036	A	C	0.0647052	0.00615228	1.41E-17	38200128
6	C6orf1	rs116141873	34,222,201	T	G	0.043	0.006	1.42E-11	34059833
6	RPS10-NUDT3; NUDT3	rs2780215	34,236,973	A	G	0.039	0.006	1.06E-09	34059833
6	RPS10-NUDT3; NUDT3	rs1187129	34,239,989	A	G	-0.029	0.007	1.41E-05	34059833
6	UHRF1BP1	rs6912327	34,764,922	T	C	0.0165	0.003	2.30E-08	22885924
6	UHRF1BP1	rs4646949	34,845,449	T	G	0.02	0.004	3.70E-08	22581228

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
6	FOXP4	rs777943523	41,550,466	C	CA	-0.008	0.003	1.53E-03	34059833
6	VEGFA	rs9472125	43,756,169	C	T	0.06979	0.00421857	4.38E-41	38200128
6	VEGFA	rs998584	43,757,896	A	C	0.012	0.002	2.31E-10	34059833
6	VEGFA	rs998584	43,757,896	A	C	0.0617628	0.00255302	8.55E-86	38200128
6	VEGFA	rs2396084	43,804,825	G	A	0.0225518	0.0027629	3.52E-11	38200128
6	LINC01512	rs9472135	43,809,802	T	C	0.011	0.002	4.21E-08	34059833
6	GSTA2	rs2749026	52,630,635	A	G	0.0218752	0.00266388	2.68E-11	38200128
6	BEND3	rs62427983	107,441,254	T	C	0.0194501	0.00273108	7.52E-09	38200128
6	ARMC2	rs11752394	109,189,664	G	C	0.0230349	0.00300159	4.75E-10	38200128
6	RSPO3	rs2800709	127,439,297	G	T	0.0244106	0.00254967	7.93E-15	38200128
6	RSPO3	rs1474696	127,449,246	A	G	-0.015	0.002	3.02E-16	34059833
6	RSPO3	rs2745353	127,452,935	T	C	0.015	0.002	4.63E-16	34059833
6	RSPO3	rs2745353	127,452,935	T	C	0.0143	0.002	5.50E-09	22885924
6	RSPO3	rs72959041	127,454,893	A	G	0.0652129	0.00596303	7.06E-19	38200128
6	L3MBTL3	rs9388767	130,357,553	A	G	0.0227283	0.00277178	2.86E-11	38200128
6	LOC645434	rs632057	139,834,012	T	G	0.008	0.002	1.37E-05	34059833
6	LINC01625	rs632057	139,834,012	T	G	0.0429738	0.00263213	4.64E-40	38200128
6	RGS17	rs607335	153,465,230	C	A	0.0194408	0.00258124	9.88E-10	38200128
6	SLC22A1	rs12208357	160,543,148	T	C	0.0417135	0.00501169	1.44E-11	38200128
6	LPA	rs10455872	161,010,118	A	G	0.0454608	0.00471768	5.32E-15	38200128
6	LPA	rs140570886	161,013,013	T	C	0.127163	0.010471	6.57E-23	38200128
6	LPA	rs77348928	161,013,030	G	A	0.0360485	0.00360352	4.77E-16	38200128
6	LPA	rs11751347	161,092,438	T	C	0.0674344	0.00423546	3.51E-38	38200128
6	QKI	rs73013411	164,126,233	A	C	-0.018	0.003	2.08E-08	34059833
6	QKI	rs4709746	164,133,001	T	C	-0.018	0.003	2.97E-08	34059833
6	LOC102724152	rs4709746	164,133,001	C	T	0.0307179	0.00376086	3.41E-11	38200128
7	GPR146	rs71538127	1,010,801	G	C	0.0288493	0.00388757	1.73E-09	38200128
7	ACTB	rs852388	5,574,239	C	G	0.024574	0.00314792	2.38E-10	38200128
7	AHR	rs4410790	17,284,577	C	T	0.0244792	0.00264249	5.61E-14	38200128
7	SNX13	rs10242866	17,920,613	T	C	0.0296287	0.00260253	2.52E-20	38200128
7	MIR148A	rs7786102	25,965,759	G	A	0.0288168	0.00282391	1.23E-16	38200128
7	MIR148A	rs4722551	25,991,826	T	C	0.0409096	0.0034795	1.43E-21	38200128
7	SNX10	rs1534696	26,397,239	C	A	0.0256054	0.00255258	3.97E-16	38200128
7	JAZF1-AS1	rs498475	28,256,240	G	A	0.0180623	0.00264862	3.14E-08	38200128
7	GCK	rs2070971	44,197,583	T	G	0.0310802	0.00371219	1.09E-11	38200128
7	GCK	rs3757840	44,231,216	T	G	-0.09	0.015	1.34E-09	24699409
7	GRB10	rs2282930	50,754,679	A	G	-0.011	0.003	1.67E-05	34059833
7	GRB10	rs933360	50,758,245	A	G	-0.051	0.0086	3.14E-09	24699409
7	GRB10	rs2108349	50,786,663	A	G	-0.012	0.002	1.13E-08	34059833
7	MLXIPL	rs141136126	72,852,007	G	A	0.0576356	0.00781477	2.17E-09	38200128
7	MLXIPL	rs799157	73,020,301	T	C	0.106161	0.00624446	2.74E-43	38200128
7	MLXIPL	rs17145750	73,026,378	C	T	0.141683	0.00346578	2.76E-241	38200128
7	GTF2IRD1	rs111914893	74,002,323	T	C	0.0408618	0.00585769	1.51E-08	38200128
7	HIP1	rs1167800	75,176,196	A	G	0.0156	0.003	2.60E-09	22885924
7	POR	rs2302429	75,614,777	A	G	0.0232638	0.00328621	9.23E-09	38200128
7	SSC4D	rs6465120	76,036,364	A	G	0.0184386	0.00254481	4.12E-09	38200128
7	PHTF2	rs848494	77,537,964	A	G	0.009	0.002	9.25E-06	34059833
7	KLF14	rs13234269	130,429,186	A	T	-0.011	0.002	1.27E-08	34059833
7	KLF14	rs10260148	130,430,969	T	C	0.0431246	0.00284574	9.46E-35	38200128
7	KLF14	rs972283	130,466,854	A	G	-0.011	0.002	1.09E-08	34059833
7	GIMAP7	rs11766379	150,208,971	C	T	0.0265583	0.00302912	1.12E-12	38200128
7	AOC1	rs62492368	150,537,635	A	G	0.0222278	0.00278135	8.89E-11	38200128
7	KCNH2	rs1805123	150,645,534	T	G	0.0223058	0.00295852	9.49E-10	38200128
8	PPP1R3B	rs330945	9,021,933	T	C	0.014	0.002	1.82E-11	34059833
8	LOC157273	rs7012637	9,173,209	A	G	-0.022	0.002	1.48E-29	34059833
8	LOC157273	rs7012814	9,173,358	A	G	-0.022	0.002	8.34E-30	34059833
8	LOC157273	rs7012814	9,173,358	G	A	0.038098	0.00256658	2.07E-33	38200128
8	PPP1R3B, TNKS	rs7012814	9,173,358	A	G	0.0481	[0.035-0.061] unit increase	1E-13	37291194
8	PPP1R3B	rs983309	9,177,732	T	G	0.0287	0.004	3.80E-14	22885924
8	LOC157273	rs4841132	9,183,596	A	G	0.026	0.003	3.83E-20	34059833
8	PPP1R3B	rs4841132	9,183,596	A	G	0.031	0.006	1.70E-10	22581228
8	PPP1R3B	rs2126259	9,185,146	T	C	0.0238	0.003	3.30E-13	22885924
8	PPP1R3B-DT	rs2126259	9,185,146	T	A	0.07023	[0.052-0.089] unit decrease	2E-13	37291194
8	LOC157273	rs1461729	9,187,242	A	G	0.0353563	0.00421777	1.03E-11	38200128
8	SOX7	rs7821812	10,644,101	C	G	0.049536	0.00314687	2.32E-37	38200128
8	BLK	rs12541800	11,423,072	A	G	0.011	0.002	6.17E-07	34059833
8	GATA4	rs7386288	11,536,332	T	C	0.0315801	0.00293417	2.47E-18	38200128
8	NAT2	rs4646250	18,260,598	G	A	0.0303732	0.00282028	2.36E-18	38200128
8	LOC100128993	rs12056334	19,080,151	A	C	0.005	0.003	1.16E-01	34059833
8	LPL	rs254	19,811,897	C	G	0.172996	0.00361375	4.60E-330	38200128
8	LPL	rs268	19,813,529	G	A	0.291877	0.00951768	1.11E-136	38200128
8	LPL	rs276	19,814,289	C	T	0.287757	0.00957285	2.12E-131	38200128
8	LPL,SLC18A1	rs73667496	19,937,852	C	T	0.0986799	0.0057617	6.59E-44	38200128
8	LPL,SLC18A1	rs7015766	19,939,049	C	T	0.263208	0.00496166	8.39E-405	38200128
8	LPL,SLC18A1	rs55682243	19,977,311	C	G	0.133134	0.00828409	7.2E-39	38200128
8	NKX2-6	rs13258890	23,615,445	T	C	0.013	0.003	2.77E-08	34059833
8	CDCA2	rs73221948	25,464,670	T	G	0.0210291	0.00292112	5.17E-09	38200128
8	ANK1	rs12549902	41,509,259	A	G	-0.06	0.01	1.01E-08	24699409
8	CYP7A1	rs2081687	59,388,565	T	C	0.023803	0.00269371	7.49E-13	38200128
8	LINC01289	rs1149470	64,608,119	T	A	0.0220737	0.0029985	2.32E-09	38200128
8	EYA1	rs13269725	72,459,889	G	A	0.0418588	0.00473827	7.59E-13	38200128
8	KCNB2	rs35957544	73,440,371	G	T	0.0174022	0.00257888	4.36E-08	38200128
8	TRPS1	rs2737226	116,639,474	T	C	0.0227621	0.00261188	1.53E-12	38200128
8	TRIB1	rs72647336	126,445,055	A	G	0.1094	0.00593777	1.56E-50	38200128
8	TRIB1	rs6999569	126,475,770	A	G	0.107897	0.0025522	6.83E-258	38200128
8	TRIB1	rs72655677	126,484,897	G	A	0.0995734	0.00609368	4E-40	38200128
8	TRIB1	rs78309295	126,528,722	G	A	0.0654236	0.00863073	7.71E-10	38200128

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
8	TRIB1	rs139827355	126,632,998	G	A	0.0493393	0.00674368	2.91E-09	38200128
8	TRIB1	rs7826687	126,645,689	G	C	0.0427737	0.00281803	7.4E-35	38200128
8	GPIHBP1	rs7832515	144,306,379	A	G	0.0313039	0.00328913	1.14E-14	38200128
9	LINC01230	rs1509195	1,033,958	C	T	0.022176	0.0027702	8.27E-11	38200128
9	GLIS3	rs4339696	4,295,880	T	G	0.009	0.002	1.52E-07	34059833
9	CDKN2B-AS1 - DMRTA1	rs10811661	22,134,094	T	A			8E-10	37116407
9	TLE4	rs11138325	82,294,364	T	C	-0.012	0.002	5.39E-08	34059833
9	RMU1	rs696825	86,583,076	C	T	0.0230535	0.00292935	1.71E-10	38200128
9	GADD45G	rs10797119	92,202,495	C	T	0.0231408	0.00256724	2.59E-13	38200128
9	ECM2	rs12686780	95,382,297	T	C	0.0260032	0.00335317	3.12E-10	38200128
9	NAMA	rs62565259	102,162,570	C	T	0.0247574	0.00340829	3.77E-09	38200128
9	ABCA1	rs4149307	107,589,744	C	T	0.0306419	0.00351979	1.62E-12	38200128
9	ABCA1	rs2275543	107,651,174	C	T	0.0374047	0.00421788	6.21E-13	38200128
9	AKNA	rs1044531	117,098,650	C	T	0.0316438	0.00453361	1.48E-08	38200128
9	ABO	rs75179845	136,132,954	T	C	-0.022	0.004	6.05E-11	34059833
9	ABO	rs8176693	136,137,657	T	C	0.02	0.003	1.10E-10	34059833
9	ABO	rs2519093	136,141,870	C	T	0.0297786	0.00328922	2.04E-13	38200128
10	NRP1	rs2776937	33,606,189	A	G	0.0206949	0.00298887	1.93E-08	38200128
10	RN7SKP196 - LINC00844	rs60453193	60,632,252	A	G	0.430581	[0.28-0.58] unit increase	0.00000004	37291194
10	SLC16A9	rs1171615	61,469,090	T	C	0.0236422	0.00302238	2.19E-10	38200128
10	JMJD1C	rs10761762	65,184,717	T	C	0.008	0.002	1.98E-05	34059833
10	JMJD1C	rs7924036	65,191,645	G	T	0.0374777	0.00254667	7.21E-33	38200128
10	PLA2G12B	rs11000468	74,711,376	C	T	0.0223074	0.00296811	1.07E-09	38200128
10	PLA2G12B	rs3829126	74,714,177	T	G	0.0307816	0.00438716	1.25E-08	38200128
10	PTEN	rs118164457	89,680,631	T	C	-0.035	0.006	3.86E-10	34059833
10	PTEN	rs12769346	89,764,490	T	G	-0.015	0.003	1.20E-08	34059833
10	HHEX,IDE	rs7923866	94,482,076	C	T	-0.12	0.015	4.16E-16	24699409
10	EXOC6	rs9919491	94,754,759	A	T	0.0212953	0.00290286	2.64E-09	38200128
10	CYP26A1	rs2068888	94,839,642	G	A	0.041442	0.00255583	1.55E-39	38200128
10	CYP26A1	rs7916761	94,941,927	T	C	0.0182124	0.00258622	1.1E-08	38200128
10	FFAR4	rs10786114	95,309,022	C	T	0.0419758	0.00384745	8.54E-19	38200128
10	CRTAC1	rs565108	99,772,190	C	T	0.0238302	0.00256423	4.67E-14	38200128
10	NT5C2	rs11191559	104,867,686	T	C	-0.014	0.003	1.27E-05	34059833
10	GPAM	rs2792751	113,940,329	C	T	0.0394203	0.00285272	3.53E-29	38200128
10	GPAM	rs4306236	113,980,294	T	G	0.0379195	0.00364056	2.87E-17	38200128
10	TCF7L2	rs7903146	114,758,349	T	C	-0.012	0.002	1.24E-09	34059833
10	TCF7L2	rs7903146	114,758,349	C	T	0.0181	0.003	6.10E-11	22885924
10	ADRB1	rs2773469	115,798,895	A	G	0.0293092	0.00289113	1.94E-16	38200128
10	MIR5694	rs7071062	122,930,612	T	C	0.019	0.007	1.19E-02	34059833
10	FGFR2	rs878409	122,999,550	G	A	0.018614	0.00256409	3.85E-09	38200128
11	ANO9, B4GALNT4	rs1117291242	380,315	T	C	0.0465064	0.00677175	2.51E-08	38200128
11	PNPLA2	rs140201358	823,586	G	C	0.0769547	0.010917	1.07E-08	38200128
11	KCNQ1	rs2237895	2,857,194	A	C			3E-11	37116407
11	AMPD3	rs12793175	10,384,303	A	G	0.0234076	0.00344032	3.37E-08	38200128
11	ARNTL	rs6486122	13,361,524	T	C	0.0243473	0.00274947	6.7E-13	38200128
11	PDE3B	rs79634051	14,561,945	G	C	0.0551675	0.00767501	5.46E-09	38200128
11	ANO3	rs1461396	26,281,664	G	C	0.0353251	0.00524722	4.69E-08	38200128
11	BDNF	rs61888800	27,722,278	T	G	0.0289022	0.00290723	7.22E-16	38200128
11	SLC35C1	rs3808976	45,827,350	G	A	0.0230574	0.00314024	2.55E-09	38200128
11	AMBRA1	rs147244995	46,417,679	C	T	0.0951763	0.0109368	1.65E-12	38200128
11	AMBRA1	rs55971594	46,474,963	A	G	0.0545966	0.00578232	1.84E-14	38200128
11	ACP2	rs326222	47,259,668	C	T	0.0526524	0.00276862	1.01E-53	38200128
11	P2RX3, TNKS1BP1	rs10792091	57,119,156	C	T	0.0261933	0.00367179	7.1E-09	38200128
11	FADS1	rs102275	61,557,803	C	T	0.0765793	0.00266614	3.8E-120	38200128
11	EML3	rs11231156	62,366,454	A	G	0.0247274	0.00263727	2.78E-14	38200128
11	MACROD1	rs2845885	63,869,062	T	C	-0.02	0.004	1.18E-08	34059833
11	VEGFB	rs56271783	64,004,723	C	G	0.089768	0.00618519	5.16E-32	38200128
11	KAT5	rs10750766	65,473,798	A	C	0.0290322	0.00280867	4.97E-17	38200128
11	RIN1	rs144718240	66,094,785	T	C	0.0452433	0.00616048	2.53E-09	38200128
11	CPT1A	rs11605837	68,597,886	T	G	0.0233185	0.00275109	6.08E-12	38200128
11	PDE2A	rs3781926	72,350,595	T	C	0.009	0.002	3.26E-05	34059833
11	SNRPGP16 - MTNR1B	rs1387153	92,673,828	T	C	0.045202	[0.032-0.058] unit increase	1E-11	37291194
11	MTNR1B	rs10830963	92,708,710	G	C	-0.17	0.016	6.71E-28	24699409
11	ZC3H12C	rs6589112	109,971,929	C	T	0.0195487	0.00279146	1.33E-08	38200128
11	PPP2R1B	rs117847213	111,421,906	A	G	0.0552327	0.00650405	5.55E-12	38200128
11	PPP2R1B	rs615642	111,649,421	G	A	0.0196409	0.00263911	1.55E-09	38200128
11	LINC02702	rs11215942	116,325,337	A	G	0.0669308	0.00609362	4.99E-19	38200128
11	LINC02702	rs79859462	116,379,996	A	G	0.0684905	0.00880893	2.81E-10	38200128
11	LINC02702	rs117794084	116,433,496	T	G	0.16877	0.0100943	6.33E-42	38200128
11	LINC02702	rs519000	116,511,522	T	C	0.0489442	0.00342156	3.79E-31	38200128
11	LINC02702	rs480823	116,525,730	C	T	0.205468	0.0047722	2.09E-267	38200128
11	LINC02702	rs11824135	116,559,553	T	G	0.255061	0.00512564	1.83E-356	38200128
11	APOA5	rs6589567	116,670,676	A	C	0.195814	0.00411457	3.19E-326	38200128
11	APOA4	rs12721043	116,692,293	C	A	0.247856	0.0121012	5.02E-62	38200128
11	SIK3	rs61907602	116,810,655	G	C	0.1207	0.00713446	6.93E-43	38200128
11	SIK3	rs11216236	116,889,658	T	C	0.0880026	0.00619819	1.04E-30	38200128
11	PCSK7	rs142334475	117,088,573	G	A	0.116315	0.0118873	2.03E-15	38200128
11	CEP164	rs573455	117,267,884	G	A	0.022103	0.00255033	2.03E-12	38200128
11	DSCAML1	rs117604511	117,382,799	C	A	0.0768542	0.00901377	4.57E-12	38200128
11	HYOU1	rs1003081	118,913,993	T	C	0.0218031	0.00256489	5.29E-12	38200128
11	MIR100HG	rs1622638	121,800,971	A	G	0.0205276	0.00260643	1.65E-10	38200128
12	CCND2	rs117233107	4,328,521	G	A	0.0878987	0.0110248	9.84E-11	38200128
12	CHD4,LPAR5	rs10774439	6,731,818	G	A	0.0276134	0.00331948	1.48E-11	38200128
12	PDE3A	rs11045171	20,470,199	A	G	0.04133	0.00321559	1.82E-25	38200128
12	PDE3A	rs4762753	20,579,969	G	T	0.024887	0.00318382	2.26E-10	38200128
12	PDE3A	rs12369443	20,582,651	A	G	0.01	0.002	6.66E-06	34059833
12	PDE3A	rs11045247	20,592,624	A	G	0.0346795	0.00488395	8.33E-09	38200128

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
12	<i>SLCO1B1</i>	rs67981690	21,343,886	G	A	0.0303598	0.00381306	1.04E-10	38200128
12	<i>GYS2</i>	rs2054435	21,696,684	A	G	-0.015	0.003	9.50E-09	34059833
12	<i>GYS2</i>	rs6487237	21,699,928	A	C	0.015	0.003	4.68E-09	34059833
12	<i>ITPR2</i>	rs10842703	26,456,188	T	A	0.022332	0.00296351	9.68E-10	38200128
12	<i>ITPR2</i>	rs10842708	26,474,867	A	G	-0.01	0.002	1.08E-05	34059833
12	<i>ALG10</i>	rs11052977	34,035,030	A	C	0.0184327	0.00260984	9.99E-09	38200128
12	<i>HDAC7</i>	rs111264094	48,202,696	C	G	0.057	0.009	1.64E-09	34059833
12	<i>INHBC,INHBE</i>	rs7966846	57,653,582	C	A	0.0220367	0.00282464	2.44E-10	38200128
12	<i>INHBC</i>	rs2122982	57,781,893	G	A	0.0413563	0.00298114	2.15E-29	38200128
12	<i>FAM19A2</i>	rs10506418	61,488,772	A	G	-0.62	0.13	1.90E-08	27416945
12	<i>HMG2</i>	rs1351394	66,351,826	T	C	-0.011	0.002	2.71E-09	34059833
12	<i>HMG2</i>	rs7968682	66,371,880	T	G	0.011	0.002	3.17E-09	34059833
12	<i>SYT1</i>	rs73343765	79,157,553	A	G	-0.19	0.053	2.14E-04	34059833
12	<i>IGF1</i>	rs1402013	102,740,822	A	G	-0.009	0.002	1.31E-06	34059833
12	<i>IGF1</i>	rs35767	102,875,569	G	A	0.013	0.006	2.20E-09	20081858
12	<i>IGF1</i>	rs860598	102,898,446	A	G	0.018	0.003	6.88E-12	34059833
12	<i>IGF1</i>	rs35747	102,912,558	A	G	0.017	0.003	2.68E-11	34059833
12	<i>RIC8B</i>	rs11113118	107,199,142	A	G	0.0230064	0.00294329	2.26E-10	38200128
12	<i>ACACB</i>	rs7298135	109,698,566	A	T	0.0251002	0.00327426	4.96E-10	38200128
12	<i>SH2B3</i>	rs653178	112,007,756	C	T	0.0224944	0.0025495	8.11E-13	38200128
12	<i>ZCCHC8</i>	rs116896792	122,948,907	C	T	0.0422638	0.0044306	9.92E-15	38200128
12	<i>HCA1</i>	rs526276	123,192,454	C	T	0.0391756	0.0033126	8.3E-22	38200128
12	<i>CCDC62</i>	rs138436155	123,285,110	C	G	0.0529468	0.00654242	5.14E-11	38200128
12	<i>SETD8</i>	rs10773000	123,736,084	G	T	0.0299301	0.00270811	3.02E-19	38200128
12	<i>DNAH10</i>	rs7133378	124,409,502	A	G	-0.013	0.002	6.00E-11	34059833
12	<i>CCDC92</i>	rs11057397	124,419,728	C	T	0.0449404	0.0026966	1.15E-41	38200128
12	<i>ZNF664-FAM101A; ZNF664</i>	rs7975482	124,481,690	A	G	0.012	0.002	1.97E-10	34059833
12	<i>ZNF664-RFLNA</i>	rs10773049	124,506,631	T	C	0.0456075	0.00260935	1.18E-45	38200128
12	<i>NCOR2</i>	rs837500	125,077,567	C	T	0.0189759	0.00266579	7.65E-09	38200128
12	<i>SCARB1</i>	rs921919	125,265,201	A	G	0.0317463	0.00276063	1.05E-20	38200128
12	<i>SCARB1</i>	rs112403212	125,303,254	T	C	0.0283816	0.00368809	4.26E-10	38200128
12	<i>SCARB1</i>	rs61941660	125,319,181	C	T	0.0414455	0.00454689	1.4E-13	38200128
12	<i>SCARB1</i>	rs7298751	125,380,232	A	G	0.0280479	0.00387146	4.14E-09	38200128
13	<i>FGF9</i>	rs12583553	22,332,822	A	T	0.55	0.12	3.60E-09	27416945
13	<i>DLEU2</i>	rs41284816	50,655,989	G	T	0.071498	0.00951314	1.07E-09	38200128
13	<i>DLEU1,DLEU2,KPNA3</i>	rs1327645	51,122,503	A	G	0.021732	0.00290817	1.33E-09	38200128
13	<i>LINC00348</i>	rs12863082	71,824,582	C	T	0.0207071	0.00300742	2.31E-08	38200128
13	<i>GPR180</i>	rs9561643	95,253,131	C	A	0.0191134	0.00274234	1.55E-08	38200128
13	<i>LINC00460 - RPL35P9</i>	rs17254590	107,037,344	G	C	2.52	[NR]	0.00000002	30327367
13	<i>COL4A2</i>	rs9521730	111,031,180	A	G	-0.009	0.002	1.15E-06	34059833
13	<i>GAS6</i>	rs7140110	114,544,024	C	T	0.031184	0.00278709	1.1E-19	38200128
13	<i>LINC00452</i>	rs75073260	114,599,617	T	G	0.0361357	0.00370071	2.31E-15	38200128
14	<i>NID2</i>	rs6572807	52,480,621	G	A	0.0193781	0.00287666	4.6E-08	38200128
14	<i>SGPP1</i>	rs7157785	64,235,556	T	G	0.0265152	0.00347129	5.72E-10	38200128
14	<i>FOXP3</i>	rs8021491	90,034,799	T	C	0.0183758	0.00268448	2.79E-08	38200128
14	<i>SLC25A29,YY1</i>	rs61993685	100,765,823	T	C	0.0378248	0.00477626	1.31E-10	38200128
14	<i>AKT1</i>	rs2494748	105,258,892	T	C	0.0194199	0.00262062	1.82E-09	38200128
15	<i>C15orf54,ENSG00000259450</i>	rs275179	39,447,529	A	G	0.0246741	0.00359241	2.5E-08	38200128
15	<i>GCHFR</i>	rs72735627	41,057,507	C	T	0.0232954	0.00437318	1.85E-09	38200128
15	<i>SPTBN5</i>	rs2925339	42,091,212	G	A	0.0245757	0.00271378	2.01E-13	38200128
15	<i>MAP1A</i>	rs139974673	44,027,885	C	T	0.196545	0.00800442	2.51E-88	38200128
15	<i>TCF12</i>	rs935328	57,538,801	T	A	0.0212468	0.00291282	3.24E-09	38200128
15	<i>LIPC</i>	rs1601935	58,671,765	T	G	0.0248295	0.00269677	7.96E-14	38200128
15	<i>LINC02349</i>	rs12440800	61,960,302	T	A	0.0210613	0.00293435	5.74E-09	38200128
15	<i>C2CD4A</i>	rs4502156	62,383,155	T	C	-0.092	0.014	1.14E-10	24699409
15	<i>NPM1P47 - C2CD4B</i>	rs7167878	62,396,189	A	C	0.04253	[0.03-0.055] unit decrease	7E-12	37291194
15	<i>LACTB</i>	rs2937859	63,366,282	G	A	0.0339049	0.00320269	8.69E-18	38200128
15	<i>USP3</i>	rs17184382	63,792,486	A	C	0.0251802	0.00257286	2E-15	38200128
15	<i>HERC1</i>	rs117044596	64,002,266	G	A	0.0489714	0.00677225	4.42E-09	38200128
15	<i>LINC01169</i>	rs4776793	66,872,114	T	C	0.0219862	0.00266086	2.02E-11	38200128
16	<i>LMF1</i>	rs12924608	950,007	T	C	0.0223239	0.00262308	5E-12	38200128
16	<i>MGRN1</i>	rs12921195	4,677,604	A	C	0.0316385	0.00380557	1.52E-11	38200128
16	<i>NTAN1</i>	rs4074872	15,117,299	A	G	0.0388621	0.00323048	1.8E-22	38200128
16	<i>PDXDC1</i>	rs12928099	15,150,505	C	A	0.0389922	0.00279415	1E-29	38200128
16	<i>TAOK2</i>	rs3814883	29,994,922	T	C	0.0249413	0.00255677	2.46E-15	38200128
16	<i>ZNF646</i>	rs34898535	31,025,641	C	T	0.0193591	0.00262845	2.28E-09	38200128
16	<i>RBL2</i>	rs2024449	53,494,617	T	C	0.01	0.002	4.81E-07	34059833
16	<i>FTO</i>	rs1421085	53,800,954	C	T	0.02	0.003	1.90E-15	22885924
16	<i>NUP93</i>	rs11643205	56,787,882	T	C	0.0416853	0.00594432	1.27E-08	38200128
16	<i>HERPUD1</i>	rs72786786	56,985,514	G	A	0.151343	0.00279684	4.12E-421	38200128
16	<i>CETP</i>	rs7499892	57,006,590	T	C	0.17128	0.00332693	2.15E-381	38200128
16	<i>CETP</i>	rs11644475	57,007,652	A	G	0.0633244	0.00773506	3.08E-11	38200128
16	<i>NLR5</i>	rs11648592	57,083,232	A	G	0.0739214	0.00935557	1.44E-10	38200128
16	<i>NRN1L</i>	rs55781197	67,940,350	A	G	0.048112	0.00398739	1.23E-22	38200128
16	<i>NFAT5</i>	rs862320	69,651,866	C	T	0.0215868	0.00259383	1.45E-11	38200128
16	<i>HP</i>	rs3794695	72,097,827	T	C	0.0323246	0.00324823	6.75E-16	38200128
16	<i>HP</i>	rs7191623	72,212,044	G	A	0.0219363	0.00313144	1.31E-08	38200128
16	<i>CMIP</i>	rs2925979	81,534,790	T	C	0.0506561	0.00277754	1.5E-49	38200128
16	<i>FAM92B</i>	rs79311290	85,150,163	G	A	0.0368533	0.00433717	5.4E-12	38200128
16	<i>BANP</i>	rs12927305	88,006,413	T	C	0.0215341	0.0025548	7.95E-12	38200128
17	<i>VPSS3</i>	rs34345377	489,296	G	C	0.0237952	0.00321406	1.89E-09	38200128
17	<i>SLC2A4</i>	rs117643180	7,185,779	A	C	0.1453	[0.1-0.19] unit increase	5E-11	37291194
17	<i>TNFSF12</i>	rs9902027	7,440,984	C	T	0.0263675	0.00305374	2.45E-12	38200128
17	<i>PEMT</i>	rs7215055	17,458,353	G	A	0.0534071	0.0052582	1.7E-16	38200128
17	<i>PEMT</i>	rs56157833	17,478,433	T	A	0.0239995	0.00338081	8.41E-09	38200128
17	<i>STARD3</i>	rs931992	37,821,435	G	T	0.020419	0.00270173	8.65E-10	38200128
17	<i>MLX</i>	rs12938909	40,787,764	G	C	0.0296854	0.00282334	1.44E-17	38200128

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
17	<i>DXH8,LINC00910,NBR1</i>	rs113905686	41,469,457	C	A	0.0359473	0.005263	2.99E-08	38200128
17	<i>CD300LG</i>	rs72836561	41,926,126	T	C	0.202804	0.00730342	2.01E-112	38200128
17	<i>CD300LG</i>	rs72836567	41,945,776	A	G	0.0448238	0.00347404	1.19E-25	38200128
17	<i>TMEM101</i>	rs2523159	42,094,734	A	G	0.0303566	0.0033396	1.63E-13	38200128
17	<i>SKAP1</i>	rs11650182	46,272,609	A	G	0.0396309	0.00502247	1.53E-10	38200128
17	<i>GIP</i>	rs595767	46,957,987	G	A	0.0230144	0.00255098	2.47E-13	38200128
17	<i>ZNFB62</i>	rs34666276	47,379,486	C	T	0.0223107	0.00265435	9.08E-12	38200128
17	<i>APOH</i>	rs1801689	64,210,580	A	C	0.0601647	0.00742132	4.76E-11	38200128
17	<i>BPTF</i>	rs12451511	65,874,861	G	T	0.0326168	0.00321083	1.68E-16	38200128
17	<i>ABCA8</i>	rs34931250	66,879,927	T	C	0.0489221	0.00534614	1.13E-13	38200128
17	<i>KCNJ2</i>	rs4519367	68,470,163	A	G	0.0175032	0.00255102	2.59E-08	38200128
17	<i>FAM100B,RNF157</i>	rs56257305	74,207,943	G	A	0.0365624	0.00473336	3.66E-10	38200128
17	<i>PGS1</i>	rs4969179	76,391,454	T	G	0.0279033	0.00260663	3.75E-18	38200128
18	<i>USP14</i>	rs3931630	148,913	G	A	0.0214553	0.00285302	1.05E-09	38200128
18	<i>THOC1</i>	rs6506033	289,209	C	T	0.040338	0.00491891	2.85E-11	38200128
18	<i>CTAGE1,GATA6</i>	rs4800392	19,908,497	C	A	0.0208211	0.0025629	4.34E-11	38200128
18	<i>LIPG</i>	rs2000813	47,093,864	C	T	0.0269876	0.00278016	3.36E-15	38200128
18	<i>LIPG</i>	rs77960347	47,109,955	A	G	0.0904947	0.0110919	3.59E-11	38200128
18	<i>LIPG</i>	rs1970696	47,169,989	T	C	0.0364443	0.00334601	9.75E-19	38200128
18	<i>MIR122</i>	rs41292412	56,118,358	T	C	0.104353	0.011836	8.43E-13	38200128
18	<i>PMAIP1</i>	rs11664369	57,739,072	T	C	0.0287823	0.00288263	5.41E-16	38200128
18	<i>MC4R</i>	rs78274649	58,053,794	G	A	0.0672668	0.00912826	2.24E-09	38200128
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	0.014	0.003	1.78E-09	34059833
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	-0.05	0.01	1.90E-08	27416945
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	0.0176385	0.00262519	4.98E-08	38200128
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	0.0374	[0.024-0.051] unit decrease	0.00000004	37291194
19	<i>PLAS4</i>	rs2289863	4,028,783	T	C	0.0207199	0.00296124	1.37E-08	38200128
19	<i>INSR</i>	rs1799815	7,125,519	A	G	0.033	0.006	9.24E-08	34059833
19	<i>INSR</i>	rs11085216	7,195,539	G	A	0.0256018	0.00281993	1.75E-13	38200128
19	<i>INSR</i>	rs4804413	7,222,655	T	C	0.029957	0.00257233	3.4E-21	38200128
19	<i>INSR</i>	rs8101064	7,293,119	T	C	0.0550407	0.00721174	5.91E-10	38200128
19	<i>MAP2K7</i>	rs2115107	7,968,168	A	G	0.0246862	0.00261689	1.94E-14	38200128
19	<i>MAP2K7</i>	rs4804833	7,970,635	A	G	0.01	0.002	6.59E-06	34059833
19	<i>CERS4</i>	rs11880745	8,268,451	T	G	0.0212664	0.0030925	2.41E-08	38200128
19	<i>ANGPTL4</i>	rs116843064	8,429,323	G	A	0.260439	0.00923145	5.57E-116	38200128
19	<i>ANGPTL4</i>	rs62117489	8,442,202	C	A	0.0713997	0.00554606	1.52E-25	38200128
19	<i>RAB11B</i>	rs2967614	8,458,145	G	A	0.025346	0.00263598	6.08E-15	38200128
19	<i>KANK2</i>	rs111831594	11,294,359	G	A	0.038376	0.00458179	1.07E-11	38200128
19	<i>DOCK6</i>	rs138572354	11,338,309	A	C	0.0387898	0.00536721	4.51E-09	38200128
19	<i>TM6SF2</i>	rs58542926	19,379,549	C	T	0.108415	0.00483858	7.28E-74	38200128
19	<i>TM6SF2</i>	rs188247550	19,396,616	C	T	0.135155	0.0116437	4.57E-21	38200128
19	<i>MAU2</i>	rs3934667	19,431,423	G	T	0.0279094	0.00281107	7.87E-16	38200128
19	<i>GATAD2A</i>	rs111406374	19,505,990	A	G	0.0555574	0.00819699	3.8E-08	38200128
19	<i>PEPD</i>	rs62102718	33,891,013	T	A	0.0300086	0.00282226	6.26E-18	38200128
19	<i>PEPD</i>	rs10422861	33,894,846	T	C	-0.013	0.002	6.65E-11	34059833
19	<i>PEPD</i>	rs731839	33,899,065	A	G	-0.012	0.002	3.87E-11	34059833
19	<i>PEPD</i>	rs731839	33,899,065	G	A	0.0148	0.002	5.10E-12	22885924
19	<i>HPN,HPN-AS1</i>	rs58895965	35,551,428	A	C	0.0287323	0.00335922	3.91E-12	38200128
19	<i>HPN,HPN-AS1</i>	rs2305746	35,556,300	G	A	0.0400082	0.00509326	1.84E-10	38200128
19	<i>MAP3K10</i>	rs339525	40,696,513	T	G	-0.007	0.003	2.07E-04	34059833
19	<i>PLAUR</i>	rs4760	44,153,100	G	A	0.0256077	0.00350928	3.2E-09	38200128
19	<i>APOC1</i>	rs483082	45,416,178	T	G	0.109491	0.00300535	4.62E-192	38200128
19	<i>APOC1</i>	rs1064725	45,422,561	T	G	0.0805094	0.00661905	5.64E-23	38200128
19	<i>APOC1P1</i>	rs60049679	45,429,708	C	G	0.0838314	0.00521724	7.43E-39	38200128
19	<i>APOC1P1</i>	rs8106813	45,431,658	G	A	0.0594672	0.00273246	8.63E-70	38200128
19	<i>RELB</i>	rs2376867	45,500,925	T	C	0.0192588	0.00272332	9.57E-09	38200128
19	<i>GIPR</i>	rs4802269	46,167,469	A	G	0.0187168	0.0026742	1.35E-08	38200128
19	<i>GIPR</i>	rs11671664	46,172,278	A	G	-0.17	0.026	2.63E-11	24699409
19	<i>IRF2BP1,MYPOP,NANOS2</i>	rs34934360	46,398,989	G	A	0.033703	0.00396352	5.21E-12	38200128
19	<i>ZC3H4</i>	rs3810291	47,569,003	A	G	0.0211385	0.00271614	2.7E-10	38200128
19	<i>ZC3H4</i>	rs200172871	47,592,967	C	CT	0.011	0.003	1.71E-05	34059833
19	<i>FGF21</i>	rs838133	49,259,529	A	G	0.0254721	0.00263828	4.72E-15	38200128
19	<i>LILRB5</i>	rs12975366	54,759,361	C	T	0.0210794	0.00259646	4.47E-11	38200128
19	<i>LILRA3</i>	rs367070	54,800,500	A	G	0.0307663	0.00306135	3.5E-16	38200128
19	<i>FIZ1</i>	rs12610709	56,102,362	A	G	0.0290922	0.00339012	3.33E-12	38200128
20	<i>MIMT1</i>	rs8102873	57,488,423	T	C	0.0193655	0.00258224	1.16E-09	38200128
20	<i>TCF15</i>	rs282146	555,352	A	G	0.0178678	0.00262714	3.41E-08	38200128
20	<i>TCF15</i>	rs144033177	571,467	C	A	0.0803563	0.0104396	4.22E-10	38200128
20	<i>CASC20</i>	rs979012	6,623,374	T	C	0.011	0.002	4.81E-07	34059833
20	<i>ACSS2</i>	rs6088461	32,905,161	T	G	0.0186846	0.00258386	4.42E-09	38200128
20	<i>ARHGAP40</i>	rs6027072	37,284,070	A	G	-0.39	0.12	4.40E-09	27416945
20	<i>MAFB</i>	rs2207132	39,142,516	A	G	0.0497346	0.00707453	1.17E-08	38200128
20	<i>MYBL2</i>	rs285171	42,337,875	C	G	-0.012	0.003	8.94E-06	34059833
20	<i>HNF4A</i>	rs1800961	43,042,364	T	C	0.0660432	0.00733364	2.73E-13	38200128
20	<i>PLTP</i>	rs435306	44,538,484	T	G	0.044549	0.00293994	9.57E-35	38200128
20	<i>PLTP</i>	rs6073958	44,551,855	C	T	0.0935597	0.00318762	2.27E-125	38200128
20	<i>EYA2</i>	rs1999536	45,581,777	C	G	-0.012	0.002	1.32E-09	34059833
20	<i>EYA2</i>	rs1206760	45,582,472	A	G	-0.011	0.002	8.82E-10	34059833
20	<i>EYA2</i>	rs55966194	45,599,090	C	G	0.0241327	0.00282908	4.46E-12	38200128
20	<i>SULF2</i>	rs6018652	46,340,974	G	A	0.0249611	0.00314761	1.24E-10	38200128
20	<i>TSHZ2</i>	rs6068280	51,235,613	G	A	0.0196953	0.00272426	4.46E-09	38200128
20	<i>PFND4</i>	rs6013915	52,810,377	A	G	-0.84	0.19	1.50E-09	27416945
20	<i>BMP7</i>	rs6123685	55,836,040	G	A	0.0233031	0.00292125	9.62E-11	38200128
20	<i>PCK1</i>	rs1042521	56,136,536	G	A	0.0201125	0.00254906	1.53E-10	38200128
20	<i>GNAS</i>	rs185799410	57,466,093	T	G	0.055617	0.0081041	2.57E-08	38200128
20	<i>OPRL1</i>	rs8126001	62,711,459	C	T	0.0203217	0.00255421	1.08E-10	38200128
21	<i>NRIP1</i>	rs2223041	16,422,603	T	C	0.0177511	0.00264224	0.00000005	38200128

CHR	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)
21	<i>D21S2088E</i>	rs200678953	24,493,294	T	TATATGTTATATAC	0.014	0.003	2.04E-08	34059833
22	<i>ISX</i>	rs10483182	35,135,106	A	G	-1.16	0.18	7.80E-12	27416945
22	<i>MAFF</i>	rs2267373	38,600,542	T	C	0.0323984	0.00258297	2.49E-24	38200128
22	<i>FAM227A</i>	rs5757161	38,990,662	A	G	0.025544	0.00270528	1.83E-14	38200128

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error

This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.

The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 11. Summary of genome-wide significance for variants associated with insulin-related traits in previous studies.

Chr	Gene	SNP	Pos (h37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB BP_38	TWB EA	TWB NEA	TWB EAF	TWB BETA	TWB SE	TWB P
1	MTOR - UBIAD1	rs2295080	11,322,628	T	G	0.0394	[0.026-0.053] unit decrease	0.00000001	37291194	1	11262571	G	T	0.19762	-0.00689	0.00254	7.20E-03
1	ARID1A	rs114165349	27,021,913	C	G	0.138022		0.00851415	1.61E-39	38200128							
1	NR0B2	rs11581460	27,242,009	G	A	0.02000011		0.00261802	5.68E-10	38200128							
1	PABPC4-AS1	rs3768321	40,035,928	T	G	0.0480953		0.00320619	4.38E-34	38200128	1	39570256	T	G	0.11091	0.01727	0.00321 4.70E-08
1	MYCL	rs61781290	40,393,160	G	A	0.0221266		0.00288512	4.88E-10	38200128	1	39927488	G	A	0.38225	0.00027	0.00207 9.20E-01
1	CDKN2C	rs72904737	51,351,846	G	A	0.034614		0.00451929	5.14E-10	38200128	1	50886174	A	G	0.09971	-0.00919	0.00335 4.60E-03
1	SSBP3	rs213494	54,877,103	T	C	0.0179418		0.00266691	4.79E-08	38200128	1	54411430	C	T	0.34551	-0.00485	0.00214 2.60E-02
1	ANGPTL3	rs10889333	62,957,030	G	A	0.0658915		0.00267004	3.37E-89	38200128	1	62491359	A	G	0.21069	-0.03369	0.00246 2.10E-05
1	PTGER3	rs650194	71,414,863	A	G	0.0192074		0.00269257	7.11E-09	38200128	1	70949180	A	G	0.27745	0.00474	0.00225 4.80E-02
1	NEGR1	rs2613505	72,835,410	T	C	0.0218899		0.00320724	3.06E-08	38200128	1	72369727	C	T	0.01350	0.00434	0.00872 7.50E-01
1	ELTD1	rs1857095	80,246,020	T	C	0.08		0.12	7.90E-09	27416945	1	79780335	C	T	0.17517	0.00108	0.00265 8.00E-01
1	CCDC18	rs1365297	93,858,292	A	G	0.034367		0.00328643	2.15E-17	38200128	1	93392735	G	A	0.30667	-0.01006	0.00219 6.10E-06
1	DPYD	rs1938566	98,478,981	C	T	0.0248702		0.00342705	3.9E-09	38200128	1	98013425	C	T	0.05617	-0.01085	0.00438 2.00E-02
1	CELSR2	rs646776	109,818,530	T	C	0.0306472		0.00306179	4.58E-16	38200128	1	109275908	C	T	0.06791	-0.00830	0.00398 4.70E-02
1	CSF1	rs333947	110,470,764	A	G	0.0315368		0.00356226	6.79E-13	38200128							
1	BOLA1	rs1044808	149,871,905	G	C	0.0431286		0.00464337	4.82E-14	38200128							
1	CTSS	rs6677420	150,946,490	A	G	0.0207841		0.00266617	2.52E-10	38200128	1	150974014	A	G	0.35732	0.00092	0.00210 6.20E-01
1	UBAP2L	rs2282227	154,243,097	G	A	0.0246886		0.00279484	7.62E-13	38200128	1	154270621	A	G	0.47126	-0.00917	0.00202 2.20E-05
1	DNM3	rs2227198	172,360,164	A	G	0.0196965		0.00257	5.01E-10	38200128	1	172391024	A	G	0.13026	0.01006	0.00299 2.50E-04
1	C1orf220	rs6700266	178,508,930	G	A	0.0206853		0.00268859	4.29E-10	38200128	1	178539795	A	G	0.36584	-0.00782	0.00209 6.60E-04
1	OPTC	rs36043408	203,511,492	G	A	0.0188793		0.00254854	1.84E-09	38200128	1	203542364	G	A	0.48684	0.00683	0.00202 2.90E-04
1	CNTN2	rs3903399	205,041,542	C	T	0.0239229		0.00311982	4.91E-10	38200128	1	205072414	C	T	0.44847	0.00710	0.00205 6.00E-04
1	LYPLAL1	rs6674544	219,628,973	A	G	0.018		0.002	6.97E-21	34059833							
1	LYPLAL1	rs2820436	219,640,680	C	A	0.0153		0.003	4.40E-09	22885924	1	219467338	A	C	0.20735	-0.00131	0.00248 4.20E-01
1	LYPLAL1-AS1	rs1538742	219,668,252	A	C	0.0278115		0.00258198	2.33E-18	38200128	1	219494910	A	C	0.31842	0.00507	0.00217 1.30E-02
1	LYPLAL1	rs2785980	219,700,519	T	C	0.017		0.004	2.00E-08	22581228	1	219527177	C	T	0.24707	-0.00583	0.00234 7.00E-03
1	LYPLAL1	rs4846565	219,722,104	G	A	0.0132		0.002	1.80E-09	22885924	1	219548762	A	G	0.23857	-0.00657	0.00236 4.40E-03
1	LYPLAL1-AS1	rs6678052	219,755,057	G	A	0.0230707		0.00294198	1.98E-10	38200128	1	219581715	G	A	0.07860	0.01184	0.00374 2.10E-03
1	MTARC1	rs2642438	220,970,028	A	G	0.0274332		0.00278243	1.24E-15	38200128	1	220796686	A	G	0.20094	0.00776	0.00252 3.70E-04
1	LINC01352	rs61830291	221,001,142	C	A	0.0299533		0.00433367	2.04E-08	38200128							
1	WNT9A	rs68160490	228,078,132	G	A	0.0198132		0.00264393	1.2E-09	38200128							
1	GALNT2	rs6684677	230,206,963	C	T	0.0250347		0.00311266	6.75E-11	38200128	1	230071216	C	T	0.44795	0.00625	0.00203 2.90E-03
1	GALNT2	rs10779835	230,299,949	T	C	0.084208		0.00261652	2.51E-150	38200128	1	230164203	C	T	0.23461	-0.01017	0.00239 4.00E-06
1	GALNT2	rs632557	230,398,102	A	G	0.0911647		0.00640068	6.79E-31	38200128							
1	GALNT2	rs2273967	230,415,293	C	T	0.0256008		0.00293879	1.56E-12	38200128	1	230279547	T	C	0.16574	-0.01104	0.00273 3.10E-05
2	TMEM18	rs5017305	630,902	A	T	0.014		0.003	1.07E-08	34059833	2	630902	A	T	0.07198	-0.00569	0.00390 8.30E-02
2	COLEC11	rs3820897	3,642,361	C	T	0.0345696		0.00334351	4.88E-17	38200128							
2	APOB	rs676210	21,231,524	G	A	0.106411		0.00315015	2.11E-165	38200128	2	21008652	G	A	0.27346	0.00602	0.00226 2.40E-02
2	ASXL2	rs34820121	26,098,259	C	A	0.0199492		0.00269358	1.86E-09	38200128	2	25875390	C	A	0.09046	0.00536	0.00350 8.70E-02
2	KCNK3	rs935168	26,914,787	A	G	0.0182814		0.00268182	3.18E-08	38200128							
2	DYSL5	rs61007968	27,177,428	C	G	0.011		0.003	2.63E-06	34059833	2	26954560	C	G	0.14447	0.00057	0.00286 7.30E-01
2	GCKR	rs6714780	27,189,063	A	G	0.0771431		0.00572893	8.63E-28	38200128							
2	GCKR	rs115961201	27,704,896	G	A	0.0853067		0.00684541	4.89E-24	38200128							
2	GCKR	rs1260326	27,730,940	T	C	-0.023		0.002	8.42E-38	34059833	2	27508073	T	C	0.49277	0.05943	0.00201 4.30E-204
2	GCKR	rs1260326	27,730,940	T	C	0.107618		0.00260329	1.11E-246	38200128	2	27508073	T	C	0.49277	0.05943	0.00201 4.30E-204
2	GCKR	rs62131877	27,740,328	C	T	0.076273		0.00578796	1.1E-26	38200128							
2	GCKR	rs780094	27,741,237	C	T	0.035		0.004	3.00E-24	20081858	2	27518370	T	C	0.48050	0.05774	0.00201 9.10E-192
2	STRN	rs3770781	37,078,839	A	G	0.0178168		0.00257503	1.97E-08	38200128	2	36851696	A	G	0.44921	0.00866	0.00205 3.10E-05
2	LHCGR	rs17326656	48,962,291	T	G	0.0275696		0.00299784	8.5E-14	38200128	2	48735152	T	G	0.01107	-0.00310	0.00963 7.00E-01
2	CEP68	rs2723065	65,279,414	A	G	0.0273314		0.00262887	3.28E-17	38200128	2	65052280	G	A	0.31207	-0.00669	0.00218 6.10E-04
2	CEP68	rs2252867	65,296,280	T	C	0.007		0.002	1.46E-05	34059833	2	65069146	C	T	0.31902	-0.00634	0.00216 1.40E-03
2	BCL2L11	rs6708784	111,927,379	A	G	0.0182037		0.00255468	7.39E-09	38200128	2	111169802	G	A	0.45369	-0.00528	0.00203 1.20E-02
2	LINC01101	rs954244	121,309,231	G	C	0.0228021		0.00292135	2.4E-10	38200128	2	120551655	G	C	0.30132	0.01411	0.00222 5.80E-11
2	LINC01101	rs11688682	121,347,612	G	C	0.0216681		0.00296417	3E-09	38200128							
2	TMEM163	rs60802178	135,268,836	G	A	0.0255716		0.00343656	1.56E-09	38200128	2	134511265	A	G	0.26906	-0.00030	0.00229 9.70E-01
2	YSK4	rs1530559	135,755,629	A	G	0.0145		0.003	3.40E-08	22885924	2	134998059	A	G	0.13967	0.00223	0.00290 5.20E-01
2	LINC01911	rs77164426	147,514,456	G	A	29.65	[NR]	5E-09	30327367	2	146756888	G	A	0.06341	-0.00674	0.00414 1.00E-01	
2	ACVR1C	rs12694933	158,525,226	T	C	0.027102		0.0039218	2.05E-08	38200128	2	157668714	C	T	0.10944	-0.00648	0.00323 4.00E-02
2	GRB14	rs62173875	165,462,543	C	T	0.0197975		0.00258416	5.09E-10	38200128	2	164606033	C	T	0.28801	0.00751	0.00224 3.40E-04
2	COBLL1	rs6713419	165,508,300	T	C	0.019		0.002	1.44E-24	34059833	2	164651790	C	T	0.10318	-0.02118	0.00330 3.30E-10
2	GRB14	rs10195252	165,513,091	T	C	0.0174		0.002	1.30E-16	22885924	2	164656581	C	T	0.10330	-0.02077	0.00330 8.20E-10
2	COBLL1	rs75265117	165,518,799	C	G	0.028		0.003	1.54E-24	34059833							
2	COBLL1	rs1128249	165,528,624	T	G	-0.02		0.002	7.71E-28	34059833	2	164672114	T	G	0.10328	-0.02107	0.00330 4.40E-10
2	COBLL1	rs13389219	165,528,876	T	C	-0.02		0.002	5.84E-28	34059833	2	164672366	T	C	0.10338	-0.02142	0.00330 2.10E-10
2	GRB14	rs13389219	165,528,876	C	T	0.0544298		0.00260495	1.78E-64	38200128	2	164672366	T	C	0.10338	-0.02142	0.00330 2.10E-10
2	GRB14, COBLL1	rs6707980	165,551,201	T	C	0.039		0.004	4.30E-20	22581228							
2	COBLL1	rs12692738	165,558,252	T	C	0.05806	[0.044-0.072] unit decrease	2E-15	37291194	2	164701742	C	T	0.06360	-0.02162	0.00412 2.40E-07	
2	COBLL1	rs355849	165,625,830	T	C	0.0510286		0.00405324	1.69E-24	38200128							
2	ERICH2																

Chr	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB_BP_38	TWB_EA	TWB_NEA	TWB_EAF	TWB_BETA	TWB_SE	TWB_P
2	LOC646736	rs2972145	227,101,309	T	C	-0.025	0.002	6.08E-38	34059833	2	226236593	T	C	0.06942	-0.01802	0.00396	3.10E-05
2	NYAP2 - MIR5702	rs2972144	227,101,411	A	C	0.06398	[0.051-0.077] unit increase	2E-22	37291194	2	226236695	A	G	0.06939	-0.01799	0.00396	3.10E-05
2	IRS1	rs2972143	227,116,365	G	A	0.0142	0.003	3.20E-08	22885924	2	226251649	A	G	0.07194	-0.01507	0.00389	4.90E-04
2	IRS1	rs17508368	227,651,446	T	C	0.0019	0.004	2.12E-06	34059833	2	226786730	T	C	0.19635	0.00521	0.00257	3.90E-02
2	PID1	rs7596814	230,128,204	G	T	0.019079	0.00280031	3.23E-08	38200128	2	229263488	T	G	0.10228	0.00091	0.00331	7.20E-01
2	HDLBP	rs59104589	242,237,902	C	T	0.0203313	0.00265168	4.92E-10	38200128	2	241298487	C	T	0.47280	0.00671	0.00201	1.20E-03
3	ITPR1	rs9812100	4,763,301	G	A	0.0173925	0.00255379	3.27E-08	38200128	3	4721617	A	G	0.13982	-0.00833	0.00291	3.30E-03
3	SYN2	rs308971	12,116,620	A	G	-0.022	0.003	3.91E-13	34059833	3	12075120	G	A	0.20484	-0.00223	0.00251	5.00E-01
3	PPARG	rs11712037	12,344,730	C	G	0.028	0.003	2.10E-21	34059833	3	12303231	G	C	0.03713	-0.03291	0.00533	6.10E-11
3	PPARG	rs12485478	12,351,223	G	A	0.0628043	0.00794243	1.4E-10	38200128	3	12309974	G	A	0.32108	0.01104	0.00216	1.30E-07
3	PPARG	rs35000407	12,351,521	T	G	0.026	0.003	1.50E-21	34059833	3	12310022	G	T	0.03963	-0.03390	0.00516	3.00E-12
3	PPARG	rs2067819	12,359,049	G	A	0.0347225	0.00310197	1.06E-19	38200128	3	12317550	A	G	0.03969	-0.03339	0.00516	5.30E-12
3	PPARG	rs11128603	12,385,828	A	G	0.06367	[0.046-0.081] unit decrease	5E-13	37291194	3	12344329	G	A	0.03960	-0.03407	0.00516	2.30E-12
3	PPARG	rs17036328	12,390,484	T	C	0.0212	0.003	3.60E-12	22885924	3	12348985	C	T	0.03967	-0.03401	0.00516	2.40E-12
3	PPARG	rs3103310	12,473,045	G	A	0.0262696	0.00302865	1.95E-12	38200128								
3	BTBD	rs13097947	15,846,011	T	C	0.021207	0.00271413	2.3E-10	38200128								
3	TRAIP	rs9819511	49,884,261	T	C	0.014	0.002	2.26E-08	34059833	3	49846828	T	C	0.15313	0.00207	0.00282	5.50E-01
3	MSTIR	rs11130227	49,993,319	G	A	0.0188406	0.0026065	4.48E-09	38200128	3	49955886	G	A	0.14184	0.00039	0.00289	9.70E-01
3	STAB1	rs57172722	52,391,182	G	C	0.0375819	0.00558247	4.69E-08	38200128	3	52357166	G	C	0.10501	-0.00455	0.00334	1.20E-01
3	NISCH	rs6800707	52,516,293	G	C	0.0434857	0.00325265	2.03E-27	38200128	3	52482277	C	G	0.01398	-0.00974	0.00858	2.30E-01
3	ITIH3	rs17331151	52,844,534	T	C	-0.016	0.003	1.52E-08	34059833	3	52810518	T	C	0.04502	-0.00949	0.00487	5.10E-02
3	EIF4E3,FOXPI	rs830620	71,679,148	C	T	0.0187587	0.00258091	3.69E-09	38200128								
3	ADCY5	rs11708067	123,065,778	A	G	-0.014	0.002	1.30E-09	34059833								
3	TPRA1	rs79983121	127,306,462	T	C	0.0234998	0.00318749	2.2E-09	38200128								
3	PCCB	rs684773	135,956,305	C	A	0.0433159	0.0030067	1.44E-31	38200128	3	136237463	A	C	0.11925	-0.01051	0.00312	1.30E-03
3	PAQR9	rs12638256	142,655,290	A	G	0.0174842	0.00256115	3.04E-08	38200128	3	142936448	A	G	0.49812	-0.00034	0.00205	6.70E-01
3	LINC01214	rs62271373	150,066,540	A	T	0.026	0.005	1.60E-08	34059833								
3	LINC01214,TSC22D2	rs62271373	150,066,540	A	T	0.0669914	0.00546369	2.55E-23	38200128								
3	LINC00880	rs9817452	156,795,414	G	T	0.0269754	0.00262829	8.22E-17	38200128	3	157077625	G	T	0.45364	0.00770	0.00203	4.40E-05
3	SLC2A2	rs5402	170,727,739	A	T	0.0270032	0.00392356	2.34E-08	38200128								
3	LINC02068	rs79287178	172,294,500	A	G	0.0647525	0.00769167	8.43E-12	38200128								
3	BCL6	rs7631606	187,628,006	T	G	0.0210464	0.00290824	4.3E-09	38200128	3	187910218	G	T	0.03867	-0.00683	0.00534	2.20E-01
3	UBXN7-AS1	rs13094241	196,190,893	T	G	0.0205999	0.00286045	5.11E-09	38200128								
4	DGKQ,JDUA	rs13101828	965,720	A	G	0.0181539	0.00256066	8.78E-09	38200128								
4	HGFAC	rs13108218	3,443,931	A	G	0.0278127	0.00263906	1.21E-17	38200128								
4	DOK7	rs731450	3,490,328	T	C	0.0245397	0.0026997	1.63E-13	38200128	4	3488601	C	T	0.06961	-0.00503	0.00398	2.20E-01
4	CYTLL	rs4450871	4,990,298	A	G	0.019929	0.00255946	2.65E-10	38200128	4	4988571	A	G	0.45443	0.00638	0.00203	2.10E-03
4	LCORL	rs71603401	18,034,463	G	A	0.0376217	0.00374037	3.31E-16	38200128	4	18032840	G	A	0.13284	0.00457	0.00302	8.50E-02
4	RBPJ	rs73243877	26,047,616	G	A	0.0442274	0.00340472	5.62E-26	38200128								
4	UBE2K	rs105582	39,700,173	C	T	0.0196344	0.00254957	4.13E-10	38200128	4	39698553	C	T	0.33866	0.00205	0.00215	3.20E-01
4	KIT	rs2159935	55,521,017	G	A	0.0226027	0.0025458	5.84E-13	38200128	4	54654850	A	G	0.37222	-0.00132	0.00209	2.40E-01
4	SHROOM3	rs7675258	77,413,179	A	G	0.0189195	0.00255136	1.78E-09	38200128	4	76492026	A	G	0.29515	0.00686	0.00222	7.70E-04
4	AFF1	rs7775228	87,985,166	T	C	0.0456982	0.00260878	7.52E-46	38200128	4	87064014	T	C	0.40409	0.01173	0.00206	4.40E-09
4	AFF1	rs447990	88,033,352	G	T	0.0231078	0.00261764	7.89E-13	38200128	4	87112200	G	T	0.18440	0.00042	0.00260	8.20E-01
4	FAM13A	rs10011342	89,672,077	A	G	0.0247207	0.00331979	1.52E-09	38200128	4	88750926	G	A	0.26143	-0.00482	0.00230	3.70E-02
4	FAM13A	rs2276936	89,726,283	A	C	-0.012	0.002	4.25E-11	34059833	4	88805132	A	C	0.28002	-0.00392	0.00226	7.50E-02
4	FAM13A	rs7775380	89,739,808	A	G	-0.012	0.002	1.48E-11	34059833	4	88818657	A	G	0.28094	-0.00434	0.00226	5.10E-02
4	FAM13A	rs3822072	89,741,269	A	G	0.0116	0.002	1.80E-08	22885924	4	88820118	A	G	0.32425	-0.00407	0.00216	5.60E-02
4	FAM13A	rs4425336	89,753,225	A	G	0.0208542	0.00309845	4.73E-08	38200128	4	88832074	A	G	0.41055	0.00505	0.00205	6.40E-03
4	ADH4	rs6848050	100,053,733	C	T	0.0209222	0.00277039	8.9E-10	38200128								
4	SLC39A8	rs13107325	103,188,709	T	C	0.0702962	0.00484448	5.3E-32	38200128								
4	TET2	rs974801	106,071,064	G	A	0.0139	0.002	3.30E-11	22885924	4	105149907	A	G	0.40966	-0.00253	0.00205	1.40E-01
4	TET2	rs9884482	106,081,636	T	C	-0.013	0.002	2.88E-11	34059833	4	105160479	T	C	0.40439	-0.00254	0.00205	1.40E-01
4	TET2	rs9884482	106,081,636	C	T	0.0165	0.002	1.40E-11	22885924	4	105160479	T	C	0.40439	-0.00254	0.00205	1.40E-01
4	TET2; TET2-AS1	rs10010325	106,106,353	A	C	0.012	0.002	4.05E-11	34059833	4	105185196	C	A	0.47248	-0.00219	0.00203	1.90E-01
4	MCUB	rs78025076	110,569,620	T	C	0.0764923	0.00901604	5.81E-12	38200128								
4	HHIP-AS1	rs7654571	145,321,006	A	G	0.012	0.002	7.77E-08	34059833	4	144399854	A	G	0.34329	0.00198	0.00212	4.70E-01
4	HHIP	rs11727676	145,659,064	T	C	-0.02	0.004	2.90E-08	34059833								
4	PDGFC	rs6855363	157,670,537	T	C	0.013	0.002	4.04E-08	34059833	4	156749385	C	T	0.30284	-0.00745	0.00221	1.00E-03
4	PDGFC	rs1816164	157,696,636	C	T	0.0214634	0.003048	1.1E-08	38200128	4	156775484	T	C	0.24125	-0.01133	0.00237	5.00E-07
4	PDGFC	rs4691380	157,720,124	C	T	0.021	0.004	5.30E-09	22581228	4	156798972	T	C	0.30132	-0.00754	0.00220	6.50E-04
4	PDGFC	rs6822892	157,734,675	A	G	0.0138	0.002	2.60E-10	22885924	4	156813523	G	A	0.30196	-0.00755	0.00220	6.50E-04
5	ARL15	rs4865796	53,272,664	A	G	0.017	0.002	7.33E-17	34059833	5	53976834	G	A	0.12823	-0.01338	0.00302	2.10E-05
5	ARL15	rs4865796	53,272,664	A	G	0.0154	0.002	2.20E-12	22885924	5	53976834	G	A	0.12823	-0.01338	0.00302	2.10E-05
5	ARL15	rs80138475	53,304,991	T	C	0.0303003	0.0040373	1.13E-09	38200128								
5	LOC101928448	rs459193	55,806,751	A	G	-0.018	0.002	1.12E-18	34059833	5	56510924	A	G	0.47054	-0.02213	0.00202	1.80E-29
5	ANKRD55-MAP3K1	rs459193	55,806,751	G	A	0.0147	0.002	1.20E-10	22885924	5	56510924	A	G	0.47054	-0.02213	0.00202	1.80E-29
5	RPL26P19 - C5orf67	rs459193	55,806,751	A	G	0.041777	[0.028-0.055] unit increase	7E-10	37291194	5	56510924	A	G	0.47054	-0.02213	0.00202	1.80E-29
5	C5orf67	rs392794	55,808,342	T	C	0.0475555	0.00292417	9.23E-40	38200128	5	56512515	C	T	0.47070	-0.02221	0.00202	9.60E-30
5																	

Chr	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB_BP_38	TWB_EA	TWB_NEA	TWB_EAF	TWB_BETA	TWB_SE	TWB_P
5	LOC101927697	rs1023667	157,968,901	A	G	-0.01	0.002	5.70E-07	34059833	5	158541893	A	G	0.43290	-0.00485	0.00204	9.00E-03
5	EBF1	rs1030472	157,994,544	G	A	0.0335843	0.00311769	2.31E-18	38200128	5	158567536	G	A	0.32032	0.00884	0.00216	2.90E-05
6	E2F3	rs4134963	20,486,798	C	T	0.0247133	0.00326148	7.82E-10	38200128	6	20486567	T	C	0.08917	-0.01128	0.00354	2.20E-03
6	CDKAL1	rs7754840	20,661,250	G	A		3E-12	37116407	6	20661019	C	G	0.35911	0.00606	0.00210	1.60E-03	
6	CDKAL1	rs7756992	20,679,709	G	A	-0.11	0.015	3.07E-13	24699409	6	20679478	G	A	0.45856	0.00567	0.00203	1.90E-03
6	HLA-C	rs2074493	31,239,776	C	A	0.0496279	0.00304462	6.18E-40	38200128	6	31271999	C	A	0.33919	0.01686	0.00246	9.10E-14
6	HLA-B	rs2394987	31,327,217	A	C	0.0476286	0.00404853	1.35E-21	38200128	6	31359440	A	C	0.28694	0.00825	0.00232	1.10E-04
6	MICB	rs3093999	31,484,550	A	T	-0.014	0.003	1.31E-07	34059833	6	31516773	A	T	0.07432	-0.00228	0.00386	4.70E-01
6	HLA-DQA1	rs11751024	32,586,236	A	C	0.0365969	0.00260322	3.84E-30	38200128	6	32618459	A	C	0.26843	0.00034	0.00255	8.90E-01
6	HLA-DQB1	rs114786106	32,596,878	G	A	0.0989186	0.00655355	1.73E-34	38200128	6	32629101	G	A	0.11195	0.00406	0.00345	1.80E-01
6	HMGAI	rs114760566	34,192,036	A	C	0.0647052	0.00615228	1.41E-17	38200128								
6	C6orf1	rs116141873	34,222,201	T	G	0.043	0.006	1.42E-11	34059833	6	34254424	T	G	0.01131	-0.01019	0.00956	3.40E-01
6	RPS10-NUDT3; NUDT3	rs2780215	34,236,973	A	G	-0.039	0.006	1.06E-09	34059833	6	34269196	G	A	0.08273	-0.02099	0.00372	2.60E-09
6	RPS10-NUDT3; NUDT3	rs1187129	34,239,989	A	G	-0.029	0.007	1.41E-05	34059833	6	34272212	A	G	0.08432	-0.01942	0.00368	2.90E-08
6	UHRF1BP1	rs6912327	34,764,922	T	C	0.0165	0.003	2.30E-08	22885924	6	34797145	C	T	0.48089	0.00096	0.00203	7.60E-01
6	UHRF1BP1	rs4646949	34,845,449	T	G	0.02	0.004	3.70E-08	22581228	6	34877672	T	G	0.28261	0.00050	0.00227	5.70E-01
6	FOXP4	rs777943523	41,550,466	C	CA	-0.008	0.003	1.53E-03	34059833								
6	VEGFA	rs9472125	43,756,169	C	T	0.06979	0.00421857	4.38E-41	38200128								
6	VEGFA	rs998584	43,757,896	A	C	0.012	0.002	2.31E-10	34059833	6	43790159	C	A	0.44372	-0.01921	0.00203	2.60E-22
6	VEGFA	rs998584	43,757,896	A	C	0.0617628	0.00255302	8.55E-86	38200128	6	43790159	C	A	0.44372	-0.01921	0.00203	2.60E-22
6	VEGFA	rs2396084	43,804,825	G	A	0.0225518	0.0027629	3.52E-11	38200128	6	43837088	A	G	0.21935	-0.01263	0.00244	1.60E-07
6	LINC01512	rs9472135	43,809,802	T	C	0.011	0.002	4.21E-08	34059833	6	43842065	C	T	0.13319	-0.00762	0.00296	9.80E-03
6	GSTA2	rs2749026	52,630,635	A	G	0.0218752	0.00266388	2.68E-11	38200128	6	52765837	A	G	0.11040	0.01784	0.00322	2.80E-08
6	BEND3	rs62427983	107,441,254	T	C	0.0194501	0.00273108	7.52E-09	38200128	6	107120050	C	T	0.15125	-0.00355	0.00281	1.70E-01
6	ARMC2	rs11752394	109,189,664	G	C	0.0230349	0.00300159	4.75E-10	38200128	6	108868461	C	G	0.41621	-0.00127	0.00205	4.80E-01
6	RSP03	rs2800709	127,439,297	G	T	0.0244106	0.00254967	7.93E-15	38200128	6	127118152	T	G	0.36941	-0.00066	0.00211	7.00E-01
6	RSP03	rs1474696	127,449,246	A	G	-0.015	0.002	3.02E-16	34059833	6	127128101	A	G	0.35592	-0.00115	0.00211	5.80E-01
6	RSP03	rs2745353	127,452,935	T	C	0.015	0.002	4.63E-16	34059833	6	127131790	C	T	0.36522	-0.00165	0.00210	4.00E-01
6	RSP03	rs2745353	127,452,935	T	C	0.0143	0.002	5.50E-09	22885924	6	127131790	C	T	0.36522	-0.00165	0.00210	4.00E-01
6	RSP03	rs72959041	127,454,893	A	G	0.0652129	0.00596303	7.06E-19	38200128								
6	L3MBTL3	rs9388767	130,357,553	A	G	0.0227283	0.00277178	2.86E-11	38200128	6	130036408	G	A	0.32977	-0.00299	0.00240	1.90E-01
6	LOC645434	rs632057	139,834,012	T	G	0.008	0.002	1.37E-05	34059833	6	139512875	G	T	0.31796	-0.00845	0.00217	1.40E-05
6	LINC01625	rs632057	139,834,012	T	G	0.0429738	0.00263213	4.64E-40	38200128	6	139512875	G	T	0.31796	-0.00845	0.00217	1.40E-05
6	RGS17	rs607335	153,465,230	C	A	0.0194408	0.00258124	9.88E-10	38200128	6	153144095	A	C	0.05292	-0.00561	0.00450	1.30E-01
6	SLC22A1	rs12208357	160,543,148	T	C	0.0417135	0.00501169	1.44E-11	38200128								
6	LPA	rs10455872	161,010,118	A	G	0.0454608	0.00471768	5.32E-15	38200128								
6	LPA	rs140570886	161,013,013	T	C	0.127163	0.010471	6.57E-23	38200128	6	160591981	C	T	0.02491	-0.00474	0.00649	5.50E-01
6	LPA	rs77348928	161,013,030	G	A	0.0360485	0.00360352	4.77E-16	38200128								
6	LPA	rs11751347	161,092,438	T	C	0.0674344	0.00423546	3.51E-38	38200128								
6	QKI	rs73013411	164,126,233	A	C	-0.018	0.003	2.08E-08	34059833	6	163705201	A	C	0.08707	-0.00712	0.00357	2.10E-02
6	QKI	rs4709746	164,133,001	T	C	-0.018	0.003	2.97E-08	34059833	6	163711969	T	C	0.08821	-0.00775	0.00356	1.20E-02
6	LOC102724152	rs4709746	164,133,001	C	T	0.0307179	0.00376086	3.41E-11	38200128	6	163711969	T	C	0.08821	-0.00775	0.00356	1.20E-02
7	GPR146	rs71538127	1,010,801	G	C	0.0288493	0.00388757	1.73E-09	38200128	7	971165	G	C	0.03283	0.01068	0.00570	4.40E-02
7	ACTB	rs852388	5,574,239	C	G	0.024574	0.00314792	2.38E-10	38200128								
7	AHR	rs4410790	17,284,577	C	T	0.0244792	0.00264249	5.61E-14	38200128	7	17244953	C	T	0.43829	0.00748	0.00204	6.90E-05
7	SNX13	rs10242866	17,920,613	T	C	0.0296287	0.00260253	2.52E-20	38200128	7	17880990	C	T	0.45850	-0.00583	0.00203	3.50E-03
7	MIR148A	rs7786102	25,965,759	G	A	0.0288168	0.00282391	1.23E-16	38200128								
7	MIR148A	rs4722551	25,991,826	T	C	0.0409096	0.0034795	1.43E-21	38200128	7	25952206	C	T	0.01974	-0.03232	0.00726	6.30E-06
7	SNX10	rs1534696	26,397,239	C	A	0.0256054	0.00255258	3.97E-16	38200128								
7	JAZF1-AS1	rs498475	28,256,240	G	A	0.0180623	0.00264862	3.14E-08	38200128	7	28216621	A	G	0.01978	0.00469	0.00723	5.90E-01
7	GCK	rs2070971	44,197,583	T	G	0.0310802	0.00371219	1.09E-11	38200128	7	44157984	T	G	0.25603	0.01495	0.00236	3.70E-10
7	GCK	rs3757840	44,231,216	T	G	-0.09	0.015	1.34E-09	24699409	7	44191617	T	G	0.46544	-0.02059	0.00202	1.20E-24
7	GRB10	rs2282930	50,754,679	A	G	-0.011	0.003	1.67E-05	34059833	7	50686982	G	A	0.48915	-0.00093	0.00202	6.90E-01
7	GRB10	rs933360	50,758,245	A	G	-0.051	0.0086	3.14E-09	24699409	7	50690548	C	T	0.25383	0.00205	0.00232	3.30E-01
7	GRB10	rs2108349	50,786,663	A	G	-0.012	0.002	1.13E-08	34059833	7	50718966	G	A	0.30315	0.00149	0.00220	4.80E-01
7	MLXIPL	rs141136126	72,852,007	G	A	0.0576356	0.00781477	2.17E-09	38200128								
7	MLXIPL	rs799157	73,020,301	T	C	0.106161	0.00624446	2.74E-43	38200128								
7	MLXIPL	rs17145750	73,026,378	C	T	0.141683	0.00346578	2.76E-241	38200128	7	73612048	T	C	0.09985	-0.06947	0.00336	4.20E-99
7	GTF2IRD1	rs111914893	74,002,323	T	C	0.0408618	0.00585769	1.51E-08	38200128								
7	HIP1	rs1167800	75,176,196	A	G	0.0156	0.003	2.60E-09	22885924								
7	POR	rs2302429	75,614,777	A	G	0.0232638	0.00328621	9.23E-09	38200128	7	75985459	A	G	0.27965	0.00224	0.00225	3.20E-01
7	SSC4D	rs6465120	76,036,364	A	G	0.0184386	0.00254481	4.12E-09	38200128	7	76407047	G	A	0.46823	0.00090	0.00203	6.00E-01
7	PHF2	rs848494	77,537,964	A	G	0.009	0.002	9.25E-06	34059833	7	77908647	G	A	0.14852	-0.00188	0.00284	4.70E-01
7	KLF14	rs13234269	130,429,186	A	T	-0.011	0.002	1.27E-08	34059833	7	130744427	T	A	0.31105	-0.01605	0.00219	2.00E-13
7	KLF14	rs10260148	130,430,969	T	C	0.0431246	0.00284574	9.46E-35	38200128	7	130746210	T	C	0.39923	0.01463	0.00210	1.60E-12
7	KLF14	rs972283	130,466,854	A	G	-0.011	0.002	1.09E-08	34059833	7	130782095	A	G	0.31436	-0.01243	0.00217	1.00E-08
7	GIMAP7	rs11766379	150,208,971	C	T	0.0265583	0.00302912	1.12E-12	38200128	7	150511883	C	T	0.14076	0.00933	0.00297	1.90E-03
7	AOC1	rs62492368	150,537,635	A	G	0.0222278	0.00278135	8.89E-11	38200128								
7	KCNH2	rs1805123	150,645,534	T	G	0.0223058	0.00295852	9.49E-10	38200128</								

Chr	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB_BP_38	TWB_EA	TWB_NEA	TWB_EAF	TWB_BETA	TWB_SE	TWB_P
8	LOC157273	rs1461729	9,187,242	A	G	0.0355363	0.00421777	1.03E-11	38200128								
8	SOX7	rs7821812	10,644,101	C	G	0.049536	0.00314687	2.32E-37	38200128	8	10786591	C	G	0.03141	0.01491	0.00576	1.60E-02
8	BLK	rs12541800	11,423,072	A	G	0.011	0.002	6.17E-07	34059833	8	11565563	A	G	0.01504	0.01399	0.00831	1.10E-01
8	GATA4	rs7386288	11,536,332	T	C	0.0315801	0.00293417	2.47E-18	38200128	8	11678823	T	C	0.12346	0.10084	0.00308	2.00E-03
8	NAT2	rs4646250	18,260,598	G	A	0.0303732	0.00282028	2.36E-18	38200128	8	18403088	A	G	0.30644	-0.01159	0.00218	2.60E-08
8	LOC100128993	rs12056334	19,080,151	A	C	0.005	0.003	1.16E-01	34059833								
8	LPL	rs254	19,811,897	C	G	0.172996	0.00361375	4.60E-330	38200128	8	19954386	G	C	0.21829	-0.04104	0.00247	1.00E-66
8	LPL	rs268	19,813,529	G	A	0.291877	0.00951768	1.11E-136	38200128								
8	LPL	rs276	19,814,289	C	T	0.287757	0.00957285	2.12E-131	38200128								
8	LPL,SLC18A1	rs73667496	19,937,852	C	T	0.0986799	0.0057617	6.59E-44	38200128	8	20080341	T	C	0.07577	-0.00630	0.00382	1.40E-01
8	LPL,SLC18A1	rs7015766	19,939,049	C	T	0.263208	0.00496166	8.39E-405	38200128								
8	LPL,SLC18A1	rs55682243	19,977,311	C	G	0.133134	0.00828409	7.2E-39	38200128								
8	NKX2-6	rs13258890	23,615,445	T	C	0.013	0.003	2.77E-08	34059833	8	23757932	C	T	0.10230	0.00133	0.00339	7.40E-01
8	CDC42	rs73221948	25,464,670	T	G	0.0210291	0.00292112	5.17E-09	38200128								
8	ANK1	rs12549902	41,509,259	A	G	-0.06	0.01	1.01E-08	24699409	8	41651740	A	G	0.36791	-0.00712	0.00209	5.10E-04
8	CYP7A1	rs2081687	59,388,565	T	C	0.023803	0.00269371	7.49E-13	38200128	8	58476006	T	C	0.21939	0.00873	0.00243	3.00E-04
8	LINC01289	rs1149470	64,608,119	T	A	0.0220737	0.0029985	2.32E-09	38200128	8	63695561	T	A	0.02801	-0.00080	0.00613	9.70E-01
8	EYA1	rs13269725	72,459,889	G	A	0.0418588	0.00473827	7.59E-13	38200128	8	71547654	G	A	0.12793	0.01277	0.00302	7.70E-06
8	KCNB2	rs35957544	73,440,371	G	T	0.0174022	0.00257888	4.36E-08	38200128	8	72528136	G	A	0.21227	-0.00678	0.00247	1.30E-02
8	TRPS1	rs2737226	116,639,474	T	C	0.0227621	0.00261188	1.53E-12	38200128	8	115627247	T	C	0.12851	0.00571	0.00301	1.20E-01
8	TRIB1	rs72647336	126,445,055	A	G	0.1094	0.00593777	1.56E-50	38200128								
8	TRIB1	rs6999569	126,475,770	A	G	0.107897	0.0025522	6.83E-258	38200128	8	125463528	G	A	0.14480	-0.02318	0.00289	2.40E-16
8	TRIB1	rs72655677	126,484,897	G	A	0.0995734	0.00609368	4E-40	38200128								
8	TRIB1	rs78309295	126,528,722	G	A	0.0654236	0.00863073	7.71E-10	38200128								
8	TRIB1	rs139827355	126,632,998	G	A	0.0493393	0.00674368	2.91E-09	38200128								
8	TRIB1	rs7826687	126,645,689	G	C	0.0427737	0.00281803	7.4E-35	38200128	8	125633445	G	C	0.45713	0.00865	0.00205	8.90E-06
8	GPIHBP1	rs7832515	144,306,379	A	G	0.0313039	0.00328913	1.14E-14	38200128								
9	LINC01230	rs1509195	1,033,958	C	T	0.022176	0.0027702	8.27E-11	38200128	9	1033958	C	T	0.44936	0.01037	0.00205	8.30E-07
9	GLIS3	rs4339696	4,295,880	T	G	0.009	0.002	1.52E-07	34059833	9	4295880	G	A	0.42661	-0.00596	0.00204	4.30E-01
9	CDC2NB-AS1 - DMRTA1	rs10811661	22,134,094	T	A			8E-10	37116407	9	22134095	C	T	0.41568	-0.00543	0.00205	1.10E-02
9	TELE4	rs11138325	82,294,364	T	C	-0.012	0.002	5.39E-08	34059833								
9	RMII	rs696825	86,583,076	C	T	0.0230535	0.00292935	1.71E-10	38200128	9	83968161	T	C	0.29661	-0.00746	0.00221	6.50E-04
9	GADD45G	rs10797119	92,202,495	C	T	0.0231408	0.00256724	2.59E-13	38200128	9	89587580	C	T	0.24001	0.00874	0.00237	5.40E-04
9	ECM2	rs12686780	95,382,297	T	C	0.0260032	0.00335317	3.12E-10	38200128	9	92620015	C	T	0.29509	-0.00403	0.00222	4.50E-02
9	NAMA	rs62565259	102,162,570	C	T	0.0247574	0.00340829	3.77E-09	38200128								
9	ABCA1	rs4149307	107,589,744	C	T	0.0306419	0.00351979	1.62E-12	38200128	9	104827463	C	T	0.26163	-0.01097	0.00230	7.40E-07
9	ABCA1	rs2275543	107,651,174	C	T	0.0374047	0.00421788	6.21E-13	38200128	9	104888893	C	T	0.06553	-0.01714	0.00408	1.40E-05
9	AKNA	rs1044531	117,098,650	C	T	0.0316438	0.00453361	1.48E-08	38200128								
9	ABO	rs75179845	136,132,954	T	C	-0.022	0.004	6.05E-11	34059833	9	133257567	C	T	0.16605	0.01196	0.00271	1.50E-06
9	ABO	rs8176693	136,137,657	T	C	0.02	0.003	1.10E-10	34059833	9	133262254	A	C	0.16582	0.01198	0.00271	1.30E-06
9	ABO	rs2519093	136,141,870	C	T	0.0297786	0.00328922	2.04E-13	38200128	9	133266456	T	C	0.18121	-0.00005	0.00262	8.10E-01
10	NRP1	rs2776937	33,606,189	A	G	0.0206949	0.00298887	1.93E-08	38200128	10	33317261	A	G	0.40566	0.00292	0.00205	1.60E-01
10	RN7SKP196 - LINC00844	rs60453193	60,632,252	A	G	0.430581	[0.28-0.58] unit increase	0.00000004	37291194								
10	SLC16A9	rs1171615	61,469,090	T	C	0.0236422	0.00302238	2.19E-10	38200128								
10	JMJD1C	rs10761762	65,184,717	T	C	0.008	0.002	1.98E-05	34059833	10	63424957	C	T	0.35848	-0.00868	0.00210	9.30E-06
10	JMJD1C	rs7924036	65,191,645	G	T	0.0374777	0.00254667	7.21E-33	38200128	10	63431885	G	T	0.33260	0.01905	0.00214	1.10E-21
10	PLA2G12B	rs11000468	74,711,376	C	T	0.0223074	0.00296811	1.07E-09	38200128								
10	PLA2G12B	rs3829126	74,714,177	T	G	0.0307816	0.00438716	1.25E-08	38200128								
10	PTEN	rs118164457	89,680,631	T	C	-0.035	0.006	3.86E-10	34059833								
10	PTEN	rs12769346	89,764,490	T	G	-0.015	0.003	1.20E-08	34059833	10	88004733	G	T	0.40207	0.00458	0.00205	1.10E-02
10	HHEX,IDE	rs7923866	94,482,076	C	T	-0.12	0.015	4.16E-16	24699409	10	92722319	C	T	0.19099	0.00968	0.00257	9.50E-05
10	EXOC6	rs9919491	94,754,759	A	T	0.0212953	0.00290286	2.64E-09	38200128	10	92995002	A	T	0.07424	0.00804	0.00387	7.70E-02
10	CYP26A1	rs2068888	94,839,642	G	A	0.041442	0.00255583	1.55E-39	38200128	10	93079885	G	A	0.18984	0.02008	0.00258	1.30E-15
10	CYP26A1	rs7916761	94,941,927	T	C	0.0182124	0.00258622	1.1E-08	38200128								
10	FFAR4	rs10786114	95,309,022	C	T	0.0419758	0.00384745	8.54E-19	38200128	10	93549265	C	T	0.11128	0.00682	0.00321	3.00E-02
10	CRTAC1	rs565108	99,772,190	C	T	0.0238302	0.00256423	4.67E-14	38200128	10	98012433	C	T	0.23318	0.00134	0.00243	5.60E-01
10	NTSC2	rs11191559	104,867,686	T	C	-0.014	0.003	1.27E-05	34059833	10	103107929	T	C	0.29173	-0.00389	0.00222	8.00E-02
10	GPAM	rs2792751	113,940,329	C	T	0.0394203	0.00285272	3.53E-29	38200128	10	112180571	T	C	0.28388	-0.00813	0.00224	5.60E-04
10	GPAM	rs4306236	113,980,294	T	G	0.0379195	0.00364056	2.87E-17	38200128	10	112220536	T	G	0.36454	0.00605	0.00210	3.20E-03
10	TCF7L2	rs7903146	114,758,349	T	C	-0.012	0.002	1.24E-09	34059833	10	112998590	T	C	0.02308	-0.00636	0.00672	4.60E-01
10	TCF7L2	rs7903146	114,758,349	C	T	0.0181	0.003	6.10E-11	22885924	10	112998590	T	C	0.02308	-0.00636	0.00672	4.60E-01
10	ADRB1	rs2773469	115,798,895	A	G	0.0293092	0.00289113	1.94E-16	38200128	10	114039136	A	G	0.26208	0.00450	0.00230	3.50E-02
10	MIR5694	rs7071062	122,930,612	T	C	0.019	0.007	1.19E-02	34059833	10	121171098	C	T	0.36586	0.001535	0.00209	3.70E-13
10	FGFR2	rs878409	122,999,550	G	A	0.018614	0.00256409	3.85E-09	38200128	10	121240036	A	G	0.49653	-0.01260	0.00202	2.00E-10
11	ANO9, B4GALNT4	rs117291242	380,315	T	C	0.0465064	0.00677175	2.51E-08	38200128								
11	PNPLA2	rs140201358	823,586	G	C	0.0769547	0.010917	1.07E-08	38200128								
11	KCNQ1	rs2237895	2,857,194	A	C			3E-11	37116407	11	2835964	C	A	0.34977	0.00764	0.00210	1.50E-04
11	AMPD3	rs12793175	10,384,303	A	G	0.0234076	0.00344032	3.37E-08	38200128	11	10362756	A	G	0.09958	-0.00104	0.00337	9.40E-01
11	ARNTL	rs6486122	13,361,524	T	C	0.0243473	0.00274947	6.7E-13	38200128	11	13339977	T	C	0.36710	0.01331	0.00208	1.80E-10
11	PDE3B	rs79634051	14,561,945	G	C	0.0551675	0.00767501	5.46E-09	38200128								
11	ANO3	rs1461396	26,281,664	G	C	0.0353251	0.005										

Chr	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB BP_38	TWB EA	TWB NEA	TWB EAF	TWB BETA	TWB SE	TWB P
11	MACROD1	rs2845885	63,869,062	T	C	-0.02	0.004	1.18E-08	34059833	11	64101590	C	T	0.40807	0.00325	0.00204	9.80E-02
11	VEGFB	rs56271783	64,004,723	C	G	0.089768	0.00618519	5.16E-32	38200128								
11	KAT5	rs10750766	65,473,798	A	C	0.0290322	0.00280867	4.97E-17	38200128	11	65706327	A	C	0.34009	0.00294	0.00214	2.00E-01
11	RIN1	rs144718240	66,094,785	T	C	0.0452433	0.00616048	2.53E-09	38200128								
11	CPT1A	rs11605837	68,597,886	T	G	0.0233185	0.00275109	6.08E-12	38200128	11	68830418	T	G	0.17682	0.00459	0.00263	7.00E-02
11	PDE2A	rs3781926	72,350,595	T	C	0.009	0.002	3.26E-05	34059833	11	72639551	C	T	0.45901	0.00013	0.00203	8.20E-01
11	SNRPGP16 - MTNR1B	rs1387153	92,673,828	T	C	0.045202	[0.032-0.058] unit increase	1E-11	37291194	11	92940662	T	C	0.45703	0.00811	0.00201	5.00E-05
11	MTNR1B	rs10830963	92,708,710	G	C	-0.17	0.016	6.71E-28	24699409	11	92975544	G	C	0.43301	0.01123	0.00202	1.40E-08
11	ZC3H12C	rs6589112	109,971,929	C	T	0.0195487	0.00279146	1.33E-08	38200128	11	110101204	T	C	0.11954	-0.00071	0.00309	7.10E-01
11	PPP2R1B	rs117847213	111,421,906	A	G	0.0552327	0.00650405	5.55E-12	38200128								
11	PPP2R1B	rs615642	111,649,421	G	A	0.0196409	0.00263911	1.55E-09	38200128	11	111778697	G	A	0.23759	0.00238	0.00236	2.70E-01
11	LINC02702	rs11215942	116,325,337	A	G	0.0669308	0.00609362	4.99E-19	38200128								
11	LINC02702	rs79859462	116,379,996	A	G	0.0684905	0.00880893	2.81E-10	38200128	11	116509279	A	G	0.02210	0.04163	0.00686	6.30E-10
11	LINC02702	rs117794084	116,433,496	T	G	0.16877	0.0100943	6.33E-42	38200128								
11	LINC02702	rs519000	116,511,522	T	C	0.0489442	0.00342156	3.79E-31	38200128								
11	LINC02702	rs480823	116,525,730	C	T	0.205468	0.0047722	2.09E-267	38200128	11	116655013	C	T	0.11553	0.05687	0.00317	2.00E-73
11	LINC02702	rs11824135	116,559,553	T	G	0.255061	0.00512564	1.83E-356	38200128	11	116688837	T	G	0.20171	0.01450	0.00254	1.80E-09
11	APOA5	rs6589567	116,670,676	A	C	0.195814	0.00411457	3.19E-326	38200128								
11	APOA4	rs12721043	116,692,293	C	A	0.247856	0.0121012	5.02E-62	38200128								
11	SIK3	rs61907602	116,810,655	G	C	0.1207	0.00713446	6.93E-43	38200128								
11	SIK3	rs11216236	116,889,658	T	C	0.0880026	0.00619819	1.04E-30	38200128								
11	PCSK7	rs142334475	117,088,573	G	A	0.116315	0.0118873	2.03E-15	38200128								
11	CEP164	rs573455	117,267,884	G	A	0.022103	0.00255033	2.03E-12	38200128	11	117397168	G	A	0.31587	-0.00556	0.00218	1.00E-02
11	DSCAML1	rs117604511	117,382,799	C	A	0.0768542	0.00901377	4.57E-12	38200128								
11	HYOU1	rs1003081	118,913,993	T	C	0.0218031	0.00256489	5.29E-12	38200128								
11	MIR100HG	rs1622638	121,800,971	A	G	0.0205276	0.00260643	1.65E-10	38200128	11	121930263	A	G	0.05321	-0.00603	0.00447	2.00E-01
12	CCND2	rs117233107	4,328,521	G	A	0.0878987	0.0110248	9.84E-11	38200128								
12	CHD4.LPAR5	rs10774439	6,731,818	G	A	0.0276134	0.00331948	1.48E-11	38200128								
12	PDE3A	rs11045171	20,470,199	A	G	0.04133	0.00321559	1.82E-25	38200128								
12	PDE3A	rs4762753	20,579,969	G	T	0.024887	0.00318382	2.26E-10	38200128	12	20427035	T	G	0.05946	-0.00745	0.00428	5.30E-02
12	PDE3A	rs12369443	20,582,651	A	G	0.01	0.002	6.66E-06	34059833	12	20429717	G	A	0.07661	-0.00872	0.00382	9.90E-03
12	PDE3A	rs11045247	20,592,624	A	G	0.0346795	0.00488395	8.33E-09	38200128	12	20439690	A	G	0.05297	0.01678	0.00451	2.70E-04
12	SLCO1B1	rs67981690	21,343,886	G	A	0.0303598	0.00381306	1.04E-10	38200128	12	21190952	G	A	0.13430	0.01024	0.00300	5.00E-04
12	GLYS2	rs2054435	21,696,684	A	G	-0.015	0.003	9.50E-09	34059833	12	21543750	A	G	0.21104	-0.00580	0.00248	1.80E-02
12	GLYS2	rs6487237	21,699,928	A	C	0.015	0.003	4.68E-09	34059833	12	21546994	C	A	0.21793	-0.00513	0.00245	3.00E-02
12	ITPR2	rs10842703	26,456,188	T	A	0.022332	0.00296351	9.68E-10	38200128	12	26303255	A	T	0.29543	-0.00248	0.00221	2.20E-01
12	ITPR2	rs10842708	26,474,867	A	G	-0.01	0.002	1.08E-05	34059833	12	26321934	A	G	0.29558	-0.00250	0.00221	2.10E-01
12	ALG10	rs11052977	34,035,030	A	C	0.0184327	0.00260984	9.99E-09	38200128	12	33882095	C	A	0.05356	0.00511	0.00449	3.60E-01
12	HDAC7	rs111264094	48,202,696	C	G	0.057	0.009	1.64E-09	34059833								
12	INHBC,INHBE	rs7966846	57,653,582	C	A	0.0220367	0.00282464	2.44E-10	38200128	12	57259799	C	A	0.38897	0.00161	0.00207	2.30E-01
12	INHBC	rs1222982	57,781,893	G	A	0.0413563	0.00298114	2.15E-29	38200128	12	57388110	A	G	0.08951	-0.00830	0.00353	1.80E-02
12	FAM19A2	rs10506418	61,488,772	A	G	-0.62	0.13	1.90E-08	27416945	12	61094991	A	G	0.12800	0.00360	0.00302	2.80E-01
12	HMG.A2	rs1351394	66,351,826	T	C	-0.011	0.002	2.71E-09	34059833	12	65958046	T	C	0.08615	-0.00031	0.00360	9.70E-01
12	HMG.A2	rs7968682	66,371,880	T	G	0.011	0.002	3.17E-09	34059833	12	65978100	G	C	0.08216	-0.00039	0.00370	9.00E-01
12	SYT1	rs73343765	79,157,553	A	G	-0.19	0.053	2.14E-04	34059833								
12	IGF1	rs1402013	102,740,822	A	G	-0.009	0.002	1.31E-06	34059833	12	102347044	A	G	0.46523	-0.00037	0.00203	8.70E-01
12	IGF1	rs35767	102,875,569	G	A	0.013	0.006	2.20E-09	20081858	12	102481791	A	G	0.35862	-0.00335	0.00210	1.00E-01
12	IGF1	rs860598	102,898,446	A	G	0.018	0.003	6.88E-12	34059833	12	102504668	G	A	0.34862	-0.00314	0.00213	1.50E-01
12	IGF1	rs35747	102,912,558	A	G	0.017	0.003	2.68E-11	34059833	12	102518780	G	A	0.34376	-0.00291	0.00212	1.80E-01
12	RIC8B	rs11113118	107,199,142	A	G	0.0230064	0.00294329	2.26E-10	38200128	12	106805364	A	G	0.33929	0.00784	0.00214	8.00E-05
12	ACACB	rs7298135	109,698,566	A	T	0.0251002	0.00327426	4.96E-10	38200128	12	109260761	T	A	0.25330	-0.01094	0.00234	8.20E-08
12	SH2B3	rs653178	112,007,756	C	T	0.0224944	0.0025495	8.11E-13	38200128								
12	ZCCHC8	rs116896792	122,948,907	C	T	0.0422638	0.0044306	9.92E-15	38200128								
12	HCAR1	rs526276	123,192,454	C	T	0.0391756	0.0033126	8.3E-22	38200128	12	122707907	T	C	0.49821	-0.00508	0.00203	5.10E-03
12	CCDC62	rs138436155	123,285,110	C	G	0.0529468	0.00654242	5.14E-11	38200128								
12	SETD8	rs10773000	123,736,084	G	T	0.0299301	0.00270811	3.02E-19	38200128	12	123251537	T	G	0.30043	-0.00289	0.00222	7.80E-02
12	DNAH10	rs7133378	124,409,502	A	G	-0.013	0.002	6.00E-11	34059833	12	123924955	A	G	0.11494	-0.00645	0.00316	4.90E-02
12	CCDC92	rs11057397	124,419,728	C	T	0.0449404	0.0026966	1.15E-41	38200128	12	123935181	T	C	0.11457	-0.00714	0.00317	2.80E-02
12	ZNF664-FAM101A; ZNF664	rs7975482	124,481,690	A	G	0.012	0.002	1.97E-10	34059833	12	123997143	G	A	0.07304	-0.01480	0.00388	2.00E-04
12	ZNF664-RFLNA	rs10773049	124,506,631	T	C	0.0456075	0.00260935	1.18E-45	38200128	12	124022084	T	C	0.45516	0.00838	0.00203	2.70E-05
12	NCOR2	rs837500	125,077,567	C	T	0.0189759	0.00266579	7.65E-09	38200128								
12	SCARB1	rs921919	125,265,201	A	G	0.0317463	0.00276063	1.05E-20	38200128								
12	SCARB1	rs112403212	125,303,254	T	C	0.0283816	0.00368809	4.26E-10	38200128	12	124818708	T	C	0.10859	0.00253	0.00326	4.10E-01
12	SCARB1	rs61941660	125,319,181	C	T	0.0414455	0.00454689	1.4E-13	38200128								
12	SCARB1	rs7298751	125,380,232	A	G	0.0280479	0.00387146	4.14E-09	38200128								
13	FGF9	rs12583553	22,332,822	A	T	0.55	0.12	3.60E-09	27416945								
13	DLEU2	rs41284816	50,655,989	G	T	0.071498	0.00951314	1.07E-09	38200128								
13	DLEU1,DLEU2,KPNA3	rs1327645	51,122,503	A	G	0.021732	0.00290817	1.33E-09	38200128	13	50548367	G	A	0.13809	-0.00388	0.00297	1.80E-01
13	LINC00348	rs12863082	71,824,582	C	T	0.0207071	0.00300742	2.31E-08	38200128	13	71250450	C	T	0.01788	-0.00737	0.00762	6.00E-01
13	GPR180	rs9561643	95,253,131	C	A	0.0191134	0.00274234	1.55E-08	38200128								
13	LINC00460 - RPL35P9	rs17254590	107,037,344	G	C	2.52	[NR]	0.00000002	30327367				</				

Chr	Gene	SNP	Pos (h37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB BP_38	TWB EA	TWB_NEA	TWB_EAF	TWB_BETA	TWB_SE	TWB_P
15	<i>C15orf34,ENSG00000259450</i>	rs275179	39,447,529	A	G	0.0246741	0.00359241	2.5E-08	38200128	15	39155328	A	G	0.37062	0.00582	0.00210	6.20E-03
15	<i>GCHFR</i>	rs72735627	41,057,507	C	T	0.0323954	0.00437318	1.85E-09	38200128								
15	<i>SPTBN5</i>	rs2925339	42,091,212	G	A	0.0245757	0.00271378	2.01E-13	38200128	15	41799014	A	G	0.01962	-0.00577	0.00728	2.60E-01
15	<i>MAP1A</i>	rs139974673	44,027,885	C	T	0.196545	0.00800442	2.51E-88	38200128								
15	<i>TCF12</i>	rs935328	57,538,801	T	A	0.0212468	0.00291282	3.24E-09	38200128	15	57246603	A	T	0.16721	-0.00178	0.00272	4.70E-01
15	<i>LIPC</i>	rs1601935	58,671,765	T	G	0.0248295	0.00269677	7.96E-14	38200128	15	58379566	G	T	0.31707	0.02107	0.00222	3.40E-22
15	<i>LINC02349</i>	rs12440800	61,960,302	T	A	0.0210613	0.00293435	5.74E-09	38200128	15	61668103	T	A	0.26528	0.00767	0.00233	2.00E-03
15	<i>C2CD4A</i>	rs4502156	62,383,155	T	C	-0.092	0.014	1.14E-10	24699409	15	62090956	C	T	0.48069	-0.00218	0.00202	2.00E-01
15	<i>NPM1P47 - C2CD4B</i>	rs7167878	62,396,189	A	C	0.04253	[0.03-0.055] unit decrease	7E-12	37291194	15	62103990	A	C	0.34056	-0.00461	0.00213	1.50E-02
15	<i>LACTB</i>	rs2937859	63,366,282	G	A	0.0339049	0.00320269	8.69E-18	38200128								
15	<i>USP3</i>	rs17184382	63,792,486	A	C	0.0251802	0.00257286	2E-15	38200128	15	63500287	C	A	0.05155	-0.01047	0.00457	1.30E-02
15	<i>HERC1</i>	rs117044596	64,002,266	G	A	0.0489714	0.00677225	4.42E-09	38200128								
15	<i>LINC01169</i>	rs4776793	66,872,114	T	C	0.0219862	0.00266086	2.02E-11	38200128	15	66579776	T	C	0.41799	0.00171	0.00208	3.10E-01
16	<i>LMF1</i>	rs12924608	950,007	T	C	0.0223239	0.00262308	5E-12	38200128								
16	<i>MGRN1</i>	rs12921195	4,677,604	A	C	0.0316385	0.00380557	1.52E-11	38200128								
16	<i>NTAN1</i>	rs4074872	15,117,299	A	G	0.0388261	0.00323048	1.8E-22	38200128								
16	<i>PDXDC1</i>	rs12928099	15,150,505	C	A	0.0389922	0.00279415	1E-29	38200128								
16	<i>TAOK2</i>	rs3814883	29,994,922	T	C	0.0249413	0.00255677	2.46E-15	38200128								
16	<i>ZNF646</i>	rs34898535	31,025,641	C	T	0.0193591	0.00262845	2.28E-09	38200128	16	31014320	C	T	0.11120	0.00615	0.00322	4.50E-02
16	<i>RBL2</i>	rs2024449	53,494,617	T	C	0.01	0.002	4.81E-07	34059833	16	53460705	C	T	0.19914	0.00355	0.00252	1.80E-01
16	<i>FTO</i>	rs1421085	53,800,954	C	T	0.02	0.003	1.90E-15	22885924	16	53767042	C	T	0.12616	0.00939	0.00304	8.40E-04
16	<i>NUP93</i>	rs11643205	56,787,882	T	C	0.0416853	0.00594432	1.27E-08	38200128	16	56753970	C	T	0.03983	0.00885	0.00517	1.20E-01
16	<i>HERPUD1</i>	rs72786786	56,985,514	G	A	0.151343	0.00279684	4.12E-421	38200128								
16	<i>CETP</i>	rs7499892	57,006,590	T	C	0.17128	0.00332693	2.15E-381	38200128	16	56972678	T	C	0.17122	0.01159	0.00268	3.40E-06
16	<i>CETP</i>	rs11644475	57,007,652	A	G	0.0633244	0.00773506	3.08E-11	38200128								
16	<i>NLRCS</i>	rs11648592	57,083,232	A	G	0.0739214	0.00935557	1.44E-10	38200128								
16	<i>NRN1L</i>	rs55781197	67,940,350	A	G	0.048112	0.00398739	1.23E-22	38200128	16	67906447	G	A	0.01778	-0.01778	0.00765	5.40E-02
16	<i>NEAT5</i>	rs862320	69,651,866	C	T	0.0215868	0.00259383	1.45E-11	38200128	16	69617963	T	C	0.09579	-0.00785	0.00344	3.00E-02
16	<i>HP</i>	rs3794695	72,097,827	T	C	0.0323246	0.00324823	6.75E-16	38200128	16	72063928	T	C	0.24752	0.00786	0.00237	1.60E-04
16	<i>HP</i>	rs7191623	72,212,044	G	A	0.0219363	0.00313144	1.31E-08	38200128	16	72178145	A	G	0.19671	0.00478	0.00255	1.80E-02
16	<i>CMIP</i>	rs2925979	81,534,790	T	C	0.0506561	0.00277754	1.5E-49	38200128	16	81501185	T	C	0.42882	0.01393	0.00204	3.70E-13
16	<i>FAM92B</i>	rs79311290	85,150,163	G	A	0.0368533	0.00433717	5.4E-12	38200128								
16	<i>BANP</i>	rs12927305	88,006,413	T	C	0.0215341	0.0025548	7.95E-12	38200128	16	87972807	T	C	0.03995	0.00643	0.00517	2.20E-01
17	<i>IPSS3</i>	rs34345377	489,296	G	C	0.0237952	0.00321406	1.89E-09	38200128	17	586056	G	C	0.02701	0.00559	0.00623	5.80E-01
17	<i>SLC2A4</i>	rs117643180	7,185,779	A	C	0.1453	[0.1-0.19] unit increase	5E-11	37291194								
17	<i>TNFSF12</i>	rs9902027	7,440,984	C	T	0.0263675	0.00305374	2.45E-12	38200128								
17	<i>PEMT</i>	rs7215055	17,458,353	G	A	0.0534071	0.0052582	1.7E-16	38200128								
17	<i>PEMT</i>	rs56157833	17,478,433	T	A	0.0239995	0.00338081	8.41E-09	38200128								
17	<i>STARD3</i>	rs931992	37,821,435	G	T	0.020419	0.00270173	8.65E-10	38200128	17	39665182	T	G	0.36605	-0.00119	0.00211	5.80E-01
17	<i>MLX</i>	rs12938909	40,787,764	G	C	0.0296854	0.00282334	1.44E-17	38200128	17	42635746	G	C	0.43999	0.00758	0.00204	1.30E-04
17	<i>DHX8,LINC00910,NBR1</i>	rs113905686	41,469,457	C	A	0.0359473	0.005263	2.99E-08	38200128								
17	<i>CD300LG</i>	rs72836561	41,926,126	T	C	0.202804	0.00730342	2.01E-112	38200128								
17	<i>CD300LG</i>	rs72836567	41,945,776	A	G	0.0448238	0.00347404	1.19E-25	38200128								
17	<i>TMEM101</i>	rs2523159	42,094,734	A	G	0.0303566	0.0033396	1.63E-13	38200128	17	44017366	A	G	0.06404	-0.01200	0.00413	2.80E-03
17	<i>SKAP1</i>	rs11650182	46,272,609	A	G	0.0396309	0.00502247	1.53E-10	38200128								
17	<i>GIP</i>	rs595767	46,957,987	G	A	0.0230144	0.00255098	2.47E-13	38200128	17	48880625	A	G	0.30493	-0.00165	0.00221	2.40E-01
17	<i>ZNF652</i>	rs34666276	47,379,486	C	T	0.0223107	0.00265435	9.08E-12	38200128	17	49302124	C	T	0.25581	0.00419	0.00232	2.50E-02
17	<i>APOH</i>	rs1801689	64,210,580	A	C	0.0601647	0.00742132	4.76E-11	38200128								
17	<i>BPTF</i>	rs12451511	65,874,861	G	T	0.0326168	0.00321083	1.68E-16	38200128	17	67878745	T	G	0.34530	-0.01328	0.00213	1.70E-10
17	<i>ABCA8</i>	rs34931250	66,879,927	T	C	0.0489221	0.00534614	1.13E-13	38200128								
17	<i>KCNJ2</i>	rs4519367	68,470,163	A	G	0.0175032	0.00255102	2.59E-08	38200128	17	70474022	A	G	0.31065	0.00766	0.00219	6.60E-04
17	<i>FAM100B,RNF157</i>	rs56257305	74,207,943	G	A	0.0365624	0.00473336	3.66E-10	38200128								
17	<i>PGS1</i>	rs4969179	76,391,454	T	G	0.0279033	0.00260663	3.75E-18	38200128	17	78395373	G	T	0.44851	-0.00874	0.00203	1.00E-05
18	<i>USP14</i>	rs3931630	148,913	G	A	0.0214553	0.00285302	1.05E-09	38200128								
18	<i>THOC1</i>	rs6506033	289,209	C	T	0.040338	0.00491891	2.85E-11	38200128	18	289209	T	C	0.03783	-0.01789	0.00530	3.30E-04
18	<i>CTAGE1,GATA6</i>	rs4800392	19,908,497	C	A	0.0208211	0.0025629	4.34E-11	38200128	18	22328534	A	C	0.31109	-0.00502	0.00220	3.00E-02
18	<i>LIPG</i>	rs2000813	47,093,864	C	T	0.0269876	0.00278016	3.36E-15	38200128	18	49567494	T	C	0.34353	0.00173	0.00215	3.30E-01
18	<i>LIPG</i>	rs77960347	47,109,955	A	G	0.0904947	0.0110919	3.59E-11	38200128								
18	<i>LIPG</i>	rs1970696	47,169,989	T	C	0.0364443	0.00334601	9.75E-19	38200128	18	49643619	T	C	0.12767	-0.00336	0.00304	3.30E-01
18	<i>MIR122</i>	rs41292412	56,118,358	T	C	0.104353	0.011836	8.43E-13	38200128								
18	<i>PMAIP1</i>	rs11664369	57,739,072	T	C	0.0287823	0.00288263	5.41E-16	38200128	18	60071840	T	C	0.18070	0.00799	0.00264	1.60E-03
18	<i>MC4R</i>	rs78274649	58,053,794	G	A	0.0672668	0.00912826	2.24E-09	38200128								
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	0.014	0.003	1.78E-09	34059833	18	63178651	C	T	0.47128	-0.00947	0.00202	4.00E-07
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	-0.05	0.01	1.90E-08	27416945	18	63178651	C	T	0.47128	-0.00947	0.00202	4.00E-07
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	0.0176385	0.00262519	4.98E-08	38200128	18	63178651	C	T	0.47128	-0.00947	0.00202	4.00E-07
18	<i>BCL2</i>	rs12454712	60,845,884	T	C	0.0374	[0.024-0.051] unit decrease	0.00000004	37291194	18	63178651	C	T	0.47128	-0.00947	0.00202	4.00E-07
19	<i>PIAS4</i>	rs2289863	4,028,783	T	C	0.0207199	0.00296124	1.37E-08	38200128								
19	<i>INSR</i>	rs1799815	7,125,519	A	G	0.033	0.006	9.24E-08	34059833								
19	<i>INSR</i>	rs11085216	7,195,539	G	A	0.0256018	0.00281993	1.75E-13	38200128	19	7195528	G	A	0.32956	0.00375	0.00215	8.10E-02
19	<i>INSR</i>	rs4804413	7,222,655	T	C	0.029957											

Chr	Gene	SNP	Pos (b37)	EA	NEA	BETA or OR	SE or 95% CI	P	Reference (PMID)	CHR	TWB_BP_38	TWB_EA	TWB_NEA	TWB_EAF	TWB_BETA	TWB_SE	TWB_P
19	<i>TM6SF2</i>	rs58542926	19,379,549	C	T	0.108415	0.00483858	7.28E-74	38200128	19	19268740	T	C	0.06647	-0.05250	0.00405	1.40E-39
19	<i>TM6SF2</i>	rs188247550	19,396,616	C	T	0.135155	0.0116437	4.57E-21	38200128								
19	<i>MAU2</i>	rs3934667	19,431,423	G	T	0.0279094	0.00281107	7.87E-16	38200128	19	19320614	T	G	0.31402	-0.01271	0.00219	2.30E-09
19	<i>GATAD2A</i>	rs111406374	19,505,990	A	G	0.0555574	0.00819699	3.8E-08	38200128								
19	<i>PEPD</i>	rs62102718	33,891,013	T	A	0.0300086	0.00282226	6.26E-18	38200128								
19	<i>PEPD</i>	rs10422861	33,894,846	T	C	-0.013	0.002	6.65E-11	34059833	19	33403940	T	C	0.43355	-0.00971	0.00204	1.70E-06
19	<i>PEPD</i>	rs731839	33,899,065	A	G	-0.012	0.002	3.87E-11	34059833	19	33408159	A	G	0.43414	-0.00974	0.00203	1.60E-06
19	<i>PEPD</i>	rs731839	33,899,065	G	A	0.0148	0.002	5.10E-12	22885924	19	33408159	A	G	0.43414	-0.00974	0.00203	1.60E-06
19	<i>HPN,HPN-AS1</i>	rs58895965	35,551,428	A	C	0.0287323	0.00335922	3.91E-12	38200128								
19	<i>HPN,HPN-AS1</i>	rs2305746	35,556,300	G	A	0.0400082	0.00509326	1.84E-10	38200128	19	35065396	A	G	0.16037	-0.02082	0.00275	4.00E-15
19	<i>MAP3K10</i>	rs339525	40,696,513	T	G	-0.007	0.003	2.07E-04	34059833								
19	<i>PLAUR</i>	rs4760	44,153,100	G	A	0.0256077	0.00350928	3.2E-09	38200128								
19	<i>APOC1</i>	rs483082	45,416,178	T	G	0.109491	0.00300535	4.62E-192	38200128	19	44912921	T	G	0.17399	0.06144	0.00266	1.30E-123
19	<i>APOC1</i>	rs1064725	45,422,561	T	G	0.0805094	0.00661905	5.64E-23	38200128								
19	<i>APOC1P1</i>	rs60049679	45,429,708	C	G	0.0838314	0.00521724	7.43E-39	38200128								
19	<i>APOC1P1</i>	rs8106813	45,431,658	G	A	0.0594672	0.00273246	8.63E-70	38200128								
19	<i>RELB</i>	rs2376867	45,500,925	T	C	0.0192588	0.00272332	9.57E-09	38200128	19	44997667	T	C	0.48135	-0.00822	0.00206	9.90E-05
19	<i>GIPIR</i>	rs4802269	46,167,469	A	G	0.0187168	0.0026742	1.35E-08	38200128								
19	<i>GIPIR</i>	rs11671664	46,172,278	A	G	-0.17	0.026	2.63E-11	24699409								
19	<i>IRF2BP1,MYPOP,NANOS2</i>	rs34934360	46,398,989	G	A	0.033703	0.00396352	5.21E-12	38200128								
19	<i>ZC3H4</i>	rs3810291	47,569,003	A	G	0.0211385	0.00271614	2.7E-10	38200128	19	47065746	A	G	0.27592	0.00684	0.00225	1.20E-03
19	<i>ZC3H4</i>	rs200172871	47,592,967	C	CT	0.011	0.003	1.71E-05	34059833								
19	<i>FGF21</i>	rs838133	49,259,529	A	G	0.0254721	0.00263828	4.72E-15	38200128								
19	<i>LILRB5</i>	rs12975366	54,759,361	C	T	0.0210794	0.00259646	4.47E-11	38200128								
19	<i>LILRA3</i>	rs367070	54,800,500	A	G	0.0307663	0.00306135	3.5E-16	38200128								
19	<i>FIZ1</i>	rs12610709	56,102,362	A	G	0.0290922	0.00339012	3.33E-12	38200128	19	55590996	A	G	0.15493	0.01400	0.00280	2.80E-07
19	<i>MIMT1</i>	rs8102873	57,488,423	T	C	0.0193655	0.00258224	1.16E-09	38200128								
20	<i>TCF15</i>	rs282146	555,352	A	G	0.0178678	0.00262714	3.41E-08	38200128								
20	<i>TCF15</i>	rs144033177	571,467	C	A	0.0803563	0.0104396	4.22E-10	38200128								
20	<i>CASC20</i>	rs979012	6,623,374	T	C	0.011	0.002	4.81E-07	34059833	20	6642727	T	C	0.09466	0.00469	0.00346	1.50E-01
20	<i>ACSS2</i>	rs6088461	32,905,161	T	G	0.0186846	0.00258386	4.42E-09	38200128	20	34317355	T	G	0.16278	0.00325	0.00277	2.30E-01
20	<i>ARHGAP40</i>	rs6027072	37,284,070	A	G	-0.39	0.12	4.40E-09	27416945								
20	<i>MAFB</i>	rs2207132	39,142,516	A	G	0.0497346	0.00707453	1.17E-08	38200128								
20	<i>MYBL2</i>	rs285171	42,337,875	C	G	-0.012	0.003	8.94E-06	34059833	20	43709235	C	G	0.17428	-0.00852	0.00266	6.30E-04
20	<i>HNF4A</i>	rs1800961	43,042,364	T	C	0.0660432	0.00733364	2.73E-13	38200128	20	44413724	T	C	0.01470	-0.01089	0.00840	1.30E-01
20	<i>PLTP</i>	rs435306	44,538,484	T	G	0.044549	0.00293994	9.57E-35	38200128	20	45909845	G	T	0.40887	-0.01554	0.00205	3.60E-15
20	<i>PLTP</i>	rs6073958	44,551,855	C	T	0.0935597	0.00318762	2.27E-125	38200128	20	45923216	C	T	0.12656	0.03164	0.00305	2.10E-27
20	<i>EYA2</i>	rs1999536	45,581,777	C	G	-0.012	0.002	1.32E-09	34059833	20	46953138	C	G	0.24063	0.00110	0.00236	6.00E-01
20	<i>EYA2</i>	rs1206760	45,582,472	A	G	-0.011	0.002	8.82E-10	34059833	20	46953833	A	G	0.24068	0.00109	0.00236	6.10E-01
20	<i>EYA2</i>	rs55966194	45,599,090	C	G	0.0241327	0.00282908	4.46E-12	38200128								
20	<i>SULF2</i>	rs6018652	46,340,974	G	A	0.0249611	0.00314761	1.24E-10	38200128								
20	<i>TSHZ2</i>	rs6068280	51,235,613	G	A	0.0196953	0.00272426	4.46E-09	38200128	20	52619074	A	G	0.41425	-0.00374	0.00208	4.60E-02
20	<i>PFND4</i>	rs6013915	52,810,377	A	G	-0.84	0.19	1.50E-09	27416945								
20	<i>BMP7</i>	rs6123685	55,836,040	G	A	0.0233031	0.00292125	9.62E-11	38200128								
20	<i>PCSK1</i>	rs1042521	56,136,536	G	A	0.0201125	0.00254906	1.53E-10	38200128								
20	<i>GNAS</i>	rs185799410	57,466,093	T	G	0.055617	0.0081041	2.57E-08	38200128								
20	<i>OPRL1</i>	rs8126001	62,711,459	C	T	0.0203217	0.00255421	1.08E-10	38200128								
21	<i>NR1P1</i>	rs2223041	16,422,603	T	C	0.0177511	0.00264224	0.00000005	38200128	21	15050282	C	T	0.15790	-0.00268	0.00278	3.70E-01
21	<i>D21S2088E</i>	rs200678953	24,493,294	T	TATATGTTATATAC	0.014	0.003	2.04E-08	34059833								
22	<i>ISX</i>	rs10483182	35,135,106	A	G	-1.16	0.18	7.80E-12	27416945								
22	<i>MAFF</i>	rs2267373	38,600,542	T	C	0.0323984	0.00258297	2.49E-24	38200128	22	38204535	C	T	0.37440	-0.01097	0.00208	2.90E-07
22	<i>FAM227A</i>	rs5757161	38,990,662	A	G	0.025544	0.00270528	1.83E-14	38200128	22	38594657	A	G	0.46865	0.00719	0.00203	7.50E-05

EA = effect allele, NEA = non-effect allele, Chr = chromosome, BETA = Beta coefficients, SE = standard error, P = p-value
This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.
The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 12. Summary of 197 novel genes exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

CHR	Gene	Pos1 (b38)	Pos2 (b38)	IR	TG	HDL-C	T2D	AD	FG	BMI	TG:HDL-C
1	SFPQ	35,183,599	35,193,142		x						
1	ZMYM4	35,268,966	35,421,944								
1	MACF1	39,084,166	39,487,138		x	x	x			x	
1	BMP8A	39,491,645	39,529,869		x		x			x	
1	PPIEL	39,522,279	39,559,698		x	x	x				
1	HEYL	39,623,430	39,639,676			x		x		x	
1	USP1	62,436,303	62,451,804		x						
1	ATG4C	62,784,105	62,865,271		x						
1	SMG5	156,249,223	156,282,829							x	
1	VHLL	156,298,623	156,299,637								
1	CCT3	156,308,960	156,338,415							x	
1	TSACC	156,337,313	156,346,994								
2	SDC1	20,200,796	20,225,433		x					x	
2	LDAH	20,684,013	20,823,130		x		x				
2	TMEM214	27,032,905	27,041,697								
2	AGBL5	27,051,622	27,070,622		x						
2	OST4	27,070,473	27,071,699								
2	EMILIN1	27,078,566	27,086,397								
2	KHK	27,086,742	27,100,751								
2	CGREF1	27,099,352	27,119,127		x						
2	ABHD1	27,123,788	27,130,812								
2	PREB	27,130,755	27,134,674								
2	PRR30	27,136,846	27,139,464		x						
2	TCF23	27,149,076	27,152,951		x						
2	SLC5A6	27,199,586	27,212,307		x	x					
2	CAD	27,217,389	27,243,786		x						
2	TRIM54	27,282,428	27,307,439		x						
2	MPV17	27,309,491	27,323,102		x						
2	GTF3C2	27,325,848	27,357,034		x						
2	PPM1G	27,381,198	27,409,683		x				x	x	
2	NRBP1	27,428,605	27,442,257		x				x	x	
2	SPATA31H1	27,576,521	27,582,722								
2	ZNF512	27,582,968	27,623,215		x		x				
2	GPN1	27,628,647	27,650,846		x					x	
2	SUPT7L	27,650,809	27,663,840								
2	SLC4A1AP	27,663,470	27,694,980		x						
2	MRPL33	27,771,716	27,779,741		x				x		
2	RBKS	27,781,363	27,890,396		x						
2	BABAM2	27,888,709	28,338,901		x	x			x	x	
2	SIX3	44,941,897	44,946,077				x		x	x	
2	INHBB	120,346,142	120,351,807								
2	NOSTRIN	168,786,538	168,865,339		x				x		
2	SPC25	168,870,890	168,890,434		x				x		
2	G6PC2	168,901,239	168,910,000						x		
2	ABCB11	168,922,938	169,031,323						x		
3	TIMP4	12,153,067	12,159,351								
3	KBTBD8	66,998,302	67,011,208		x	x				x	
4	SPON2	1,166,932	1,208,962								
4	MSANTD1	3,249,039	3,256,615							x	
4	RG512	3,314,146	3,439,913		x					x	
4	LRPAP1	3,503,596	3,532,497								
4	FAM184B	17,632,085	17,781,512				x				
4	DCAF16	17,800,654	17,810,758				x				
4	NCAPG	17,810,812	17,844,864		x						
4	UGT2B15	68,646,596	68,670,776		x	x					
4	KLHL8	87,160,103	87,220,608		x						
4	TLL1	165,873,257	166,104,457							x	
5	HSD17B4	119,452,442	119,542,335			x					
5	HAVCR1	157,029,519	157,058,959		x						

CHR	Gene	Pos1 (b38)	Pos2 (b38)	IR	TG	HDL-C	T2D	AD	FG	BMI	TG:HDL-C
6	RREB1	7,107,596	7,251,980		x	x	x		x		
6	TRIM27	28,903,001	28,923,991								
6	OR10C1	29,439,938	29,440,977								
6	MAS1L	29,486,765	29,487,902								
6	UBD	29,555,611	29,559,925								
6	GABBR1	29,602,227	29,633,185		x			x		x	
6	MOG	29,656,980	29,672,372					x		x	
6	HLA-F	29,723,339	29,727,296								
6	HCG4	29,791,030	29,793,073								
6	ZNRD1ASP	30,001,011	30,061,189								
6	TRIM31	30,102,896	30,113,090		x	x				x	
6	TRIM40	30,136,107	30,148,735			x				x	
6	TRIM15	30,163,205	30,172,696								
6	TRIM26	30,184,454	30,213,494		x						
6	HCG17	30,234,038	30,326,134		x						
6	HCG18	30,287,396	30,327,156								
6	RPP21	30,345,128	30,346,858								
6	ABCF1	30,571,392	30,591,532								
6	PPP1R10	30,600,399	30,617,307							x	
6	ATAT1	30,626,835	30,646,821								
6	DHX16	30,653,118	30,673,053								
6	FLOT1	30,727,733	30,742,676								
6	IER3	30,743,198	30,744,550								
6	DDR1	30,884,083	30,900,156								
6	GTF2H4	30,908,199	30,914,103								
6	VARS2	30,914,204	30,926,458								
6	SFTA2	30,931,349	30,932,175								
6	MUC21	30,983,707	30,989,898		x						
6	MUC22	31,005,951	31,035,402		x						
6	HCG22	31,053,449	31,059,878				x				
6	C6orf15	31,111,222	31,112,555		x						
6	HCG27	31,197,759	31,203,968			x	x	x			
6	MICA	31,399,783	31,415,316		x	x				x	
6	GRM4	34,018,642	34,155,622			x				x	
6	GSTA1	52,791,379	52,803,866								
7	POLD2	44,114,679	44,123,570						x		
7	MYL7	44,138,863	44,141,317				x		x		
7	YKT6	44,200,978	44,214,294				x		x		
7	CAMK2B	44,217,149	44,325,631		x		x		x		
7	AUTS2	69,598,918	70,793,068				x	x		x	
7	POM121	72,879,334	72,951,440		x					x	
7	NSUN5	73,302,515	73,308,867								
7	FKBP6	73,328,151	73,358,637		x						
7	FZD9	73,433,778	73,436,120		x	x					
7	BAZ1B	73,440,397	73,522,285		x	x					
7	BCL7B	73,536,352	73,557,735			x					
7	TBL2	73,568,945	73,578,683		x	x				x	
7	VPS37D	73,667,843	73,672,110		x	x					
7	DNAJC30	73,680,917	73,683,451		x						
7	ABHD11	73,736,094	73,738,860		x						
7	CLDN3	73,768,996	73,770,270		x						
7	TMEM270	73,861,158	73,865,893								
7	ELN	74,027,788	74,069,906								
7	RFC2	74,231,501	74,254,458		x						
7	CLIP2	74,289,474	74,405,943								
7	GNAT3	80,458,670	80,511,926								
7	CD36	80,602,187	80,679,277		x	x					
7	SEMA3C	80,742,537	80,919,351			x					
7	CDK6	92,604,920	92,836,627			x					
8	INTS10	19,817,406	19,852,075		x	x	x				
8	KCNU1	36,784,323	36,936,126		x	x	x				
8	SDCBP	58,553,168	58,582,860								

CHR	Gene	Pos1 (b38)	Pos2 (b38)	IR	TG	HDL-C	T2D	AD	FG	BMI	TG:HDL-C
8	NSMAF	58,583,504	58,659,845		x						
8	SLC30A8	116,950,272	117,176,714		x		x		x	x	
9	DMRT2	1,050,345	1,057,554		x						
9	PTPN3	109,375,693	109,498,313		x						
9	PALM2	109,640,787	109,951,476								
10	AKR1C4	5,196,834	5,218,947		x	x					
10	NRBF2	63,133,246	63,155,031		x						
10	REEP3	63,521,362	63,625,123		x	x	x			x	
10	KIF11	92,593,067	92,655,395								
10	WDR11	120,851,174	120,909,526			x	x				
11	DAGLA	61,680,432	61,747,002							x	
11	MYRF	61,752,648	61,788,517		x	x					
11	TMEM258	61,789,129	61,792,613		x	x			x		
11	FEN1	61,792,636	61,797,242								
11	FADS2	61,816,202	61,867,354		x	x	x		x		
11	FADS3	61,873,522	61,891,545		x	x					
11	RAB3IL1	61,897,295	61,920,269		x						
11	BUD13	116,748,169	116,772,998		x	x					
11	APOC3	116,829,907	116,833,071		x	x					
11	APOA1	116,835,752	116,837,622		x	x				x	
11	PAFAH1B2	117,144,283	117,178,173		x	x				x	
11	SIDT2	117,179,222	117,197,445		x	x					
11	LOC100652768	117,195,612	117,201,914								
11	TAGLN	117,199,323	117,204,792		x	x					
11	RNF214	117,232,624	117,285,688		x	x					
11	BACE1	117,285,685	117,316,256		x	x					
11	NLRX1	119,168,333	119,184,016								
12	FAM222A	109,714,381	109,770,507			x					
12	ANKRD13A	109,999,429	110,039,430			x					
12	IFT81	110,124,334	110,218,795			x				x	
12	ATP2A2	110,281,226	110,351,092			x					
12	CUX2	111,034,023	111,350,556		x	x				x	
14	C14orf166	51,989,509	52,004,702								
14	SERPINA5	94,581,368	94,593,120								
15	AQP9	58,138,208	58,185,911			x					
15	TLE3	70,047,790	70,097,917		x	x				x	
15	PCSK6	101,303,927	101,489,984		x	x	x				
17	ZNHIT3	36,486,626	36,499,310		x		x			x	
17	MYO19	36,495,754	36,535,457				x			x	
17	PIGW	36,535,554	36,539,301								
17	GGNBP2	36,544,887	36,589,846							x	
17	DHRS11	36,591,795	36,600,804							x	
17	CLTC	59,619,688	59,696,956								
17	PTRH2	59,697,305	59,707,495								
17	VMP1	59,707,501	59,840,591		x						
17	MIR21	59,841,265	59,841,337								
17	TUBD1	59,859,479	59,892,945		x	x					
17	RPS6KB1	59,893,045	59,950,425		x						
17	RNFT1	59,952,361	59,964,756								
17	C17orf58	67,991,098	67,993,649		x					x	
17	KPNA2	68,035,731	68,046,854			x				x	
17	LINC00674	68,101,554	68,135,929								
19	MARCHF2	8,413,305	8,439,017			x	x				
19	HNRNPM	8,444,918	8,489,118			x					
19	PRAM1	8,490,055	8,502,654								
19	NCAN	19,211,972	19,252,252		x					x	
19	HAPLN4	19,255,640	19,262,787		x					x	
19	NDUFA13	19,516,209	19,528,204								
19	YJEFN3	19,528,860	19,537,584								
19	CILP2	19,538,264	19,546,659		x					x	
19	PBX4	19,561,706	19,618,916		x					x	
19	GMIP	19,629,472	19,643,667		x						

CHR	Gene	Pos1 (b38)	Pos2 (b38)	IR	TG	HDL-C	T2D	AD	FG	BMI	TG:HDL-C
19	CEBPA	33,299,933	33,302,564		x	x					
19	CEBPG	33,373,668	33,382,686								
19	NECTIN2	44,846,135	44,889,228		x	x	x	x		x	
19	TOMM40	44,891,219	44,903,689		x	x		x		x	
19	APOE	44,905,781	44,909,393		x	x	x	x		x	
19	APOC2	44,946,051	44,949,565		x	x		x			
20	LINC00261	22,560,553	22,578,642				x		x		
20	FOXA2	22,581,003	22,585,463						x		
20	LOC101929685	22,587,521	22,607,517								
20	ZNF335	45,948,652	45,972,194		x	x					
20	MMP9	46,008,907	46,016,561								
20	SLC12A5	46,021,689	46,060,150		x	x					
22	MIRLET7BHG	46,085,996	46,113,928								
22	PPARA	46,150,595	46,243,756		x					x	

AD = Alzheimer's disease; b38 = Genome Research Consortium human build 38; BMI = body mass index; CHR = chromosome; FG = fasting glucose; HDL-C = high-density lipoprotein cholesterol; IR = insulin resistance; NA = not available; Pos = position; T2D = type 2 diabetes; TG = triglycerides; TG:HDL-C = the triglyceride to high-density lipoprotein cholesterol ratio;

x: Previous GWASs reported in the NHGRI-EBI GWAS Catalog have identified various phenotypes that reach genome-wide significance ($P < 5 \times 10^{-8}$). This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test. The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 13. Linkage disequilibrium (LD) between top SNPs exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

Gene1	SNP1	Gene2	SNP2	LD (R^2)
GCKR	rs1260326	SPATA31H1	rs1919127	0.4702
GCKR	rs1260326	ZNF512	rs12989678	0.4644
GCKR	rs1260326	GPN1	rs34502053	0.2377
GCKR	rs1260326	SUPT7L	rs4666010	0.1309
GCKR	rs1260326	SLC4A1AP	rs13021208	0.1940
GCKR	rs1260326	RBKS	rs898034	0.1506
GCKR	rs1260326	MRPL33	rs3792253	0.1110
MLXIPL	rs3812316	FZD9	rs1178947	0.7352
MLXIPL	rs3812316	BAZ1B	rs111837003	0.7517
MLXIPL	rs3812316	BCL7B	rs7793710	0.8312
MLXIPL	rs3812316	TBL2	rs13246490	0.8350
APOA5	rs651821	BUD13	rs6589565	0.6649
APOA5	rs651821	APOC3	rs5128	0.0945
APOA5	rs651821	APOA1	rs12718464	0.0079
APOA5	rs651821	PAFAH1B2	rs7925256	0.0509
APOA5	rs651821	SIDT2	rs6589603	0.0383
APOA5	rs651821	TAGLN	rs588534	0.0300
APOC1	rs5117	NECTIN2	rs283811	0.5174
APOC1	rs5117	TOMM40	rs157582	0.5458
APOC1	rs5117	APOE	rs440446	0.2215

R^2 = plink --bfile file_name --ld SNP1 SNP2 --out outfile

Supplementary Table 14. Conditional analyses for the top 20 novel genes exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P (conditional)	P (original)
Conditional analysis on GCKR rs1260326										
2	<i>SPATA31H1</i>	rs1919127	27,578,626	C	T	0.47	0.01	0.003	0.014	6.90E-114
2	<i>ZNF512</i>	rs12989678	27,598,615	T	C	0.47	0.01	0.003	3.30E-03	1.30E-115
2	<i>GPN1</i>	rs34502053	27,631,657	A	G	0.32	0.01	0.002	3.30E-03	7.90E-68
2	<i>SUPT7L</i>	rs4666010	27,655,819	T	C	0.42	0.01	0.002	1.20E-03	9.90E-45
2	<i>SLC4A1AP</i>	rs13021208	27,678,861	T	C	0.34	0.01	0.002	4.00E-03	1.60E-57
2	<i>RBKS</i>	rs898034	27,867,953	T	C	0.47	0.00	0.002	0.140	1.50E-38
2	<i>MRPL33</i>	rs3792253	27,779,135	T	C	0.41	0.01	0.002	5.80E-03	2.20E-37
Conditional analysis on MLXIPL rs3812316										
7	<i>FZD9</i>	rs1178947	73,435,848	C	T	0.09	0.02	0.007	0.048	5.80E-69
7	<i>BAZ1B</i>	rs111837003	73,493,129	T	C	0.09	0.02	0.007	0.062	1.20E-71
7	<i>BCL7B</i>	rs7793710	73,557,201	G	C	0.10	0.01	0.008	0.280	1.10E-83
7	<i>TBL2</i>	rs13246490	73,578,020	T	C	0.10	0.01	0.008	0.320	2.60E-84
Conditional analysis on APOA5 rs651821										
11	<i>BUD13</i>	rs6589565	116,769,521	A	G	0.20	-0.06	0.004	2.60E-45	7.3E-445
11	<i>APOC3</i>	rs5128	116,832,924	G	C	0.29	0.02	0.002	3.50E-11	2.80E-152
11	<i>APOA1</i>	rs12718464	116,836,685	A	G	0.04	-0.04	0.005	1.10E-13	3.10E-39
11	<i>PAFAH1B2</i>	rs7925256	117,174,619	T	C	0.29	0.01	0.002	1.60E-04	8.00E-75
11	<i>SIDT2</i>	rs6589603	117,185,123	C	T	0.50	-0.01	0.002	1.30E-04	1.10E-59
11	<i>TAGLN</i>	rs588534	117,197,788	G	A	0.46	-0.01	0.002	6.30E-05	3.40E-51
Conditional analysis on APOC1 rs5117										
19	<i>NECTIN2</i>	rs283811	44,885,243	G	A	0.17	0.02	0.004	2.80E-09	1.60E-94
19	<i>TOMM40</i>	rs157582	44,892,962	T	C	0.17	0.02	0.004	1.70E-08	7.50E-94
19	<i>APOE</i>	rs440446	44,905,910	G	C	0.39	0.03	0.002	1.40E-37	1.70E-106

A conditional analysis was conducted using mixed linear models implemented in BOLT-LMM, adjusted for an additional lead SNP genotype (e.g., GCKR rs1260326), sex, and the top 10 principal components (PCs).

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error
This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.
The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 15. Heritability and genetic correlations for the TyG index, TG:HDL-C ratio, and log(TG:HDL-C) ratio.

A. Heritability

	h² (stdev)	Lambda GC	Mean Chi²	Intercept	Ratio
TyG index	0.1742 (0.027)	1.3101	1.5787	1.0553 (0.0118)	0.0955 (0.0204)
TG:HDL	0.156 (0.0253)	1.3101	1.5258	1.0579 (0.0115)	0.1101 (0.0218)
log(TG:HDL)	0.1991 (0.0277)	1.3685	1.6669	1.0657 (0.0128)	0.0986 (0.0192)

B. Genetic correlation

Phenotype 1	Phenotype 2	Correlation	Correlation SE	P-value
TyG index	TG:HDL	0.9673	0.0106	0
TyG index	log(TG:HDL)	0.9635	0.0096	0
TG:HDL	log(TG:HDL)	0.9989	0.0028	0

h² = heritability; Lambda GC = Genomic Control Lambda; SE = standard error; stdev = standard deviation; TG:HDL-C = the ratio of triglycerides to high-density lipoprotein cholesterol; TyG index = the triglyceride-glucose index; log(TG:HDL-C) = the logarithm-transformed TG:HDL-C ratio.

This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test. The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.

Supplementary Table 16. Results of the fine mapping analysis in 10 distinct regions of interest for the TyG index.

CHR	BP region	N SNPs of region	CS	N SNPs of CS	Purity	CS coverage	SNPs (Only the first three are shown)
1	61003238~ 64003238	7584	1	51	0.95327	0.9538	rs56342264, rs10889336, rs12042319
			1	13	0.98899	0.95302	rs1318006, rs56213756, rs56403064
2	19491280~ 22491280	6758	2	2	0.98569	0.99999	rs13306194, rs57825321
			3	9	0.92086	0.97282	rs1107851, rs11096641, rs12478327
			1	1	1	1	rs1260326
2	26008073 ~ 29367953	5713	2	1	1	0.99998	rs143881585
			3	7	0.7405	0.95317	rs143644163, rs3792250, rs76395430
			4	120	0.75469	0.95079	rs375337766, rs139395522, rs813592
4	1888545 ~ 4888545	6123	1	6	0.81225	0.95004	rs13127597, rs1894442, rs12644442
			2	5	0.98325	0.99998	rs28766336, rs28478452, rs1076903
7	72106007 ~ 75106007	3412	1	7	0.99965	0.99847	rs3812316, rs77048596, rs13246993
			1	27	0.98345	0.95047	rs6586884, rs6999813, rs77237194
			2	6	0.88616	0.95015	rs1041983, rs4921915, rs11267998
8	18399789 ~ 21520643	9894	3	4	0.93644	0.96396	rs10106652, rs34351848, rs6999158
			4	15	0.99186	0.96668	rs7001307, rs73210856, rs73210858
			5	25	0.9507	0.9526	rs2410617, rs2410616, rs17091872
			6	1	1	0.97156	rs149001621
8	123969835 ~ 126969835	7630	1	9	0.97056	0.95227	rs2954021, rs2954029, rs2980869
			2	24	0.87388	0.95818	rs11990424, rs72724629, rs72724628
			1	1	1	0.99524	rs651821
			2	1	1	0.99943	rs3135507
11	115134723 ~ 118855903	9846	3	2	0.99362	1	rs2075291, rs3741297
			4	2	0.99425	0.99856	rs10750098, rs5128
			5	136	0.66752	0.95037	rs181948358, rs7942637, rs142032672
			1	2	0.9922	0.96246	rs2070895, rs1077835
15	56887979 ~ 59931740	8004	2	2	0.92322	0.97507	rs1532085, rs261291
			3	7	0.94344	0.97645	rs10162642, rs11071371, rs28690720
19	17768740 ~ 20768740	6603	1	1	1	1	rs58542926
			2	1	1	0.96601	rs374807806
			1	2	0.99951	1	rs483082, rs438811
			2	1	1	0.97139	rs440446
19	43378777 ~ 46429300	6668	3	1	1	0.9843	rs370920052
			4	4	0.91849	0.95451	rs2288911, rs4803775, rs11669173
			5	6	0.98608	0.98483	rs7259350, rs7259004, rs111271293

BP = base pair; CHR = chromosome; CS= credible set.

“Purity” is defined as the minimum absolute pairwise correlation (Pearson’s r) among SNPs in the credible set.

The “coverage” of credible sets refers to the probability that the causal variant is contained in the credible set.

Supplementary Table 17. Results of the association of IR-related polygenic risk scores (PRSs) with the TyG index in the testing set.

Phenotype	Reference (Author, year)	Population n	GWAS Sample Size	GWAS SNPs	PRS SNPs	R ² -R ² Null	R ²	P	BETA
TyG_index	-	TWB	95,977	6,753,571	854,050	10.57%	23.80%	< E-200	0.164
TG	Graham et al., 2021	EAS	146,492	15,255,562	994,587	8.10%	21.33%	< E-200	0.145
HDL	Graham et al., 2021	EAS	146,492	16,536,398	994,587	1.99%	15.22%	2.74E-164	-0.071
T2D	Spracklen et al., 2020	EAS	433,540	11,825,584	992,246	1.12%	14.34%	1.41E-92	0.054
Random glucose	Sakaue et al., 2021	EAS	133,336	13,476,509	976,877	0.32%	13.55%	8.74E-28	0.029
HbA1c	Sakaue et al., 2021	EAS	71,221	13,466,143	976,877	0.25%	13.48%	4.86E-22	0.025
NAFLD	Ghodsian N et al., 2021	EUR	778,614	6,797,908	929,100	0.15%	13.38%	7.98E-14	0.02
Fasting glucose	Manning AK et al., 2012	EUR	58,070	2,628,881	923,817	0.09%	13.32%	4.55E-09	0.015
SBP	Sakaue et al., 2021	EAS	145,505	13,477,770	976,877	0.07%	13.29%	7.75E-07	0.013
BMI	Sakaue et al., 2021	EAS	163,835	13,479,178	976,877	0.06%	13.29%	3.18E-06	0.012
IR	Williamson A et al., 2023	EUR	53,334	9,558,719	961,804	0.03%	13.26%	1.22E-03	0.008
LDL	Graham et al., 2021	EAS	146,492	15,226,956	994,587	0.03%	13.25%	1.87E-03	0.008
DBP	Sakaue et al., 2021	EAS	145,515	13,477,770	976,877	0.01%	13.24%	2.68E-02	0.006

BETA = Beta coefficients; BMI = Body Mass Index; DBP = Diastolic Blood Pressure; EAS = East Asian; EUR = European; HDL = High-Density Lipoprotein; HbA1c = Hemoglobin A1c; IR = Insulin Resistance; GWAS = Genome-Wide Association Study; LDL = Low-Density Lipoprotein; NAFLD = Non-Alcoholic Fatty Liver Disease; PRS = polygenic risk score; SBP = Systolic Blood Pressure; TyG index = the triglyceride-glucose index; TG = triglyceride; T2D = Type 2 Diabetes; TWB = Taiwan Biobank.

The TyG index was derived using the formula $\text{Ln}[\text{fasting triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$.

GWAS of the TyG index was conducted using the training set in the Taiwan Biobank.

Null model : TyG index~SNPSEX+AGE+PC1- PC10

PRS model : TyG index~strSCORE +SNPSEX+AGE+PC1- PC10

R² (R-squared): the proportion of variance in the phenotype explained by the PRS model.

PRS SNPs: the number of SNPs included in the PRS calculation.

R²-R² Null: the difference between the R² value of the PRS model and the null model.

Supplementary Table 18. Summary of variants exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the female cohort using the Taiwan Biobank.

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	USP1 *	rs1334806	62409642	A	G	0.4451890	0.0159377	0.0025786	1.8E-10
1	USP1 *	rs72929768	62416932	T	C	0.4488940	0.0170837	0.0025833	8.2E-12
1	USP1 *	rs12406266	62426154	A	G	0.3370760	-0.0204216	0.0026682	7.1E-15
1	USP1 *	rs13375306	62426411	A	G	0.3267270	-0.0202294	0.0026983	1.8E-14
1	USP1 *	rs584998	62426557	G	A	0.4107060	-0.0172975	0.0025617	1.3E-11
1	USP1 *	rs11207965	62427445	A	C	0.3372270	-0.0205646	0.0026626	4.0E-15
1	USP1 *	rs56941198	62427538	AT	A	0.4106740	-0.0172740	0.0025596	1.3E-11
1	USP1 *	rs12023351	62427860	T	C	0.4085200	-0.0179406	0.0025604	2.3E-12
1	USP1 *	rs12045584	62429211	T	A	0.3372720	-0.0205869	0.0026613	3.6E-15
1	USP1 *	rs12025429	62430113	T	C	0.3349360	-0.0211938	0.0026652	5.9E-16
1	USP1 *	rs635897	62430748	C	A	0.4088160	-0.0180125	0.0025575	1.8E-12
1	USP1 *	rs662723	62432105	G	A	0.4104630	-0.0174159	0.0025546	1.1E-11
1	USP1 *	rs10493324	62432471	T	C	0.3247490	-0.0229849	0.0027154	1.0E-17
1	USP1 *	rs60500353	62433313	T	C	0.2121550	-0.0306867	0.0031355	5.2E-23
1	USP1 *	rs624698	62435140	G	A	0.2605930	-0.0307951	0.0028840	1.9E-28
1	USP1 *	rs624700	62435141	C	G	0.2605930	-0.0307951	0.0028840	1.9E-28
1	USP1 *	rs626787	62435572	G	C	0.2603470	-0.0307864	0.0028722	1.5E-28
1	USP1 *	rs631106	62436136	A	C	0.2601610	-0.0307031	0.0028727	2.0E-28
1	USP1	rs646179	62437203	G	A	0.3835950	-0.0237635	0.0026043	1.7E-21
1	USP1	rs9436221	62437688	C	T	0.2548680	-0.0304179	0.0028922	2.7E-27
1	USP1	rs9436222	62437692	G	C	0.2548680	-0.0304179	0.0028922	2.7E-27
1	USP1	rs9436223	62437876	T	C	0.2548260	-0.0305608	0.0028917	1.4E-27
1	USP1	rs12029068	62438624	T	C	0.2548260	-0.0305608	0.0028917	1.4E-27
1	USP1	rs9436661	62438904	G	T	0.2548260	-0.0305608	0.0028917	1.4E-27
1	USP1	rs11588261	62439265	A	G	0.2548280	-0.0305614	0.0028916	1.4E-27
1	USP1	rs10493322	62440222	T	C	0.2134620	-0.0336852	0.0030712	3.9E-29
1	USP1	rs60688353	62440418	CAA	C	0.2134670	-0.0337135	0.0030712	3.5E-29
1	USP1	rs638714	62440818	T	G	0.2544050	-0.0306797	0.0028935	8.8E-28
1	USP1	rs638305	62440866	T	G	0.2550260	-0.0305686	0.0028901	1.4E-27
1	USP1	chr1:62441011_A_AT	62441011	AT	A	0.2403340	-0.0304829	0.0029817	3.4E-26
1	USP1	rs637723	62441057	T	C	0.2523590	-0.0311044	0.0029072	4.3E-28
1	USP1	rs656297	62441924	G	A	0.2550260	-0.0305686	0.0028901	1.4E-27
1	USP1	rs642845	62442564	C	T	0.2624470	-0.0291920	0.0028758	1.2E-25
1	USP1	rs641540	62442867	G	A	0.2550260	-0.0305686	0.0028901	1.4E-27
1	USP1	rs527281380	62444278	A	AAAG	0.2271350	-0.0325739	0.0030378	2.5E-28
1	USP1	rs1553145497	62445632	GTGTA	G	0.2550860	-0.0303086	0.0028920	4.6E-27
1	USP1	rs10647753	62445634	GTA	G	0.2554110	-0.0303822	0.0028926	3.6E-27
1	USP1	rs598253	62445670	C	T	0.2550150	-0.0305953	0.0028902	1.2E-27
1	USP1	rs11207969	62446080	G	A	0.2550150	-0.0305953	0.0028902	1.2E-27
1	USP1	rs659656	62446449	G	C	0.2550150	-0.0305953	0.0028902	1.2E-27
1	USP1	rs10158897	62447248	T	C	0.2134770	-0.0336360	0.0030724	4.8E-29
1	USP1	rs783291	62449307	A	G	0.2550400	-0.0305945	0.0028901	1.2E-27
1	USP1	rs11207970	62449802	T	C	0.2124320	-0.0337902	0.0030802	3.7E-29
1	USP1	rs583609	62451125	C	T	0.2550460	-0.0306023	0.0028901	1.2E-27
1	USP1 *	rs597470	62452125	G	T	0.2550400	-0.0306006	0.0028901	1.2E-27
1	USP1 *	rs597078	62452186	A	G	0.2545730	-0.0306893	0.0028933	1.0E-27
1	USP1 *	rs597076	62452194	A	T	0.2545730	-0.0306893	0.0028933	1.0E-27
1	USP1 *	rs630144	62453193	G	A	0.2550430	-0.0306104	0.0028902	1.1E-27
1	DOCK7 *	chr1:62453356_GT_G	62453356	G	GT	0.2522870	-0.0311047	0.0029268	9.8E-28
1	DOCK7 *	rs79346928	62454307	CAT	C	0.2135140	-0.0337015	0.0030710	3.5E-29
1	DOCK7 *	rs636523	62454337	G	A	0.2132930	-0.0333247	0.0030732	1.4E-28
1	DOCK7 *	rs636497	62454358	G	A	0.2550600	-0.0305519	0.0028901	1.4E-27
1	DOCK7 *	rs624660	62454717	A	C	0.2556250	-0.0306052	0.0028912	1.1E-27
1	DOCK7	rs634341	62455751	C	T	0.2521870	-0.0302555	0.0029086	7.1E-27
1	DOCK7	rs3913007	62455915	C	T	0.2135140	-0.0337094	0.0030711	3.4E-29
1	DOCK7	rs4350231	62456989	A	G	0.2114260	-0.0340351	0.0030828	1.8E-29
1	DOCK7	rs12023489	62458187	A	G	0.2545300	-0.0305901	0.0028940	1.7E-27
1	DOCK7	rs12037659	62458192	T	C	0.2129410	-0.0337660	0.0030763	4.1E-29
1	DOCK7	rs62932760	62458534	TG	T	0.2376280	-0.0303482	0.0029909	3.4E-25
1	DOCK7	rs9988450	62458777	T	C	0.2550640	-0.0305511	0.0028902	1.4E-27
1	DOCK7	rs77064258	62460056	T	C	0.1775650	-0.0302680	0.0033156	7.5E-21
1	DOCK7	rs1305520	62460386	A	T	0.2552870	-0.0306987	0.0028914	8.1E-28
1	DOCK7	rs7547965	62460700	G	A	0.2553320	-0.0305975	0.0028912	1.3E-27
1	DOCK7	chr1:62462070_CA_C	62462070	C	CA	0.2335560	-0.0322639	0.0030356	1.3E-27
1	DOCK7	rs1167996	62462126	T	G	0.2526430	-0.0310855	0.0029019	2.8E-28
1	DOCK7	rs998403	62462878	A	G	0.2116760	-0.0339371	0.0030803	2.3E-29
1	DOCK7	rs11356503	62463707	T	TA	0.2116760	-0.0339371	0.0030803	2.3E-29
1	DOCK7	rs1177541	62464221	G	A	0.2537040	-0.0308073	0.0028970	7.0E-28
1	DOCK7	rs77083979	62464435	A	G	0.2032920	-0.0327021	0.0031272	1.4E-26
1	DOCK7	rs11207972	62464553	G	A	0.2537290	-0.0307878	0.0028967	7.5E-28

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs1167998	62465961	C	A	0.2591310	-0.0298436	0.0028754	1.3E-26
1	DOCK7	rs77907749	62466449	T	C	0.2033440	-0.0325532	0.0031264	2.2E-26
1	DOCK7	rs1168001	62468087	G	A	0.2537540	-0.0306705	0.0028965	1.1E-27
1	DOCK7	rs12124284	62468356	A	G	0.2119510	-0.0338259	0.0030790	3.1E-29
1	DOCK7	rs1168002	62468637	A	G	0.2546980	-0.0309397	0.0028991	3.9E-28
1	DOCK7	rs1168003	62469175	G	A	0.2537540	-0.0306705	0.0028965	1.1E-27
1	DOCK7	rs12043877	62469328	T	C	0.2033380	-0.0325224	0.0031265	2.4E-26
1	DOCK7	rs1007205	62471241	T	C	0.2536910	-0.0307118	0.0028978	1.0E-27
1	DOCK7	rs10889330	62473795	C	G	0.2537510	-0.0306656	0.0028965	1.1E-27
1	DOCK7	rs1979722	62474426	A	G	0.2117330	-0.0337700	0.0030796	3.9E-29
1	DOCK7	rs11442941	62474595	T	TG	0.2536430	-0.0306609	0.0028977	1.3E-27
1	DOCK7	chr1:62475497_GA_G	62475497	GA	G	0.2573420	-0.0304963	0.0029075	8.8E-27
1	DOCK7	rs10889331	62477336	G	T	0.2537480	-0.0306619	0.0028966	1.1E-27
1	DOCK7	rs1168009	62478283	G	A	0.2539560	-0.0306540	0.0028982	1.1E-27
1	DOCK7	rs1168010	62478308	G	A	0.2540300	-0.0306049	0.0028983	1.4E-27
1	DOCK7	rs35913674	62479276	CA	C	0.2542970	-0.0308317	0.0028963	7.4E-28
1	DOCK7	rs1183260	62479747	A	G	0.2535070	-0.0306063	0.0028971	1.4E-27
1	DOCK7	rs6587976	62479960	T	C	0.2535070	-0.0306063	0.0028971	1.4E-27
1	DOCK7	rs1305521	62483363	A	G	0.2547810	-0.0308290	0.0028968	7.1E-28
1	DOCK7	rs11207974	62484289	C	T	0.2534730	-0.0306646	0.0028973	1.2E-27
1	DOCK7	rs10889332	62485187	T	C	0.2534020	-0.0306915	0.0028996	1.2E-27
1	DOCK7	rs2489835	62489300	T	C	0.2534020	-0.0307423	0.0028976	9.0E-28
1	DOCK7	rs1690761	62490191	C	T	0.2533770	-0.0306642	0.0028979	1.2E-27
1	DOCK7	rs10889333	62491359	A	G	0.2116740	-0.0338379	0.0030800	3.0E-29
1	DOCK7	rs10889334	62491528	G	C	0.2116790	-0.0338552	0.0030801	2.8E-29
1	DOCK7	rs10789112	62492087	C	T	0.2116820	-0.0338850	0.0030805	2.7E-29
1	DOCK7	rs1183851	62492987	T	C	0.3789750	-0.0238163	0.0026084	9.8E-22
1	DOCK7	rs10889335	62494430	G	A	0.2034840	-0.0327088	0.0031430	2.3E-26
1	DOCK7	rs1168041	62494579	T	C	0.2184060	-0.0296446	0.0030460	4.5E-23
1	DOCK7	chr1:62494664_T_TG	62494664	TG	T	0.1568900	-0.0301580	0.0035382	3.4E-18
1	DOCK7	rs1168040	62494904	T	C	0.2532860	-0.0312814	0.0028985	1.3E-28
1	DOCK7	rs1168036	62497063	A	G	0.2519060	-0.0308378	0.0029016	1.1E-27
1	DOCK7	rs1002687	62498066	G	A	0.2534310	-0.0307282	0.0029002	1.4E-27
1	DOCK7	chr1:62498080_A_AT	62498080	A	AT	0.2615280	-0.0306634	0.0029242	1.1E-26
1	DOCK7	rs1168034	62498243	G	C	0.2521010	-0.0308068	0.0029007	1.1E-27
1	DOCK7	chr1:62499937_GA_G	62499937	GA	G	0.2528210	-0.0309076	0.0029047	1.0E-27
1	DOCK7	rs35529421	62499950	A	T	0.2058320	-0.0342419	0.0031271	4.8E-29
1	DOCK7	rs1168032	62502076	A	G	0.2519880	-0.0306277	0.0029013	1.8E-27
1	DOCK7	rs1168031	62502316	C	T	0.2521010	-0.0308068	0.0029007	1.1E-27
1	DOCK7	chr1:62502762_A_AT	62502762	AT	A	0.2103620	-0.0339267	0.0030864	4.3E-29
1	DOCK7	rs1168030	62502820	C	T	0.2522170	-0.0308041	0.0029016	1.1E-27
1	DOCK7	rs56342264	62503238	T	TA	0.2104770	-0.0339330	0.0030857	4.3E-29
1	DOCK7	rs1168029	62503731	G	A	0.2531000	-0.0304118	0.0028997	4.5E-27
1	DOCK7	rs1168028	62503760	G	A	0.2520980	-0.0308001	0.0029007	1.1E-27
1	DOCK7	rs1168027	62504513	T	C	0.2519030	-0.0308311	0.0029016	1.1E-27
1	DOCK7	rs1168026	62505325	T	C	0.2520980	-0.0308001	0.0029007	1.1E-27
1	DOCK7	chr1:62506471_CT_C	62506471	CT	C	0.2550370	-0.0304551	0.0029042	5.6E-27
1	DOCK7	rs7527004	62506557	G	A	0.2521670	-0.0307855	0.0029013	1.2E-27
1	DOCK7	rs12027778	62507642	G	C	0.1935610	-0.0327343	0.0031858	1.3E-25
1	DOCK7	rs1184865	62508124	A	G	0.2520900	-0.0307921	0.0029007	1.2E-27
1	DOCK7	rs1168042	62508479	A	T	0.2518980	-0.0308190	0.0029016	1.1E-27
1	DOCK7	rs35836805	62508787	T	TTTAC	0.2101060	-0.0340021	0.0030886	4.3E-29
1	DOCK7	rs11207976	62511080	A	G	0.2518950	-0.0308081	0.0029016	1.2E-27
1	DOCK7	rs11207977	62511636	T	C	0.2106590	-0.0337754	0.0030879	1.0E-28
1	DOCK7	rs1781212	62511748	G	A	0.2542380	-0.0301355	0.0029112	1.6E-26
1	DOCK7	rs1168044	62511887	A	C	0.2552000	-0.0302486	0.0029034	1.4E-26
1	DOCK7	rs1690755	62514490	A	G	0.2522090	-0.0307696	0.0029004	1.2E-27
1	DOCK7	rs10557760	62514728	CACA	C	0.2522160	-0.0308507	0.0029014	9.6E-28
1	DOCK7	rs10889336	62514739	C	T	0.2105930	-0.0339756	0.0030864	3.8E-29
1	DOCK7	rs10889337	62514936	A	G	0.2520900	-0.0307921	0.0029007	1.2E-27
1	DOCK7	rs12090886	62515769	G	A	0.2520900	-0.0307921	0.0029007	1.2E-27
1	DOCK7	rs11207979	62517323	A	G	0.2519030	-0.0307447	0.0029015	1.4E-27
1	DOCK7	rs1168046	62518022	A	C	0.2518020	-0.0307499	0.0029018	1.4E-27
1	DOCK7	rs1168047	62518080	C	T	0.2519030	-0.0307447	0.0029015	1.4E-27
1	DOCK7	rs10889338	62519226	T	C	0.2102790	-0.0339223	0.0030869	4.8E-29
1	DOCK7	rs1168050	62521284	C	T	0.2519460	-0.0307352	0.0029016	1.6E-27
1	DOCK7	rs1690766	62521618	T	C	0.2519090	-0.0307225	0.0029014	1.6E-27
1	DOCK7	rs1781195	62523301	T	C	0.2524510	-0.0305059	0.0028999	4.8E-27
1	DOCK7	rs1627591	62524136	C	T	0.2519090	-0.0307225	0.0029014	1.6E-27
1	DOCK7	rs11577840	62525698	T	C	0.2519090	-0.0307225	0.0029014	1.6E-27
1	DOCK7	rs12062275	62526234	T	C	0.2519090	-0.0307225	0.0029014	1.6E-27
1	DOCK7	rs11207980	62527078	C	T	0.2105840	-0.0339966	0.0030879	3.3E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs4915838	62527397	G	A	0.2519060	-0.0307146	0.0029014	1.6E-27
1	DOCK7	rs12403207	62527949	T	C	0.2524970	-0.0309600	0.0029060	8.4E-28
1	DOCK7	rs12039115	62529592	T	C	0.2018730	-0.0326579	0.0031343	3.0E-26
1	DOCK7	rs1168015	62530375	C	G	0.2519000	-0.0307013	0.0029014	1.7E-27
1	DOCK7	rs1168013	62531167	C	G	0.2518800	-0.0306686	0.0029012	1.9E-27
1	DOCK7	rs10458569	62531930	A	C	0.1824590	-0.0310172	0.0032598	4.0E-22
1	DOCK7	rs35664253	62532065	C	CAG	0.2519000	-0.0307013	0.0029014	1.7E-27
1	DOCK7	chr1:62533439_A_AT	62533439	A	AT	0.2520230	-0.0308416	0.0029019	1.1E-27
1	DOCK7	rs4915840	62533924	C	G	0.2520670	-0.0307147	0.0029025	1.7E-27
1	DOCK7	rs61393465	62535060	G	GC	0.2102830	-0.0338785	0.0030867	5.5E-29
1	DOCK7	rs1168018	62535449	A	C	0.2518950	-0.0307256	0.0029014	1.5E-27
1	DOCK7	rs1168017	62536880	A	G	0.2519000	-0.0307013	0.0029014	1.7E-27
1	DOCK7	rs76176236	62538722	C	T	0.1218130	-0.0254854	0.0038729	9.2E-12
1	DOCK7	rs56115463	62540080	A	C	0.2010440	-0.0325617	0.0031423	5.5E-26
1	DOCK7	rs7548877	62540279	T	C	0.2519290	-0.0306702	0.0029017	1.9E-27
1	DOCK7	rs11207981	62540416	C	A	0.2521500	-0.0307957	0.0029030	1.3E-27
1	DOCK7	rs1168023	62540924	A	T	0.2519320	-0.0306643	0.0029017	1.9E-27
1	DOCK7	rs66827188	62541132	TTATAGA ^A	T	0.2524480	-0.0305073	0.0029043	3.5E-27
1	DOCK7	rs1781221	62541171	A	C	0.2519470	-0.0306590	0.0029019	1.9E-27
1	DOCK7	rs11207982	62541511	T	C	0.2103100	-0.0338772	0.0030871	5.6E-29
1	DOCK7	rs1184547	62541557	G	A	0.2519320	-0.0306643	0.0029017	1.9E-27
1	DOCK7	rs1168022	62542050	A	T	0.2519290	-0.0306693	0.0029017	1.9E-27
1	DOCK7	rs1168021	62544229	A	G	0.2528600	-0.0305753	0.0029004	3.3E-27
1	DOCK7	rs1168020	62544285	C	T	0.2531020	-0.0304313	0.0029030	5.2E-27
1	DOCK7	rs1179765	62544439	G	C	0.2519290	-0.0306693	0.0029017	1.9E-27
1	DOCK7	rs12074528	62545200	T	C	0.2519290	-0.0306693	0.0029017	1.9E-27
1	DOCK7	rs10889339	62546385	A	G	0.2521970	-0.0307493	0.0029025	1.3E-27
1	DOCK7	rs10889340	62546400	A	C	0.2520890	-0.0306728	0.0029022	1.9E-27
1	DOCK7	rs11207983	62546436	C	T	0.2519290	-0.0306693	0.0029017	1.9E-27
1	DOCK7	rs2029763	62547463	G	A	0.2103070	-0.0338840	0.0030871	5.5E-29
1	DOCK7	rs11207984	62547725	C	T	0.2519290	-0.0306693	0.0029017	1.9E-27
1	DOCK7	rs11207985	62548115	A	G	0.2519660	-0.0307281	0.0029017	1.6E-27
1	DOCK7	rs10789113	62549528	T	A	0.2103150	-0.0338828	0.0030871	5.5E-29
1	DOCK7	chr1:62550719_AT_A	62550719	AT	A	0.2633040	-0.0304294	0.0029243	5.8E-27
1	DOCK7	rs11207986	62552499	T	C	0.2519380	-0.0306670	0.0029018	2.0E-27
1	DOCK7	rs10889342	62553181	T	C	0.2081910	-0.0339904	0.0031027	4.7E-29
1	DOCK7	rs11207988	62553316	T	A	0.1900160	-0.0340806	0.0032558	1.7E-26
1	DOCK7	rs7519785	62554248	G	A	0.2519690	-0.0306408	0.0029015	2.2E-27
1	DOCK7	rs10159255	62555145	A	C	0.2103500	-0.0338482	0.0030868	6.4E-29
1	DOCK7	rs2131925	62560271	G	T	0.2530270	-0.0303802	0.0028992	5.7E-27
1	DOCK7	rs2131926	62560340	C	T	0.2521370	-0.0306504	0.0029002	2.1E-27
1	DOCK7	rs10889343	62560758	T	G	0.2521370	-0.0306504	0.0029002	2.1E-27
1	DOCK7	rs4329540	62561353	C	T	0.2527760	-0.0306598	0.0028984	2.2E-27
1	DOCK7	chr1:62562233_CTTT_C	62562233	C	CTTT	0.2105220	-0.0337772	0.0030851	7.7E-29
1	DOCK7	rs4915621	62563762	A	G	0.2521230	-0.0306183	0.0029002	2.4E-27
1	DOCK7	rs12025714	62565940	A	C	0.1980350	-0.0316224	0.0031658	3.5E-24
1	DOCK7	rs6693353	62565945	A	C	0.2521090	-0.0306741	0.0029003	1.9E-27
1	DOCK7	rs139360475	62566892	AACAG	A	0.4583530	-0.0213714	0.0025516	6.4E-18
1	DOCK7	rs10889344	62568270	T	C	0.2521070	-0.0306835	0.0029004	1.8E-27
1	DOCK7	rs10789114	62568551	C	T	0.2091060	-0.0336793	0.0030973	1.6E-28
1	DOCK7	rs7555577	62568692	A	C	0.2519590	-0.0308766	0.0029070	1.0E-27
1	DOCK7	rs10789115	62570458	A	G	0.2521040	-0.0306881	0.0029003	1.8E-27
1	DOCK7	rs12735272	62571136	G	A	0.2521040	-0.0306881	0.0029003	1.8E-27
1	DOCK7	rs12116574	62572166	T	C	0.2067140	-0.0329938	0.0031141	5.6E-27
1	DOCK7	rs142666378	62572632	T	TGG	0.2521040	-0.0306881	0.0029003	1.8E-27
1	DOCK7	rs6696502	62573862	C	T	0.2521040	-0.0306881	0.0029003	1.8E-27
1	DOCK7	rs12038768	62575057	T	G	0.2105210	-0.0338057	0.0030852	6.8E-29
1	DOCK7	rs11207990	62575415	T	C	0.2520950	-0.0306973	0.0029004	1.8E-27
1	DOCK7	rs11207992	62576129	G	T	0.2105210	-0.0338057	0.0030852	6.8E-29
1	DOCK7	rs1472257	62576455	A	G	0.2520870	-0.0306966	0.0029005	1.8E-27
1	DOCK7	rs10789116	62577067	G	A	0.2105210	-0.0338057	0.0030852	6.8E-29
1	DOCK7	rs1748201	62579835	A	C	0.2508910	-0.0307175	0.0029073	2.1E-27
1	DOCK7	rs1748200	62580368	T	C	0.2522830	-0.0307729	0.0029003	1.2E-27
1	DOCK7	rs1629122	62580907	C	A	0.2523460	-0.0306099	0.0029006	2.5E-27
1	DOCK7	chr1:62582603_C_CCCCA	62582603	CCCCA	C	0.2076910	-0.0331375	0.0031586	2.1E-26
1	DOCK7	rs9436224	62582604	C	A	0.2303510	-0.0297459	0.0030586	2.0E-23
1	DOCK7	rs34465969	62582605	C	A	0.2278900	-0.0294964	0.0030602	4.3E-23
1	DOCK7	rs35194512	62582606	C	A	0.1870080	-0.0337888	0.0032832	8.8E-26
1	DOCK7	rs11207995	62583880	C	A	0.2131130	-0.0335862	0.0030826	1.2E-28
1	DOCK7	rs1748195	62583922	G	C	0.2459630	-0.0293187	0.0029245	9.1E-25
1	DOCK7	rs12042319	62584148	A	G	0.2104780	-0.0339473	0.0030856	4.0E-29
1	DOCK7	rs3850634	62584927	G	T	0.2105740	-0.0337549	0.0030848	8.0E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs12030293	62586017	T	C	0.2020580	-0.0325789	0.0031327	3.7E-26
1	DOCK7	rs12048208	62589609	A	G	0.2005530	-0.0330006	0.0031474	1.6E-26
1	DOCK7	rs11207996	62589799	A	G	0.2108500	-0.0338638	0.0030877	6.8E-29
1	DOCK7	rs1748197	62590441	A	G	0.2228870	-0.0331221	0.0030212	1.7E-28
1	DOCK7	rs2366636	62590999	A	G	0.2228870	-0.0331221	0.0030212	1.7E-28
1	DOCK7	rs1748199	62591465	C	T	0.2228870	-0.0331221	0.0030212	1.7E-28
1	DOCK7	rs79439217	62594366	TAAGAA	T	0.2520190	-0.0307534	0.0029029	1.9E-27
1	DOCK7	rs6690733	62594640	C	A	0.2519770	-0.0306262	0.0029013	2.3E-27
1	DOCK7	rs79151558	62595131	G	A	0.0366879	-0.0414612	0.0067331	1.1E-09
1	DOCK7	rs11207997	62596235	T	C	0.2520190	-0.0306687	0.0029010	2.0E-27
1	ANGPTL3, DOCK7	rs34483103	62604866	A	TTAATG	0.2101030	-0.0338838	0.0030916	5.8E-29
1	DOCK7	rs10789117	62606594	C	A	0.2538290	-0.0303748	0.0028968	4.5E-27
1	DOCK7	rs59952505	62607196	C	CA	0.2538570	-0.0306884	0.0028957	1.3E-27
1	DOCK7	rs6675401	62608304	T	C	0.2535580	-0.0305793	0.0028954	2.3E-27
1	DOCK7	rs6678483	62608771	A	C	0.2535580	-0.0305793	0.0028954	2.3E-27
1	DOCK7	rs71776858	62608856	C	CTCAT	0.2103620	-0.0335744	0.0030880	1.7E-28
1	DOCK7	rs10889347	62610155	A	G	0.2535490	-0.0306029	0.0028955	2.1E-27
1	DOCK7	rs10889348	62612551	T	A	0.2104960	-0.0334961	0.0030887	2.0E-28
1	DOCK7	rs10889349	62616248	G	A	0.2473070	-0.0312816	0.0029303	1.4E-27
1	DOCK7	rs2031373	62617618	A	C	0.3860910	-0.0234560	0.0025971	4.9E-21
1	DOCK7	rs61471917	62618359	A	G	0.2535490	-0.0305711	0.0028955	2.4E-27
1	DOCK7	rs10889350	62619595	T	C	0.2538300	-0.0303878	0.0028969	4.4E-27
1	DOCK7	chr1:62619812_T_TA	62619812	TA	T	0.3772580	-0.0234918	0.0026387	1.6E-20
1	DOCK7	rs12239736	62620326	A	T	0.2095290	-0.0336157	0.0030983	1.8E-28
1	DOCK7	rs12239737	62620330	A	T	0.1545500	-0.0323772	0.0035612	1.2E-20
1	DOCK7	rs6587980	62625187	T	C	0.2519380	-0.0307322	0.0029032	2.1E-27
1	DOCK7	rs11207998	62625800	C	G	0.2018340	-0.0325094	0.0031348	4.7E-26
1	DOCK7	rs10157265	62627946	T	C	0.2535220	-0.0305665	0.0028959	2.4E-27
1	DOCK7	rs34211669	62627990	G	GT	0.2102590	-0.0336704	0.0030876	1.2E-28
1	DOCK7	rs11485618	62628536	G	A	0.2102350	-0.0337194	0.0030875	9.7E-29
1	DOCK7	rs10789118	62629021	G	A	0.2102320	-0.0336933	0.0030874	1.1E-28
1	DOCK7	rs7520810	62630040	T	C	0.2534230	-0.0305015	0.0028968	2.8E-27
1	DOCK7	rs12025800	62631110	G	C	0.2535270	-0.0305806	0.0028959	2.3E-27
1	DOCK7	rs141409973	62631753	AG	A	0.2535270	-0.0305806	0.0028959	2.3E-27
1	DOCK7	rs10789119	62632564	A	G	0.2102490	-0.0336976	0.0030873	1.0E-28
1	DOCK7	rs11207999	62632970	C	A	0.2535270	-0.0305806	0.0028959	2.3E-27
1	DOCK7	rs10889352	62633352	C	T	0.2102320	-0.0336933	0.0030874	1.1E-28
1	DOCK7	rs2366638	62633906	A	G	0.2535270	-0.0305806	0.0028959	2.3E-27
1	DOCK7	rs377031118	62634374	GA	G	0.2530020	-0.0304488	0.0028998	4.7E-27
1	DOCK7	rs10789120	62635452	A	G	0.2096710	-0.0333009	0.0030916	4.3E-28
1	DOCK7	rs1570694	62637546	G	A	0.2102110	-0.0336028	0.0030875	1.5E-28
1	DOCK7	rs6657050	62639582	G	A	0.2526740	-0.0304115	0.0029007	4.3E-27
1	DOCK7	rs12047226	62639867	C	T	0.2102030	-0.0336080	0.0030875	1.4E-28
1	DOCK7	rs113795489	62640503	A	AAAGC	0.2101990	-0.0336065	0.0030875	1.4E-28
1	DOCK7	rs7538689	62640577	A	G	0.3864710	-0.0232018	0.0025916	1.3E-20
1	DOCK7	rs7539035	62641096	A	C	0.2535100	-0.0305591	0.0028960	2.4E-27
1	DOCK7	rs995000	62641855	T	C	0.2093500	-0.0330657	0.0030919	1.1E-27
1	DOCK7	rs10789121	62642348	C	T	0.3864110	-0.0232542	0.0025918	1.1E-20
1	DOCK7	rs11208000	62642703	G	A	0.2502270	-0.0306312	0.0029161	2.7E-27
1	DOCK7	rs66531495	62643009	A	GGCCACA	0.2503960	-0.0308984	0.0029197	1.6E-27
1	DOCK7	rs993013	62645398	G	T	0.2547850	-0.0307464	0.0028935	1.2E-27
1	DOCK7	rs1168085	62646649	C	G	0.2535270	-0.0305735	0.0028960	2.3E-27
1	DOCK7	rs1168086	62646718	A	G	0.2535270	-0.0305735	0.0028960	2.3E-27
1	DOCK7	rs746735	62647840	C	A	0.2538490	-0.0303481	0.0028981	5.2E-27
1	DOCK7	rs1168089	62648048	T	C	0.2524940	-0.0299557	0.0028995	2.3E-26
1	DOCK7	rs33999917	62650370	GA	G	0.2525360	-0.0300460	0.0028987	1.6E-26
1	DOCK7	rs1168093	62650556	G	A	0.2525390	-0.0300459	0.0028987	1.7E-26
1	DOCK7	rs112957492	62651339	C	T	0.2092080	-0.0331146	0.0030914	8.5E-28
1	DOCK7	rs35107877	62651507	A	AG	0.2525500	-0.0300337	0.0028986	1.7E-26
1	DOCK7	rs10889353	62652525	C	A	0.2098850	-0.0328589	0.0030899	2.1E-27
1	DOCK7	rs1168097	62654700	C	T	0.2569210	-0.0301208	0.0028932	2.1E-26
1	DOCK7	rs60286666	62655430	T	TC	0.2537430	-0.0306243	0.0028969	2.1E-27
1	DOCK7	rs1168098	62655623	G	A	0.2534270	-0.0307150	0.0028989	1.7E-27
1	DOCK7	rs1168099	62657188	C	A	0.2537690	-0.0305467	0.0028964	2.7E-27
1	DOCK7	rs4495740	62658794	G	T	0.2092360	-0.0330930	0.0030913	9.4E-28
1	DOCK7	rs1168100	62658871	T	C	0.4523520	-0.0203083	0.0025511	2.6E-16
1	DOCK7	rs1168102	62662034	C	T	0.2525730	-0.0300575	0.0028984	1.7E-26
1	DOCK7	rs1168103	62662410	C	T	0.2526910	-0.0300296	0.0028989	2.0E-26
1	DOCK7	rs1168104	62662654	A	G	0.2525650	-0.0300308	0.0028985	1.9E-26
1	DOCK7	rs10889354	62663411	C	T	0.2092770	-0.0332403	0.0030925	6.0E-28
1	DOCK7	rs11208001	62664760	T	C	0.2517400	-0.0296068	0.0029206	2.2E-25
1	DOCK7	rs12024419	62664854	A	G	0.1816790	-0.0309041	0.0032698	8.4E-22

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs2479464	62665320	G	A	0.2526060	-0.0299322	0.0028998	2.7E-26
1	DOCK7	rs1168132	62667797	T	A	0.2525500	-0.0300287	0.0028999	2.0E-26
1	DOCK7	rs4587594	62668259	A	G	0.2092290	-0.0331202	0.0030920	9.0E-28
1	DOCK7	rs28399032	62669953	C	G	0.2091820	-0.0332656	0.0030927	6.0E-28
1	DOCK7	rs1168128	62670175	C	G	0.2526100	-0.0301130	0.0029019	1.6E-26
1	DOCK7	rs181835401	62670284	A	G	0.2511630	-0.0302553	0.0029103	1.3E-26
1	DOCK7	rs1168124	62674059	C	T	0.2523950	-0.0302161	0.0029008	1.0E-26
1	DOCK7	rs11208004	62679768	A	G	0.2094090	-0.0329435	0.0030954	1.8E-27
1	DOCK7	rs4459145	62680578	A	C	0.2473090	-0.0303344	0.0029349	2.0E-26
1	DOCK7	rs7531579	62681369	C	A	0.2089710	-0.0334863	0.0030953	3.1E-28
1	DOCK7	chr1:62686882_G_GA	62686882	GA	G	0.1959150	-0.0328860	0.0032097	3.0E-25
1	DOCK7	rs56280080	62687528	T	TCAGAA	0.2084140	-0.0334804	0.0031085	3.9E-28
1	DOCK7	rs4344355	62688282	T	C	0.2091720	-0.0338213	0.0031097	1.5E-28
1	DOCK7 *	rs10889356	62689678	A	G	0.2086230	-0.0338098	0.0031075	1.4E-28
1	DOCK7 *	rs1168114	62690372	A	G	0.2173110	-0.0325630	0.0030696	7.2E-27
1	DOCK7 *	rs1168113	62690427	T	C	0.2365810	-0.0304746	0.0029772	1.0E-24
1	DOCK7 *	rs35834397	62693541	TA	T	0.2275040	-0.0306381	0.0030142	2.1E-24
1	DOCK7 *	rs10889357	62694611	T	C	0.1945980	-0.0329054	0.0031890	6.8E-26
1	DOCK7 *	rs1168107	62695502	A	T	0.2275540	-0.0306633	0.0030142	1.9E-24
1	DOCK7 *	rs12136083	62697402	C	T	0.1946630	-0.0330924	0.0031880	3.4E-26
1	DOCK7 *	rs9659790	62700090	G	A	0.2275510	-0.0306578	0.0030130	1.6E-24
1	DOCK7 *	rs11208006	62704195	T	C	0.2275510	-0.0305660	0.0030131	2.4E-24
1	DOCK7 *	rs12041843	62704478	G	T	0.1787580	-0.0307182	0.0033128	2.4E-21
1	DOCK7 *	rs6682423	62705392	C	T	0.2275180	-0.0306217	0.0030128	2.0E-24
1	DOCK7 *	rs6666816	62705528	C	T	0.2275150	-0.0306166	0.0030128	2.0E-24
1	DOCK7 *	rs880694	62707613	C	T	0.2276020	-0.0306706	0.0030122	1.6E-24
1	DOCK7 *	rs10889360	62708247	T	C	0.1946490	-0.0330254	0.0031876	3.8E-26
1	DOCK7 *	rs11208007	62710412	T	A	0.1946910	-0.0330560	0.0031873	3.2E-26
1	DOCK7 *	rs4409689	62711694	C	T	0.2275350	-0.0306358	0.0030127	1.8E-24
1	DOCK7 *	rs60152331	62711868	G	T	0.3717010	-0.0230698	0.0026386	3.7E-19
1	DOCK7 *	rs7518497	62712025	C	A	0.1946440	-0.0330386	0.0031876	3.5E-26
1	DOCK7 *	rs9787151	62713467	C	T	0.2276040	-0.0306463	0.0030120	1.6E-24
1	DOCK7 *	rs9787156	62713541	G	A	0.2276160	-0.0306513	0.0030119	1.5E-24
1	DOCK7 *	rs12043910	62715877	A	G	0.1863140	-0.0318202	0.0032418	1.2E-23
1	DOCK7 *	rs6686331	62716464	C	T	0.2275720	-0.0308150	0.0030131	9.3E-25
1	DOCK7 *	rs75650238	62717743	C	CCA	0.1857890	-0.0319936	0.0032475	9.9E-24
1	DOCK7 *	rs6661669	62720298	T	C	0.2278400	-0.0308531	0.0030128	9.7E-25
1	DOCK7 *	rs76609868	62720544	C	A	0.1840190	-0.0315661	0.0032628	3.8E-23
1	DOCK7 *	rs12031537	62722415	A	C	0.1846070	-0.0316846	0.0032521	3.5E-23
1	DOCK7 *	rs7517372	62723893	G	A	0.2131360	-0.0286602	0.0030905	1.4E-20
1	DOCK7 *	rs4915624	62725847	G	A	0.2169250	-0.0295696	0.0030615	4.6E-22
1	DOCK7 *	rs76794398	62725894	A	G	0.1847210	-0.0316346	0.0032486	3.6E-23
1	DOCK7 *	rs4915853	62725906	C	A	0.2257950	-0.0306420	0.0030182	2.7E-24
1	DOCK7 *	rs199747920	62727151	ATT TTC	A	0.2173460	-0.0293419	0.0030596	8.7E-22
1	DOCK7 *	rs149188767	62727166	CTTTTCT	C	0.2255270	-0.0274171	0.0030569	3.0E-19
1	DOCK7 *	chr1:62727171_CT_C	62727171	C	CT	0.2152630	-0.0293078	0.0030777	1.5E-21
1	DOCK7 *	rs12029452	62727599	C	A	0.1847230	-0.0316357	0.0032485	3.6E-23
1	DOCK7 *	rs12026283	62728242	A	T	0.1847230	-0.0316357	0.0032485	3.6E-23
1	DOCK7 *	rs2149116	62728301	G	A	0.3757230	-0.0230827	0.0026420	8.5E-19
1	DOCK7 *	rs12023282	62728306	A	G	0.1847530	-0.0316349	0.0032487	3.6E-23
1	DOCK7 *	rs6664692	62729989	C	T	0.2138510	-0.0290766	0.0030791	2.2E-21
1	DOCK7 *	rs11208009	62730021	C	T	0.2222950	-0.0303760	0.0030365	7.2E-24
1	DOCK7 *	rs10889364	62731143	T	C	0.1848410	-0.0317013	0.0032476	2.9E-23
1	DOCK7 *	rs12049254	62731481	C	G	0.1848610	-0.0316890	0.0032474	3.0E-23
1	DOCK7 *	rs76753312	62733237	C	G	0.1849040	-0.0317715	0.0032456	1.8E-23
1	DOCK7 *	chr1:62733488_GA_G	62733488	GA	G	0.1859390	-0.0318307	0.0032460	1.9E-23
1	DOCK7 *	rs4630152	62733601	C	T	0.2145750	-0.0292955	0.0030707	7.3E-22
1	DOCK7 *	rs150990100	62733676	TG	T	0.2241350	-0.0307949	0.0030385	1.7E-24
1	DOCK7 *	rs61775961	62733677	G	T	0.2237700	-0.0307810	0.0030413	2.0E-24
1	DOCK7 *	rs61775962	62733679	A	G	0.2237700	-0.0307810	0.0030413	2.0E-24
1	DOCK7 *	rs6679002	62734265	G	T	0.2232320	-0.0305757	0.0030265	2.4E-24
1	DOCK7 *	rs12024044	62734645	A	G	0.1854720	-0.0317328	0.0032405	2.1E-23
1	DOCK7 *	rs12025111	62735769	A	G	0.1854010	-0.0319221	0.0032412	1.2E-23
1	DOCK7 *	rs12028944	62735867	A	T	0.1854590	-0.0317412	0.0032408	2.0E-23
1	ATG4C *	chr1:62736501_AT_A	62736501	AT	A	0.1962640	-0.0305076	0.0032405	1.1E-21
1	ATG4C *	rs12121288	62736790	G	A	0.2141170	-0.0293370	0.0030781	6.8E-22
1	ATG4C *	rs72915166	62736922	A	G	0.2137800	-0.0294789	0.0030830	5.3E-22
1	ATG4C *	rs78731792	62736973	A	G	0.1848300	-0.0317142	0.0032564	3.1E-23
1	ATG4C *	rs66676942	62737728	A	AT	0.1822790	-0.0321756	0.0032995	2.7E-23
1	ATG4C *	rs10789123	62737950	T	A	0.2109130	-0.0299032	0.0031361	8.7E-22
1	ATG4C *	rs12027341	62738235	A	G	0.1804190	-0.0324772	0.0033225	3.2E-23
1	ATG4C *	rs77870744	62738693	C	T	0.1821770	-0.0320345	0.0033167	1.2E-22

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	ATG4C *	rs10889365	62744078	T	A	0.3246090	-0.0173452	0.0027173	4.1E-11
1	ATG4C *	rs12124310	62745143	G	A	0.4739670	-0.0160259	0.0025746	8.0E-11
1	ATG4C *	rs11208013	62745229	G	T	0.3045850	-0.0158178	0.0027641	2.2E-09
1	ATG4C *	rs10889366	62746055	C	T	0.3047220	-0.0157932	0.0027626	2.2E-09
1	ATG4C *	rs7517722	62747351	A	G	0.3246070	-0.0172607	0.0027135	4.1E-11
1	ATG4C *	rs7546804	62749346	C	T	0.3051780	-0.0156277	0.0027554	3.0E-09
1	ATG4C *	rs35245250	62749539	A	G	0.3087390	-0.0154510	0.0027648	5.1E-09
1	ATG4C *	rs61765877	62749542	T	C	0.3090110	-0.0154098	0.0027634	5.4E-09
1	ATG4C *	rs61765878	62749543	T	G	0.3090780	-0.0152742	0.0027669	8.0E-09
1	ATG4C *	rs2149115	62749703	A	G	0.3254440	-0.0171361	0.0027067	4.6E-11
1	ATG4C *	chr1:62750578_GT_G	62750578	GT	G	0.3286450	-0.0170345	0.0027188	6.1E-11
1	ATG4C *	chr1:62750950_T_TA	62750950	T	TA	0.3276570	-0.0171003	0.0027010	5.7E-11
1	ATG4C *	rs10789124	62753106	A	C	0.3066910	-0.0155481	0.0027382	2.5E-09
1	ATG4C *	rs10749734	62754277	G	A	0.3269490	-0.0169661	0.0026919	5.0E-11
1	ATG4C *	rs6663281	62755520	T	C	0.3067180	-0.0155864	0.0027380	2.3E-09
1	ATG4C *	rs6702274	62756495	C	A	0.3267080	-0.0170632	0.0026917	4.0E-11
1	ATG4C *	rs11208019	62757051	A	G	0.3265960	-0.0169924	0.0026922	5.0E-11
1	ATG4C *	rs12085904	62758431	T	C	0.3067230	-0.0156371	0.0027378	2.0E-09
1	ATG4C *	rs34837685	62758629	C	CG	0.3067250	-0.0156334	0.0027377	2.0E-09
1	ATG4C *	rs12567340	62759440	T	C	0.3267100	-0.0171091	0.0026915	3.5E-11
1	ATG4C *	rs6688416	62759580	A	C	0.3271150	-0.0170692	0.0026929	4.0E-11
1	ATG4C *	rs6688417	62759584	A	G	0.3267100	-0.0171091	0.0026915	3.5E-11
1	ATG4C *	rs11810184	62759727	A	G	0.4722020	-0.0151865	0.0025659	6.2E-10
1	ATG4C *	rs6664372	62759780	C	G	0.3068460	-0.0155836	0.0027382	2.3E-09
1	ATG4C *	rs11208021	62759863	T	C	0.3266990	-0.0170948	0.0026915	3.6E-11
1	ATG4C *	rs6664677	62760028	C	T	0.3266990	-0.0170948	0.0026915	3.6E-11
1	ATG4C *	rs11208023	62760152	C	T	0.3266990	-0.0170948	0.0026915	3.6E-11
1	ATG4C *	rs11208024	62760241	T	C	0.3270150	-0.0171601	0.0026921	3.5E-11
1	ATG4C *	rs10889371	62760321	T	C	0.3067780	-0.0156776	0.0027379	1.8E-09
1	ATG4C *	rs3532757	62760475	T	TAA	0.3266990	-0.0170948	0.0026915	3.6E-11
1	ATG4C *	rs10789125	62761091	T	C	0.3267010	-0.0170952	0.0026915	3.7E-11
1	ATG4C *	rs10889372	62761709	C	T	0.3269470	-0.0170875	0.0026930	4.0E-11
1	ATG4C *	rs34399640	62762493	G	GT	0.3271820	-0.0169622	0.0026933	5.1E-11
1	ATG4C *	rs11208025	62762659	A	G	0.3265640	-0.0170284	0.0026923	4.3E-11
1	ATG4C *	rs10889374	62762771	A	T	0.3067050	-0.0156222	0.0027376	2.1E-09
1	ATG4C *	rs10889375	62763157	G	A	0.3264510	-0.0169012	0.0026951	5.7E-11
1	ATG4C *	rs11208026	62763202	C	G	0.3261250	-0.0168395	0.0026932	6.8E-11
1	ATG4C *	rs6656747	62764464	A	G	0.3067030	-0.0156151	0.0027375	2.1E-09
1	ATG4C *	rs11208027	62765214	G	A	0.3263870	-0.0169161	0.0026926	5.6E-11
1	ATG4C *	rs12138091	62765246	T	A	0.3065760	-0.0156117	0.0027376	2.0E-09
1	ATG4C *	rs11807368	62765730	G	T	0.3263880	-0.0169495	0.0026926	5.0E-11
1	ATG4C *	rs10889376	62766178	C	G	0.3060830	-0.0153154	0.0027433	5.1E-09
1	ATG4C *	rs11579171	62768057	C	T	0.3274790	-0.0168690	0.0026926	6.9E-11
1	ATG4C *	rs7543380	62768997	T	A	0.3031150	-0.0157908	0.0027460	1.4E-09
1	ATG4C *	rs4396149	62776025	C	T	0.3260160	-0.0168320	0.0027092	9.6E-11
1	ATG4C	rs7540030	62784304	A	G	0.3027060	-0.0156832	0.0027495	1.8E-09
1	ATG4C	rs12750156	62790022	C	T	0.3248420	-0.0170518	0.0026999	4.8E-11
1	ATG4C	rs6657707	62792979	C	T	0.3236710	-0.0170129	0.0027014	5.5E-11
1	ATG4C	rs12129919	62795685	C	T	0.3248610	-0.0170020	0.0027006	5.3E-11
1	ATG4C	rs10736399	62798112	T	C	0.3026240	-0.0156311	0.0027497	2.1E-09
1	ATG4C	rs11208032	62799494	G	C	0.3236750	-0.0170091	0.0027014	5.6E-11
1	ATG4C	rs6587990	62806788	T	A	0.3248470	-0.0169988	0.0026943	4.7E-11
1	ATG4C	rs12752360	62808188	C	G	0.3248430	-0.0169881	0.0026943	4.8E-11
1	ATG4C	rs11579518	62808587	G	A	0.3252340	-0.0167611	0.0026952	8.6E-11
1	ATG4C	rs11208035	62808867	T	C	0.3238840	-0.0169852	0.0026955	5.0E-11
1	ATG4C	rs6683832	62811233	G	A	0.3028830	-0.0156206	0.0027437	1.9E-09
1	ATG4C	rs6686232	62811426	C	T	0.3238630	-0.0169781	0.0026957	5.2E-11
1	ATG4C	rs12120847	62812209	G	A	0.3236660	-0.0169072	0.0026971	6.3E-11
1	ATG4C	rs10749735	62812321	A	G	0.3236660	-0.0169072	0.0026971	6.3E-11
1	ATG4C	rs11208036	62812347	G	A	0.3236660	-0.0169072	0.0026971	6.3E-11
1	ATG4C	rs6665932	62813093	A	G	0.3236690	-0.0169026	0.0026971	6.3E-11
1	ATG4C	rs6657235	62813424	T	C	0.3236690	-0.0169026	0.0026971	6.3E-11
1	ATG4C	rs6660873	62814582	T	A	0.3236710	-0.0168976	0.0026971	6.4E-11
1	ATG4C	chr1:62815181_CT_C	62815181	CT	C	0.4738280	-0.0151967	0.0025393	3.7E-10
1	ATG4C	rs6682286	62815748	G	A	0.3236710	-0.0168976	0.0026971	6.4E-11
1	ATG4C	rs7539616	62817334	C	T	0.4773260	-0.0149562	0.0025309	6.0E-10
1	ATG4C	rs12134455	62817783	A	G	0.3236750	-0.0169075	0.0026971	6.2E-11
1	ATG4C	rs11208037	62817845	A	G	0.3240790	-0.0168149	0.0026983	8.1E-11
1	ATG4C	rs11208038	62817875	A	G	0.3236750	-0.0169075	0.0026971	6.2E-11
1	ATG4C	rs2366820	62818249	C	T	0.3237790	-0.0169250	0.0026976	6.0E-11
1	ATG4C	rs2366821	62818466	G	C	0.3244910	-0.0167337	0.0026987	8.4E-11
1	ATG4C	rs7528963	62820576	G	A	0.4963150	0.0159168	0.0025595	5.5E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	ATG4C	rs11208040	62821867	T	A	0.3236360	-0.0169814	0.0026977	5.1E-11
1	ATG4C	rs7519205	62824457	G	A	0.3338910	-0.0166067	0.0026761	1.9E-10
1	ATG4C	rs6664673	62824892	G	C	0.3033790	-0.0155680	0.0027435	2.1E-09
1	ATG4C	rs6587991	62825003	C	A	0.3243450	-0.0169302	0.0026955	5.8E-11
1	ATG4C	rs7414021	62826201	A	G	0.3035350	-0.0156557	0.0027475	2.1E-09
1	ATG4C	rs10159426	62827199	C	G	0.3107330	-0.0155374	0.0027280	3.2E-09
1	ATG4C	rs10789129	62827786	T	C	0.3020020	-0.0153551	0.0027494	4.1E-09
1	ATG4C	rs34117354	62827807	T	TC	0.3020020	-0.0153551	0.0027494	4.1E-09
1	ATG4C	rs7512374	62828034	C	T	0.3233060	-0.0167955	0.0026986	9.2E-11
1	ATG4C	rs7512529	62828075	G	A	0.3228740	-0.0167463	0.0027011	1.1E-10
1	ATG4C	rs7524508	62828183	T	A	0.3233040	-0.0168014	0.0026986	9.1E-11
1	ATG4C	rs6663165	62829519	C	T	0.3123260	-0.0150157	0.0027233	1.1E-08
1	ATG4C	rs6687943	62830098	A	T	0.3119170	-0.0150233	0.0027232	1.1E-08
1	ATG4C	rs6679582	62830600	T	C	0.3118430	-0.0150372	0.0027227	1.0E-08
1	ATG4C	rs10889383	62831090	C	T	0.3118400	-0.0150368	0.0027227	1.0E-08
1	ATG4C	rs11587081	62831444	A	G	0.3328340	-0.0164423	0.0026789	3.1E-10
1	ATG4C	rs2366822	62831549	G	T	0.3118450	-0.0150352	0.0027227	1.0E-08
1	ATG4C	rs5774617	62831628	CT	C	0.2850650	-0.0154176	0.0028136	1.5E-08
1	ATG4C	rs56799376	62832193	G	GTTTTA	0.3119400	-0.0149729	0.0027230	1.2E-08
1	ATG4C	rs7527905	62832439	G	A	0.3328280	-0.0164564	0.0026789	3.0E-10
1	ATG4C	rs10889384	62835981	G	A	0.3118530	-0.0150688	0.0027226	9.8E-09
1	ATG4C	rs10889385	62836344	T	A	0.3328640	-0.0164620	0.0026786	2.9E-10
1	ATG4C	rs11208043	62836820	C	T	0.3340200	-0.0162823	0.0026811	4.2E-10
1	ATG4C	rs2886770	62837115	A	G	0.3023720	-0.0154391	0.0027467	3.1E-09
1	ATG4C	rs2886771	62837769	A	G	0.3233540	-0.0168111	0.0026983	8.7E-11
1	ATG4C	rs12567999	62837928	T	C	0.3233540	-0.0168111	0.0026983	8.7E-11
1	ATG4C	rs10493327	62838174	C	T	0.3233540	-0.0168111	0.0026983	8.7E-11
1	ATG4C	rs10889386	62839848	C	G	0.3023720	-0.0154391	0.0027467	3.1E-09
1	ATG4C	rs6695607	62840561	T	G	0.3233540	-0.0168111	0.0026983	8.7E-11
1	ATG4C	rs6683423	62840983	G	A	0.3118760	-0.0150485	0.0027223	1.0E-08
1	ATG4C	rs12743698	62841289	C	T	0.3328600	-0.0164544	0.0026786	3.0E-10
1	ATG4C	rs3737892	62841632	A	G	0.3328600	-0.0164544	0.0026786	3.0E-10
1	ATG4C	rs3737893	62841713	T	C	0.3233480	-0.0168089	0.0026983	8.7E-11
1	ATG4C	rs6665455	62842772	A	G	0.3023720	-0.0154391	0.0027467	3.1E-09
1	ATG4C	rs4448545	62843657	G	A	0.3328600	-0.0164544	0.0026786	3.0E-10
1	ATG4C	rs71045858	62844156	T	TG	0.3023720	-0.0154391	0.0027467	3.1E-09
1	ATG4C	rs11208045	62844194	A	G	0.3233540	-0.0168111	0.0026983	8.7E-11
1	ATG4C	rs11208046	62844526	C	T	0.3233540	-0.0168111	0.0026983	8.7E-11
1	ATG4C	rs71045859	62845712	AT	A	0.3336670	-0.0163989	0.0026774	3.5E-10
1	ATG4C	rs12748640	62846102	T	C	0.3328600	-0.0164544	0.0026786	3.0E-10
1	ATG4C	rs11208047	62846165	G	A	0.3118760	-0.0150485	0.0027223	1.0E-08
1	ATG4C	rs71045860	62847231	A	AAAAC	0.3328640	-0.0164412	0.0026785	3.1E-10
1	ATG4C	rs56692911	62848150	T	TTTTG	0.3249050	-0.0167909	0.0027007	9.7E-11
1	ATG4C	rs6587992	62849801	A	G	0.3328490	-0.0164481	0.0026785	3.0E-10
1	ATG4C	rs6587993	62850012	T	C	0.3328490	-0.0164481	0.0026785	3.0E-10
1	ATG4C	rs6587994	62850077	G	A	0.3328490	-0.0164481	0.0026785	3.0E-10
1	ATG4C	rs7529145	62850858	A	G	0.3251740	-0.0160725	0.0027259	1.2E-09
1	ATG4C	rs7529146	62850860	A	G	0.3135590	-0.0143300	0.0027410	4.6E-08
1	ATG4C	rs6699457	62851169	C	G	0.3118760	-0.0150274	0.0027221	1.0E-08
1	ATG4C	rs6670072	62852531	T	C	0.3328450	-0.0164313	0.0026785	3.1E-10
1	ATG4C	rs6676821	62854495	T	G	0.3233470	-0.0167865	0.0026982	9.1E-11
1	ATG4C	rs6677051	62854650	T	C	0.3233490	-0.0167869	0.0026982	9.1E-11
1	ATG4C	rs1333733	62856890	A	G	0.3119440	-0.0151404	0.0027204	8.9E-09
1	ATG4C	rs1981067	62857072	C	T	0.3328100	-0.0164251	0.0026774	3.4E-10
1	ATG4C	rs6587996	62857413	G	A	0.3329020	-0.0165238	0.0026769	2.7E-10
1	ATG4C	rs6656119	62857582	C	G	0.3329020	-0.0165238	0.0026769	2.7E-10
1	ATG4C	rs7527423	62859046	T	A	0.3329020	-0.0165238	0.0026769	2.7E-10
1	ATG4C	rs71045861	62859699	CT	C	0.3335330	-0.0162632	0.0026799	5.2E-10
1	ATG4C	rs6676637	62860283	T	G	0.3234040	-0.0168500	0.0026966	8.4E-11
1	ATG4C	rs7521483	62860645	C	A	0.3329020	-0.0165238	0.0026769	2.7E-10
1	ATG4C	rs2184192	62861191	T	G	0.4729350	-0.0150332	0.0025366	6.3E-10
1	ATG4C	rs1333736	62861764	T	A	0.3234040	-0.0168500	0.0026966	8.4E-11
1	ATG4C	rs6670694	62862187	G	A	0.3234040	-0.0168500	0.0026966	8.4E-11
1	ATG4C	rs6683732	62862408	T	C	0.3234230	-0.0168012	0.0026968	9.2E-11
1	ATG4C	rs7540205	62863117	T	C	0.3239030	-0.0168275	0.0026972	8.3E-11
1	ATG4C	rs1360677	62863273	T	C	0.3026250	-0.0154399	0.0027450	3.2E-09
1	ATG4C	rs1360678	62863380	T	C	0.3234320	-0.0168141	0.0026968	9.0E-11
1	ATG4C	rs7531329	62863788	G	A	0.3026390	-0.0154659	0.0027446	3.1E-09
1	ATG4C	rs3211074	62864546	G	A	0.3329400	-0.0165003	0.0026770	2.8E-10
1	ATG4C *	rs17097064	62865621	T	G	0.3329400	-0.0165003	0.0026770	2.8E-10
1	ATG4C *	rs5774621	62866019	TA	T	0.3120850	-0.0150673	0.0027206	9.9E-09
1	ATG4C *	rs1413242	62866193	C	T	0.3119730	-0.0151022	0.0027207	9.5E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	ATG4C *	rs998096	62866234	A	C	0.3328830	-0.0164914	0.0026775	2.8E-10
1	ATG4C *	rs12128286	62866524	A	C	0.3329300	-0.0164682	0.0026772	3.0E-10
1	ATG4C *	rs1931079	62866953	G	A	0.3329440	-0.0164738	0.0026771	2.9E-10
1	ATG4C *	rs2803245	62867539	C	T	0.2923660	-0.0149670	0.0027759	2.3E-08
1	ATG4C *	rs11803404	62867652	T	C	0.3330360	-0.0164923	0.0026774	2.7E-10
1	ATG4C *	rs10640020	62867798	C	CTCTT	0.3121110	-0.0151012	0.0027209	9.7E-09
1	ATG4C *	rs1333730	62868437	G	A	0.3329680	-0.0165108	0.0026770	2.7E-10
1	ATG4C *	rs11208049	62868614	G	A	0.3330360	-0.0164298	0.0026767	3.2E-10
1	ATG4C *	rs7553110	62869374	A	G	0.3234650	-0.0168405	0.0026968	8.3E-11
1	ATG4C *	rs7555606	62869525	A	G	0.3236800	-0.0169510	0.0026967	6.2E-11
1	ATG4C *	rs11584363	62870392	A	G	0.3234650	-0.0168405	0.0026968	8.3E-11
1	ATG4C *	rs11208050	62870600	T	C	0.3234650	-0.0168405	0.0026968	8.3E-11
1	ATG4C *	chr1:62870674_A_AT	62870674	A	AT	0.3249110	-0.0161422	0.0027038	4.1E-10
1	ATG4C *	rs11208051	62870957	C	T	0.3329680	-0.0165108	0.0026770	2.7E-10
1	ATG4C *	rs28793284	62871200	G	T	0.3355620	-0.0165579	0.0026736	2.2E-10
1	ATG4C *	rs12756081	62871663	G	A	0.3329640	-0.0165133	0.0026770	2.6E-10
1	ATG4C *	rs2050248	62872447	A	T	0.3119950	-0.0151250	0.0027207	9.1E-09
1	ATG4C *	rs6587997	62872515	T	G	0.3329450	-0.0165035	0.0026772	2.7E-10
1	ATG4C *	rs11208052	62873126	A	G	0.3329980	-0.0164876	0.0026772	2.9E-10
1	ATG4C *	rs36019631	62873148	CT	C	0.3329610	-0.0164925	0.0026770	2.8E-10
1	ATG4C *	rs6657552	62873981	T	C	0.3118170	-0.0151569	0.0027218	8.9E-09
1	ATG4C *	rs6693530	62873985	G	A	0.3327680	-0.0165062	0.0026781	2.9E-10
1	ATG4C *	rs10889387	62875174	C	T	0.3116410	-0.0151688	0.0027213	8.6E-09
1	ATG4C *	rs12725996	62876411	T	A	0.3329800	-0.0167054	0.0026812	1.7E-10
1	ATG4C *	rs7515960	62876535	A	G	0.3326010	-0.0165199	0.0026776	2.7E-10
1	ATG4C *	rs6587998	62876798	C	T	0.3326010	-0.0165199	0.0026776	2.7E-10
1	ATG4C *	rs6685784	62877152	C	A	0.3326010	-0.0165199	0.0026776	2.7E-10
1	ATG4C *	rs1333734	62877305	C	T	0.3116450	-0.0151629	0.0027213	8.7E-09
1	ATG4C *	rs12749904	62877674	C	A	0.3326010	-0.0165199	0.0026776	2.7E-10
1	ATG4C *	rs1537496	62878769	A	T	0.3339710	-0.0162016	0.0026818	6.0E-10
1	ATG4C *	rs7522726	62878835	A	G	0.3116450	-0.0151629	0.0027213	8.7E-09
1	ATG4C *	rs7526246	62880316	A	T	0.3281300	-0.0161171	0.0026861	6.6E-10
1	ATG4C *	rs12728111	62880901	C	T	0.3281300	-0.0161171	0.0026861	6.6E-10
1	ATG4C *	rs12742537	62881305	G	A	0.3279120	-0.0160649	0.0026872	7.7E-10
1	ATG4C *	rs11580642	62882427	T	A	0.3281300	-0.0161171	0.0026861	6.6E-10
1	ATG4C *	rs7535496	62882885	A	T	0.3079770	-0.0149037	0.0027310	1.3E-08
1	ATG4C *	rs11804568	62885930	T	C	0.3270930	-0.0157665	0.0027075	1.5E-09
1	ATG4C *	rs11208056	62887038	C	T	0.3273420	-0.0157949	0.0027080	1.4E-09
1	ATG4C *	rs12564421	62887759	G	T	0.2930290	-0.0178481	0.0028083	2.1E-10
1	ATG4C *	rs2780871	62889202	T	C	0.2797380	-0.0176858	0.0028345	2.6E-10
1	ATG4C *	rs7512480	62893145	C	T	0.2990200	-0.0196472	0.0027789	1.4E-12
1	ATG4C *	rs2803238	62893889	G	A	0.2858340	-0.0170450	0.0027995	1.1E-09
1	ATG4C *	rs55924040	62894308	C	T	0.2699560	-0.0158208	0.0028454	2.1E-08
2	APOB *	rs9306897	20938306	T	C	0.0811215	0.0319310	0.0046733	2.7E-11
2	APOB *	rs11096689	20940780	C	T	0.0792051	0.0333087	0.0047144	8.4E-12
2	APOB *	rs4296389	20943234	C	T	0.0947741	0.0353877	0.0043576	2.3E-16
2	APOB *	rs4507059	20943569	G	A	0.0829577	0.0328527	0.0046032	3.5E-13
2	APOB *	rs10201379	20943917	C	A	0.1291440	0.0317429	0.0038067	9.5E-18
2	APOB *	rs4426495	20944222	C	T	0.1292140	0.0317014	0.0038052	1.1E-17
2	APOB *	rs10180633	20945069	G	T	0.1260270	0.0323777	0.0038510	4.6E-18
2	APOB *	rs13020417	20945074	T	G	0.0487594	0.0416053	0.0058762	2.3E-12
2	APOB *	rs10183548	20945739	G	A	0.1246830	0.0333443	0.0038565	4.2E-19
2	APOB *	rs5829761	20946172	AC	A	0.1246890	0.0333517	0.0038565	4.2E-19
2	APOB *	rs6732011	20946761	G	T	0.1245430	0.0332595	0.0038599	4.3E-19
2	APOB *	rs35424228	20947933	T	C	0.0485409	0.0418155	0.0058881	2.3E-12
2	APOB *	rs3923037	20948514	A	C	0.1227410	0.0331893	0.0038824	1.0E-18
2	APOB *	rs149034253	20951648	A	G	0.0488968	0.0419314	0.0058644	1.2E-12
2	APOB *	rs1477526787	20953510	T	TTATG	0.0457074	0.0408362	0.0060490	2.0E-11
2	APOB *	rs148458076	20955854	C	T	0.1226880	0.0335210	0.0038636	6.6E-19
2	APOB *	rs36145916	20956506	T	C	0.1220670	0.0339272	0.0038723	3.0E-19
2	APOB *	rs143375141	20956554	T	C	0.1617500	-0.0182125	0.0034525	5.4E-09
2	APOB *	rs36187918	20958070	G	A	0.1222400	0.0335135	0.0038673	5.9E-19
2	APOB *	rs36190370	20958814	A	C	0.0458014	0.0419915	0.0060366	5.8E-12
2	APOB *	rs147436013	20959450	T	G	0.1628590	-0.0184656	0.0034340	3.7E-09
2	APOB *	rs1344063	20961673	T	C	0.1257610	0.0323353	0.0038147	3.3E-18
2	APOB *	rs2337382	20961892	A	G	0.0890447	0.0384528	0.0044302	3.9E-18
2	APOB *	rs12999441	20963235	C	T	0.0441463	0.0448381	0.0061354	5.8E-13
2	APOB *	rs4665639	20964019	A	G	0.1221860	-0.0339086	0.0038544	2.1E-19
2	APOB *	rs17393586	20964727	A	G	0.0441463	0.0448381	0.0061354	5.8E-13
2	APOB *	rs6707950	20964769	T	C	0.0868230	0.0401371	0.0044817	4.0E-19
2	APOB *	rs4665790	20965698	T	A	0.1227250	0.0344206	0.0038450	5.7E-20
2	APOB *	rs17041662	20966196	C	T	0.1226630	0.0345043	0.0038460	5.1E-20

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs17397826	20966219	T	C	0.0441463	0.0448381	0.0061354	5.8E-13
2	APOB *	rs17041663	20967366	G	T	0.1220920	0.0338320	0.0038544	2.6E-19
2	APOB *	rs35695820	20967415	G	GCGCC	0.1323470	0.0300469	0.0037474	9.3E-17
2	APOB *	rs79490663	20968191	G	A	0.1598610	-0.0173948	0.0034486	2.5E-08
2	APOB *	rs6706783	20968537	A	T	0.0867430	0.0400915	0.0044820	4.3E-19
2	APOB *	rs1320144	20969240	A	C	0.1220000	0.0339075	0.0038557	2.0E-19
2	APOB *	rs1320145	20969490	G	A	0.1224650	0.0343502	0.0038502	7.6E-20
2	APOB *	rs35893087	20969651	A	G	0.1220460	0.0338908	0.0038556	2.1E-19
2	APOB *	rs72788558	20971996	C	T	0.1595240	-0.0171802	0.0034524	3.8E-08
2	APOB *	rs17041679	20972540	T	C	0.1226410	0.0336150	0.0038454	3.7E-19
2	APOB *	rs72788559	20972650	T	G	0.1588140	-0.0182501	0.0034591	6.5E-09
2	APOB *	rs34335269	20973378	A	G	0.1216470	0.0340424	0.0038593	1.3E-19
2	APOB *	rs201349382	20974609	T	TC	0.1524490	-0.0207398	0.0035115	1.4E-10
2	APOB *	rs6733447	20975264	G	A	0.1228030	0.0347763	0.0038429	1.7E-20
2	APOB *	rs55664492	20975554	T	C	0.0443722	0.0444694	0.0061210	6.2E-13
2	APOB *	rs10495713	20977647	A	G	0.1211320	0.0345105	0.0038666	6.5E-20
2	APOB *	rs7608123	20980007	T	G	0.1211210	0.0345290	0.0038664	6.2E-20
2	APOB *	rs7571469	20981609	G	C	0.1211220	0.0346351	0.0038654	5.0E-20
2	APOB *	rs10172650	20982585	A	G	0.1571590	-0.0192170	0.0034643	1.4E-09
2	APOB *	rs10164442	20982691	G	A	0.1568150	-0.0192184	0.0034667	1.5E-09
2	APOB *	rs35131127	20983042	C	T	0.0873059	0.0402098	0.0044674	3.5E-19
2	APOB *	rs9789416	20983180	A	G	0.1210790	0.0346892	0.0038654	4.4E-20
2	APOB *	rs11124924	20983403	C	G	0.1738140	-0.0178412	0.0033257	4.2E-09
2	APOB *	rs56327713	20983964	T	G	0.0873718	0.0407019	0.0044703	1.2E-19
2	APOB *	rs56403064	20984034	C	T	0.1216980	0.0352120	0.0038562	1.2E-20
2	APOB *	rs56213756	20984123	G	C	0.1213010	0.0352287	0.0038627	1.2E-20
2	APOB *	rs67212568	20985612	G	T	0.0440792	0.0449313	0.0061384	5.3E-13
2	APOB *	rs34059329	20986894	T	C	0.0874135	0.0390958	0.0044693	2.5E-18
2	APOB *	chr2:20986987_TG_T	20986987	TG	T	0.1720530	0.0269011	0.0034328	5.3E-16
2	APOB *	rs1320143	20989476	G	A	0.1200090	0.0346710	0.0038926	7.3E-20
2	APOB *	rs6721844	20989699	T	G	0.0868910	0.0394650	0.0044879	1.6E-18
2	APOB *	rs6722374	20990190	T	G	0.1192950	0.0346342	0.0039034	1.2E-19
2	APOB *	rs13014683	20990254	T	C	0.0492218	0.0416166	0.0058280	1.9E-12
2	APOB *	rs4665642	20990313	G	A	0.1193100	0.0346112	0.0039034	1.2E-19
2	APOB *	rs1318006	20991280	G	A	0.1200990	0.0354014	0.0038956	1.8E-20
2	APOB *	rs1318005	20991336	G	A	0.1197900	0.0352041	0.0039015	3.0E-20
2	APOB *	rs1318004	20991337	C	T	0.1197900	0.0352041	0.0039015	3.0E-20
2	APOB *	rs72780134	20991960	A	G	0.1683080	-0.0187666	0.0033871	9.4E-10
2	APOB *	rs12992267	20992773	T	C	0.0709511	0.0374050	0.0049242	2.2E-14
2	APOB *	rs34776010	20993375	G	C	0.0709503	0.0373736	0.0049242	2.3E-14
2	APOB *	rs79823619	20993415	C	G	0.1646640	-0.0187005	0.0034198	1.1E-09
2	APOB *	rs57947200	20994357	A	T	0.0687850	0.0373002	0.0050250	1.0E-13
2	APOB *	rs56984418	20994358	G	A	0.0708165	0.0371706	0.0049299	2.7E-14
2	APOB *	rs6756501	20995933	T	C	0.0662497	0.0369511	0.0050881	3.2E-13
2	APOB *	rs6725189	20996129	T	G	0.0664858	0.0367226	0.0050805	3.5E-13
2	APOB *	rs4665709	20998083	A	G	0.0708895	0.0366770	0.0049280	5.6E-14
2	APOB *	rs4371387	20998261	A	G	0.0708084	0.0371053	0.0049298	2.8E-14
2	APOB *	rs952274	20998485	T	G	0.0664843	0.0366473	0.0050801	3.7E-13
2	APOB *	rs62122484	21000700	A	G	0.0391041	0.0448896	0.0065161	1.7E-11
2	APOB *	rs369226260	21001217	A	T	0.0359078	0.0455050	0.0068402	4.2E-11
2	APOB *	rs371445178	21001218	T	A	0.0359082	0.0455052	0.0068402	4.2E-11
2	APOB *	rs551038752	21001219	A	T	0.0359078	0.0455050	0.0068402	4.2E-11
2	APOB	rs1042031	21002881	T	C	0.0441103	0.0448974	0.0061382	6.4E-13
2	APOB	rs1800479	21004511	G	C	0.0425028	0.0459012	0.0062600	5.2E-13
2	APOB	rs693	21009323	A	G	0.0488616	0.0308554	0.0058529	3.1E-08
2	APOB	rs3749054	21014366	T	A	0.0442076	0.0451531	0.0061347	4.5E-13
2	APOB	rs2854725	21014914	G	T	0.1554290	-0.0208844	0.0034917	6.4E-11
2	APOB	rs13003321	21017014	C	T	0.0381799	0.0403423	0.0066405	5.3E-10
2	APOB	rs12720828	21018872	T	C	0.0429317	0.0450640	0.0062242	7.7E-13
2	APOB	rs10199768	21021128	T	G	0.0480033	0.0322273	0.0059008	9.6E-09
2	APOB	rs57825321	21024193	A	T	0.1469560	-0.0259432	0.0035781	4.4E-15
2	APOB	rs13306194	21029662	A	G	0.1430420	-0.0263105	0.0036352	6.8E-15
2	APOB *	rs11893021	21050706	G	T	0.1769880	-0.0181147	0.0033728	1.6E-08
2	APOB *	rs58612563	21051291	G	A	0.1773800	-0.0182480	0.0033666	1.1E-08
2	APOB *	rs75022238	21052006	C	T	0.1774760	-0.0181587	0.0033653	1.2E-08
2	APOB *	rs111397565	21052832	CA	C	0.1775210	-0.0180543	0.0033635	1.4E-08
2	APOB *	rs57922105	21055341	T	C	0.1724310	-0.0177293	0.0033925	3.2E-08
2	APOB *	rs75565290	21055810	G	A	0.1724040	-0.0177511	0.0033910	3.1E-08
2	APOB *	rs35750610	21059021	C	T	0.0414368	0.0389983	0.0063697	6.0E-09
2	APOB *	rs75208098	21060292	C	T	0.1730540	-0.0175820	0.0033850	3.9E-08
2	APOB *	rs60857806	21061227	G	T	0.1728150	-0.0177032	0.0033873	3.2E-08
2	APOB *	rs56885855	21061405	T	C	0.1728250	-0.0176960	0.0033874	3.2E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs75953246	21061841	A	G	0.1728190	-0.0177300	0.0033873	3.1E-08
2	APOB *	rs77257367	21062230	T	C	0.1717880	-0.0179963	0.0033983	2.0E-08
2	APOB *	rs11894096	21062695	G	A	0.1706760	-0.0177070	0.0034078	4.1E-08
2	APOB *	chr2:21062703_C_CA	21062703	CA	C	0.1730670	-0.0177525	0.0033848	3.0E-08
2	APOB *	rs80196520	21078435	A	C	0.1736810	-0.0172776	0.0033611	4.7E-08
2	APOB *	rs59263713	21079390	T	G	0.1737100	-0.0172492	0.0033603	4.6E-08
2	APOB *	rs11886946	21082715	C	A	0.1741210	-0.0174420	0.0033547	3.5E-08
2	APOB *	rs79721590	21083359	C	G	0.1741200	-0.0173428	0.0033545	4.2E-08
2	APOB *	rs112680646	21084238	A	G	0.1741540	-0.0172282	0.0033533	4.8E-08
2	APOB *	rs79783818	21147375	A	T	0.1711220	-0.0172475	0.0033729	4.4E-08
2	DPYSL5	rs3820821	26932980	C	T	0.3313090	0.0145198	0.0027032	2.9E-08
2	DPYSL5	rs4665929	26932981	T	G	0.3325380	0.0143545	0.0026982	3.4E-08
2	DPYSL5	rs3820822	26932994	A	G	0.3325300	0.0143445	0.0026986	3.4E-08
2	DPYSL5	rs4665363	26933548	G	T	0.3325910	0.0145435	0.0027023	2.3E-08
2	DPYSL5	rs920437	26934528	A	G	0.3326300	0.0145529	0.0027029	2.4E-08
2	DPYSL5	rs920435	26934920	C	T	0.3318150	0.0145262	0.0027057	2.6E-08
2	DPYSL5	rs12615423	26935755	T	G	0.3324160	0.0145402	0.0027038	2.4E-08
2	DPYSL5	rs1992311	26936473	G	A	0.3323790	0.0145975	0.0027041	2.2E-08
2	DPYSL5	rs7589627	26936918	C	T	0.3354630	0.0146475	0.0027117	1.6E-08
2	DPYSL5	rs6759548	26938192	A	G	0.3323980	0.0145739	0.0027042	2.3E-08
2	DPYSL5	rs6718978	26938723	G	A	0.3323610	0.0146090	0.0027045	2.2E-08
2	DPYSL5	rs3739085	26940176	T	C	0.3284880	0.0144998	0.0027137	2.3E-08
2	DPYSL5	rs3820823	26941938	G	A	0.3281460	0.0144841	0.0027131	2.6E-08
2	DPYSL5	rs3739086	26942334	C	T	0.3349070	0.0157633	0.0027096	1.0E-09
2	DPYSL5	rs6707735	26943954	T	C	0.3277530	0.0149042	0.0027127	1.0E-08
2	DPYSL5	rs6708148	26944452	A	G	0.3279390	0.0148188	0.0027122	1.3E-08
2	DPYSL5	rs3739088	26944916	T	C	0.3285640	0.0148736	0.0027107	1.1E-08
2	CGREF1	rs4665372	27102969	A	T	0.2435030	0.0156474	0.0029454	4.4E-08
2	ABHD1 *	rs7605526	27122616	A	G	0.2368030	0.0163639	0.0030259	4.7E-08
2	ABHD1	rs4665946	27125063	A	C	0.2997100	0.0197119	0.0027721	7.6E-13
2	ABHD1	rs4665947	27125161	C	T	0.3009290	0.0199963	0.0027773	3.5E-13
2	ABHD1	rs6741646	27125330	T	C	0.3076030	0.0194456	0.0027404	6.5E-13
2	ABHD1	rs12467319	27125819	C	T	0.2995590	0.0190823	0.0027528	1.7E-12
2	ABHD1	rs1866561	27128411	G	A	0.2996080	0.0196982	0.0027488	2.8E-13
2	ABHD1	rs2304678	27130639	C	G	0.1636400	0.0211158	0.0034231	1.5E-10
2	PREB	rs71401560	27131111	TA	T	0.1637380	0.0215761	0.0034247	6.6E-11
2	PREB	rs11695930	27132103	T	C	0.1626470	0.0208746	0.0034355	3.4E-10
2	PREB	rs2289358	27133123	T	G	0.1630580	0.0215026	0.0034383	8.2E-11
2	PREB	rs2289359	27133410	C	T	0.1631190	0.0216131	0.0034388	6.4E-11
2	PREB *	rs11678061	27134751	T	C	0.1630740	0.0217051	0.0034414	6.7E-11
2	PRR30	rs111121	27137019	C	T	0.2945110	0.0163504	0.0027936	3.2E-09
2	PRR30	rs2304680	27138378	T	C	0.1580140	0.0211761	0.0034850	4.4E-10
2	PRR30	rs3795961	27139079	A	G	0.1581540	0.0210668	0.0034856	5.4E-10
2	PRR30 *	rs11691585	27139503	G	A	0.1603890	0.0216735	0.0034682	1.6E-10
2	PRR30 *	rs7574004	27140243	C	T	0.2951500	0.0171613	0.0027965	5.7E-10
2	PRR30 *	chr2:27141287_CT_C	27141287	C	CT	0.2915800	0.0185409	0.0028262	3.4E-11
2	PRR30 *	rs2439076	27142694	T	C	0.2946920	0.0172913	0.0027924	3.8E-10
2	PRR30 *	rs1659677	27142747	A	G	0.2947390	0.0173367	0.0027925	3.5E-10
2	PRR30 *	rs1659711	27143540	C	A	0.2989220	0.0173813	0.0027845	2.9E-10
2	TCF23 *	rs1298360	27144930	T	C	0.1581100	0.0215369	0.0034855	2.4E-10
2	TCF23 *	rs4665950	27145435	A	G	0.1581090	0.0215496	0.0034856	2.3E-10
2	TCF23 *	rs1275518	27145623	G	A	0.1604870	0.0219987	0.0034682	8.8E-11
2	TCF23 *	rs1275515	27147364	C	T	0.1604590	0.0220864	0.0034686	7.5E-11
2	TCF23 *	rs1275514	27147662	C	T	0.1590260	0.0218534	0.0034972	1.1E-10
2	TCF23 *	rs7606672	27147737	C	G	0.1604520	0.0220061	0.0034693	9.0E-11
2	TCF23 *	rs1275513	27148102	T	C	0.2958310	0.0179703	0.0027941	8.5E-11
2	TCF23	rs1275511	27150802	T	C	0.3058510	0.0159666	0.0027781	8.4E-09
2	TCF23	rs1275510	27150871	A	G	0.1574050	0.0223453	0.0034988	6.9E-11
2	TCF23	rs1275509	27151141	G	A	0.3071820	0.0155666	0.0027729	2.0E-08
2	TCF23	rs1275508	27151551	C	A	0.1571980	0.0222206	0.0034993	7.8E-11
2	SLCSA6 *	rs74684611	27191771	C	T	0.1037010	-0.0256494	0.0042335	1.2E-10
2	CAD *	rs118130043	27245399	G	A	0.0440855	0.0380313	0.0062422	2.0E-10
2	MPV17	rs146502189	27322314	T	G	0.0319616	-0.0393854	0.0071902	5.2E-09
2	GTF3C2	rs201232671	27348271	G	A	0.0406016	0.0424557	0.0065038	1.5E-11
2	PPM1G	rs140391935	27387603	T	C	0.0452531	0.0417033	0.0061396	9.4E-13
2	PPM1G	rs79803862	27399271	A	T	0.0668252	-0.0347350	0.0051455	2.3E-13
2	PPM1G *	rs1728918	27412596	A	G	0.2091290	0.0275645	0.0031019	1.1E-19
2	NRBP1 *	rs147530299	27419228	A	AGTGGC	0.1583650	0.0281324	0.0034834	3.6E-16
2	IFT172	rs117414910	27455222	T	C	0.0475382	0.0415964	0.0059881	2.3E-13
2	IFT172	rs140257887	27456289	T	C	0.0271450	-0.0432511	0.0077582	3.4E-09
2	GCKR	rs201393954	27500983	T	TC	0.0254037	-0.0433981	0.0080246	7.5E-09
2	GCKR	rs1260326	27508073	T	C	0.4929810	0.0566666	0.0025223	1.2E-118

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	GCKR	rs3817588	27508345	C	T	0.3569530	-0.0526127	0.0026390	2.4E-93
2	GCKR	rs146716184	27508726	C	T	0.0698178	0.0274679	0.0049967	8.2E-09
2	GCKR	rs148527487	27509703	AT	A	0.3526870	-0.0517680	0.0026642	2.6E-88
2	GCKR	rs6547692	27512105	G	A	0.4916900	0.0561338	0.0025290	1.4E-115
2	GCKR	rs780096	27518205	C	G	0.4909030	0.0561374	0.0025243	7.9E-116
2	GCKR	rs780095	27518238	A	G	0.4895710	0.0563159	0.0025264	1.7E-116
2	GCKR	rs780094	27518370	T	C	0.4807160	0.0549414	0.0025240	1.9E-111
2	GCKR	rs780093	27519736	T	C	0.4832970	0.0545955	0.0025240	4.5E-110
2	GCKR	rs780092	27520287	G	A	0.3593560	-0.0519373	0.0026323	2.1E-91
2	GCKR	rs814295	27520348	G	A	0.3611670	-0.0517883	0.0026285	4.2E-91
2	GCKR	rs74928908	27521222	G	A	0.3582890	-0.0517219	0.0026361	2.5E-90
2	GCKR *	rs1260334	27525730	C	A	0.4867190	0.0548359	0.0025369	1.5E-109
2	GCKR *	rs1260333	27525757	A	G	0.4859110	0.0542442	0.0025202	9.7E-109
2	GCKR *	rs1313566	27526037	G	A	0.4836410	0.0543509	0.0025392	4.5E-108
2	GCKR *	rs11336847	27526125	AT	A	0.4839380	0.0545474	0.0025472	8.0E-108
2	GCKR *	rs6744393	27527272	T	C	0.3586620	-0.0510756	0.0026679	4.2E-86
2	GCKR *	rs2950835	27527678	A	G	0.4852000	0.0536252	0.0025587	2.0E-103
2	GCKR *	rs2911711	27527679	T	A	0.4852070	0.0536047	0.0025587	2.4E-103
2	GCKR *	rs78680773	27528695	C	A	0.3565790	-0.0510079	0.0026686	1.1E-85
2	GCKR *	rs6753534	27530004	C	T	0.4856310	0.0470912	0.0025637	9.6E-81
2	GCKR *	rs74450311	27531758	C	CAT	0.3752680	-0.0348471	0.0026116	3.5E-43
2	GCKR *	rs62131879	27532245	G	T	0.3759530	-0.0349054	0.0026102	2.6E-43
2	GCKR *	rs7606605	27532849	T	A	0.2109390	0.0265940	0.0031376	6.4E-19
2	GCKR *	rs4665987	27532958	A	G	0.4717400	0.0410906	0.0025315	2.1E-63
2	GCKR *	rs10181342	27534476	G	A	0.3758140	-0.0349141	0.0026104	2.5E-43
2	GCKR *	rs4665988	27538569	A	C	0.4719350	0.0410822	0.0025306	2.1E-63
2	GCKR *	rs116443177	27541255	T	C	0.3776370	-0.0349624	0.0026083	1.4E-43
2	GCKR *	rs62131881	27541914	T	G	0.3756740	-0.0349000	0.0026098	2.5E-43
2	GCKR *	rs62131882	27542613	C	T	0.3772910	-0.0349862	0.0026066	1.2E-43
2	GCKR *	rs12473139	27542720	C	T	0.4729100	0.0412979	0.0025290	3.5E-64
2	GCKR *	rs4665991	27543417	A	G	0.4724630	0.0411855	0.0025312	9.3E-64
2	GCKR *	rs67080990	27544621	G	GC	0.4730580	0.0412395	0.0025297	5.8E-64
2	GCKR *	rs62141278	27545514	T	C	0.3780530	-0.0348455	0.0026077	2.7E-43
2	GCKR *	rs59210625	27546607	C	A	0.2111440	0.0265069	0.0031362	7.1E-19
2	GCKR *	rs62141279	27548548	T	C	0.3767350	-0.0350870	0.0026090	9.9E-44
2	C2orf16 *	chr2:27550224_C_CT	27550224	CT	C	0.3726880	-0.0349270	0.0026310	2.1E-42
2	C2orf16 *	rs2384627	27551582	A	G	0.3758060	-0.0346868	0.0026091	1.1E-42
2	C2orf16 *	rs202103665	27553764	A	AT	0.4710930	0.0409262	0.0025294	5.1E-63
2	C2orf16 *	rs62141281	27554784	T	G	0.3766830	-0.0347217	0.0026057	4.9E-43
2	C2orf16 *	rs6751087	27555149	C	T	0.3766840	-0.0347232	0.0026057	4.8E-43
2	C2orf16 *	rs12995461	27555300	C	A	0.4714040	0.0408438	0.0025282	8.4E-63
2	C2orf16 *	rs10169065	27555693	G	A	0.4714040	0.0408438	0.0025282	8.4E-63
2	C2orf16 *	rs10179872	27555705	A	G	0.4702510	0.0407966	0.0025296	1.3E-62
2	C2orf16 *	rs79414972	27558930	G	A	0.3643680	-0.0332046	0.0026515	2.6E-38
2	C2orf16 *	rs62141288	27560331	A	G	0.3549640	-0.0328997	0.0026699	2.4E-36
2	C2orf16 *	rs200969564	27560335	GAC	G	0.3549640	-0.0328997	0.0026699	2.4E-36
2	C2orf16 *	rs62141290	27560525	C	T	0.3750540	-0.0346834	0.0026119	1.1E-42
2	C2orf16 *	rs4665382	27560934	C	T	0.4714130	0.0408435	0.0025286	8.9E-63
2	C2orf16 *	rs62141291	27561167	T	C	0.3767050	-0.0346421	0.0026053	7.9E-43
2	C2orf16 *	rs62141292	27561433	C	A	0.3767010	-0.0346422	0.0026053	7.9E-43
2	C2orf16 *	rs7570476	27561791	T	C	0.4713530	0.0407544	0.0025284	1.7E-62
2	C2orf16 *	rs10208529	27563321	T	A	0.4713640	0.0407422	0.0025284	1.9E-62
2	C2orf16 *	rs60854669	27564062	C	T	0.3766890	-0.0346682	0.0026053	7.0E-43
2	C2orf16 *	rs965813	27566994	A	T	0.3766540	-0.0346571	0.0026055	7.3E-43
2	C2orf16 *	rs4665383	27566868	G	C	0.4713710	0.0407420	0.0025284	1.9E-62
2	C2orf16 *	rs59876138	27569456	C	A	0.3766650	-0.0346730	0.0026055	6.8E-43
2	C2orf16 *	rs7577311	27571054	T	G	0.4715940	0.0408016	0.0025293	1.4E-62
2	C2orf16 *	rs6704596	27574060	G	A	0.3766780	-0.0346749	0.0026055	6.6E-43
2	C2orf16	rs1919127	27578626	C	T	0.4713400	0.0406802	0.0025276	2.4E-62
2	C2orf16	rs1919128	27578892	G	A	0.4713990	0.0406632	0.0025273	2.7E-62
2	C2orf16	rs3811644	27579938	G	A	0.3766550	-0.0347419	0.0026053	4.4E-43
2	ZNF512	rs6734059	27585287	C	T	0.3767530	-0.0347628	0.0026051	3.9E-43
2	ZNF512	rs12478841	27588855	G	A	0.4721640	0.0405246	0.0025276	6.8E-62
2	ZNF512	rs6760250	27589385	A	G	0.4721640	0.0405246	0.0025276	6.8E-62
2	ZNF512	rs62138963	27591507	T	C	0.3766510	-0.0347455	0.0026050	4.3E-43
2	ZNF512	rs62138964	27591571	T	C	0.3766510	-0.0347455	0.0026050	4.3E-43
2	ZNF512	rs145275920	27591660	T	C	0.0579396	-0.0485623	0.0054207	1.6E-19
2	ZNF512	rs13022873	27592643	C	A	0.4720150	0.0404159	0.0025288	1.5E-61
2	ZNF512	rs76013440	27593448	A	G	0.3757230	-0.0345156	0.0026093	2.4E-42
2	ZNF512	rs62138965	27593726	C	T	0.3758250	-0.0344919	0.0026087	2.5E-42
2	ZNF512	rs13010586	27594950	A	G	0.4721710	0.0405266	0.0025276	6.8E-62
2	ZNF512	rs1919129	27595854	G	C	0.3766420	-0.0347330	0.0026050	4.7E-43

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ZNF512	rs62138966	27596305	A	G	0.3763730	-0.0347453	0.0026056	4.8E-43
2	ZNF512	rs12989678	27598615	T	C	0.4716220	0.0411053	0.0025351	3.7E-63
2	ZNF512	rs78378018	27599416	GAC	G	0.3767740	-0.0346797	0.0026057	6.6E-43
2	ZNF512	rs117655217	27600099	C	T	0.0577253	-0.0484558	0.0054228	2.9E-19
2	ZNF512	rs56725354	27601301	C	G	0.3766410	-0.0347377	0.0026050	4.6E-43
2	ZNF512	rs62138968	27601618	G	C	0.3766390	-0.0347410	0.0026050	4.6E-43
2	ZNF512	rs112927528	27601644	TTTTTG	T	0.3754100	-0.0349826	0.0026101	2.0E-43
2	ZNF512	rs12467476	27602848	C	T	0.4708610	0.0404146	0.0025289	1.6E-61
2	ZNF512	rs12464616	27604225	T	C	0.4721120	0.0405322	0.0025278	6.6E-62
2	ZNF512	rs2141372	27604329	T	G	0.3766740	-0.0347752	0.0026053	4.2E-43
2	ZNF512	rs66497975	27604459	T	GTCATGT	0.4706610	0.0408235	0.0025320	1.8E-62
2	ZNF512	rs6719960	27607200	G	A	0.3766450	-0.0347593	0.0026052	4.5E-43
2	ZNF512	rs6547735	27608740	C	T	0.3766440	-0.0347926	0.0026053	3.7E-43
2	ZNF512	rs2384656	27609188	G	A	0.4721250	0.0405779	0.0025278	4.7E-62
2	ZNF512	rs1881397	27609418	G	A	0.3770480	-0.0350209	0.0026065	1.1E-43
2	ZNF512	chr2:27609869_CA_C	27609869	C	CA	0.3957830	-0.0335955	0.0026327	1.3E-39
2	ZNF512	rs112427483	27610460	T	TATATAT	0.3322690	-0.0381142	0.0027335	3.0E-46
2	ZNF512	rs74175068	27610635	C	T	0.4583080	0.0404361	0.0025836	6.3E-59
2	ZNF512	rs34016998	27610820	T	C	0.4714540	0.0404956	0.0025274	7.4E-62
2	ZNF512	rs12987055	27611285	C	T	0.4716540	0.0405579	0.0025278	5.6E-62
2	ZNF512	rs13405762	27611748	C	A	0.3743960	-0.0342623	0.0026151	9.4E-42
2	ZNF512	rs78170284	27612215	A	G	0.3770190	-0.0344797	0.0026055	1.7E-42
2	ZNF512	rs13020949	27613738	T	C	0.4715430	0.0403196	0.0025289	2.5E-61
2	ZNF512	chr2:27614806_CT_C	27614806	C	CT	0.3766560	-0.0345620	0.0026087	1.3E-42
2	ZNF512	rs1881395	27615682	A	G	0.3766140	-0.0345445	0.0026089	1.6E-42
2	ZNF512	rs4666000	27616502	C	T	0.4714420	0.0403996	0.0025302	1.6E-61
2	ZNF512	rs2068834	27616672	C	T	0.4709740	0.0403948	0.0025307	1.7E-61
2	ZNF512	rs7571558	27616965	G	C	0.3766850	-0.0345163	0.0026091	1.7E-42
2	ZNF512	rs4666001	27617672	G	A	0.1562720	0.0203453	0.0034796	9.9E-10
2	ZNF512	rs4666002	27617773	C	G	0.4707330	0.0404266	0.0025324	1.5E-61
2	ZNF512	rs62138971	27617887	A	G	0.3754370	-0.0342621	0.0026223	8.0E-42
2	ZNF512	rs1881396	27621734	G	T	0.3716310	-0.0352920	0.0026265	6.0E-44
2	GPN1	rs3749147	27629051	A	G	0.3132380	0.0338782	0.0027216	1.6E-37
2	GPN1	rs146892484	27629283	C	CG	0.4171910	0.0263973	0.0025651	1.2E-25
2	GPN1	rs34502053	27631657	A	G	0.3159320	0.0341990	0.0027159	1.1E-38
2	GPN1	rs10173720	27632530	A	T	0.4187320	0.0262430	0.0025582	1.3E-25
2	GPN1	rs6719175	27636484	A	T	0.3145200	0.0342466	0.0027294	2.5E-38
2	GPN1	rs77350364	27643272	A	G	0.4180880	0.0258486	0.0025657	1.0E-24
2	GPN1	rs12474585	27648726	C	T	0.4181970	0.0261132	0.0025642	2.8E-25
2	GPN1	rs35605899	27649445	A	AATAT	0.3347350	0.0306057	0.0026807	7.3E-32
2	GPN1	rs8731	27650459	C	G	0.4177440	0.0261345	0.0025643	2.8E-25
2	SUPT7L	chr2:27652149_AAAAT_A	27652149	AAAAT	A	0.4169200	0.0260712	0.0025707	4.5E-25
2	SUPT7L	rs67775899	27652169	TAAA	T	0.4175980	0.0260991	0.0025733	4.9E-25
2	SUPT7L	rs10202364	27652175	T	A	0.4181360	0.0261013	0.0025697	4.6E-25
2	SUPT7L	rs4666010	27655819	T	C	0.4176550	0.0261315	0.0025642	2.5E-25
2	SLC4A1AP	rs2272406	27669156	T	A	0.3346330	0.0306981	0.0026789	4.4E-32
2	SLC4A1AP	rs76586169	27674968	G	A	0.4172810	0.0260906	0.0025637	3.1E-25
2	SLC4A1AP	rs13021208	27678861	T	C	0.3347660	0.0313312	0.0026799	3.5E-33
2	SLC4A1AP	rs72613829	27680120	C	T	0.4164970	0.0265056	0.0025650	6.3E-26
2	SLC4A1AP	rs13023094	27687839	C	A	0.3347810	0.0306044	0.0026777	5.6E-32
2	SLC4A1AP	rs12998770	27690321	C	T	0.3350110	0.0305630	0.0026780	6.0E-32
2	SLC4A1AP *	rs80322731	27697569	G	A	0.2080760	0.0266037	0.0031552	1.0E-18
2	SLC4A1AP *	rs13030973	27705930	C	T	0.3319120	0.0310155	0.0026782	8.5E-33
2	SLC4A1AP *	rs4665385	27707970	C	T	0.4129870	0.0264172	0.0025610	6.0E-26
2	SLC4A1AP *	rs6727388	27709720	G	A	0.3311810	0.0314255	0.0026801	1.6E-33
2	SLC4A1AP *	rs4616435	27710775	T	C	0.3318840	0.0310053	0.0026784	9.1E-33
2	SLC4A1AP *	rs58199976	27711657	T	C	0.4120210	0.0268441	0.0025617	1.0E-26
2	SLC4A1AP *	rs6727215	27711864	A	G	0.3311460	0.0314122	0.0026802	1.8E-33
2	SLC4A1AP *	rs4665386	27712485	C	A	0.4135000	0.0264916	0.0025605	4.7E-26
2	SLC4A1AP *	rs6742571	27719021	G	A	0.4192870	0.0261858	0.0025635	1.8E-25
2	SLC4A1AP *	chr2:27724905_CT_C	27724905	C	CT	0.4116840	0.0253160	0.0026014	3.1E-23
2	SLC4A1AP *	rs1881394	27726185	G	A	0.4151920	0.0261414	0.0025853	4.3E-25
2	SLC4A1AP *	rs10432705	27727970	A	G	0.3311200	0.0316753	0.0027097	3.6E-33
2	SLC4A1AP *	rs867282	27728791	C	T	0.4149230	0.0259442	0.0025845	1.1E-24
2	SLC4A1AP *	rs2384655	27729368	T	A	0.4149690	0.0259318	0.0025844	1.2E-24
2	SLC4A1AP *	rs12994085	27729539	T	C	0.4149840	0.0259372	0.0025844	1.2E-24
2	SLC4A1AP *	rs12993377	27729900	C	G	0.4149800	0.0259359	0.0025845	1.2E-24
2	MRPL33 *	rs12624148	27733614	C	T	0.4151900	0.0257798	0.0025883	3.0E-24
2	MRPL33 *	rs6753736	27735988	G	C	0.4205380	0.0245734	0.0025823	1.8E-22
2	MRPL33 *	rs75429814	27738747	T	C	0.4110490	0.0246678	0.0026026	3.3E-22
2	MRPL33 *	rs111938697	27740266	C	T	0.4150560	0.0242922	0.0025932	9.4E-22
2	MRPL33 *	rs12714223	27740463	A	G	0.4140530	0.0239066	0.0025927	3.9E-21

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	MRPL33 *	rs36017854	27740804	AAT	A	0.4132860	0.0240080	0.0025958	3.0E-21
2	MRPL33 *	rs9678824	27741461	G	C	0.4143330	0.0237466	0.0025908	7.0E-21
2	MRPL33 *	rs13023194	27744393	C	G	0.3332340	0.0273360	0.0027028	3.2E-25
2	MRPL33 *	rs9967838	27745587	C	A	0.4143350	0.0234722	0.0025738	1.0E-20
2	MRPL33 *	chr2:27747209_A_AT	27747209	AT	A	0.4026700	0.0229887	0.0025894	9.8E-20
2	MRPL33 *	rs9677663	27749578	A	G	0.4096060	0.0238936	0.0025660	1.1E-21
2	MRPL33 *	rs57238885	27751393	C	G	0.4096960	0.0241482	0.0025655	4.6E-22
2	MRPL33 *	rs10201247	27752104	G	A	0.4096960	0.0241482	0.0025655	4.6E-22
2	MRPL33 *	rs6547796	27752527	C	T	0.4100020	0.0240693	0.0025658	6.3E-22
2	MRPL33 *	rs4666011	27758045	G	C	0.4097290	0.0241089	0.0025650	5.0E-22
2	MRPL33 *	rs10209020	27758077	T	C	0.4099530	0.0240761	0.0025657	6.0E-22
2	MRPL33 *	rs12471347	27758788	G	C	0.4098260	0.0240142	0.0025641	6.7E-22
2	MRPL33 *	rs77154381	27759252	A	G	0.4080480	0.0243464	0.0025689	2.4E-22
2	MRPL33 *	rs12477908	27764179	C	A	0.4108990	0.0238970	0.0025641	1.2E-21
2	MRPL33 *	rs13006480	27764354	G	C	0.3260940	0.0271297	0.0027143	5.8E-25
2	MRPL33 *	rs13013484	27765954	A	G	0.4098620	0.0240014	0.0025642	7.2E-22
2	MRPL33 *	rs146796793	27766610	G	A	0.0530735	-0.0435494	0.0057068	5.1E-15
2	MRPL33 *	rs4665390	27767042	C	T	0.4109150	0.0239058	0.0025656	1.3E-21
2	MRPL33 *	rs74429612	27770976	C	T	0.4109940	0.0238673	0.0025640	1.5E-21
2	MRPL33	rs3736594	27772914	C	A	0.4110180	0.0240286	0.0025640	7.1E-22
2	MRPL33	rs3792252	27773064	A	G	0.4098120	0.0240149	0.0025640	6.5E-22
2	MRPL33	rs35463245	27777857	C	G	0.4079290	0.0239142	0.0025711	1.2E-21
2	MRPL33	rs17006242	27778184	C	A	0.4108630	0.0239338	0.0025641	1.1E-21
2	MRPL33	rs3792253	27779135	T	C	0.4097310	0.0240021	0.0025645	7.2E-22
2	MRPL33 *	rs13030345	27780307	T	G	0.3063610	0.0252916	0.0027615	4.0E-21
2	RBKS	rs74327441	27784205	G	A	0.4037860	0.0234333	0.0026055	4.8E-20
2	RBKS	rs192918024	27787093	T	A	0.0295460	-0.0457773	0.0075272	2.4E-10
2	RBKS	rs7596967	27789917	T	G	0.3898190	0.0216009	0.0026138	3.4E-17
2	RBKS	rs7593136	27794925	A	G	0.4112540	0.0236168	0.0025637	3.5E-21
2	RBKS	rs6744348	27795158	A	C	0.4112690	0.0236302	0.0025634	3.4E-21
2	RBKS	rs36035825	27795264	T	G	0.4112660	0.0236366	0.0025634	3.3E-21
2	RBKS	rs4666012	27795426	A	G	0.4112620	0.0236351	0.0025634	3.3E-21
2	RBKS	rs11322614	27796225	AT	A	0.4100000	0.0233763	0.0025699	8.9E-21
2	RBKS	rs4666013	27796239	C	T	0.4112690	0.0236005	0.0025633	3.6E-21
2	RBKS	rs4666014	27796308	G	A	0.4113380	0.0235560	0.0025633	4.2E-21
2	RBKS	rs4666015	27796500	G	A	0.4112740	0.0235972	0.0025633	3.7E-21
2	RBKS	rs34181670	27796989	T	C	0.4112750	0.0235995	0.0025633	3.7E-21
2	RBKS	rs35679500	27797099	T	C	0.4112750	0.0235995	0.0025633	3.7E-21
2	RBKS	rs12623170	27797290	C	T	0.4117900	0.0233110	0.0025625	1.2E-20
2	RBKS	rs3935148	27798099	T	A	0.4083320	0.0237550	0.0025685	3.0E-21
2	RBKS	rs13027427	27798176	G	T	0.3793680	0.0212143	0.0026059	4.5E-17
2	RBKS	rs6745545	27798978	C	G	0.3793150	0.0212214	0.0026061	4.5E-17
2	RBKS	rs7570730	27799808	G	A	0.3792750	0.0214076	0.0026084	3.1E-17
2	RBKS	rs11127125	27800253	T	C	0.3785680	0.0212453	0.0026106	5.0E-17
2	RBKS	rs11127126	27800417	C	T	0.3792760	0.0213894	0.0026090	3.2E-17
2	RBKS	rs12473340	27800930	G	A	0.3792180	0.0213004	0.0026094	4.1E-17
2	RBKS	rs12473400	27801157	G	T	0.3800280	0.0213219	0.0026098	4.3E-17
2	RBKS	rs4630723	27801464	T	C	0.3895490	0.0195357	0.0026291	1.2E-14
2	RBKS	rs13019037	27801775	C	T	0.3793830	0.0211559	0.0026116	6.2E-17
2	RBKS	rs4632296	27802117	T	C	0.3806090	0.0212228	0.0026196	6.2E-17
2	RBKS	rs13001060	27802194	T	C	0.3823180	0.0205848	0.0026177	5.1E-16
2	RBKS	rs12995865	27802199	A	C	0.3823180	0.0205848	0.0026177	5.1E-16
2	RBKS	rs11891769	27802713	G	C	0.3794350	0.0213011	0.0026111	4.2E-17
2	RBKS	rs12465012	27805324	C	T	0.3587840	0.0183358	0.0026410	9.3E-13
2	RBKS	rs4665392	27806782	A	G	0.3586730	0.0180381	0.0026409	1.9E-12
2	RBKS	rs12986980	27807570	A	G	0.3578520	0.0182863	0.0026410	9.9E-13
2	RBKS	rs13023003	27809270	G	C	0.3582680	0.0183975	0.0026386	7.2E-13
2	RBKS	rs4233716	27811517	C	T	0.3788850	0.0163413	0.0026117	2.0E-10
2	RBKS	rs4233717	27811813	A	T	0.3788850	0.0163413	0.0026117	2.0E-10
2	RBKS	chr2:27813039_TAA_T	27813039	TAA	T	0.3785310	0.0163260	0.0026122	1.9E-10
2	RBKS	rs4666016	27814273	T	A	0.3773640	0.0164665	0.0026130	1.5E-10
2	RBKS	rs4464229	27815213	C	T	0.3790160	0.0161925	0.0026149	2.7E-10
2	RBKS	rs12617171	27815932	C	T	0.3779470	0.0162502	0.0026121	2.3E-10
2	RBKS	rs4420671	27816433	G	C	0.3780470	0.0163404	0.0026115	1.8E-10
2	RBKS	rs4493211	27816605	G	T	0.3785310	0.0162926	0.0026126	2.1E-10
2	RBKS	rs4665393	27817409	G	A	0.3780550	0.0163397	0.0026115	1.8E-10
2	RBKS	rs4666017	27817658	C	A	0.3780550	0.0163397	0.0026115	1.8E-10
2	RBKS	rs12478766	27818333	T	C	0.3780200	0.0162559	0.0026118	2.2E-10
2	RBKS	rs13026758	27818406	A	G	0.3780130	0.0163071	0.0026119	2.0E-10
2	RBKS	rs4666018	27819192	C	T	0.3832070	0.0162277	0.0026096	2.8E-10
2	RBKS	rs66523005	27822746	TAGAA	T	0.3869240	0.0165592	0.0026068	1.4E-10
2	RBKS	rs4666020	27823161	G	A	0.3868960	0.0167270	0.0026061	9.5E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	RBKS	chr2:27825136_CA_C	27825136	CA	C	0.3884020	0.0164852	0.0026113	2.2E-10
2	RBKS	rs9679543	27828084	C	T	0.3818120	0.0168976	0.0025986	5.1E-11
2	RBKS	rs10531773	27831894	GAA	G	0.3820060	0.0169497	0.0025991	4.5E-11
2	RBKS	rs4666021	27833014	A	G	0.3812540	0.0166822	0.0025996	1.0E-10
2	RBKS	rs9678430	27834262	G	C	0.3813080	0.0167119	0.0026000	9.0E-11
2	RBKS	rs12463914	27834492	C	T	0.3813210	0.0166877	0.0025994	9.9E-11
2	RBKS	rs7560060	27834657	T	C	0.3812540	0.0166822	0.0025996	1.0E-10
2	RBKS	rs4666022	27834956	T	C	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs12464988	27835359	C	T	0.3795050	0.0164235	0.0026115	2.5E-10
2	RBKS	rs13027666	27835566	T	C	0.3801390	0.0162787	0.0026090	3.4E-10
2	RBKS	rs11885959	27836033	C	G	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs4665394	27836155	T	C	0.3810990	0.0167096	0.0025999	8.8E-11
2	RBKS	rs12617110	27837044	A	G	0.3812400	0.0168417	0.0026000	6.4E-11
2	RBKS	rs12617113	27837070	A	G	0.3812400	0.0168417	0.0026000	6.4E-11
2	RBKS	rs12992890	27837964	T	C	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs34096628	27838123	A	C	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs4275987	27840089	A	G	0.3860560	0.0172311	0.0026106	2.8E-11
2	RBKS	rs4462754	27841127	C	T	0.3817660	0.0168996	0.0025986	4.7E-11
2	RBKS	rs9678336	27842537	A	G	0.3812160	0.0167544	0.0025998	7.8E-11
2	RBKS	rs74446114	27843255	C	T	0.2996440	0.0194187	0.0027765	1.2E-12
2	RBKS	rs4233718	27843493	A	G	0.3812630	0.0167736	0.0025997	7.8E-11
2	RBKS	rs11127127	27844037	G	T	0.3818750	0.0169138	0.0025986	4.7E-11
2	RBKS	rs11127128	27844103	T	A	0.3812630	0.0167736	0.0025997	7.8E-11
2	RBKS	rs77853892	27844692	A	C	0.1651000	0.0253041	0.0034635	1.0E-14
2	RBKS	rs4564736	27846676	A	T	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs11901133	27846846	T	G	0.3811960	0.0167303	0.0025998	8.3E-11
2	RBKS	rs4555299	27848323	A	G	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs35841453	27849835	T	C	0.3812540	0.0167793	0.0025997	7.7E-11
2	RBKS	rs4666024	27850112	C	G	0.3789020	0.0170734	0.0026050	3.8E-11
2	RBKS	rs4666025	27851027	C	T	0.3812540	0.0167793	0.0025997	7.7E-11
2	RBKS	rs4313931	27851834	C	T	0.3812540	0.0167793	0.0025997	7.7E-11
2	RBKS	rs4583413	27851957	C	T	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs4419196	27852431	A	G	0.3811770	0.0167483	0.0025997	7.9E-11
2	RBKS	rs4447576	27853381	T	C	0.3847600	0.0167386	0.0026116	8.8E-11
2	RBKS	rs11127129	27853841	C	G	0.3815290	0.0171044	0.0026046	3.5E-11
2	RBKS	rs7426295	27856127	G	A	0.3760040	0.0179069	0.0026096	3.9E-12
2	RBKS	rs4233719	27856477	C	A	0.3760040	0.0179069	0.0026096	3.9E-12
2	RBKS	rs4233720	27856908	A	G	0.3760850	0.0178337	0.0026095	5.1E-12
2	RBKS	rs13025314	27857347	G	A	0.3760850	0.0178337	0.0026095	5.1E-12
2	RBKS	rs4578808	27858763	G	T	0.3760850	0.0178337	0.0026095	5.1E-12
2	RBKS	rs4578809	27859627	G	A	0.3760850	0.0178337	0.0026095	5.1E-12
2	RBKS	chr2:27860975_C_CT	27860975	C	CT	0.3760950	0.0178335	0.0026096	5.2E-12
2	RBKS	rs6714106	27860977	C	T	0.3786490	0.0177719	0.0026127	8.3E-12
2	RBKS	rs7595986	27862444	A	G	0.3759480	0.0178801	0.0026094	4.2E-12
2	RBKS	rs13021285	27862480	T	C	0.3760290	0.0178069	0.0026093	5.5E-12
2	RBKS	rs77353560	27862677	A	C	0.2841980	0.0189834	0.0028274	1.3E-11
2	RBKS	rs11902158	27863898	A	G	0.3760290	0.0178069	0.0026093	5.5E-12
2	RBKS	rs13004096	27864338	C	T	0.3760290	0.0178069	0.0026093	5.5E-12
2	RBKS	rs1973116	27865051	C	T	0.3751410	0.0183424	0.0026159	1.6E-12
2	RBKS	rs4666028	27865713	T	A	0.3771360	0.0175541	0.0026089	1.1E-11
2	RBKS	rs71441095	27866981	A	G	0.4721050	-0.0255076	0.0025604	2.2E-24
2	RBKS	rs10171517	27867192	T	C	0.4722730	-0.0254520	0.0025600	2.5E-24
2	RBKS	rs898034	27867953	T	C	0.4723930	-0.0254614	0.0025595	2.4E-24
2	RBKS	rs2337373	27870055	C	T	0.3760020	0.0178993	0.0026097	4.0E-12
2	RBKS	rs13016573	27871403	C	G	0.3773480	0.0179254	0.0026136	4.1E-12
2	RBKS	rs4665398	27871903	A	T	0.3760850	0.0178566	0.0026095	4.8E-12
2	RBKS	rs12466687	27873840	C	A	0.3770470	0.0178838	0.0026129	4.6E-12
2	RBKS	rs12466717	27873925	G	A	0.3759500	0.0179061	0.0026094	4.0E-12
2	RBKS	rs4666030	27874355	C	T	0.3759450	0.0179099	0.0026094	3.9E-12
2	RBKS	rs13411592	27875857	A	G	0.3759480	0.0179140	0.0026093	3.9E-12
2	RBKS	rs35445284	27878028	A	AT	0.3766400	0.0178820	0.0026117	4.7E-12
2	RBKS	rs6706209	27879071	T	C	0.3758770	0.0180420	0.0026087	2.6E-12
2	RBKS	rs12620151	27879837	T	A	0.3759680	0.0180668	0.0026087	2.5E-12
2	RBKS	rs6547814	27880131	G	A	0.3758770	0.0180420	0.0026087	2.6E-12
2	RBKS	rs11886463	27881670	C	T	0.3759580	0.0179646	0.0026086	3.4E-12
2	RBKS	rs13413962	27881699	A	G	0.3758720	0.0180503	0.0026087	2.5E-12
2	RBKS	rs6708889	27884825	T	C	0.3758400	0.0179638	0.0026083	3.1E-12
2	RBKS	chr2:27888789_TA_T	27888789	T	TA	0.3755630	0.0181092	0.0026093	2.2E-12
2	BRE	rs7607546	27895795	A	G	0.3756390	0.0179547	0.0026041	3.2E-12
2	BRE	rs141361525	27896053	G	C	0.0554869	-0.0397052	0.0056059	2.1E-13
2	BRE	rs7592580	27898323	C	T	0.3765810	0.0176794	0.0026033	7.6E-12
2	BRE	rs17006365	27900507	G	T	0.3765280	0.0178202	0.0026048	4.0E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	BRE	rs6709765	27900893	T	A	0.3757690	0.0178943	0.0026031	3.3E-12
2	BRE	rs10177845	27901304	A	G	0.3758310	0.0178259	0.0026030	4.0E-12
2	BRE	rs34483784	27906524	G	A	0.3896720	0.0159799	0.0025911	7.6E-10
2	BRE	rs10201105	27908366	C	G	0.3896810	0.0159642	0.0025912	7.8E-10
2	BRE	rs10190494	27908376	G	A	0.3898810	0.0157590	0.0025911	1.3E-09
2	BRE	rs10204488	27909383	A	G	0.3867640	0.0161048	0.0025911	4.8E-10
2	BRE	rs2016616	27911170	G	A	0.3906690	0.0162258	0.0025946	4.0E-10
2	BRE	rs1458396	27913484	G	A	0.3895900	0.0160168	0.0025910	6.7E-10
2	BRE	rs35177396	27916281	TA	T	0.3934510	0.0149888	0.0025946	9.2E-09
2	BRE	rs2337372	27917482	G	A	0.3896260	0.0159885	0.0025911	7.8E-10
2	BRE	rs10173848	27920150	T	G	0.3864940	0.0162184	0.0025910	3.5E-10
2	BRE	rs1870325	27921200	A	G	0.3865300	0.0161928	0.0025907	3.6E-10
2	BRE	rs117290132	27923697	A	G	0.0405214	-0.0427059	0.0065078	2.9E-11
2	BRE	rs6745379	27924674	C	T	0.3875210	0.0161936	0.0025899	3.7E-10
2	BRE	rs13026003	27927931	C	T	0.3900250	0.0159305	0.0025923	8.7E-10
2	BRE	rs111357701	27928463	TTTCTC	T	0.3878890	0.0163991	0.0025991	3.5E-10
2	BRE	rs10185472	27928487	A	G	0.3891230	0.0160751	0.0025933	5.8E-10
2	BRE	rs6547815	27932328	A	T	0.3873750	0.0160781	0.0025914	5.4E-10
2	BRE	rs11886375	27932881	A	C	0.3872300	0.0160611	0.0025901	5.9E-10
2	BRE	rs10174070	27933753	G	A	0.3883590	0.0158164	0.0026079	1.8E-09
2	BRE	rs10194283	27936212	A	G	0.3873510	0.0164163	0.0025874	2.3E-10
2	BRE	rs10184052	27936777	G	A	0.3874900	0.0164389	0.0025873	2.2E-10
2	BRE	rs13400398	27939242	T	C	0.3871360	0.0164239	0.0025874	2.2E-10
2	BRE	rs13416434	27939407	C	T	0.3871370	0.0164230	0.0025874	2.2E-10
2	BRE	rs4390729	27939994	C	T	0.3904940	0.0161919	0.0025871	4.7E-10
2	BRE	rs11274834	27940623	TGCTAAC	C	0.3838990	0.0165373	0.0026015	2.6E-10
2	BRE	rs10170872	27941686	T	C	0.3870980	0.0164626	0.0025875	2.1E-10
2	BRE	rs57403744	27942131	A	G	0.1577160	0.0251915	0.0035031	3.4E-14
2	BRE	rs13399709	27944583	T	C	0.3872760	0.0163761	0.0025868	2.6E-10
2	BRE	rs7577437	27945548	G	A	0.3874500	0.0163668	0.0025869	2.6E-10
2	BRE	rs6547816	27946730	C	T	0.3887580	0.0161799	0.0025943	6.2E-10
2	BRE	rs12165240	27949258	T	A	0.3893760	0.0164854	0.0025914	2.8E-10
2	BRE	rs13382482	27949426	C	T	0.3897580	0.0166459	0.0025894	1.8E-10
2	BRE	rs7595847	27950176	A	T	0.3899330	0.0165925	0.0025896	2.0E-10
2	BRE	rs1506535	27951214	G	A	0.3900520	0.0165904	0.0025891	2.0E-10
2	BRE	rs13008539	27951540	A	C	0.3900520	0.0165904	0.0025891	2.0E-10
2	BRE	rs7584462	27953189	T	A	0.3904780	0.0165059	0.0025891	2.6E-10
2	BRE	rs7587180	27953242	G	A	0.3908910	0.0164037	0.0025883	3.4E-10
2	BRE	rs10205313	27953660	C	A	0.3891430	0.0160574	0.0025960	8.7E-10
2	BRE	chr2:27955981_G_GT	27955981	GT	G	0.3884340	0.0166151	0.0025996	2.6E-10
2	BRE	rs10559599	27958465	TTA	T	0.3906480	0.0164883	0.0025889	2.7E-10
2	BRE	rs1506537	27959034	C	G	0.3875140	0.0164221	0.0025889	2.5E-10
2	BRE	rs1506536	27959139	C	T	0.3901960	0.0164717	0.0025902	2.8E-10
2	BRE	rs2012704	27961899	A	T	0.3871480	0.0160673	0.0025910	5.4E-10
2	BRE	rs1350481	27962941	C	G	0.3868210	0.0160718	0.0025898	5.8E-10
2	BRE	rs3056502	27966214	T	TTTC	0.3844600	0.0163870	0.0025942	2.9E-10
2	BRE	rs1902966	27966413	A	G	0.3844600	0.0163870	0.0025942	2.9E-10
2	BRE	rs1841068	27968762	T	C	0.3871580	0.0164224	0.0025872	2.3E-10
2	BRE	rs10188108	27969688	G	C	0.3876190	0.0162004	0.0025861	4.0E-10
2	BRE	rs10198257	27973444	C	T	0.3757780	0.0160815	0.0026420	1.1E-09
2	BRE	rs12465000	27976557	A	G	0.3874290	0.0163684	0.0025869	2.6E-10
2	BRE	rs12465103	27976869	C	G	0.3874500	0.0163546	0.0025869	2.7E-10
2	BRE	rs2337374	27977285	A	G	0.3874490	0.0163487	0.0025869	2.7E-10
2	BRE	rs898032	27980069	G	C	0.3879850	0.0161953	0.0025865	4.1E-10
2	BRE	rs898031	27980427	T	C	0.2466640	0.0187532	0.0029560	3.2E-11
2	BRE	rs7577342	27982714	T	C	0.3881640	0.0166493	0.0025882	1.3E-10
2	BRE	rs28662360	27986053	G	A	0.3874390	0.0163055	0.0025869	3.0E-10
2	BRE	rs10209126	27986416	T	C	0.3871460	0.0163611	0.0025872	2.6E-10
2	BRE	rs13029008	27990023	A	G	0.3869200	0.0160965	0.0025873	5.4E-10
2	BRE	rs10175508	27990557	T	C	0.3870330	0.0162404	0.0025879	3.5E-10
2	BRE	rs12470614	27994460	C	T	0.3879810	0.0161749	0.0025865	4.3E-10
2	BRE	rs1458397	27996741	C	T	0.3891630	0.0159420	0.0025863	8.4E-10
2	BRE	rs1458398	27997074	G	A	0.3886330	0.0162151	0.0025850	4.0E-10
2	BRE	rs10204513	27998058	C	G	0.3888020	0.0160493	0.0025842	6.2E-10
2	BRE	rs10196483	27998315	T	A	0.3888020	0.0160493	0.0025842	6.2E-10
2	BRE	rs10204832	28005541	A	T	0.3888050	0.0160401	0.0025842	6.4E-10
2	BRE	rs10168171	28009220	G	A	0.3888080	0.0160421	0.0025842	6.3E-10
2	BRE	rs2839791	28009412	C	A	0.3883470	0.0162641	0.0025854	3.6E-10
2	BRE	rs145058190	28010531	T	C	0.0404896	-0.0443641	0.0065012	8.6E-12
2	BRE	rs58258810	28011829	GA	G	0.3874200	0.0156025	0.0025949	1.8E-09
2	BRE	rs56046821	28011834	A	T	0.3888080	0.0160421	0.0025842	6.3E-10
2	BRE	rs7602328	28012317	A	G	0.3886400	0.0162049	0.0025850	4.2E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	BRE	rs13003383	28012896	C	T	0.3885760	0.0161151	0.0025851	5.5E-10
2	BRE	rs10495761	28013088	T	C	0.3882290	0.0159784	0.0025851	7.3E-10
2	BRE	rs11127132	28013253	C	T	0.3885360	0.0160902	0.0025847	5.8E-10
2	BRE	rs6547817	28015118	T	C	0.3883520	0.0162507	0.0025854	3.7E-10
2	BRE	rs35526001	28017352	A	ATGT	0.3862990	0.0161573	0.0025911	5.2E-10
2	BRE	rs10180107	28017658	C	T	0.3876870	0.0162704	0.0025854	3.4E-10
2	BRE	rs4616436	28019441	A	G	0.3875180	0.0164367	0.0025862	2.2E-10
2	BRE	rs6725627	28019585	G	T	0.3877050	0.0162781	0.0025855	3.4E-10
2	BRE	rs12997202	28027522	A	G	0.3869180	0.0160679	0.0025861	5.5E-10
2	BRE	rs6727432	28028123	G	T	0.3877280	0.0160856	0.0025861	5.5E-10
2	BRE	rs17006439	28031825	A	G	0.1820060	0.0216242	0.0033364	7.0E-12
2	BRE	rs937812	28032435	T	C	0.3874590	0.0164147	0.0025868	2.5E-10
2	BRE	rs9309658	28033964	G	A	0.3874420	0.0164183	0.0025867	2.4E-10
2	BRE	rs7593127	28035160	A	G	0.3874420	0.0164183	0.0025867	2.4E-10
2	BRE	rs6731650	28038296	A	C	0.3870940	0.0165494	0.0025879	1.9E-10
2	BRE	rs10175826	28038517	A	G	0.3864070	0.0161082	0.0025895	4.9E-10
2	BRE	rs10200337	28038807	T	C	0.2452350	0.0193060	0.0029664	1.2E-11
2	BRE	rs6547819	28043177	G	A	0.3841170	0.0152054	0.0026114	7.4E-09
2	BRE	rs7580274	28043202	T	C	0.3841960	0.0160736	0.0026037	7.5E-10
2	BRE	rs6738887	28045600	T	C	0.3879420	0.0160262	0.0025859	6.0E-10
2	BRE	rs12614744	28046835	T	A	0.3883900	0.0158506	0.0025886	9.4E-10
2	BRE	rs13402420	28048568	G	T	0.4021620	0.0140909	0.0025703	3.2E-08
2	BRE	rs4133152	28052962	A	T	0.0417647	-0.0438504	0.0064049	5.7E-12
2	BRE	rs1395324	28053776	G	C	0.3873850	0.0165233	0.0025865	1.8E-10
2	BRE	rs1911128	28056782	G	T	0.4022960	0.0142987	0.0025695	2.0E-08
2	BRE	rs1911127	28056826	A	G	0.4023050	0.0142861	0.0025694	2.1E-08
2	BRE	rs6547820	28058678	A	G	0.3872960	0.0165137	0.0025861	1.8E-10
2	BRE	rs6758799	28061766	C	T	0.3870770	0.0164922	0.0025880	1.8E-10
2	BRE	rs10173528	28065525	T	C	0.2458740	0.0197550	0.0029627	4.2E-12
2	BRE	rs13414801	28067480	C	T	0.4020590	0.0143269	0.0025708	1.9E-08
2	BRE	rs13409819	28070432	A	C	0.3861800	0.0165161	0.0026319	5.0E-10
2	BRE	rs11691385	28076117	G	A	0.4705960	0.0165330	0.0025757	8.3E-11
2	BRE	rs6737313	28076400	G	A	0.4715080	0.0166281	0.0025765	6.6E-11
2	BRE	rs11363251	28078343	G	GC	0.4423090	0.0166452	0.0025419	4.8E-11
2	BRE	rs2337699	28080846	T	C	0.4451490	0.0167976	0.0025356	3.3E-11
2	BRE	rs11682011	28081194	A	G	0.2932060	0.0182454	0.0027876	6.2E-12
2	BRE	chr2:28082112_GA_G	28082112	G	GA	0.2929310	0.0182882	0.0027914	6.1E-12
2	BRE	rs13415164	28082796	T	C	0.2937800	0.0177282	0.0027863	2.6E-11
2	BRE	rs2337700	28084076	G	A	0.4620250	0.0145614	0.0025219	5.4E-09
2	BRE	rs12614949	28084924	A	G	0.4428480	0.0163430	0.0025366	1.1E-10
2	BRE	rs10173426	28086710	G	A	0.3126300	0.0150959	0.0027366	3.2E-09
2	BRE	rs13402525	28091991	T	G	0.2956070	0.0174516	0.0027769	3.8E-11
2	BRE	rs13405377	28092277	T	G	0.2944490	0.0181671	0.0027831	6.3E-12
2	BRE	rs13431542	28092278	T	C	0.2944490	0.0181671	0.0027831	6.3E-12
2	BRE	rs11678963	28092691	G	A	0.3126980	0.0151026	0.0027364	2.9E-09
2	BRE	rs6710214	28094574	G	A	0.3217480	0.0161280	0.0027171	1.9E-10
2	BRE	rs10182585	28094942	G	A	0.3191380	0.0170391	0.0027292	2.5E-11
2	BRE	rs7578052	28096012	G	A	0.3044070	0.0185012	0.0027504	2.0E-12
2	BRE	rs6757405	28096049	T	C	0.3033190	0.0187497	0.0027557	1.1E-12
2	BRE	rs3863	28096267	G	A	0.3028730	0.0184137	0.0027565	2.5E-12
2	BRE	rs13395259	28096429	T	C	0.4524880	0.0172541	0.0025393	9.8E-12
2	BRE	rs11679638	28096872	T	C	0.3049490	0.0185653	0.0027439	1.2E-12
2	BRE	rs7581813	28097094	G	T	0.4516640	0.0171246	0.0025289	1.1E-11
2	BRE	rs7572644	28097166	T	C	0.4515040	0.0171524	0.0025293	1.0E-11
2	BRE	rs7558946	28097314	T	C	0.4506360	0.0172533	0.0025316	6.6E-12
2	BRE	rs10209559	28099593	A	G	0.2940040	0.0181771	0.0027753	7.1E-12
2	BRE	rs10187665	28101263	G	A	0.3193120	0.0168849	0.0027192	3.4E-11
2	BRE	rs77252308	28101842	T	TC	0.2936200	0.0181132	0.0027809	9.4E-12
2	BRE	rs6705961	28102334	T	C	0.4415750	0.0163440	0.0025450	1.3E-10
2	BRE	rs9309659	28103391	C	G	0.4523320	0.0170798	0.0025461	1.7E-11
2	BRE	rs10186196	28104963	G	C	0.2934520	0.0165480	0.0027961	4.6E-10
2	COBLL1 *	rs6754919	164651333	T	C	0.1034360	-0.0236727	0.0041408	3.6E-08
2	COBLL1 *	rs6713419	164651790	C	T	0.1034400	-0.0236962	0.0041407	3.5E-08
2	COBLL1 *	rs36105243	164668241	G	C	0.1033920	-0.0235169	0.0041395	4.7E-08
2	COBLL1 *	rs7592412	164669828	C	T	0.1033870	-0.0234970	0.0041394	4.8E-08
2	COBLL1 *	rs1128249	164672114	T	G	0.1035510	-0.0235254	0.0041369	4.6E-08
2	COBLL1 *	rs13389219	164672366	T	C	0.1036650	-0.0236050	0.0041400	4.5E-08
2	G6PC2	rs2232326	168907981	C	T	0.0399488	-0.0351147	0.0064892	4.7E-08
2	G6PC2 *	rs12053049	168910638	C	T	0.2891550	0.0152202	0.0028295	3.8E-08
2	G6PC2 *	rs16856187	168913876	C	A	0.2927500	0.0153969	0.0028249	3.9E-08
2	ABCB11 *	rs71676177	168919036	A	ATTTG	0.2878060	0.0155762	0.0028185	2.2E-08
2	ABCB11 *	rs73972707	168919250	G	A	0.2879480	0.0154285	0.0028179	3.0E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ABCB11 *	rs28819151	168919319	G	A	0.2879440	0.0154358	0.0028178	3.0E-08
2	ABCB11 *	rs74870851	168919713	G	A	0.2880050	0.0154495	0.0028173	3.0E-08
2	ABCB11 *	rs78529720	168920787	G	A	0.2899460	0.0155174	0.0028083	2.9E-08
2	ABCB11	rs16856261	168947058	T	C	0.3092650	0.0149826	0.0027715	3.6E-08
3	SYN2 *	rs35355828	12225005	A	G	0.0457764	-0.0346447	0.0060545	4.5E-09
3	SYN2 *	rs11720578	12225584	T	G	0.0458285	-0.0341259	0.0060528	7.1E-09
3	PPARG	rs17036160	12288284	T	C	0.0379778	-0.0344144	0.0066124	4.7E-08
3	PPARG	rs11709077	12295008	A	G	0.0394511	-0.0361248	0.0064876	5.1E-09
3	PPARG	rs35000407	12310022	G	T	0.0391919	-0.0350088	0.0065078	1.7E-08
3	PPARG	rs2067819	12317550	A	G	0.0392637	-0.0346054	0.0065020	2.4E-08
3	PPARG	chr3:12318858_G_GT	12318858	GT	G	0.0383379	-0.0374802	0.0065941	2.8E-09
3	PPARG	rs150732434	12319385	T	TG	0.0391788	-0.0350896	0.0065086	1.6E-08
3	PPARG	rs13083375	12323809	T	G	0.0391788	-0.0350896	0.0065086	1.6E-08
3	PPARG	rs13064760	12327902	T	C	0.0391788	-0.0350896	0.0065086	1.6E-08
3	PPARG	rs2012444	12334457	T	C	0.0391807	-0.0351156	0.0065091	1.7E-08
3	PPARG	rs35240997	12337852	G	A	0.0392739	-0.0344509	0.0065022	2.7E-08
3	PPARG	rs13085211	12341766	A	G	0.0397910	-0.0350785	0.0064583	1.3E-08
3	PPARG	rs7638903	12342215	A	G	0.0391459	-0.0351321	0.0065088	1.4E-08
3	PPARG	rs11128603	12344329	G	A	0.0392070	-0.0349773	0.0065038	1.6E-08
3	PPARG	rs4684847	12344838	T	C	0.0390135	-0.0349492	0.0065192	1.8E-08
3	PPARG	rs35788455	12347409	C	CTTG	0.0392261	-0.0349286	0.0065022	1.6E-08
3	PPARG	rs17036326	12347814	G	A	0.0393725	-0.0344508	0.0064915	2.6E-08
3	PPARG	rs17036328	12348985	C	T	0.0392482	-0.0348456	0.0065006	1.7E-08
3	PPARG	rs6802898	12349708	T	C	0.0392691	-0.0346744	0.0064979	2.0E-08
3	PPARG	rs2197423	12350084	A	G	0.0392895	-0.0348287	0.0064981	1.7E-08
3	PPARG	rs7647481	12350314	A	G	0.0392261	-0.0349286	0.0065022	1.6E-08
3	PPARG	rs7649970	12350773	T	C	0.0393077	-0.0347755	0.0064951	1.8E-08
3	PPARG	rs1801282	12351626	G	C	0.0392960	-0.0345848	0.0064958	2.1E-08
3	PPARG	rs17036342	12352183	G	A	0.0391801	-0.0346357	0.0065060	2.1E-08
3	PPARG	rs1899951	12353341	T	C	0.0392239	-0.0346163	0.0065023	1.9E-08
3	PPARG	rs4684848	12354146	A	G	0.0391787	-0.0346604	0.0065056	2.0E-08
3	PPARG	rs4135250	12355346	G	A	0.0391783	-0.0346608	0.0065056	2.0E-08
3	PPARG	rs71304101	12355414	A	G	0.0391783	-0.0346608	0.0065056	2.0E-08
3	PPARG	rs2881654	12355456	A	G	0.0391783	-0.0346608	0.0065056	2.0E-08
4	RGS12	rs1894442	3384588	T	C	0.4591540	-0.0297532	0.0025541	2.8E-29
4	RGS12	rs12644442	3385844	A	G	0.4953370	0.0286102	0.0025630	5.0E-27
4	RGS12	rs4690090	3387800	T	C	0.4414560	-0.0288351	0.0025800	5.4E-27
4	RGS12	rs6828057	3388084	A	G	0.4439060	-0.0289565	0.0025798	4.5E-27
4	RGS12	rs2269496	3388419	C	T	0.2868640	0.0211628	0.0028562	4.3E-12
4	RGS12	rs13127597	3388545	C	A	0.4640290	-0.0293664	0.0025391	8.6E-29
4	RGS12	rs73193383	3390547	T	C	0.2758490	0.0235467	0.0028798	1.2E-14
4	RGS12	rs17797467	3390588	G	C	0.4666260	-0.0292263	0.0025577	4.1E-28
4	RGS12	rs13152128	3390623	A	C	0.4603830	-0.0287219	0.0025523	3.1E-27
4	RGS12	rs12510769	3392647	C	T	0.2820650	0.0236264	0.0028469	8.1E-15
4	RGS12	rs9995777	3403748	T	C	0.4480440	0.0270858	0.0026003	4.9E-24
4	RGS12	rs10027926	3412927	A	G	0.2625020	0.0246480	0.0029403	2.1E-15
4	RGS12	rs62274930	3413609	T	C	0.4725240	-0.0294072	0.0025742	7.6E-29
4	RGS12	rs16844301	3413651	A	G	0.4993650	0.0267332	0.0025689	6.2E-24
4	RGS12	rs3213506	3415757	A	G	0.4720570	-0.0297948	0.0025781	1.7E-29
4	RGS12	rs3213507	3416118	C	G	0.4983340	-0.0267238	0.0025737	4.2E-24
4	RGS12	rs17190954	3416357	G	A	0.2657660	0.0248601	0.0029234	5.4E-16
4	RGS12	rs16844307	3416438	T	C	0.4726970	-0.0298167	0.0025796	1.7E-29
4	RGS12	rs16844309	3416539	A	G	0.4722890	-0.0300293	0.0025794	5.3E-30
4	RGS12	rs12641989	3418113	A	G	0.2653950	0.0246800	0.0029263	1.0E-15
4	RGS12	rs3748037	3418544	A	G	0.2654500	0.0247905	0.0029253	7.1E-16
4	RGS12	rs3748036	3418644	T	C	0.4725230	-0.0301287	0.0025827	3.6E-30
4	RGS12	rs4690095	3419582	C	T	0.4885220	0.0292700	0.0025877	3.2E-28
4	RGS12	rs3088231	3420484	A	G	0.2641220	0.0247899	0.0029375	9.2E-16
4	RGS12	rs3789739	3421715	T	C	0.4747400	-0.0300004	0.0025896	1.9E-29
4	RGS12	rs16844330	3422504	T	C	0.1060070	0.0239402	0.0041284	1.9E-08
4	RGS12	rs58143210	3423303	T	C	0.4713890	-0.0298075	0.0025925	3.0E-29
4	HGFAC	rs2073505	3442776	A	G	0.0940681	0.0294265	0.0043449	3.0E-11
4	HGFAC *	rs28766336	3452024	T	G	0.4733030	-0.0293923	0.0025808	6.9E-30
4	HGFAC *	rs4690099	3452727	T	C	0.4641070	-0.0284875	0.0025824	4.1E-28
4	DOK7 *	rs2091626	3460173	T	G	0.4659520	-0.0285474	0.0025839	3.2E-28
4	DOK7 *	rs1076903	3460467	G	A	0.4659940	-0.0286489	0.0025842	2.0E-28
4	DOK7 *	rs28478452	3461750	A	G	0.4646770	-0.0287288	0.0025889	2.3E-28
4	DOK7	rs56738936	3468759	TGTGA	T	0.3409490	0.0204932	0.0027042	7.2E-14
4	DOK7	rs36205397	3468877	G	A	0.3814530	0.0209545	0.0026155	1.9E-15
4	DOK7	chr4:3469063_A_AGT	3469063	AGT	A	0.3799980	0.0209628	0.0026187	2.7E-15
4	DOK7	rs10007119	3471339	G	A	0.3824630	0.0210079	0.0026031	1.4E-15
4	DOK7	rs6831256	3471412	G	A	0.3829420	0.0208558	0.0026002	2.2E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
4	TLL1 *	rs17634465	166206230	C	T	0.4634190	-0.0148395	0.0025533	3.0E-09
4	TLL1 *	rs17691028	166209275	G	A	0.4365310	-0.0146319	0.0025573	8.6E-09
4	TLL1 *	rs59649146	166211072	G	A	0.4580400	-0.0137184	0.0025366	3.5E-08
4	TLL1 *	rs74718730	166225287	G	T	0.4586390	-0.0141852	0.0025377	1.7E-08
4	TLL1 *	rs78889045	166227270	A	G	0.4355470	-0.0149425	0.0025497	4.8E-09
4	TLL1 *	rs17634553	166230796	T	C	0.4346110	-0.0146808	0.0025503	8.8E-09
4	TLL1 *	rs10517883	166232518	T	C	0.4350800	-0.0145185	0.0025489	1.2E-08
4	TLL1 *	rs149723812	166235572	G	A	0.4579720	-0.0139298	0.0025376	2.7E-08
4	TLL1 *	rs184793585	166238504	T	C	0.4340330	-0.0145279	0.0025521	1.1E-08
4	TLL1 *	rs11941421	166239949	C	G	0.4409800	-0.0146473	0.0025540	9.1E-09
4	TLL1 *	rs58933593	166244458	G	C	0.4359920	-0.0146550	0.0025475	9.3E-09
4	TLL1 *	rs58312036	166249069	A	G	0.4354520	-0.0145150	0.0025557	1.3E-08
4	TLL1 *	rs78510747	166254179	T	A	0.4553330	-0.0140522	0.0025606	2.6E-08
4	TLL1 *	rs366831	166286628	G	A	0.4351950	-0.0139539	0.0025530	4.2E-08
4	TLL1 *	rs76796580	166295265	G	A	0.4420640	-0.0137524	0.0025617	4.5E-08
4	TLL1 *	rs77672162	166295763	A	G	0.4420680	-0.0137560	0.0025617	4.5E-08
4	TLL1 *	rs481882	166297056	A	G	0.4434570	-0.0137601	0.0025613	3.5E-08
4	TLL1 *	rs12511044	166299482	A	T	0.4416880	-0.0137906	0.0025773	3.5E-08
4	TLL1 *	rs374975	166301032	C	T	0.4435570	-0.0137232	0.0025595	3.7E-08
4	TLL1 *	rs420844	166302214	G	T	0.4435570	-0.0137232	0.0025595	3.7E-08
4	TLL1 *	rs34576775	166302336	C	T	0.4435570	-0.0137232	0.0025595	3.7E-08
4	TLL1 *	rs77037918	166303079	G	A	0.4435570	-0.0137232	0.0025595	3.7E-08
4	TLL1 *	rs1612523	166303083	A	G	0.4435570	-0.0137232	0.0025595	3.7E-08
4	TLL1 *	rs138620646	166304115	A	G	0.4430400	-0.0136268	0.0025608	4.8E-08
4	TLL1 *	rs75519208	166304469	T	A	0.4434840	-0.0136933	0.0025598	4.0E-08
4	TLL1 *	rs118056036	166306840	T	G	0.4429450	-0.0138724	0.0025631	3.1E-08
4	TLL1 *	rs28497438	166308672	T	A	0.4522540	-0.0139367	0.0025547	1.9E-08
4	TLL1 *	rs10030891	166309095	T	C	0.4520560	-0.0138783	0.0025548	2.2E-08
4	TLL1 *	rs61575174	166314034	T	G	0.4497670	-0.0136085	0.0025643	4.3E-08
4	TLL1 *	rs77886495	166319093	C	T	0.4520950	-0.0137608	0.0025547	2.8E-08
4	TLL1 *	rs75226936	166324700	T	C	0.4519330	-0.0137973	0.0025538	2.5E-08
4	TLL1 *	rs78104708	166324871	T	C	0.4519390	-0.0137982	0.0025538	2.5E-08
4	TLL1 *	rs77243957	166325661	T	C	0.4518480	-0.0138031	0.0025539	2.4E-08
4	TLL1 *	rs10517892	166326824	G	T	0.4519220	-0.0137991	0.0025536	2.5E-08
4	TLL1 *	rs72986496	166328118	G	A	0.4516090	-0.0137986	0.0025677	2.5E-08
4	TLL1 *	rs17691368	166328491	G	C	0.4520270	-0.0138211	0.0025529	2.4E-08
4	TLL1 *	rs117476483	166329579	C	A	0.4525570	-0.0138403	0.0025526	2.4E-08
4	TLL1 *	rs12502127	166331519	C	T	0.4527380	-0.0139239	0.0025529	1.9E-08
4	TLL1 *	rs12502129	166331525	G	T	0.4527380	-0.0139239	0.0025529	1.9E-08
4	TLL1 *	rs11100641	166333521	C	G	0.4518820	-0.0137285	0.0025530	3.0E-08
4	TLL1 *	rs11100643	166335418	A	C	0.4518720	-0.0138924	0.0025488	2.2E-08
4	TLL1 *	rs10857378	166335702	T	C	0.4518860	-0.0138893	0.0025462	2.5E-08
5	FGF10	rs17234352	44328266	C	CA	0.0700972	-0.0278609	0.0049951	2.4E-08
5	FGF10-AS1	rs16901836	44390524	G	C	0.0683349	-0.0291974	0.0050771	6.7E-09
5	ANKRD55 *	rs6881312	56500733	T	G	0.2866740	0.0151836	0.0027965	1.4E-08
5	ANKRD55 *	rs73132727	56502276	G	C	0.2888740	0.0156783	0.0027856	4.0E-09
5	ANKRD55 *	rs73132728	56504012	G	A	0.2900020	0.0156684	0.0027797	3.8E-09
5	ANKRD55 *	rs60762814	56504882	T	C	0.2888930	0.0157002	0.0027854	3.9E-09
5	ANKRD55 *	rs73132731	56505331	G	A	0.2900250	0.0156501	0.0027796	4.0E-09
5	ANKRD55 *	rs73132735	56505759	T	A	0.2892800	0.0154935	0.0027875	6.0E-09
5	ANKRD55 *	rs56198135	56507151	A	G	0.2840370	0.0149467	0.0028030	2.5E-08
5	ANKRD55 *	rs42392	56508102	G	A	0.2985580	-0.0144767	0.0027595	3.6E-08
5	ANKRD55 *	rs25757	56508377	G	C	0.2985500	-0.0144807	0.0027594	3.6E-08
5	ANKRD55 *	rs16885608	56510081	T	G	0.2896690	0.0157797	0.0027797	3.0E-09
5	ANKRD55 *	rs459193	56510924	A	G	0.4706540	-0.0230987	0.0025282	7.7E-21
5	LOC101928448	rs464605	56511543	C	T	0.4709380	-0.0230802	0.0025296	7.3E-21
5	LOC101928448	rs245143	56512322	G	A	0.2961370	-0.0144165	0.0027779	4.6E-08
5	LOC101928448	rs157507	56512451	T	C	0.3307360	-0.0178666	0.0026831	2.6E-12
5	LOC101928448	rs392794	56512515	C	T	0.4707970	-0.0231227	0.0025304	6.1E-21
5	LOC101928448	rs465002	56512648	C	T	0.4707950	-0.0231515	0.0025305	5.4E-21
5	LOC101928448	rs157510	56513139	C	A	0.3306770	-0.0178293	0.0026826	3.0E-12
5	LOC101928448	rs157512	56513300	C	T	0.4360800	-0.0215690	0.0025498	1.1E-18
5	LOC101928448	rs256903	56513311	C	A	0.4700390	-0.0232174	0.0025326	4.4E-21
5	LOC101928448	rs173964	56513638	A	G	0.4697680	-0.0233477	0.0025332	2.8E-21
5	LOC101928448	rs256904	56514478	A	T	0.4703010	-0.0231411	0.0025333	6.8E-21
5	LOC101928448	rs245142	56514622	A	G	0.3303560	-0.0177761	0.0026826	3.6E-12
5	LOC101928448	rs456867	56515265	T	C	0.3304670	-0.0178253	0.0026813	3.5E-12
5	LOC101928448	rs459447	56515514	A	G	0.3292000	-0.0179759	0.0026861	2.8E-12
5	LOC101928448	rs465983	56516303	G	A	0.4391330	-0.0216950	0.0025512	9.4E-19
5	LOC101928448	rs61142999	56516795	A	G	0.2823080	0.0154425	0.0028114	7.5E-09
5	LOC101928448	rs405176	56517885	G	A	0.3695060	-0.0186975	0.0026212	3.2E-13
5	LOC101928448	rs60202005	56518728	T	C	0.2839880	0.0158143	0.0028062	3.4E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	LOC101928448	rs56411612	56519256	T	G	0.2840240	0.0158172	0.0028064	3.4E-09
5	LOC101928448	rs455660	56521061	T	C	0.3810280	-0.0195867	0.0025968	1.1E-14
5	LOC101928448	rs76721602	56522121	A	C	0.2813150	0.0154051	0.0028553	1.2E-08
5	LOC101928448	rs76878791	56522574	G	A	0.2816010	0.0154917	0.0028670	1.5E-08
5	LOC101928448	rs3843467	56560548	T	G	0.1139560	0.0212558	0.0039749	4.4E-08
5	LOC101928448	rs11743303	56564125	G	A	0.1151090	0.0211311	0.0039574	4.3E-08
5	LOC101928448	rs3936511	56564954	G	A	0.1149850	0.0211755	0.0039589	3.8E-08
5	LOC101928448	rs3936510	56565039	T	G	0.1150210	0.0212041	0.0039581	3.6E-08
5	LOC101928448	rs5868014	56565080	G	GC	0.1149700	0.0211580	0.0039589	3.8E-08
5	LOC101928448	rs13173241	56565532	A	G	0.1150980	0.0214730	0.0039571	2.3E-08
5	LOC101928448	rs28650790	56565637	T	C	0.1149710	0.0214461	0.0039591	2.7E-08
5	TNFAIP8	rs148191234	119349730	A	T	0.0388073	-0.0399758	0.0065429	9.7E-09
5	TNFAIP8	rs144394643	119350839	G	C	0.0388404	-0.0399772	0.0065403	9.6E-09
5	TNFAIP8	rs183964200	119352576	C	A	0.0399132	-0.0390335	0.0064565	1.3E-08
5	TNFAIP8	rs137934992	119353404	A	G	0.0388073	-0.0399547	0.0065429	9.9E-09
5	TNFAIP8	rs115891073	119354432	A	G	0.0387865	-0.0401983	0.0065445	8.1E-09
5	TNFAIP8	rs147021763	119356901	G	A	0.0385325	-0.0409927	0.0065659	4.2E-09
5	TNFAIP8	rs77850120	119358547	A	T	0.0375555	-0.0419802	0.0066549	2.3E-09
5	TNFAIP8	rs147641701	119358921	T	A	0.0375340	-0.0421608	0.0066567	2.0E-09
5	TNFAIP8	rs145778841	119363651	T	C	0.0387113	-0.0425604	0.0065622	1.0E-09
5	TNFAIP8	rs143932930	119364483	T	G	0.0387109	-0.0425562	0.0065622	1.0E-09
5	TNFAIP8	rs150800682	119365445	G	C	0.0387333	-0.0430676	0.0065669	6.4E-10
5	TNFAIP8	rs9327100	119366180	G	A	0.0397600	-0.0419894	0.0064847	1.1E-09
5	TNFAIP8	rs141199457	119370335	T	TC	0.0385066	-0.0438425	0.0065869	3.1E-10
5	TNFAIP8	rs143225937	119370413	G	C	0.0385075	-0.0438391	0.0065870	3.2E-10
5	TNFAIP8	rs151300053	119374385	A	G	0.0382507	-0.0433086	0.0066059	6.8E-10
5	TNFAIP8	rs5870855	119377761	AT	A	0.1584790	-0.0266111	0.0034736	1.2E-13
5	TNFAIP8	rs59406275	119379517	A	G	0.0383418	-0.0447172	0.0065954	1.2E-10
5	TNFAIP8	rs140403040	119381339	G	A	0.0380570	-0.0444775	0.0066170	1.3E-10
5	TNFAIP8	rs143744864	119383503	A	G	0.0382319	-0.0432698	0.0065969	3.4E-10
5	TNFAIP8	rs12332329	119385999	A	G	0.1454120	-0.0270070	0.0035882	2.0E-13
5	TNFAIP8	rs6882000	119387339	A	G	0.0393544	-0.0427450	0.0065020	3.2E-10
5	TNFAIP8	rs6595187	119387914	G	A	0.1596330	-0.0261841	0.0034529	2.0E-13
5	TNFAIP8	rs139299785	119389092	C	T	0.0382480	-0.0432054	0.0065956	3.4E-10
5	TNFAIP8	rs9764678	119390967	C	T	0.1587700	-0.0261318	0.0034583	2.3E-13
5	TNFAIP8	rs7720409	119392561	A	G	0.1572830	-0.0258014	0.0034649	5.9E-13
5	TNFAIP8	rs3203922	119393258	C	G	0.1572930	-0.0257863	0.0034649	6.3E-13
5	TNFAIP8	rs1045241	119393591	T	C	0.1574090	-0.0256543	0.0034630	8.5E-13
5	TNFAIP8	rs1045242	119393632	G	A	0.1574750	-0.0260178	0.0034663	3.8E-13
5	TNFAIP8 *	rs190066550	119394689	T	C	0.0380910	-0.0423264	0.0066016	9.5E-10
5	TNFAIP8 *	rs1105769	119395372	C	A	0.2022540	-0.0196603	0.0031623	8.2E-10
5	TNFAIP8 *	rs150590141	119395425	G	C	0.0381492	-0.0420970	0.0065987	9.5E-10
5	TNFAIP8 *	rs1105770	119395552	G	T	0.2022770	-0.0197096	0.0031622	7.0E-10
5	TNFAIP8 *	rs3733856	119396243	C	T	0.0392472	-0.0417645	0.0065058	7.3E-10
5	TNFAIP8 *	rs7703744	119396492	G	C	0.1523060	-0.0258414	0.0035220	7.3E-13
5	TNFAIP8 *	rs113115500	119396633	G	GT	0.0392476	-0.0417718	0.0065058	7.3E-10
5	TNFAIP8 *	rs113771869	119398110	C	G	0.0381257	-0.0420164	0.0066009	1.0E-09
5	TNFAIP8 *	rs3813311	119399036	G	A	0.0392318	-0.0414590	0.0065062	9.4E-10
5	TNFAIP8 *	rs3813312	119399186	T	C	0.0381257	-0.0420164	0.0066009	1.0E-09
5	TNFAIP8 *	rs6876817	119400550	C	T	0.0392292	-0.0415686	0.0065066	8.6E-10
5	TNFAIP8 *	rs73790861	119401033	C	T	0.0381474	-0.0423019	0.0065996	8.0E-10
5	TNFAIP8 *	rs112064880	119401256	TG	T	0.0381474	-0.0423019	0.0065996	8.0E-10
5	TNFAIP8 *	rs113087177	119401445	G	A	0.0381474	-0.0423019	0.0065996	8.0E-10
5	TNFAIP8 *	rs6860944	119401577	G	A	0.0375146	-0.0422845	0.0066560	1.2E-09
5	TNFAIP8 *	rs75615340	119401605	C	T	0.0357667	-0.0421368	0.0068211	2.7E-09
5	TNFAIP8 *	rs796399261	119401646	G	A	0.0353376	-0.0405053	0.0068580	1.7E-08
5	TNFAIP8 *	rs138617167	119402535	C	A	0.0381017	-0.0419961	0.0066041	1.1E-09
5	TNFAIP8 *	rs149322190	119403029	T	G	0.0381021	-0.0420064	0.0066041	1.1E-09
5	TNFAIP8 *	rs76429389	119403290	A	G	0.0381013	-0.0420208	0.0066041	1.1E-09
5	TNFAIP8 *	rs142366409	119403748	C	A	0.0381017	-0.0420139	0.0066041	1.1E-09
5	TNFAIP8 *	rs139852373	119404402	G	A	0.0412456	-0.0389812	0.0063645	5.3E-09
5	TNFAIP8 *	rs149838859	119404824	A	T	0.0412048	-0.0389683	0.0063685	5.1E-09
5	TNFAIP8 *	rs56017758	119404998	A	G	0.1483100	-0.0247997	0.0035771	1.0E-11
5	TNFAIP8 *	rs143312148	119405425	A	C	0.0381011	-0.0423405	0.0066050	7.6E-10
5	TNFAIP8 *	rs148963541	119407705	G	A	0.0382248	-0.0414917	0.0065992	1.6E-09
5	TNFAIP8 *	rs145427586	119407916	G	A	0.0383782	-0.0404595	0.0065876	3.7E-09
5	TNFAIP8 *	rs138073818	119408024	G	T	0.0382248	-0.0414917	0.0065992	1.6E-09
5	TNFAIP8 *	rs182086523	119408567	C	G	0.0382248	-0.0414917	0.0065992	1.6E-09
5	TNFAIP8 *	rs141161625	119408866	T	C	0.0382248	-0.0414917	0.0065992	1.6E-09
5	TNFAIP8 *	rs145620909	119409690	A	G	0.0382252	-0.0414749	0.0065992	1.7E-09
5	TNFAIP8 *	rs181992160	119409882	G	T	0.0382244	-0.0414773	0.0065992	1.7E-09
5	TNFAIP8 *	rs142281675	119410471	A	G	0.0382248	-0.0414796	0.0065992	1.6E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	TNFAIP8 *	rs151254930	119410609	A	G	0.0382248	-0.0414796	0.0065992	1.6E-09
5	TNFAIP8 *	rs139303947	119410616	A	G	0.0381345	-0.0412742	0.0066071	2.1E-09
5	TNFAIP8 *	rs139899740	119414770	A	C	0.0380792	-0.0422630	0.0066072	8.3E-10
5	TNFAIP8 *	rs117353451	119414971	A	G	0.0380792	-0.0422630	0.0066072	8.3E-10
5	HSD17B4 *	rs35401573	119543023	T	G	0.0406206	-0.0366919	0.0064089	1.3E-08
5	TIMD4	rs11134462	156933172	G	C	0.3442680	-0.0151683	0.0026957	1.1E-08
5	TIMD4	rs10062458	156940081	T	C	0.1679680	-0.0225684	0.0034086	4.9E-12
5	TIMD4	rs7717984	156942160	C	T	0.1587670	-0.0229763	0.0034711	2.9E-12
5	TIMD4	rs13167071	156946626	G	C	0.1587890	-0.0226882	0.0034683	5.5E-12
5	TIMD4	rs11361881	156950119	CT	C	0.1593410	-0.0222350	0.0034591	1.4E-11
5	TIMD4	rs4704727	156953056	T	G	0.1593630	-0.0224868	0.0034579	8.6E-12
5	TIMD4	rs7724832	156954359	G	A	0.1593950	-0.0223878	0.0034577	9.6E-12
5	TIMD4	rs4704825	156955297	A	G	0.2104240	-0.0200374	0.0031252	8.9E-12
5	TIMD4	rs1363232	156956411	A	G	0.1594430	-0.0222420	0.0034572	1.4E-11
5	TIMD4	rs2862059	156957504	G	C	0.1644340	-0.0231129	0.0034361	2.0E-12
5	TIMD4	rs6878680	156960126	G	C	0.2111870	-0.0204698	0.0031178	2.7E-12
5	TIMD4	rs4407617	156960425	C	G	0.1592760	-0.0225811	0.0034631	6.7E-12
5	TIMD4 *	rs6882076	156963286	T	C	0.2715090	-0.0232675	0.0028483	3.8E-18
5	TIMD4 *	rs6874202	156964617	T	C	0.2714100	-0.0232522	0.0028496	4.0E-18
5	TIMD4 *	rs62382402	156964807	T	C	0.1527950	-0.0211533	0.0035232	2.4E-10
5	TIMD4 *	rs4704826	156965071	C	A	0.2714690	-0.0232286	0.0028497	4.5E-18
5	TIMD4 *	rs4704827	156965078	T	C	0.2714100	-0.0232522	0.0028496	4.0E-18
5	TIMD4 *	rs12517431	156965237	C	T	0.2713940	-0.0232865	0.0028498	3.6E-18
5	TIMD4 *	rs28735189	156967082	C	T	0.2706980	-0.0232436	0.0028602	5.9E-18
5	TIMD4 *	rs9715911	156967430	G	A	0.2706570	-0.0233492	0.0028610	4.7E-18
5	TIMD4 *	rs11745603	156967507	C	T	0.2706500	-0.0233389	0.0028611	4.9E-18
5	TIMD4 *	rs12657266	156968992	C	T	0.2702890	-0.0234102	0.0028671	4.4E-18
5	TIMD4 *	rs10043150	156969464	A	C	0.1516960	-0.0213363	0.0035448	2.1E-10
5	TIMD4 *	rs1393207	156970529	T	A	0.2700940	-0.0234323	0.0028695	4.2E-18
5	TIMD4 *	rs6882345	156970662	G	A	0.2701000	-0.0233896	0.0028694	4.7E-18
5	TIMD4 *	rs6883317	156971242	A	G	0.1515700	-0.0215365	0.0035473	1.5E-10
5	TIMD4 *	rs58198139	156972028	C	T	0.2700970	-0.0232744	0.0028706	6.7E-18
5	TIMD4 *	rs11134475	156972939	A	G	0.2700540	-0.0232381	0.0028715	7.5E-18
5	TIMD4 *	rs28722027	156973514	T	C	0.2635300	-0.0220637	0.0028943	4.8E-16
5	TIMD4 *	rs6891318	156973733	C	A	0.2636150	-0.0219765	0.0028944	6.5E-16
5	TIMD4 *	rs55776147	156973797	A	G	0.2704920	-0.0231878	0.0028715	1.0E-17
5	TIMD4 *	rs7715848	156974467	G	C	0.1512530	-0.0215973	0.0035527	1.3E-10
5	TIMD4 *	rs7702004	156974719	C	T	0.2618410	-0.0220977	0.0029049	5.2E-16
5	TIMD4 *	chr5:156975081_A_AGAGC	156975081	AGAGG	A	0.2515080	-0.0199682	0.0029906	6.1E-13
5	TIMD4 *	rs7707200	156975624	C	T	0.1322100	-0.0215148	0.0038092	1.9E-09
5	TIMD4 *	rs7379358	156976582	T	A	0.3911900	-0.0163258	0.0026506	2.3E-10
5	TIMD4 *	rs10055656	156977360	C	T	0.2585200	-0.0216612	0.0029140	2.5E-15
5	TIMD4 *	rs28575973	156977576	A	C	0.2583660	-0.0215348	0.0029149	3.6E-15
5	TIMD4 *	rs10062571	156977625	T	G	0.1455280	-0.0211849	0.0036135	6.5E-10
5	TIMD4 *	chr5:156978231_C_CT	156978231	CT	C	0.1952390	-0.0190297	0.0032180	5.3E-10
5	TIMD4 *	rs10059560	156978773	C	T	0.1965660	-0.0186403	0.0032021	8.6E-10
5	TIMD4 *	rs10050384	156978935	T	C	0.1959970	-0.0183681	0.0032053	1.6E-09
5	TIMD4 *	rs12187385	156979446	C	A	0.1964940	-0.0185920	0.0032024	9.3E-10
5	TIMD4 *	rs4704728	156979597	G	C	0.3876410	-0.0167739	0.0026289	5.0E-11
5	TIMD4 *	rs4704830	156979708	G	A	0.3876770	-0.0167564	0.0026292	5.4E-11
5	TIMD4 *	rs4704831	156979709	C	G	0.3878430	-0.0167992	0.0026290	4.8E-11
5	TIMD4 *	rs1973491	156982536	T	C	0.1303830	-0.0232920	0.0037858	1.1E-10
5	TIMD4 *	rs55682810	156984036	GA	G	0.1943260	-0.0190324	0.0032133	3.9E-10
5	TIMD4 *	rs56308765	156984044	A	C	0.1925600	-0.0190181	0.0032310	4.3E-10
5	TIMD4 *	rs7736899	156984196	A	C	0.3769960	-0.0161577	0.0026392	3.0E-10
5	TIMD4 *	rs10059263	156984250	C	T	0.1965080	-0.0179807	0.0032037	2.7E-09
5	TIMD4 *	rs10039097	156984874	C	T	0.1943300	-0.0190128	0.0032132	4.0E-10
5	TIMD4 *	rs6866930	156985611	C	G	0.3770040	-0.0161340	0.0026396	3.3E-10
5	TIMD4 *	rs55875237	156988018	T	C	0.1433450	-0.0220225	0.0036384	2.0E-10
5	TIMD4 *	rs111273781	156989163	T	C	0.1313170	-0.0229652	0.0037720	2.1E-10
5	TIMD4 *	rs10044267	156989418	A	G	0.1433580	-0.0220204	0.0036383	2.0E-10
5	TIMD4 *	rs12659077	156989695	G	T	0.3833580	-0.0173682	0.0026320	1.2E-11
5	TIMD4 *	chr5:156995894_CAA_C	156995894	C	CAA	0.1450060	-0.0226244	0.0036295	7.3E-11
5	HAVCR1 *	rs10075548	156997238	C	T	0.1444070	-0.0223404	0.0036268	1.1E-10
5	HAVCR1 *	rs66891562	156998368	C	T	0.4081780	-0.0156778	0.0025925	3.1E-10
5	HAVCR1 *	rs10079422	156998650	A	T	0.1963940	-0.0193586	0.0031990	1.6E-10
5	HAVCR1 *	rs1501906	157000648	G	A	0.4091590	-0.0156249	0.0025728	2.7E-10
5	HAVCR1 *	rs67899516	157001721	G	A	0.4089560	-0.0156958	0.0025731	2.2E-10
5	HAVCR1 *	rs7714118	157001727	G	T	0.4022670	-0.0146269	0.0025787	3.6E-09
5	HAVCR1 *	rs111847148	157001777	GACAA	G	0.4025570	-0.0147795	0.0025797	2.5E-09
5	HAVCR1 *	rs1546288	157003694	G	A	0.4089650	-0.0156222	0.0025742	2.7E-10
5	HAVCR1 *	rs66512776	157004261	C	T	0.4094740	-0.0157021	0.0025769	2.6E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
5	HAVCR1 *	rs6870058	157004262	A	G	0.4024250	-0.0145306	0.0025807	4.7E-09
5	HAVCR1 *	rs2102151	157005007	T	C	0.1975100	-0.0193708	0.0031805	1.4E-10
5	HAVCR1 *	rs7721033	157005512	T	C	0.1975240	-0.0193582	0.0031804	1.5E-10
5	HAVCR1 *	rs10036890	157006640	A	T	0.1975620	-0.0193930	0.0031800	1.4E-10
5	HAVCR1 *	rs10076109	157007151	T	C	0.1975650	-0.0194133	0.0031800	1.3E-10
5	HAVCR1 *	rs9791162	157007697	C	T	0.4091670	-0.0157491	0.0025771	2.7E-10
5	HAVCR1 *	rs10062923	157008228	A	G	0.1451570	-0.0222911	0.0036093	1.1E-10
5	HAVCR1 *	rs56012634	157008942	A	G	0.4091910	-0.0156750	0.0025774	3.2E-10
5	HAVCR1 *	rs55892205	157009022	G	A	0.4091910	-0.0156750	0.0025774	3.2E-10
5	HAVCR1 *	rs4704833	157009347	A	T	0.4091950	-0.0156774	0.0025774	3.2E-10
5	HAVCR1 *	rs1995376	157009447	A	T	0.1976890	-0.0190747	0.0031787	2.6E-10
5	HAVCR1 *	rs76296718	157009493	G	A	0.1450900	-0.0218972	0.0036106	2.2E-10
5	HAVCR1 *	rs140842228	157011602	G	T	0.4050210	-0.0156178	0.0025824	4.9E-10
5	HAVCR1 *	rs6555788	157011656	C	T	0.1936150	-0.0191230	0.0032009	3.5E-10
5	HAVCR1 *	rs6555789	157011856	T	C	0.1936220	-0.0191219	0.0032009	3.5E-10
5	HAVCR1 *	rs141319343	157011963	A	G	0.0487900	-0.0322786	0.0059032	3.4E-08
5	HAVCR1 *	rs7715158	157012073	A	G	0.1938060	-0.0189437	0.0031995	4.8E-10
5	HAVCR1 *	rs113879698	157012840	T	A	0.4052580	-0.0155382	0.0025817	5.6E-10
5	HAVCR1 *	rs80050550	157013424	C	G	0.4054700	-0.0155276	0.0025826	6.0E-10
5	HAVCR1 *	rs7736117	157013824	T	C	0.1935790	-0.0191525	0.0032005	3.3E-10
5	HAVCR1 *	rs187399190	157014301	G	A	0.4079140	-0.0151145	0.0025873	1.8E-09
5	HAVCR1 *	rs6862070	157014453	T	C	0.1904410	-0.0188258	0.0032349	1.0E-09
5	HAVCR1 *	rs4704834	157016055	A	G	0.2618800	-0.0227101	0.0028818	6.5E-17
5	HAVCR1 *	chr5:157016890_C_CT	157016890	C	CT	0.4055070	-0.0154300	0.0025826	7.2E-10
5	HAVCR1 *	rs4704836	157017430	G	A	0.4069410	-0.0156269	0.0025873	5.0E-10
5	HAVCR1 *	rs9885146	157017750	T	C	0.1409010	-0.0223733	0.0036491	1.6E-10
5	HAVCR1 *	rs6555801	157018625	A	C	0.1410910	-0.0225083	0.0036462	1.3E-10
5	HAVCR1 *	rs56330860	157019393	GA	G	0.4053030	-0.0154336	0.0025818	7.5E-10
5	HAVCR1 *	rs10462973	157022494	G	A	0.4053950	-0.0154743	0.0025823	6.6E-10
5	HAVCR1 *	rs7707445	157022737	A	G	0.1937410	-0.0193082	0.0031960	2.3E-10
5	HAVCR1 *	rs35242034	157025733	C	T	0.4053630	-0.0154954	0.0025833	6.5E-10
5	HAVCR1 *	rs6866758	157028101	T	C	0.2550460	-0.0217061	0.0029060	2.5E-15
5	HAVCR1	rs2134230	157029946	C	G	0.1938730	-0.0189722	0.0031948	4.3E-10
5	HAVCR1	rs68145045	157031185	G	A	0.4057630	-0.0151258	0.0025839	1.7E-09
5	HAVCR1	rs61047347	157032570	T	TC	0.1974130	-0.0175519	0.0031745	4.4E-09
5	HAVCR1	rs2277025	157033084	T	C	0.4060110	-0.0151025	0.0025850	1.8E-09
5	HAVCR1	rs3842063	157033162	T	TA	0.2556620	-0.0213293	0.0029038	7.9E-15
5	HAVCR1	rs6896306	157034265	G	T	0.1937040	-0.0184848	0.0032007	1.3E-09
5	HAVCR1	chr5:157038023_GA_G	157038023	G	GA	0.2138790	-0.0184284	0.0031010	6.5E-10
5	HAVCR1	rs6878732	157038245	A	T	0.2162290	-0.0188487	0.0030809	1.8E-10
5	HAVCR1	rs10059699	157039143	C	T	0.1924430	-0.0188321	0.0032113	8.2E-10
5	HAVCR1	rs200212405	157040297	TC	T	0.1901240	-0.0191796	0.0032326	5.2E-10
5	HAVCR1	rs56182597	157040299	C	A	0.1861630	-0.0204436	0.0032908	9.1E-11
5	HAVCR1	rs17054133	157040380	C	T	0.1924580	-0.0188024	0.0032111	8.6E-10
5	HAVCR1	rs6555819	157041528	A	G	0.1930970	-0.0185018	0.0032084	1.4E-09
5	HAVCR1	rs6874311	157041787	T	G	0.1931000	-0.0184972	0.0032083	1.4E-09
5	HAVCR1	rs9313418	157042213	T	C	0.1931390	-0.0183802	0.0032077	1.8E-09
5	HAVCR1	rs2270926	157042772	A	G	0.1402120	-0.0220561	0.0036581	3.8E-10
5	HAVCR1	rs10038271	157043390	T	C	0.1401140	-0.0221602	0.0036589	3.1E-10
5	HAVCR1	rs11374500	157045224	TA	T	0.1927800	-0.0183551	0.0032123	2.0E-09
5	HAVCR1	rs35931650	157046505	G	A	0.1923790	-0.0184668	0.0032072	1.9E-09
5	HAVCR1	rs62382456	157046893	A	G	0.1921370	-0.0184973	0.0032092	1.8E-09
5	HAVCR1	rs7706174	157048387	G	T	0.1921320	-0.0183981	0.0032099	2.2E-09
5	HAVCR1	rs1553318	157052312	G	C	0.1979560	-0.0199772	0.0031750	5.4E-11
5	HAVCR1	chr5:157052432_CTTG_C	157052432	C	CTTG	0.1911660	-0.0189023	0.0032163	1.0E-09
5	HAVCR1	rs77147640	157052557	CGTT	C	0.2154920	-0.0188005	0.0030860	2.9E-10
5	HAVCR1	rs11134525	157053637	A	T	0.1970290	-0.0195468	0.0031920	1.7E-10
5	HAVCR1	rs2270925	157055088	T	C	0.1872810	-0.0185900	0.0032986	4.8E-09
5	HAVCR1	rs2270924	157055090	A	T	0.1872810	-0.0185900	0.0032986	4.8E-09
5	HAVCR1	rs139106057	157056287	AT	A	0.1335480	-0.0215558	0.0037950	5.4E-09
6	HCG17, HCG18	rs117416277	30288213	C	T	0.1121940	-0.0228044	0.0042779	4.5E-08
6	RPP21 *	rs9391681	30383227	C	T	0.1098370	-0.0231315	0.0043381	2.3E-08
6	ABCF1	rs143982339	30586413	C	CAT	0.1132360	-0.0222517	0.0042587	2.8E-08
6	ABCF1 *	rs9380181	30595202	T	A	0.1169290	-0.0224959	0.0042032	1.5E-08
6	PPP1R10	rs9348841	30610096	C	T	0.1144150	-0.0222409	0.0042218	2.3E-08
6	ATAT1	rs143128695	30635406	G	A	0.1156240	-0.0232446	0.0042293	6.3E-09
6	DHX16 *	rs151195028	30673581	C	G	0.1157000	-0.0228559	0.0042257	1.1E-08
6	FLOT1	rs9380182	30735848	C	A	0.1139290	-0.0228182	0.0042433	8.0E-09
6	IER3 *	rs9391634	30807802	G	C	0.1104240	-0.0221867	0.0043172	4.0E-08
6	HLA-C *	rs9264579	31267969	A	G	0.3620360	-0.0151523	0.0028485	1.3E-08
6	HLA-C	rs2074493	31271999	C	A	0.3392180	0.0167001	0.0030771	8.0E-09
6	VEGFA *	rs4711750	43789345	T	A	0.4377050	-0.0197500	0.0025463	2.4E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
6	VEGFA *	rs998584	43790159	C	A	0.4444120	-0.0193345	0.0025443	1.2E-15
6	VEGFA *	rs6905288	43791136	G	A	0.2998500	-0.0200529	0.0027592	4.7E-14
6	VEGFA *	rs6458349	43792052	G	A	0.2149430	-0.0202116	0.0031164	2.8E-11
6	VEGFA *	rs11967262	43792590	C	G	0.4317910	-0.0197517	0.0025575	2.1E-16
6	VEGFA *	rs1358980	43796814	C	T	0.4497830	-0.0197305	0.0025401	2.9E-16
6	VEGFA *	rs1885659	43797796	A	G	0.1603740	-0.0190134	0.0035341	5.2E-09
6	RGS17	rs6901945	153078520	C	T	0.2892820	-0.0149582	0.0027939	3.4E-08
6	RGS17	rs78722146	153078605	AAAT	A	0.2891700	-0.0151605	0.0027974	2.9E-08
6	RGS17	chr6:153079082_AT_A	153079082	A	AT	0.2952790	-0.0148859	0.0027956	4.3E-08
6	RGS17	rs3910736	153091341	C	T	0.3231030	-0.0146765	0.0026955	1.7E-08
6	RGS17	rs3910737	153091342	A	G	0.3221960	-0.0147790	0.0026964	1.3E-08
6	RGS17	rs9371672	153101005	C	G	0.3195750	-0.0145681	0.0027083	2.2E-08
6	RGS17	rs6557271	153116600	T	C	0.3143530	-0.0143359	0.0027190	3.5E-08
6	RGS17	rs6932473	153117438	A	T	0.3230340	-0.0141970	0.0026977	3.6E-08
6	RGS17	rs6557273	153122024	A	G	0.3216760	-0.0143267	0.0027034	2.9E-08
6	RGS17	chr6:153122930_T_TTACTG	153122930	T	TGGAGT/	0.3214740	-0.0142221	0.0027004	3.4E-08
6	RGS17	rs9371676	153124830	C	A	0.3212780	-0.0142612	0.0027006	3.3E-08
6	RGS17	rs13215045	153126381	C	T	0.3213310	-0.0140850	0.0026995	4.5E-08
6	RGS17	rs6932847	153127172	G	A	0.3211080	-0.0141080	0.0026995	4.5E-08
7	MIR148A *	rs4722555	25973632	C	T	0.4427830	0.0139599	0.0025409	3.6E-08
7	MIR148A *	rs6970673	25975022	T	C	0.4403050	0.0139268	0.0025426	3.5E-08
7	MIR148A *	rs28537499	25975772	C	A	0.4407840	0.0139187	0.0025424	3.4E-08
7	MIR148A *	rs6461905	26000782	T	C	0.4629310	0.0137919	0.0025475	3.7E-08
7	MIR148A *	rs58292232	26001109	G	T	0.4629460	0.0138095	0.0025475	3.5E-08
7	MIR148A *	rs6979761	26002804	C	T	0.4656580	0.0138055	0.0025462	3.5E-08
7	MIR148A *	rs6959733	26002919	T	C	0.4650190	0.0138282	0.0025449	3.6E-08
7	MIR148A *	rs11367100	26003929	A	AC	0.4650310	0.0137677	0.0025441	4.2E-08
7	MIR148A *	rs7781851	26004501	A	T	0.4629930	0.0140698	0.0025559	2.9E-08
7	MIR148A *	rs7798823	26004532	T	C	0.4650330	0.0137664	0.0025441	4.2E-08
7	MIR148A *	rs11378017	26005456	GT	G	0.4668070	0.0139225	0.0025450	3.2E-08
7	MIR148A *	rs4722564	26007843	T	G	0.4666520	0.0137691	0.0025455	4.5E-08
7	MIR148A *	rs2391217	26008798	A	C	0.4663920	0.0137537	0.0025483	4.8E-08
7	MIR148A *	chr7:26036104_T_TTTTTG	26036104	TTTTTG	T	0.4561600	0.0142445	0.0025758	1.0E-08
7	MIR148A *	rs56056224	26044015	T	A	0.4622430	0.0137516	0.0025597	4.7E-08
7	NFE2L3 *	rs4722566	26080075	C	T	0.4974360	0.0136312	0.0025508	4.9E-08
7	NFE2L3 *	rs9639528	26080958	T	C	0.4968990	0.0136813	0.0025496	4.2E-08
7	NFE2L3 *	rs7805293	26081178	C	A	0.4965590	0.0136479	0.0025501	4.2E-08
7	NFE2L3 *	rs2391223	26082321	A	G	0.4959960	0.0136404	0.0025468	4.0E-08
7	GCK	rs2070971	44157984	T	G	0.2557080	0.0171495	0.0029603	3.2E-08
7	GCK	rs62460075	44161550	T	C	0.2113820	-0.0186576	0.0031615	1.8E-08
7	GCK	rs12540369	44165915	T	A	0.2330060	-0.0198834	0.0029913	8.6E-11
7	GCK	rs12535229	44166006	A	G	0.2330060	-0.0198834	0.0029913	8.6E-11
7	GCK	rs2971672	44166307	C	A	0.4588880	0.0176495	0.0025350	3.3E-11
7	GCK	rs77851840	44166756	G	GAT	0.2330160	-0.0198728	0.0029913	8.8E-11
7	GCK	rs62460076	44166795	A	T	0.2329040	-0.0198708	0.0029928	8.9E-11
7	GCK	rs62460077	44167083	T	C	0.2330160	-0.0198728	0.0029913	8.8E-11
7	GCK	rs73112269	44168408	A	G	0.2331860	-0.0199356	0.0029896	7.2E-11
7	GCK	rs16881016	44171808	C	T	0.2344940	-0.0199996	0.0029820	6.0E-11
7	GCK	rs112745774	44172019	T	C	0.2341130	-0.0198631	0.0029847	8.3E-11
7	GCK	rs60275913	44172686	T	G	0.2343180	-0.0198754	0.0029835	8.2E-11
7	GCK	rs59419319	44174275	T	C	0.2351770	-0.0202656	0.0029810	3.2E-11
7	GCK	rs3779606	44175415	C	T	0.2352990	-0.0202696	0.0029797	3.2E-11
7	GCK	rs62460080	44176272	A	G	0.2353170	-0.0202711	0.0029795	3.2E-11
7	GCK	rs17172566	44176513	A	G	0.2353170	-0.0202711	0.0029795	3.2E-11
7	GCK	rs2908290	44176538	A	G	0.4582570	0.0183684	0.0025334	3.9E-12
7	GCK	rs62459064	44176698	T	C	0.2353030	-0.0202816	0.0029795	3.1E-11
7	GCK	rs2284777	44176999	C	T	0.2350030	-0.0201649	0.0029822	4.0E-11
7	GCK	rs2284775	44177762	G	A	0.2354610	-0.0204373	0.0029794	2.2E-11
7	GCK	rs2284774	44178742	A	G	0.2354390	-0.0203946	0.0029797	2.4E-11
7	GCK	rs2300587	44179195	C	T	0.2354450	-0.0203903	0.0029798	2.5E-11
7	GCK	rs12534104	44180143	A	C	0.2256480	-0.0210638	0.0030709	2.3E-11
7	GCK	rs1990458	44183203	T	C	0.3200650	-0.0152586	0.0027585	3.5E-08
7	GCK	rs730497	44184122	A	G	0.1972990	0.0202983	0.0031769	5.0E-11
7	GCK	rs2908289	44184343	A	G	0.1972710	0.0203228	0.0031780	4.8E-11
7	GCK	rs3808319	44185252	A	G	0.3588630	-0.0163397	0.0026421	2.5E-10
7	GCK	rs2268570	44186491	G	C	0.3702090	-0.0159182	0.0026248	4.6E-10
7	GCK	rs2971670	44186502	T	C	0.1949900	0.0204511	0.0031985	5.6E-11
7	GCK *	rs1799884	44189469	T	C	0.1954630	0.0205597	0.0031907	3.7E-11
7	GCK *	rs3757840	44191617	G	T	0.4651930	-0.0217077	0.0025385	2.6E-18
7	GCK *	rs2971669	44192179	T	C	0.3546580	0.0178990	0.0026389	6.8E-12
7	GCK *	rs6975024	44192287	C	T	0.2053180	0.0192011	0.0031291	3.2E-10
7	GCK *	rs7789273	44193006	T	C	0.3708810	-0.0159591	0.0026247	4.0E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	GCK *	rs741037	44193234	A	G	0.1986290	0.0202469	0.0031753	7.3E-11
7	GCK *	rs2908286	44195138	T	C	0.1983150	0.0204081	0.0031746	4.9E-11
7	YKT6 *	rs4607517	44196069	A	G	0.1984220	0.0205125	0.0031704	3.8E-11
7	YKT6 *	rs1985469	44200725	T	A	0.1921120	0.0202117	0.0032424	1.8E-10
7	YKT6 *	rs1004558	44200808	T	C	0.1982390	0.0203165	0.0031754	5.8E-11
7	YKT6	rs2971668	44203839	C	G	0.2073520	0.0197367	0.0031207	1.1E-10
7	YKT6	rs2971667	44205461	C	T	0.1985080	0.0203943	0.0031722	4.8E-11
7	YKT6	rs10278336	44205764	G	A	0.3690190	-0.0157418	0.0026242	6.6E-10
7	YKT6	rs917793	44206254	T	A	0.1985460	0.0204313	0.0031717	4.7E-11
7	YKT6	rs3824065	44207659	T	C	0.3695810	-0.0158715	0.0026183	4.2E-10
7	YKT6	rs2908282	44209229	A	G	0.1983820	0.0204522	0.0031744	4.4E-11
7	YKT6	rs3840674	44212591	C	CTG	0.1989320	0.0203989	0.0031839	4.0E-11
7	CAMK2B *	rs878521	44216044	A	G	0.3555300	0.0178448	0.0026371	7.1E-12
7	CAMK2B	rs78359497	44217896	A	G	0.1719840	0.0201551	0.0033965	5.7E-10
7	CAMK2B	rs758982	44218344	T	C	0.1730850	0.0197906	0.0033904	8.4E-10
7	CAMK2B	rs1065359	44220107	A	G	0.3560030	-0.0166557	0.0026523	6.4E-11
7	CAMK2B	rs1127065	44220272	T	C	0.3703880	-0.0171523	0.0026247	2.1E-11
7	CAMK2B	rs732360	44222379	A	G	0.1982300	0.0185660	0.0032100	3.8E-09
7	NSUN5	rs3750074	73308628	T	C	0.0161881	-0.0683714	0.0100477	8.2E-13
7	FKBP6 *	rs200456061	73371588	T	C	0.0161285	-0.0676897	0.0100645	1.3E-12
7	FKBP6 *	rs186391487	73384030	A	G	0.0160719	-0.0679169	0.0100853	1.2E-12
7	FZD9 *	rs42123	73425622	G	T	0.1103530	-0.0546422	0.0040866	5.2E-44
7	FZD9 *	rs42122	73427493	A	G	0.0931645	-0.0625006	0.0043681	3.9E-49
7	FZD9 *	chr7:73428127_GAC_G	73428127	G	GAC	0.0872458	-0.0610424	0.0045184	4.6E-44
7	FZD9 *	rs140439318	73428135	C	CAT	0.0881012	-0.0640127	0.0045010	9.7E-49
7	FZD9 *	chr7:73428147_GAC_G	73428147	G	GAC	0.0906861	-0.0635996	0.0044438	2.4E-49
7	FZD9 *	chr7:73428394_GAC_G	73428394	G	GAC	0.0933368	-0.0596792	0.0044441	4.7E-44
7	FZD9 *	rs200948285	73429969	AC	A	0.0119923	-0.0853470	0.0116134	1.6E-14
7	FZD9 *	rs200392099	73432411	CTTT	C	0.0872634	-0.0637406	0.0044906	1.3E-48
7	FZD9 *	rs868953856	73432413	T	A	0.0750701	-0.0666917	0.0048632	1.8E-44
7	FZD9 *	rs782289776	73432414	T	C	0.0750701	-0.0666917	0.0048632	1.8E-44
7	FZD9	rs138414411	73434563	T	C	0.0212445	-0.0660192	0.0087921	1.0E-13
7	FZD9	rs1178947	73435848	C	T	0.0911038	-0.0644393	0.0044006	2.9E-51
7	BAZ1B	rs2240466	73441939	A	G	0.0923588	-0.0651459	0.0043652	3.0E-53
7	BAZ1B	rs1178979	73442100	C	T	0.0918506	-0.0651187	0.0043760	4.7E-53
7	BAZ1B	rs1178977	73442719	G	A	0.0918070	-0.0651925	0.0043769	4.0E-53
7	BAZ1B	rs34604283	73443383	C	CA	0.0917829	-0.0653027	0.0043774	2.8E-53
7	BAZ1B	rs113452856	73444805	A	G	0.0215664	-0.0634227	0.0087282	5.7E-13
7	BAZ1B	rs146626977	73448166	C	T	0.0120131	-0.0846083	0.0116028	2.1E-14
7	BAZ1B	rs13231516	73448919	G	T	0.0965915	-0.0628461	0.0042780	6.7E-52
7	BAZ1B	rs2074756	73449425	C	T	0.0120131	-0.0846083	0.0116028	2.1E-14
7	BAZ1B	rs714052	73450539	G	A	0.0969214	-0.0624699	0.0042735	2.3E-51
7	BAZ1B	rs34763247	73452286	T	A	0.0964898	-0.0630524	0.0042801	4.0E-52
7	BAZ1B	rs1306476	73454192	G	A	0.0964938	-0.0630377	0.0042803	4.4E-52
7	BAZ1B	rs71071936	73455536	CT	C	0.0925082	-0.0652035	0.0043653	2.3E-53
7	BAZ1B	rs35330527	73455877	G	A	0.0980392	-0.0622072	0.0042570	2.0E-51
7	BAZ1B	rs60982449	73459090	G	A	0.0904548	-0.0658119	0.0044115	3.3E-53
7	BAZ1B	rs2074755	73462836	C	T	0.0956971	-0.0635211	0.0042981	2.4E-52
7	BAZ1B	rs35797675	73463714	G	T	0.0980110	-0.0627140	0.0042579	3.1E-52
7	BAZ1B	rs12056034	73464315	G	A	0.0971709	-0.0621766	0.0042695	4.7E-51
7	BAZ1B	rs71556715	73467477	T	C	0.0956823	-0.0635860	0.0042983	1.8E-52
7	BAZ1B	rs62465144	73468776	C	T	0.0963800	-0.0631787	0.0042839	3.6E-52
7	BAZ1B	rs6976930	73471480	A	G	0.0911175	-0.0659812	0.0043950	7.6E-54
7	BAZ1B	rs141027825	73471893	C	G	0.0139922	-0.0770456	0.0108125	1.1E-13
7	BAZ1B	rs139267697	73475356	A	G	0.0120197	-0.0846233	0.0116001	2.1E-14
7	BAZ1B	rs35695283	73479073	G	A	0.0916530	-0.0654842	0.0043813	2.3E-53
7	BAZ1B	rs75229905	73481616	C	T	0.0963856	-0.0630129	0.0042832	6.1E-52
7	BAZ1B	rs7797566	73482065	C	A	0.0963856	-0.0630129	0.0042832	6.1E-52
7	BAZ1B	rs17145713	73490480	T	C	0.0957412	-0.0634602	0.0042974	2.6E-52
7	BAZ1B	rs111837003	73493129	T	C	0.0909384	-0.0661420	0.0043985	6.2E-54
7	BAZ1B	rs118023175	73494447	G	C	0.0120534	-0.0847526	0.0115844	1.9E-14
7	BAZ1B	rs117830225	73494457	C	G	0.0120196	-0.0846268	0.0116001	2.1E-14
7	BAZ1B	rs13244268	73497513	C	T	0.0964073	-0.0640557	0.0042941	3.3E-53
7	BAZ1B	rs67243124	73497702	A	AAAAAAC	0.0954213	-0.0635377	0.0043048	3.1E-52
7	BAZ1B	rs201533187	73497710	A	AAAAAG	0.0869941	-0.0603258	0.0045171	1.0E-42
7	BAZ1B	rs34482346	73501191	C	G	0.0956791	-0.0636241	0.0042983	1.6E-52
7	BAZ1B	chr7:73505631_GA_G	73505631	G	GA	0.0902314	-0.0648866	0.0044522	1.2E-50
7	BAZ1B	rs79862839	73507279	C	T	0.0956823	-0.0636291	0.0042984	1.6E-52
7	BAZ1B	rs13221253	73507903	G	A	0.0955710	-0.0635806	0.0043015	2.2E-52
7	BAZ1B	rs34437827	73509008	G	A	0.0956689	-0.0636382	0.0042988	1.6E-52
7	BAZ1B	rs7811265	73520180	G	A	0.0872608	-0.0663458	0.0044968	3.6E-52
7	BAZ1B *	rs62466264	73524388	C	T	0.0958823	-0.0637664	0.0042965	9.3E-53

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	BAZ1B *	rs11983997	73524914	C	G	0.0955512	-0.0635467	0.0043015	2.6E-52
7	BAZ1B *	rs80189144	73525609	C	T	0.0955512	-0.0635467	0.0043015	2.6E-52
7	BCL7B *	rs143934761	73533607	G	A	0.0212474	-0.0635778	0.0087811	5.5E-13
7	BCL7B	rs142030730	73542085	T	C	0.0130550	-0.0564498	0.0111452	3.9E-08
7	BCL7B	rs17145732	73555938	G	T	0.0996371	-0.0651915	0.0042260	1.8E-56
7	BCL7B	rs13233571	73556901	T	C	0.0954702	-0.0677996	0.0043041	2.8E-58
7	BCL7B	rs7793710	73557201	G	C	0.0954193	-0.0679836	0.0043057	1.6E-58
7	BCL7B	rs13234157	73557398	A	C	0.0944912	-0.0672387	0.0043392	1.0E-56
7	BCL7B *	rs13244614	73559524	A	C	0.0953871	-0.0680478	0.0043070	1.2E-58
7	BCL7B *	rs140173690	73560328	A	C	0.0172033	-0.0652019	0.0097148	2.6E-12
7	BCL7B *	rs111269058	73561372	T	C	0.0953957	-0.0680644	0.0043071	1.1E-58
7	BCL7B *	rs13225333	73561688	T	C	0.0953666	-0.0680686	0.0043074	1.2E-58
7	BCL7B *	rs13225347	73561718	T	C	0.0953911	-0.0681021	0.0043072	9.8E-59
7	BCL7B *	rs13225450	73561793	T	C	0.0952655	-0.0679418	0.0043100	1.8E-58
7	BCL7B *	rs34594435	73562919	T	C	0.0953968	-0.0680927	0.0043071	1.0E-58
7	BCL7B *	rs6946689	73563307	A	T	0.0954798	-0.0680573	0.0043065	1.1E-58
7	TBL2 *	rs12539316	73563568	G	A	0.0965971	-0.0666911	0.0042881	1.4E-56
7	TBL2 *	rs12539351	73563782	G	A	0.0906421	-0.0709436	0.0044077	1.5E-60
7	TBL2 *	rs147472118	73563984	T	C	0.0192800	-0.0791758	0.0091823	2.8E-17
7	TBL2 *	rs17145738	73568544	T	C	0.0955379	-0.0680257	0.0043036	1.4E-58
7	TBL2	rs13232120	73568980	T	A	0.0955380	-0.0680244	0.0043041	1.3E-58
7	TBL2	rs14415	73570450	C	T	0.0955380	-0.0680244	0.0043041	1.3E-58
7	TBL2	rs190174185	73572316	C	G	0.0115010	-0.0819652	0.0118623	5.3E-12
7	TBL2	rs2286276	73573024	T	C	0.0956621	-0.0677365	0.0043009	4.0E-58
7	TBL2	rs35659126	73573739	T	C	0.0952682	-0.0680791	0.0043094	1.5E-58
7	TBL2	chr7:73574811_C_CA	73574811	CA	C	0.0960776	-0.0670931	0.0043004	2.7E-57
7	TBL2	rs11974409	73575060	G	A	0.0953571	-0.0678968	0.0043087	2.5E-58
7	TBL2	rs12540011	73577374	A	G	0.0954022	-0.0682027	0.0043081	9.7E-59
7	TBL2	rs13246490	73578020	T	C	0.0953885	-0.0682976	0.0043084	7.3E-59
7	TBL2 *	rs66553475	73579219.CTGCTGC	T	T	0.0947737	-0.0680521	0.0043231	4.3E-58
7	TBL2 *	chr7:73581580_C_CA	73581580	CA	C	0.0833701	-0.0659673	0.0046428	1.7E-47
7	TBL2 *	rs66506038	73581613	C	T	0.0954149	-0.0683012	0.0043077	7.0E-59
7	TBL2 *	rs67644909	73581624	T	C	0.0939555	-0.0681930	0.0043434	7.6E-58
7	TBL2 *	rs9638180	73584622	G	A	0.0954652	-0.0681923	0.0043074	1.0E-58
7	TBL2 *	rs9638181	73584713	G	A	0.0954652	-0.0681923	0.0043074	1.0E-58
7	TBL2 *	rs9638182	73584775	G	T	0.0954652	-0.0681923	0.0043074	1.0E-58
7	MLXIPL *	rs35173225	73586691	T	C	0.0954757	-0.0681722	0.0043094	1.2E-58
7	MLXIPL *	rs187404224	73588697	G	A	0.0953909	-0.0682704	0.0043083	8.3E-59
7	MLXIPL *	rs185081604	73588973	C	A	0.0953909	-0.0682704	0.0043083	8.3E-59
7	MLXIPL *	rs145099458	73589985	T	C	0.0907904	-0.0664272	0.0044267	4.7E-53
7	MLXIPL *	rs35866503	73591446	T	C	0.0953909	-0.0682704	0.0043083	8.3E-59
7	MLXIPL *	rs13225660	73592058	T	C	0.0953909	-0.0682704	0.0043083	8.3E-59
7	MLXIPL *	chr7:73592757_C_CA	73592757	CA	C	0.0885608	-0.0682901	0.0044903	9.4E-55
7	MLXIPL	rs1051921	73593613	A	G	0.0953909	-0.0682661	0.0043083	8.4E-59
7	MLXIPL	rs13247874	73596112	T	C	0.0971839	-0.0693583	0.0042754	2.0E-61
7	MLXIPL	rs35332062	73597712	A	G	0.0979886	-0.0694160	0.0042569	5.7E-62
7	MLXIPL	rs79624003	73598455	G	A	0.0979198	-0.0698575	0.0042594	1.2E-62
7	MLXIPL	rs35732917	73598939	C	T	0.0978018	-0.0701714	0.0042628	3.8E-63
7	MLXIPL	rs13235543	73599571	T	C	0.0977241	-0.0703013	0.0042639	2.7E-63
7	MLXIPL	rs13240065	73601039	A	G	0.0966862	-0.0698033	0.0042925	6.2E-62
7	MLXIPL	rs34346326	73601851	C	T	0.0975721	-0.0701234	0.0042687	7.3E-63
7	MLXIPL	rs879969597	73602094	G	GCCTT	0.0106688	-0.0684899	0.0125517	3.3E-08
7	MLXIPL	rs13240994	73602532	C	T	0.0882111	-0.0755773	0.0044873	2.0E-66
7	MLXIPL	rs13226650	73602675	G	A	0.0976930	-0.0701624	0.0042687	6.8E-63
7	MLXIPL	rs35368205	73603327	T	C	0.0884796	-0.0747224	0.0044545	2.3E-66
7	MLXIPL	rs34166762	73604194	C	T	0.0890542	-0.0786136	0.0044514	2.0E-72
7	MLXIPL	rs61010704	73605645	G	A	0.0863666	-0.0798861	0.0045022	2.6E-73
7	MLXIPL	rs3812316	73606007	G	C	0.0863675	-0.0799304	0.0045015	2.1E-73
7	MLXIPL	rs6968170	73606346	A	G	0.0864137	-0.0799214	0.0045003	2.1E-73
7	MLXIPL	rs77048596	73607881	A	G	0.0863983	-0.0798669	0.0045010	2.8E-73
7	MLXIPL	rs13246993	73608416	A	G	0.0863956	-0.0798435	0.0045012	3.0E-73
7	MLXIPL	rs141854486	73608603	A	AAG	0.0780183	-0.0784432	0.0047475	1.0E-64
7	MLXIPL	rs12531645	73609551	A	G	0.0863098	-0.0796895	0.0045033	6.7E-73
7	MLXIPL	rs35512732	73610432	T	TC	0.0863986	-0.0798296	0.0045012	3.2E-73
7	MLXIPL	rs13234131	73611645	G	A	0.0995177	-0.0748566	0.0042186	7.0E-72
7	MLXIPL	rs13234378	73611821	T	A	0.0999729	-0.0746184	0.0042138	9.0E-72
7	MLXIPL	rs17145750	73612048	T	C	0.0998803	-0.0747865	0.0042119	4.3E-72
7	MLXIPL	rs7808877	73613120	G	C	0.0997085	-0.0746855	0.0042160	1.0E-71
7	MLXIPL	rs139002804	73613553	A	G	0.0117308	-0.0916140	0.0117549	5.0E-16
7	MLXIPL	rs33951980	73615107	T	C	0.0997097	-0.0746781	0.0042160	1.0E-71
7	MLXIPL	rs2074768	73615773	C	A	0.0996984	-0.0745719	0.0042164	1.5E-71
7	MLXIPL	rs13229619	73615845	A	G	0.0996984	-0.0745719	0.0042164	1.5E-71

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	MLXIPL	rs7798357	73617935	C	G	0.0996531	-0.0743100	0.0042181	5.3E-71
7	MLXIPL	rs7785479	73618505	C	T	0.0996486	-0.0743302	0.0042181	4.8E-71
7	MLXIPL	rs34062580	73619229	A	G	0.0996497	-0.0743285	0.0042181	4.9E-71
7	MLXIPL	rs6975495	73619700	G	A	0.0996531	-0.0743590	0.0042183	4.4E-71
7	MLXIPL	rs71556736	73620599	T	C	0.0997334	-0.0741214	0.0042167	1.3E-70
7	MLXIPL	rs7800944	73621527	C	T	0.1000960	-0.0733536	0.0042112	2.7E-69
7	MLXIPL	rs1207541622	73621799	C	T	0.0122029	-0.1101540	0.0116319	3.2E-22
7	MLXIPL	rs2736909	73621803	G	C	0.0122029	-0.1101540	0.0116319	3.2E-22
7	MLXIPL	rs55747707	73623036	A	G	0.0996370	-0.0742273	0.0042207	8.6E-71
7	MLXIPL	rs34060476	73623626	G	A	0.0996063	-0.0741776	0.0042216	1.0E-70
7	MLXIPL *	rs35493868	73625076	G	C	0.0996086	-0.0741979	0.0042220	9.5E-71
7	MLXIPL *	rs34121855	73626484	G	T	0.0976332	-0.0742218	0.0042678	1.3E-69
7	MLXIPL *	rs62466318	73627755	T	C	0.1079670	-0.0676350	0.0040738	2.3E-63
7	MLXIPL *	chr7:73627972_GCTTT_G	73627972	G	GCTTT	0.1082690	-0.0672530	0.0040724	9.7E-63
7	MLXIPL *	rs117739002	73628073	T	C	0.0178740	-0.0764340	0.0095486	4.4E-15
7	MLXIPL *	rs6460047	73628113	C	T	0.1094460	-0.0664802	0.0040547	7.2E-62
7	MLXIPL *	rs7805504	73628255	C	T	0.1093400	-0.0668440	0.0040566	1.9E-62
7	MLXIPL *	rs7786376	73628284	G	A	0.1107000	-0.0669482	0.0040371	2.7E-63
7	MLXIPL *	rs35340690	73628738	C	G	0.1520410	-0.0439414	0.0035517	9.6E-37
7	MLXIPL *	rs34958196	73628771	A	G	0.1394610	-0.0510856	0.0036725	2.5E-45
7	MLXIPL *	rs34430945	73629335	C	T	0.1389480	-0.0510378	0.0036769	3.4E-45
7	MLXIPL *	rs34321592	73630874	A	G	0.1672500	-0.0435217	0.0034117	4.2E-39
7	MLXIPL *	rs7784668	73631153	C	T	0.1384030	-0.0509108	0.0036864	8.1E-45
7	MLXIPL *	rs78815801	73631608	C	T	0.1288250	-0.0525646	0.0038388	4.8E-44
7	MLXIPL *	rs1412452301	73631935 CTTCCTT	C	C	0.1656660	-0.0434194	0.0034350	2.3E-38
7	MLXIPL *	rs17145813	73632428	A	C	0.1652540	-0.0430573	0.0034429	1.3E-37
7	MLXIPL *	rs17145817	73632449	G	A	0.1652540	-0.0430712	0.0034429	1.2E-37
7	MLXIPL *	rs36091304	73633181	C	T	0.1635060	-0.0441075	0.0034668	1.0E-38
7	MLXIPL *	rs34899589	73633190	C	T	0.1620150	-0.0437895	0.0034872	6.9E-38
7	MLXIPL *	rs35855035	73633221	T	C	0.1619140	-0.0431573	0.0034867	9.5E-37
7	MLXIPL *	rs35703204	73633518	T	C	0.1650260	-0.0431002	0.0034502	1.7E-37
7	MLXIPL *	rs13230514	73633765	G	A	0.1648020	-0.0429975	0.0034509	2.4E-37
7	MLXIPL *	rs62466323	73634348	A	G	0.1647830	-0.0425928	0.0034522	9.9E-37
7	MLXIPL *	rs13234805	73634852	A	G	0.1343670	-0.0511360	0.0037604	2.1E-43
7	MLXIPL *	rs13222090	73635057	C	T	0.1649700	-0.0420896	0.0034499	5.0E-36
7	VPS37D *	rs371515311	73660465	A	G	0.0173240	-0.0604330	0.0096863	4.9E-11
7	WBSR28 *	rs73144858	73922565	G	C	0.0199115	-0.0532712	0.0090786	7.5E-10
7	ELN *	rs188072556	73999294	T	C	0.0168609	-0.0602919	0.0098257	8.7E-11
7	CLIP2	rs151126504	74392493	T	C	0.0208372	-0.0494306	0.0089103	5.1E-09
7	KLF14 *	rs6973807	130739211	G	A	0.3077310	-0.0205371	0.0027887	1.8E-13
7	KLF14 *	rs6974400	130739314	A	G	0.3077270	-0.0205530	0.0027876	1.7E-13
7	KLF14 *	rs6974288	130739451	G	A	0.3078720	-0.0205576	0.0027858	1.5E-13
7	KLF14 *	rs11762784	130739885	A	G	0.3079880	-0.0202970	0.0027816	2.7E-13
7	KLF14 *	rs3996350	130742296	C	G	0.3089680	-0.0203575	0.0027631	1.6E-13
7	KLF14 *	rs13234269	130744427	A	T	0.3098820	-0.0207008	0.0027501	4.5E-14
7	KLF14 *	rs4731701	130746171	T	C	0.3086950	-0.0204861	0.0027628	7.3E-14
7	KLF14 *	rs10260148	130746210	T	C	0.3986690	0.0205335	0.0026265	1.7E-15
7	KLF14 *	rs34072724	130747710	A	G	0.3107550	-0.0206763	0.0027339	2.9E-14
7	KLF14 *	rs6971365	130747722	C	T	0.4010230	0.0204404	0.0026164	1.9E-15
7	KLF14 *	rs13241165	130747779	T	A	0.3107930	-0.0206703	0.0027338	2.9E-14
7	KLF14 *	rs4731702	130748625	T	C	0.3106630	-0.0207291	0.0027312	2.4E-14
7	KLF14 *	rs11976955	130748835	G	C	0.4024400	0.0200392	0.0026173	5.3E-15
7	KLF14 *	rs6961342	130749185	A	C	0.4024140	0.0200348	0.0026164	5.8E-15
7	KLF14 *	rs35722851	130749741	C	T	0.3096250	-0.0208664	0.0027434	1.9E-14
7	KLF14 *	rs35057928	130749767	C	T	0.3092160	-0.0209395	0.0027445	1.6E-14
7	KLF14 *	rs34282904	130749770	A	G	0.3094650	-0.0208678	0.0027437	1.9E-14
7	KLF14 *	rs287621	130750422	T	C	0.4009880	0.0202592	0.0026151	3.5E-15
7	KLF14 *	chr7:130751316_A_AAT	130751316	AAT	A	0.3102950	-0.0209781	0.0027393	1.3E-14
7	KLF14 *	rs34084575	130751643	TA	T	0.3112040	-0.0209133	0.0027355	1.5E-14
7	KLF14 *	rs11979110	130751700	T	C	0.3111300	-0.0208577	0.0027354	1.7E-14
7	KLF14 *	rs13230111	130752365	G	A	0.3104730	-0.0210266	0.0027357	9.9E-15
7	KLF14 *	rs7810507	130752717	A	G	0.4015930	0.0203146	0.0026121	2.5E-15
7	KLF14 *	rs13233731	130752930	A	G	0.3104170	-0.0209446	0.0027357	1.2E-14
7	KLF14 *	rs13234407	130753455	A	G	0.3104360	-0.0209202	0.0027355	1.3E-14
7	KLF14 *	rs7783857	130754299	G	C	0.4209880	0.0213096	0.0025695	3.7E-17
7	KLF14 *	rs13241538	130755103	C	G	0.3112620	-0.0210812	0.0027306	6.6E-15
7	KLF14 *	rs13228906	130757125	A	G	0.3109530	-0.0209665	0.0027345	9.2E-15
7	KLF14 *	rs6467314	130757382	G	C	0.4198280	0.0213690	0.0025658	2.8E-17
7	KLF14 *	rs17185445	130757868	T	C	0.3112550	-0.0210332	0.0027363	8.3E-15
7	KLF14 *	rs3996352	130760175	G	A	0.3089750	-0.0210716	0.0027453	6.4E-15
7	KLF14 *	rs13240528	130760369	A	C	0.3088510	-0.0212012	0.0027462	4.6E-15
7	KLF14 *	chr7:130760669_C_CT	130760669	CT	C	0.3011530	-0.0203931	0.0027928	1.6E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	KLF14 *	rs17789506	130760815	A	G	0.3092690	-0.0210557	0.0027461	6.9E-15
7	KLF14 *	rs35712907	130761088	T	TA	0.3092380	-0.0210738	0.0027470	6.7E-15
7	KLF14 *	rs11765979	130761118	C	A	0.3092440	-0.0210752	0.0027471	6.6E-15
7	KLF14 *	rs1364422	130761222	T	C	0.4217010	0.0212554	0.0025558	2.1E-17
7	KLF14 *	rs59326756	130762371	G	A	0.4235560	0.0207205	0.0025601	1.7E-16
7	KLF14 *	rs12667251	130764699	G	A	0.3434390	-0.0180483	0.0026979	5.7E-12
7	KLF14 *	rs185963	130765392	C	T	0.3416720	-0.0177772	0.0027001	1.0E-11
7	KLF14 *	rs288484	130765438	A	G	0.3416280	-0.0177065	0.0027002	1.3E-11
7	KLF14 *	rs172306	130765628	G	A	0.3434730	-0.0180326	0.0026972	6.4E-12
7	KLF14 *	rs577195	130765902	C	G	0.3416250	-0.0177175	0.0026999	1.2E-11
7	KLF14 *	rs1665759	130766738	T	C	0.3416770	-0.0177183	0.0026996	1.2E-11
7	KLF14 *	rs1646629	130766864	C	T	0.3414900	-0.0176959	0.0027002	1.3E-11
7	KLF14 *	rs1646631	130766912	G	A	0.3416210	-0.0177694	0.0026992	1.0E-11
7	KLF14 *	rs56258902	130767225	C	CTTTA	0.3138800	-0.0176722	0.0027612	7.4E-11
7	KLF14 *	rs10238574	130767468	T	C	0.3416040	-0.0177714	0.0026989	1.1E-11
7	KLF14 *	rs1596972	130768623	A	G	0.3417150	-0.0176444	0.0026975	1.4E-11
7	KLF14 *	rs1562398	130773172	C	G	0.3392660	-0.0167822	0.0027089	1.6E-10
7	KLF14 *	rs34748838	130774483	T	C	0.3152320	-0.0169143	0.0027484	3.1E-10
7	KLF14 *	rs6968740	130775517	G	T	0.3422070	-0.0173352	0.0026921	2.8E-11
7	KLF14 *	rs6951054	130775721	T	G	0.3422080	-0.0173150	0.0026920	2.9E-11
7	KLF14 *	rs35964477	130777099	A	AT	0.3155970	-0.0168926	0.0027469	3.4E-10
7	KLF14 *	rs4425698	130777483	T	C	0.3423010	-0.0173590	0.0026904	2.6E-11
7	KLF14 *	rs1596973	130777524	G	A	0.3423020	-0.0173145	0.0026902	2.9E-11
7	KLF14 *	rs6467315	130778433	C	G	0.3179760	-0.0165781	0.0027554	6.9E-10
7	KLF14 *	rs6949956	130778566	T	G	0.3418650	-0.0170560	0.0026861	5.2E-11
7	KLF14 *	rs6968233	130778697	G	A	0.3420020	-0.0171639	0.0026852	4.0E-11
7	KLF14 *	rs10954284	130778999	A	T	0.3152520	-0.0164284	0.0027412	9.1E-10
7	KLF14 *	rs10245520	130779072	T	C	0.3419020	-0.0169373	0.0026843	7.2E-11
7	KLF14 *	rs6972634	130779366	A	G	0.3421620	-0.0169486	0.0026840	6.8E-11
7	KLF14 *	rs6467316	130779837	C	T	0.3418210	-0.0167717	0.0026851	1.0E-10
7	KLF14 *	rs6467317	130779901	A	G	0.3428250	-0.0169262	0.0026836	7.2E-11
7	KLF14 *	rs9641894	130780295	T	G	0.3421030	-0.0170019	0.0026817	5.7E-11
7	KLF14 *	rs34188023	130780856	G	GT	0.3428290	-0.0169398	0.0026796	6.1E-11
7	KLF14 *	rs1447059	130780895	A	G	0.3423450	-0.0170382	0.0026800	5.1E-11
7	KLF14 *	rs1447060	130781332	A	G	0.3400100	-0.0169780	0.0026809	7.0E-11
7	KLF14 *	rs972283	130782095	A	G	0.3134020	-0.0169165	0.0027235	3.1E-10
7	KLF14 *	rs972284	130782207	C	T	0.3412680	-0.0172982	0.0026738	2.3E-11
8	NAT2 *	rs35548819	183711107	C	T	0.4721960	0.0177974	0.0025507	2.0E-12
8	NAT2 *	rs2172426	18371511	C	T	0.4418700	-0.0190809	0.0025501	6.8E-15
8	NAT2 *	rs1845736	18372655	T	C	0.4392340	-0.0186092	0.0025487	3.1E-14
8	NAT2 *	rs13267304	18374424	T	C	0.4903270	0.0180919	0.0025235	3.1E-13
8	NAT2 *	rs7835476	18375604	A	C	0.4903930	0.0180364	0.0025232	3.4E-13
8	NAT2 *	rs7006687	18376073	C	T	0.4634400	-0.0185397	0.0025272	3.6E-14
8	NAT2 *	rs4481648	18378050	G	T	0.4621850	-0.0181871	0.0025425	1.7E-13
8	NAT2 *	rs2047252	18380477	T	C	0.4869040	0.0183790	0.0025685	3.8E-14
8	NAT2 *	rs10448136	18382184	A	C	0.1748560	-0.0175769	0.0033409	4.0E-08
8	NAT2 *	rs13266992	18382187	C	T	0.4766050	0.0176111	0.0025670	5.7E-13
8	NAT2 *	rs59416053	18383290	C	G	0.4744170	0.0171001	0.0025550	1.8E-12
8	NAT2 *	rs35354956	18383809	C	T	0.4764820	0.0173418	0.0025469	7.9E-13
8	NAT2 *	rs13277738	18383997	T	C	0.4735930	0.0170073	0.0025494	2.0E-12
8	NAT2 *	rs13262341	18385587	G	A	0.4780440	0.0175797	0.0025456	3.4E-13
8	NAT2 *	rs10109286	18386093	C	T	0.4752610	0.0176068	0.0025463	2.8E-13
8	NAT2 *	rs10095072	18387152	T	G	0.4995010	0.0182623	0.0025398	2.3E-14
8	NAT2 *	rs10095159	18387174	G	A	0.5002360	-0.0181366	0.0025439	4.1E-14
8	NAT2 *	rs75501607	18387243	T	C	0.4991120	0.0180381	0.0025377	3.8E-14
8	NAT2 *	rs13282367	18387476	G	T	0.4799830	0.0171215	0.0025436	1.2E-12
8	NAT2 *	rs10085931	18387939	A	G	0.5004160	-0.0187771	0.0025487	4.5E-15
8	NAT2 *	rs11780884	18388543	A	G	0.4917360	0.0178588	0.0025480	7.1E-14
8	NAT2 *	rs4646243	18390099	C	T	0.4757880	0.0173778	0.0025311	3.9E-13
8	NAT2 *	rs4646267	18390403	G	A	0.4758080	0.0173353	0.0025309	4.1E-13
8	NAT2 *	rs4646246	18391151	G	A	0.4736340	0.0172954	0.0025342	5.2E-13
8	NAT2	rs55686478	18392865	A	G	0.4723490	0.0170456	0.0025401	1.2E-12
8	NAT2	rs35583283	18396999	C	G	0.4782420	0.0173905	0.0025413	4.6E-13
8	NAT2	rs1041983	18400285	T	C	0.4317230	-0.0190461	0.0025468	3.1E-15
8	NAT2	rs1799931	18400860	A	G	0.1585450	-0.0200263	0.0034519	2.5E-09
8	NAT2 *	rs971473	18401450	T	C	0.1661790	-0.0187279	0.0033889	8.7E-09
8	NAT2 *	rs79409592	18403606	T	C	0.1657800	-0.0185943	0.0033942	1.2E-08
8	NAT2 *	rs115942586	18404518	C	T	0.1660900	-0.0186106	0.0033909	1.1E-08
8	NAT2 *	rs4646254	18404549	G	A	0.4805740	0.0174156	0.0025365	6.2E-13
8	NAT2 *	rs4646257	18405036	T	C	0.4798130	0.0176209	0.0025360	3.6E-13
8	NAT2 *	rs12674710	18406153	C	A	0.4804000	0.0175272	0.0025368	4.7E-13
8	NAT2 *	rs2088200	18407894	G	C	0.1691310	-0.0180541	0.0033713	2.4E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	NAT2 *	rs74303991	18408156	A	G	0.1615680	-0.0190489	0.0034327	1.0E-08
8	NAT2 *	rs12676857	18409062	C	T	0.4731470	0.0171548	0.0025457	1.8E-12
8	NAT2 *	rs2898475	18409186	C	T	0.4290570	-0.0133881	0.0025676	3.3E-08
8	NAT2 *	rs2410561	18409264	A	G	0.4731000	0.0172207	0.0025457	1.5E-12
8	NAT2 *	rs2410562	18409322	C	T	0.4290550	-0.0133898	0.0025676	3.3E-08
8	NAT2 *	rs7837608	18409337	A	G	0.4290550	-0.0133898	0.0025676	3.3E-08
8	NAT2 *	rs2898476	18409414	A	G	0.4725140	0.0172439	0.0025467	1.4E-12
8	NAT2 *	rs7460653	18409473	C	G	0.4743830	0.0170625	0.0025470	2.8E-12
8	NAT2 *	rs10103029	18409828	G	A	0.4749650	0.0170478	0.0025454	2.8E-12
8	NAT2 *	rs10103148	18409919	C	A	0.4764770	0.0167719	0.0025459	6.4E-12
8	NAT2 *	rs10087857	18409951	C	G	0.4749340	0.0169993	0.0025456	3.3E-12
8	NAT2 *	rs10088333	18410368	A	G	0.4749110	0.0169631	0.0025456	3.6E-12
8	NAT2 *	rs1603290	18411760	G	A	0.4245930	-0.0136974	0.0025701	2.1E-08
8	NAT2 *	rs10089958	18411833	G	A	0.4775170	0.0172614	0.0025449	1.5E-12
8	NAT2 *	rs57180587	18412071	T	A	0.4770180	0.0173351	0.0025454	1.2E-12
8	NAT2 *	rs12543818	18414402	G	T	0.4341060	-0.0137357	0.0025619	1.9E-08
8	NAT2 *	rs12545528	18414438	T	G	0.4337540	-0.0136110	0.0025604	2.5E-08
8	NAT2 *	chr8:18414568_A_AT	18414568	AT	A	0.3806720	-0.0154341	0.0026251	6.6E-10
8	NAT2 *	rs4921911	18414597	T	C	0.3876030	-0.0158067	0.0025920	1.7E-10
8	NAT2 *	rs4921912	18414623	G	A	0.3880030	-0.0157720	0.0025903	1.8E-10
8	NAT2 *	rs4921913	18414867	T	C	0.4802190	-0.0188392	0.0025246	8.0E-15
8	NAT2 *	rs4921914	18414928	T	C	0.4843080	-0.0186225	0.0025330	2.0E-14
8	NAT2 *	rs4921915	18414956	A	G	0.4813770	-0.0190919	0.0025252	4.2E-15
8	NAT2 *	rs11267998	18414993	TGAGCTG	C	0.4843670	-0.0187111	0.0025265	1.6E-14
8	NAT2 *	rs35246381	18415025	T	C	0.4842740	-0.0187586	0.0025252	1.3E-14
8	NAT2 *	rs35570672	18415125	C	T	0.4839330	-0.0187326	0.0025259	1.4E-14
8	NAT2 *	rs1495741	18415371	A	G	0.4831950	-0.0189128	0.0025249	7.9E-15
8	NAT2 *	rs1495742	18415391	T	C	0.2672220	-0.0184949	0.0028564	3.6E-11
8	NAT2 *	rs13254811	18415508	G	A	0.4687450	0.0171193	0.0025433	2.4E-12
8	NAT2 *	rs1495743	18415790	C	G	0.4838220	-0.0188348	0.0025281	1.1E-14
8	NAT2 *	rs6998197	18416486	T	C	0.3137760	-0.0146805	0.0027398	4.1E-08
8	NAT2 *	rs7815666	18416695	T	C	0.3136050	-0.0147049	0.0027403	4.4E-08
8	NAT2 *	rs7828813	18416714	C	G	0.3140070	-0.0146444	0.0027382	4.9E-08
8	NAT2 *	rs7815698	18416746	T	A	0.3140980	-0.0147190	0.0027388	4.3E-08
8	NAT2 *	rs35942058	18416888	A	G	0.4690900	0.0172242	0.0025465	2.8E-12
8	NAT2 *	rs34987019	18416933	C	T	0.4691000	0.0172237	0.0025466	2.9E-12
8	NAT2 *	rs7812546	18417104	A	T	0.4684930	0.0170922	0.0025516	5.2E-12
8	NAT2 *	rs34537991	18417174	C	G	0.4703550	0.0172650	0.0025494	3.0E-12
8	NAT2 *	rs7828489	18417249	G	T	0.4789830	0.0178273	0.0025506	6.4E-13
8	NAT2 *	rs12545875	18417281	C	T	0.1704970	-0.0187660	0.0033673	1.0E-08
8	NAT2 *	rs7816847	18417679	C	A	0.4708270	0.0173422	0.0025451	1.6E-12
8	NAT2 *	rs8180964	18417979	T	C	0.1513360	-0.0195955	0.0035454	2.2E-08
8	NAT2 *	rs4560828	18418784	T	A	0.4707970	0.0172824	0.0025525	3.0E-12
8	NAT2 *	rs13255048	18419130	A	G	0.4687200	0.0176841	0.0025504	7.8E-13
8	NAT2 *	rs35492904	18419249	A	G	0.2416420	-0.0190150	0.0029782	1.6E-10
8	NAT2 *	chr8:18419370_AAACAAC	18419370	AAACAAC	A	0.4667980	0.0170567	0.0025547	5.5E-12
8	NAT2 *	rs1466753	18419609	T	C	0.2623860	-0.0187135	0.0028863	3.2E-11
8	NAT2 *	rs983776	18420448	C	T	0.2667570	-0.0180217	0.0028760	1.4E-10
8	NAT2 *	rs983777	18420469	G	A	0.2510420	-0.0184824	0.0029393	2.0E-10
8	NAT2 *	rs7005648	18420698	T	A	0.4732070	0.0174643	0.0025489	1.0E-12
8	NAT2 *	rs150364778	18421641	T	CACAAGT	0.1498210	-0.0200262	0.0035800	1.1E-08
8	NAT2 *	rs17642824	18421743	A	G	0.1464580	-0.0210081	0.0036136	2.7E-09
8	INTS10 *	rs74549553	19874863	C	G	0.0759314	-0.0285322	0.0048363	1.5E-09
8	INTS10 *	rs4922113	19877440	A	G	0.1205330	-0.0259597	0.0039427	3.4E-11
8	INTS10 *	rs75070501	19880081	G	A	0.1183440	-0.0302899	0.0039590	8.6E-15
8	INTS10 *	rs17410407	19881732	T	G	0.1165140	-0.0294655	0.0039772	4.4E-14
8	INTS10 *	rs77829308	19883675	T	C	0.1143140	-0.0296388	0.0040138	5.7E-14
8	INTS10 *	chr8:19884251_C_CA	19884251	CA	C	0.1121560	-0.0302439	0.0040619	3.1E-14
8	INTS10 *	rs73607783	19884693	A	T	0.1236570	-0.0297770	0.0038947	8.1E-15
8	INTS10 *	rs79341217	19885706	T	C	0.1009930	-0.0336193	0.0042258	2.6E-16
8	INTS10 *	rs74974359	19885743	C	T	0.0692580	-0.0317297	0.0050273	8.6E-11
8	INTS10 *	rs10503666	19887085	C	G	0.0871865	-0.0389890	0.0044792	2.9E-19
8	INTS10 *	rs17482310	19889365	T	G	0.0971381	-0.0328630	0.0042745	4.2E-15
8	INTS10 *	rs79396901	19890937	C	T	0.0875660	-0.0390867	0.0044662	2.4E-19
8	INTS10 *	rs138094414	19892729	C	G	0.0839860	-0.0379678	0.0045477	6.9E-18
8	INTS10 *	rs112861901	19893440	C	T	0.0873295	-0.0390869	0.0044703	1.7E-19
8	INTS10 *	rs12550077	19893888	A	G	0.0827718	-0.0380994	0.0045772	7.8E-18
8	LPL *	rs17482386	19896010	G	A	0.0989222	-0.0358110	0.0042441	6.4E-18
8	LPL *	chr8:19896793_C_CT	19896793	CT	C	0.1039980	-0.0364613	0.0041668	3.5E-19
8	LPL *	rs1919482	19897207	T	A	0.0999496	-0.0336053	0.0042260	1.6E-16
8	LPL *	rs76085257	19897616	A	C	0.0829549	-0.0378097	0.0045676	9.6E-18
8	LPL *	rs73597688	19897664	A	C	0.0969337	-0.0357654	0.0042823	7.7E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs73597690	19898115	A	C	0.0888328	-0.0365263	0.0044458	1.3E-17
8	LPL *	rs12543154	19898466	T	G	0.0877882	-0.0372597	0.0044657	5.3E-18
8	LPL *	rs10091649	19898910	G	T	0.0920516	-0.0384272	0.0043980	6.8E-20
8	LPL *	rs73597699	19899081	T	C	0.0789256	-0.0377536	0.0047173	6.8E-17
8	LPL *	rs10102717	19899302	T	C	0.0896820	-0.0377563	0.0044454	4.1E-19
8	LPL *	rs1441771	19899789	T	C	0.0892744	-0.0386685	0.0044576	8.9E-20
8	LPL *	rs1441770	19899808	A	G	0.0895465	-0.0383834	0.0044510	1.4E-19
8	LPL *	rs183801835	19904479	C	T	0.0206401	-0.0567883	0.0088980	4.8E-12
8	LPL *	rs77032723	19906481	T	C	0.1289430	-0.0385522	0.0038125	1.3E-26
8	LPL *	rs192423215	19907403	C	G	0.0197858	-0.0602689	0.0090775	7.4E-13
8	LPL *	rs60526148	19909692	T	C	0.1538940	-0.0415135	0.0035214	6.5E-35
8	LPL *	rs3988301	19912868	G	T	0.1585590	-0.0419290	0.0034813	1.8E-36
8	LPL *	rs28834434	19917379	A	C	0.1515710	-0.0419715	0.0035165	4.7E-36
8	LPL *	rs4466415	19919470	C	A	0.1628940	-0.0411776	0.0034296	2.5E-36
8	LPL *	rs77899453	19922799	A	G	0.1511500	-0.0421060	0.0035259	4.0E-36
8	LPL *	rs2119692	19922946	C	G	0.1522450	-0.0413143	0.0035158	3.2E-35
8	LPL *	rs3866470	19927611	A	G	0.0166912	-0.0632202	0.0098502	3.8E-12
8	LPL *	rs7816032	19929380	T	C	0.1575790	-0.0407548	0.0034574	2.8E-35
8	LPL *	rs139001474	19931094	A	T	0.1615630	-0.0412566	0.0034340	1.6E-36
8	LPL *	rs149764042	19931164	C	G	0.0688274	-0.0661864	0.0050255	4.4E-44
8	LPL *	rs4592053	19931255	G	A	0.1619530	-0.0411238	0.0034316	2.0E-36
8	LPL *	rs150331294	19932487	A	T	0.1570060	-0.0407276	0.0034676	3.9E-35
8	LPL *	rs182893294	19933207	C	T	0.0135247	-0.0667752	0.0109591	4.4E-10
8	LPL *	rs9694336	19933560	T	C	0.1501230	-0.0424406	0.0035427	1.5E-36
8	LPL *	rs145353248	19933835	T	C	0.1500250	-0.0425783	0.0035429	9.5E-37
8	LPL	rs3779787	19940405	T	G	0.1576420	-0.0398841	0.0034743	6.0E-34
8	LPL	rs1534649	19942130	T	G	0.1575550	-0.0416153	0.0034729	1.2E-36
8	LPL	rs112127208	19944019	G	T	0.1561400	-0.0417555	0.0034808	1.5E-36
8	LPL	rs10104051	19944891	T	C	0.1563510	-0.0417506	0.0034791	1.2E-36
8	LPL	rs3779788	19945582	T	C	0.1554220	-0.0417129	0.0034877	3.6E-36
8	LPL	rs56321069	19946485	A	T	0.1547450	-0.0429202	0.0035025	4.9E-38
8	LPL	rs8176337	19949160	G	C	0.1540650	-0.0440357	0.0035264	3.2E-39
8	LPL	rs74304285	19950519	A	G	0.1525490	-0.0446905	0.0035671	1.0E-39
8	LPL	rs113023641	19950620	A	G	0.1524780	-0.0447270	0.0035688	9.2E-40
8	LPL	rs73667472	19952184	C	T	0.0605676	-0.0706857	0.0053429	5.5E-45
8	LPL	rs343	19953276	A	C	0.1498180	-0.0192541	0.0036051	3.4E-08
8	LPL	rs249	19953495	C	T	0.0610371	-0.0734106	0.0053127	2.6E-48
8	LPL	rs250	19953512	ATG	A	0.1533810	-0.0195677	0.0035727	1.3E-08
8	LPL	rs254	19954386	G	C	0.2187150	-0.0395087	0.0030939	3.8E-41
8	LPL	rs255	19954390	C	T	0.2187290	-0.0395674	0.0030940	2.9E-41
8	LPL	rs256	19954456	T	C	0.2194130	-0.0398650	0.0030857	4.3E-42
8	LPL	rs263	19955301	T	C	0.2209060	-0.0403293	0.0030535	1.2E-43
8	LPL	rs264	19955669	A	G	0.2104240	-0.0368160	0.0030974	2.3E-35
8	LPL	rs269	19956156	G	T	0.2200390	-0.0421646	0.0030754	1.4E-46
8	LPL	rs271	19956191	A	G	0.2193780	-0.0422078	0.0030780	1.3E-46
8	LPL	chr8:19956458_G_GT	19956458	GT	G	0.2161000	-0.0419206	0.0031118	1.0E-44
8	LPL	rs285	19957678	T	C	0.3525480	-0.0344099	0.0027018	1.1E-40
8	LPL	rs287	19958045	G	A	0.2042800	-0.0541790	0.0031283	1.1E-71
8	LPL	rs289	19958108	C	T	0.2041810	-0.0544341	0.0031256	2.0E-72
8	LPL	rs291	19958341	C	T	0.2051660	-0.0547079	0.0031199	1.2E-73
8	LPL	chr8:19958567_T_TA	19958567	TA	T	0.2043010	-0.0536853	0.0031279	1.3E-70
8	LPL	rs295	19958727	C	A	0.2054360	-0.0545165	0.0031173	2.5E-73
8	LPL	rs297	19958860	C	T	0.2041710	-0.0544108	0.0031256	2.3E-72
8	LPL	rs301	19959423	C	T	0.2039720	-0.0549728	0.0031290	1.3E-73
8	LPL	rs304	19959850	G	T	0.1985890	-0.0544245	0.0031826	1.3E-69
8	LPL	rs305	19959890	G	A	0.2032610	-0.0549152	0.0031348	3.1E-73
8	LPL	rs308	19959965	G	T	0.0805049	-0.0779361	0.0046373	3.3E-69
8	LPL	rs314	19960531	A	G	0.2041180	-0.0548933	0.0031290	1.9E-73
8	LPL	rs117026536	19961262	T	G	0.1048750	-0.0807264	0.0041151	1.0E-92
8	LPL	rs320	19961566	G	T	0.2044830	-0.0546517	0.0031238	5.9E-73
8	LPL	rs322	19961706	C	A	0.2047410	-0.0543413	0.0031286	5.0E-72
8	LPL	rs325	19961817	C	T	0.1042730	-0.0822145	0.0041203	1.1E-95
8	LPL	rs326	19961928	G	A	0.2046450	-0.0546762	0.0031226	4.1E-73
8	LPL	rs327	19962025	G	T	0.2048530	-0.0545550	0.0031250	1.0E-72
8	LPL	rs328	19962213	G	C	0.1042510	-0.0821410	0.0041209	1.4E-95
8	LPL	rs331	19962894	A	G	0.2030430	-0.0551356	0.0031305	9.4E-74
8	LPL	rs12679834	19962922	C	T	0.1042340	-0.0823291	0.0041215	5.7E-96
8	LPL	rs117199990	19963405	T	C	0.1019510	-0.0825909	0.0041694	2.3E-94
8	LPL	rs145391587	19963422	C	A	0.1009990	-0.0832700	0.0041892	4.1E-95
8	LPL	rs75278536	19963914	G	T	0.1038890	-0.0822810	0.0041277	1.3E-95
8	LPL	rs146265243	19963956	G	GT	0.1039090	-0.0823091	0.0041282	1.2E-95
8	LPL	rs77069344	19964271	G	T	0.1038890	-0.0822810	0.0041277	1.3E-95

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL	rs11570891	19965299	T	C	0.1041590	-0.0822167	0.0041230	1.2E-95
8	LPL	rs3208305	19966137	T	A	0.1972140	-0.0556919	0.0031743	2.5E-73
8	LPL	rs1803924	19966163	T	C	0.1041640	-0.0822273	0.0041229	1.2E-95
8	LPL	rs3735964	19966534	A	C	0.1042140	-0.0821069	0.0041213	1.8E-95
8	LPL	rs13702	19966981	C	T	0.2012010	-0.0555946	0.0031425	2.6E-74
8	LPL	rs1059611	19967052	C	T	0.1042370	-0.0820085	0.0041208	2.8E-95
8	LPL	rs10645926	19967115	CTT	C	0.1042000	-0.0820737	0.0041215	2.0E-95
8	LPL	rs15285	19967156	T	C	0.2006870	-0.0559683	0.0031441	4.5E-75
8	LPL *	rs3916027	19967357	A	G	0.2006230	-0.0559599	0.0031451	5.9E-75
8	LPL *	rs77150190	19968791	C	G	0.0954420	-0.0812301	0.0042837	6.8E-86
8	LPL *	rs77729186	19968807	G	A	0.0954420	-0.0812301	0.0042837	6.8E-86
8	LPL *	rs2197089	19968862	A	G	0.3459050	-0.0338624	0.0026522	1.5E-39
8	LPL *	rs79108221	19969190	T	C	0.0953812	-0.0811280	0.0042846	1.1E-85
8	LPL *	rs1563590475	19969589	A	ACTT	0.0806788	-0.0781302	0.0046766	2.3E-67
8	LPL *	rs10105606	19970337	A	C	0.2003820	-0.0558360	0.0031455	1.4E-74
8	LPL *	rs1569209	19972659	G	T	0.0218086	-0.0768936	0.0086294	1.4E-19
8	LPL *	rs1011685	19973258	T	C	0.1032090	-0.0818853	0.0041396	3.5E-94
8	LPL *	rs10096633	19973410	T	C	0.1033250	-0.0819098	0.0041375	2.3E-94
8	LPL *	rs17482753	19975135	T	G	0.1027380	-0.0819016	0.0041484	1.2E-93
8	LPL *	rs78963197	19979135	C	T	0.0995264	-0.0789395	0.0042250	5.0E-84
8	LPL *	rs74855321	19979473	T	C	0.1018030	-0.0814320	0.0041675	3.2E-92
8	LPL *	rs4464984	19980958	T	C	0.1963080	-0.0555122	0.0031818	1.9E-72
8	LPL *	rs58946909	19982830	A	G	0.1026030	-0.0814091	0.0041547	2.7E-92
8	LPL *	rs75551077	19982897	C	G	0.1026640	-0.0813355	0.0041535	3.3E-92
8	LPL *	rs1554519534	19985625	CA	C	0.0565447	-0.0834115	0.0055788	2.2E-53
8	LPL *	rs17091891	19985660	C	T	0.0926301	-0.0817876	0.0043760	4.4E-84
8	LPL *	rs17410914	19985951	A	C	0.0999581	-0.0827443	0.0042031	1.1E-93
8	LPL *	rs117227752	19986350	A	G	0.1027900	-0.0823095	0.0041479	9.7E-95
8	LPL *	rs59147390	19986368	C	T	0.1027880	-0.0823103	0.0041479	9.6E-95
8	LPL *	rs184371102	19986419	T	G	0.0790396	-0.0778005	0.0046752	3.5E-68
8	LPL *	rs12678919	19986711	G	A	0.1030880	-0.0818909	0.0041418	3.5E-94
8	LPL *	rs7819706	19986904	G	A	0.1026040	-0.0823811	0.0041530	9.6E-95
8	LPL *	rs115129770	19986928	G	C	0.1026040	-0.0823811	0.0041530	9.6E-95
8	LPL *	rs149670831	19986936	C	CT	0.1026040	-0.0823811	0.0041530	9.6E-95
8	LPL *	rs7841189	19987865	T	C	0.1030540	-0.0822763	0.0041471	2.4E-94
8	LPL *	rs78458743	19988803	G	T	0.1027100	-0.0822759	0.0041508	1.5E-94
8	LPL *	rs114566157	19988978	G	C	0.1027100	-0.0822759	0.0041508	1.5E-94
8	LPL *	rs139894713	19989069	A	C	0.0217933	-0.0777694	0.0086314	6.0E-20
8	LPL *	rs12682115	19989549	A	G	0.1027100	-0.0822759	0.0041508	1.5E-94
8	LPL *	rs78013771	19989712	C	T	0.1027100	-0.0822759	0.0041508	1.5E-94
8	LPL *	rs76496571	19989930	A	C	0.1027640	-0.0824765	0.0041497	4.7E-95
8	LPL *	rs10503669	19990179	A	C	0.1028450	-0.0824076	0.0041446	4.6E-95
8	LPL *	rs17410962	19990569	A	G	0.1027690	-0.0824450	0.0041492	5.4E-95
8	LPL *	rs117604010	19990885	A	G	0.0794234	-0.0782112	0.0046637	4.5E-69
8	LPL *	rs17489185	19990988	C	G	0.1027700	-0.0824493	0.0041492	5.3E-95
8	LPL *	rs17410983	19991182	T	C	0.1027720	-0.0824434	0.0041492	5.5E-95
8	LPL *	rs17489226	19991367	T	A	0.1027730	-0.0824413	0.0041492	5.5E-95
8	LPL *	rs17410996	19991761	G	T	0.1026790	-0.0823429	0.0041509	1.2E-94
8	LPL *	rs75801420	19992159	G	T	0.1027540	-0.0822668	0.0041512	1.5E-94
8	LPL *	rs17091905	19992246	A	G	0.1027600	-0.0824805	0.0041495	4.3E-95
8	LPL *	rs114964604	19992478	G	A	0.1018840	-0.0819900	0.0041695	3.4E-93
8	LPL *	rs73600084	19992481	C	T	0.1018840	-0.0819900	0.0041695	3.4E-93
8	LPL *	rs76975037	19993997	A	C	0.1027140	-0.0822182	0.0041510	2.3E-94
8	LPL *	rs17489268	19994534	A	T	0.2002380	-0.0554873	0.0031542	1.8E-73
8	LPL *	rs17411024	19994623	A	G	0.1025660	-0.0821627	0.0041541	3.0E-94
8	LPL *	rs17091909	19994645	T	G	0.1026870	-0.0821636	0.0041521	2.9E-94
8	LPL *	rs147729680	19994665	T	TTC	0.2003630	-0.0555528	0.0031534	1.1E-73
8	LPL *	rs17411031	19994799	G	C	0.2002740	-0.0555062	0.0031536	1.4E-73
8	LPL *	rs17411045	19994851	C	T	0.2001300	-0.0555513	0.0031557	1.2E-73
8	LPL *	rs17489282	19995007	T	C	0.2003110	-0.0555461	0.0031540	1.3E-73
8	LPL *	rs4922117	19995075	C	T	0.2002710	-0.0555116	0.0031536	1.3E-73
8	LPL *	rs1822200	19995318	T	G	0.2002710	-0.0555116	0.0031536	1.3E-73
8	LPL *	rs1372344	19995428	T	A	0.2002710	-0.0555116	0.0031536	1.3E-73
8	LPL *	rs1992442	19995878	C	A	0.2004070	-0.0554140	0.0031543	2.4E-73
8	LPL *	rs2410618	19995989	A	G	0.2002610	-0.0555512	0.0031538	1.0E-73
8	LPL *	rs1992443	19996076	A	G	0.2002610	-0.0555512	0.0031538	1.0E-73
8	LPL *	rs920588	19996756	T	C	0.2002800	-0.0556055	0.0031537	7.8E-74
8	LPL *	rs920589	19996850	T	G	0.2002590	-0.0555637	0.0031537	9.8E-74
8	LPL *	rs4425772	19996989	T	C	0.1996960	-0.0555275	0.0031579	2.2E-73
8	LPL *	rs4628269	19996998	T	C	0.1996960	-0.0555275	0.0031579	2.2E-73
8	LPL *	rs2410619	19997042	A	C	0.2002590	-0.0555637	0.0031537	9.8E-74
8	LPL *	rs4320561	19997126	A	C	0.2001000	-0.0553623	0.0031555	3.5E-73

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs2410620	19997149	T	C	0.2001000	-0.0553623	0.0031555	3.5E-73
8	LPL *	rs2410621	19997171	C	T	0.2001000	-0.0553623	0.0031555	3.5E-73
8	LPL *	rs2410623	19997378	G	A	0.2002730	-0.0555610	0.0031537	9.9E-74
8	LPL *	rs17411113	19997495	G	C	0.1027270	-0.0819642	0.0041523	9.1E-94
8	LPL *	rs79734126	19997519	T	C	0.0788984	-0.0778979	0.0046790	3.3E-68
8	LPL *	rs34564316	19997710	T	C	0.2003200	-0.0554458	0.0031565	1.8E-73
8	LPL *	rs17411126	19997761	C	T	0.2002850	-0.0555839	0.0031535	8.3E-74
8	LPL *	rs17411133	19997820	A	T	0.2003130	-0.0554883	0.0031532	1.4E-73
8	LPL *	rs17489373	19997833	A	G	0.2003220	-0.0554937	0.0031532	1.4E-73
8	LPL *	rs17411168	19998089	C	T	0.2005150	-0.0553288	0.0031497	1.8E-73
8	LPL *	rs34932218	19998150	G	A	0.2005610	-0.0553318	0.0031493	1.6E-73
8	LPL *	rs140426714	19998333	G	GTATTTT	0.1992290	-0.0552797	0.0031625	9.6E-73
8	LPL *	rs2165558	19998749	G	T	0.2204700	-0.0503879	0.0030882	3.1E-63
8	LPL *	rs4523270	19999028	C	T	0.2006140	-0.0552573	0.0031482	2.4E-73
8	LPL *	rs2103325	20000832	T	C	0.2002970	-0.0553348	0.0031490	1.6E-73
8	LPL *	rs1581675	20000988	A	T	0.2003040	-0.0553584	0.0031489	1.4E-73
8	LPL *	rs4490856	20001609	C	T	0.3535930	-0.0370605	0.0026582	2.6E-47
8	LPL *	rs2119690	20002028	A	G	0.2003840	-0.0553948	0.0031482	1.0E-73
8	LPL *	rs2165556	20002116	T	C	0.2003870	-0.0554150	0.0031481	9.2E-74
8	LPL *	rs12541912	20002280	C	G	0.2007840	-0.0552881	0.0031459	1.4E-73
8	LPL *	rs74869266	20002686	C	A	0.0218948	-0.0783910	0.0086093	2.1E-20
8	LPL *	rs79236614	20002949	G	C	0.1025340	-0.0818536	0.0041527	1.0E-93
8	LPL *	rs34818360	20003236	A	G	0.2001010	-0.0552928	0.0031500	2.5E-73
8	LPL *	rs4083261	20003715	C	T	0.2007870	-0.0554151	0.0031460	7.1E-74
8	LPL *	rs3844510	20003850	C	A	0.2004430	-0.0555577	0.0031478	5.1E-74
8	LPL *	rs2410625	20004709	T	C	0.2004200	-0.0555705	0.0031479	4.3E-74
8	LPL *	rs4644277	20005059	C	T	0.2004200	-0.0555705	0.0031479	4.3E-74
8	LPL *	rs4389957	20005235	A	G	0.3541680	-0.0358467	0.0026543	8.5E-45
8	LPL *	rs1441766	20005277	T	A	0.2020790	-0.0554034	0.0031449	4.8E-74
8	LPL *	rs1441764	20005513	T	C	0.2007870	-0.0554151	0.0031460	7.1E-74
8	LPL *	rs6586884	20005847	C	T	0.1026820	-0.0825598	0.0041510	3.4E-95
8	LPL *	rs6999813	20005960	A	T	0.1026820	-0.0825598	0.0041510	3.4E-95
8	LPL *	rs2119689	20005996	T	C	0.2004200	-0.0555705	0.0031479	4.3E-74
8	LPL *	chr8:20006328_G_GA	20006328	GA	G	0.1979580	-0.0564867	0.0031698	2.6E-75
8	LPL *	rs1441763	20007045	C	T	0.2004200	-0.0555705	0.0031479	4.3E-74
8	LPL *	rs1441762	20007176	A	G	0.2005900	-0.0556069	0.0031491	4.1E-74
8	LPL *	rs1441761	20007237	C	G	0.1997470	-0.0555275	0.0031535	1.4E-73
8	LPL *	rs1441760	20007238	T	C	0.1997470	-0.0555275	0.0031535	1.4E-73
8	LPL *	chr8:20007371_T_TAAA	20007371	TAAA	T	0.1933760	-0.0558405	0.0032127	1.1E-72
8	LPL *	rs2083637	20007664	G	A	0.2003590	-0.0555768	0.0031481	4.4E-74
8	LPL *	rs2083636	20007752	G	T	0.2008530	-0.0554608	0.0031456	5.7E-74
8	LPL *	rs77237194	20007944	T	A	0.1027190	-0.0825345	0.0041502	4.2E-95
8	LPL *	rs35495249	20007998	A	C	0.1992340	-0.0557849	0.0031577	3.1E-74
8	LPL *	rs894211	20008236	T	C	0.1993160	-0.0557738	0.0031569	3.7E-74
8	LPL *	rs894210	20008332	A	G	0.3555520	-0.0362972	0.0026510	5.6E-46
8	LPL *	rs765547	20008763	A	G	0.2004710	-0.0555888	0.0031475	4.7E-74
8	LPL *	rs765548	20009083	T	C	0.2004680	-0.0555986	0.0031476	4.4E-74
8	LPL *	rs765549	20009120	G	A	0.2007750	-0.0554212	0.0031465	8.9E-74
8	LPL *	rs1441758	20009367	T	A	0.2004680	-0.0555986	0.0031476	4.4E-74
8	LPL *	rs139547332	20009665	CT	C	0.0793428	-0.0784392	0.0046665	2.5E-69
8	LPL *	rs9644637	20009709	C	T	0.2004680	-0.0555986	0.0031476	4.4E-74
8	LPL *	rs9644638	20009889	T	C	0.2000350	-0.0555719	0.0031517	1.1E-73
8	LPL *	rs11986942	20009934	G	C	0.2007750	-0.0554212	0.0031465	8.9E-74
8	LPL *	rs34327087	20009983	T	G	0.2004050	-0.0555634	0.0031481	4.8E-74
8	LPL *	rs34345068	20010025	T	G	0.2004220	-0.0555566	0.0031478	5.3E-74
8	LPL *	rs2009493	20010342	A	G	0.2004730	-0.0555961	0.0031476	4.8E-74
8	LPL *	rs1837843	20010591	T	C	0.1965840	-0.0548322	0.0031729	3.3E-71
8	LPL *	rs1837842	20010779	C	T	0.2004730	-0.0555961	0.0031476	4.8E-74
8	LPL *	rs1441757	20010866	C	G	0.2004730	-0.0555961	0.0031476	4.8E-74
8	LPL *	rs1441755	20011377	C	T	0.2004730	-0.0555961	0.0031476	4.8E-74
8	LPL *	rs1441754	20011428	A	G	0.1996820	-0.0559707	0.0031551	8.9E-75
8	LPL *	rs4406409	20011460	C	T	0.1995060	-0.0547969	0.0031591	9.5E-72
8	LPL *	rs1441753	20011553	A	G	0.2004730	-0.0555961	0.0031476	4.8E-74
8	LPL *	rs4126104	20011855	T	G	0.2004730	-0.0555961	0.0031476	4.8E-74
8	LPL *	rs1919484	20012165	A	G	0.2004340	-0.0555507	0.0031480	5.9E-74
8	LPL *	rs35687633	20012476	G	A	0.2000970	-0.0556307	0.0031535	8.3E-74
8	LPL *	rs34942551	20012504	G	T	0.2001060	-0.0556396	0.0031536	8.0E-74
8	LPL *	rs34499461	20012516	C	G	0.1999640	-0.0556015	0.0031552	1.3E-73
8	LPL *	rs35369244	20012533	C	G	0.1999650	-0.0556004	0.0031553	1.3E-73
8	LPL *	rs35739466	20012576	A	G	0.1969350	-0.0546444	0.0031777	2.1E-70
8	LPL *	rs35617716	20012752	A	T	0.1974310	-0.0547016	0.0031675	7.5E-71
8	LPL *	rs35237252	20012760	A	C	0.1974880	-0.0546045	0.0031669	1.5E-70

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs1569213	20013224	A	G	0.1775440	-0.0515279	0.0033669	8.8E-57
8	LPL *	rs78810414	20013602	T	C	0.0846616	-0.0810357	0.0045467	3.5E-78
8	LPL *	rs1372343	20013809	T	C	0.1850600	-0.0519786	0.0032587	1.5E-61
8	LPL *	rs1372342	20013820	A	T	0.1850670	-0.0519848	0.0032586	1.4E-61
8	LPL *	rs1372341	20013821	A	T	0.1850670	-0.0519848	0.0032586	1.4E-61
8	LPL *	rs1372340	20013861	A	G	0.1818020	-0.0514594	0.0032826	8.6E-60
8	LPL *	rs2410627	20014002	C	T	0.1854220	-0.0521636	0.0032552	3.4E-62
8	LPL *	rs7461115	20014029	G	C	0.1854220	-0.0521636	0.0032552	3.4E-62
8	LPL *	rs2410628	20014118	T	C	0.1854030	-0.0519873	0.0032553	7.3E-62
8	LPL *	rs2410629	20014126	C	T	0.1855190	-0.0520103	0.0032538	6.1E-62
8	LPL *	rs2898495	20014381	G	A	0.1855050	-0.0520370	0.0032540	5.4E-62
8	LPL *	rs4593558	20014497	G	A	0.1855180	-0.0520234	0.0032538	5.9E-62
8	LPL *	rs6986010	20015269	C	T	0.1855090	-0.0520497	0.0032540	5.1E-62
8	LPL *	rs35465966	20016045	A	C	0.1851540	-0.0522013	0.0032571	2.4E-62
8	LPL *	rs34693282	20016055	G	A	0.1854130	-0.0520253	0.0032549	6.4E-62
8	LPL *	rs17489539	20016071	A	T	0.1852530	-0.0520653	0.0032568	5.6E-62
8	LPL *	rs4922118	20016634	T	C	0.1851970	-0.0524465	0.0032624	1.3E-62
8	LPL *	rs4922119	20016642	T	C	0.1851970	-0.0524465	0.0032624	1.3E-62
8	LPL *	rs4375019	20016987	A	T	0.1815580	-0.0513230	0.0032828	1.1E-59
8	LPL *	rs141287949	20017421	A	AAGAC	0.0851426	-0.0811078	0.0045293	6.2E-79
8	LPL *	rs4333617	20017493	G	A	0.1821460	-0.0509182	0.0032788	4.4E-59
8	LPL *	rs2410630	20017589	T	C	0.1822090	-0.0508405	0.0032787	6.7E-59
8	LPL *	rs6586886	20017897	A	G	0.1823120	-0.0508174	0.0032763	7.2E-59
8	LPL *	rs73208815	20018604	C	G	0.1821280	-0.0508966	0.0032768	6.5E-59
8	LPL *	rs28675909	20018723	T	A	0.0850812	-0.0813305	0.0045301	4.3E-79
8	LPL *	rs79198716	20018753	T	C	0.0852765	-0.0809835	0.0045248	9.3E-79
8	LPL *	chr8:20018790_G_GA	20018790	GA	G	0.1835530	-0.0506071	0.0032759	4.7E-58
8	LPL *	rs78300069	20019013	T	C	0.0857733	-0.0809570	0.0045108	4.1E-79
8	LPL *	rs76737188	20019083	C	G	0.0894961	-0.0810184	0.0044193	4.1E-82
8	LPL *	rs7016880	20019235	C	G	0.0895806	-0.0807590	0.0044168	8.5E-82
8	LPL *	rs7007609	20019286	C	T	0.0894961	-0.0810184	0.0044193	4.1E-82
8	LPL *	rs7007797	20019459	G	T	0.0894961	-0.0810184	0.0044193	4.1E-82
8	LPL *	rs7004149	20019697	G	A	0.0894961	-0.0810184	0.0044193	4.1E-82
8	LPL *	rs7004158	20019722	G	A	0.0894961	-0.0810184	0.0044193	4.1E-82
8	LPL *	rs6983430	20019742	C	G	0.0894961	-0.0810184	0.0044193	4.1E-82
8	LPL *	rs77219697	20019950	C	T	0.0894978	-0.0809904	0.0044198	4.6E-82
8	LPL *	rs12678603	20020221	T	C	0.0857921	-0.0810756	0.0045123	2.1E-79
8	LPL *	rs12678604	20020262	G	C	0.0857487	-0.0811037	0.0045123	2.1E-79
8	LPL *	rs1534650	20020643	C	T	0.3491830	-0.0353531	0.0026722	1.5E-44
8	LPL *	rs7013777	20020845	C	T	0.1867610	-0.0515695	0.0032470	2.6E-61
8	LPL *	rs4922120	20021087	G	A	0.3486010	-0.0348458	0.0026702	1.7E-43
8	LPL *	rs112994260	20021193	A	T	0.0894450	-0.0811608	0.0044219	2.6E-82
8	LPL *	rs142117848	20021359	A	C	0.0894460	-0.0811620	0.0044219	2.6E-82
8	LPL *	rs4335137	20021363	T	A	0.1877290	-0.0513781	0.0032399	4.8E-61
8	LPL *	rs1819092	20021566	C	T	0.1867570	-0.0516751	0.0032471	1.4E-61
8	LPL *	rs1819094	20021804	G	C	0.1833280	-0.0507792	0.0032718	5.1E-59
8	LPL *	rs75082673	20022298	A	G	0.0857022	-0.0811469	0.0045137	1.7E-79
8	LPL *	rs11989309	20022819	T	C	0.0893919	-0.0811205	0.0044231	2.9E-82
8	LPL *	rs75675187	20023215	T	C	0.0893794	-0.0811369	0.0044235	2.8E-82
8	LPL *	rs74511360	20023529	A	G	0.0856733	-0.0810215	0.0045148	3.1E-79
8	LPL *	rs78404258	20023547	G	A	0.0894472	-0.0809376	0.0044226	7.1E-82
8	LPL *	rs74615535	20023725	A	G	0.0893691	-0.0810485	0.0044240	4.3E-82
8	LPL *	rs60223219	20024290	G	A	0.0894173	-0.0810211	0.0044232	5.1E-82
8	LPL *	rs35048052	20024541	AT	A	0.3497720	-0.0349191	0.0026654	1.1E-43
8	LPL *	rs7816447	20025439	C	T	0.0880538	-0.0808076	0.0044614	2.4E-80
8	LPL *	rs1919487	20026019	A	T	0.1828190	-0.0509548	0.0032739	3.1E-59
8	LPL *	rs73208819	20026413	C	T	0.2242220	0.0149680	0.0030304	4.6E-08
8	LPL *	rs114650503	20026746	A	G	0.0856406	-0.0808926	0.0045157	5.2E-79
8	LPL *	rs9644639	20027436	G	C	0.0856078	-0.0810073	0.0045175	3.6E-79
8	LPL *	rs2410631	20028057	T	A	0.1842400	-0.0500623	0.0032633	1.8E-57
8	LPL *	rs2410632	20028146	A	G	0.1841190	-0.0500310	0.0032646	2.3E-57
8	LPL *	rs11984636	20028215	C	T	0.0862570	-0.0802143	0.0045061	8.4E-78
8	LPL *	rs11984698	20028423	C	T	0.0862000	-0.0801962	0.0045084	1.0E-77
8	LPL *	rs35147888	20028593	T	TG	0.1841780	-0.0500791	0.0032640	1.7E-57
8	LPL *	rs11995475	20029177	T	C	0.0861903	-0.0802383	0.0045083	9.0E-78
8	LPL *	rs75469215	20029651	T	A	0.0856193	-0.0789450	0.0045303	1.4E-74
8	LPL *	rs4543558	20030818	G	C	0.1840760	-0.0504058	0.0032675	3.5E-58
8	LPL *	rs2178296	20031614	T	G	0.1675470	-0.0515469	0.0033805	1.2E-56
8	LPL *	rs78358410	20031888	G	T	0.1000320	-0.0773413	0.0042452	9.0E-81
8	LPL *	rs10103634	20033101	A	G	0.2496630	-0.0345681	0.0029232	3.3E-36
8	LPL *	rs139315015	20035786	G	A	0.1137450	-0.0611770	0.0039831	8.8E-59
8	LPL *	rs28841897	20036993	C	T	0.3374030	-0.0349563	0.0026905	2.4E-42

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs149001621	20039893	T	C	0.0109157	0.0749414	0.0122316	1.5E-10
8	LPL *	rs4244457	20041535	T	C	0.3276280	-0.0356494	0.0026885	6.8E-44
8	LPL *	rs76259755	20041650	C	T	0.1132310	-0.0624981	0.0039848	2.4E-61
8	LPL *	rs7826306	20043160	C	G	0.3298920	-0.0345560	0.0026885	1.5E-41
8	LPL *	rs6993414	20045407	G	A	0.1140670	-0.0627219	0.0039714	2.6E-62
8	LPL *	rs74983646	20045739	A	G	0.0982015	-0.0594630	0.0042507	1.7E-49
8	LPL *	rs78299715	20048393	G	C	0.0487096	-0.0314263	0.0058735	1.4E-08
8	LPL *	rs118099376	20048449	A	G	0.0168599	-0.0747314	0.0098201	9.0E-15
8	LPL *	rs11991231	20050401	C	T	0.1139230	-0.0626079	0.0039753	8.2E-62
8	LPL *	rs66462329	20054549	A	G	0.2420340	-0.0363372	0.0029543	5.4E-39
8	LPL *	rs115849089	20054859	A	G	0.1104220	-0.0608189	0.0040298	3.4E-57
8	LPL *	rs4585763	20055743	T	A	0.3273550	-0.0355863	0.0027045	1.2E-43
8	SLC18A1 *	rs6586891	20057087	A	C	0.3231100	-0.0344552	0.0027148	2.0E-40
8	SLC18A1 *	rs10104610	20058043	C	G	0.2424560	-0.0364733	0.0029523	2.4E-39
8	SLC18A1 *	rs66778572	20058609	A	G	0.2415050	-0.0361408	0.0029586	1.6E-38
8	SLC18A1 *	rs4128744	20062144	T	C	0.1116190	-0.0607992	0.0040126	8.6E-58
8	SLC18A1 *	rs4637851	20065099	A	G	0.3423740	-0.0356659	0.0027032	1.4E-43
8	SLC18A1 *	rs6999158	20070502	A	T	0.2641310	-0.0368190	0.0029049	4.5E-41
8	SLC18A1 *	rs10106652	20070649	A	G	0.2626840	-0.0369387	0.0029105	2.9E-41
8	SLC18A1 *	rs9644568	20071071	A	G	0.1128480	-0.0604965	0.0039811	2.4E-58
8	SLC18A1 *	rs34351848	20071686	T	TC	0.2618460	-0.0376698	0.0029331	4.3E-42
8	SLC18A1 *	rs13281248	20077573	A	G	0.0554087	-0.0768615	0.0055927	7.2E-48
8	SLC18A1 *	rs13257289	20077715	C	T	0.0566277	-0.0750702	0.0055547	4.8E-46
8	TRIB1 *	rs6999569	125463528	G	A	0.1451880	-0.0230675	0.0036159	1.6E-10
8	TRIB1 *	rs2980856	125464137	G	C	0.1449220	-0.0228630	0.0036151	2.4E-10
8	TRIB1 *	rs2954017	125464631	T	C	0.4340420	0.0264054	0.0025463	2.0E-26
8	TRIB1 *	rs2954018	125464911	C	T	0.2960190	0.0208683	0.0027689	1.5E-14
8	TRIB1 *	rs2980855	125465234	C	T	0.1449330	-0.0228868	0.0036148	2.4E-10
8	TRIB1 *	rs2980854	125465255	T	C	0.1449330	-0.0228868	0.0036148	2.4E-10
8	TRIB1 *	rs2954019	125465517	A	G	0.1447730	-0.0229842	0.0036171	2.0E-10
8	TRIB1 *	rs2001945	125465736	G	C	0.4341020	0.0263955	0.0025462	2.1E-26
8	TRIB1 *	rs2980853	125466108	A	C	0.4405150	0.0261260	0.0025430	6.9E-26
8	TRIB1 *	rs2001846	125466208	T	C	0.4341020	0.0263932	0.0025466	2.1E-26
8	TRIB1 *	rs2001845	125466402	A	G	0.2960460	0.0207890	0.0027694	2.0E-14
8	TRIB1 *	rs2001844	125466503	A	G	0.4405910	0.0260592	0.0025436	9.0E-26
8	TRIB1 *	rs6982636	125467073	G	A	0.4406950	0.0260383	0.0025431	9.5E-26
8	TRIB1 *	rs6982502	125467120	C	T	0.4341360	0.0263015	0.0025462	2.7E-26
8	TRIB1 *	rs2980886	125467846	G	A	0.4407330	0.0260347	0.0025430	1.0E-25
8	TRIB1 *	rs4871603	125468125	C	T	0.3027680	0.0201567	0.0027508	9.1E-14
8	TRIB1 *	rs2980882	125468458	A	G	0.4407790	0.0260449	0.0025433	9.6E-26
8	TRIB1 *	rs2980880	125468730	G	A	0.2962650	0.0207005	0.0027673	2.4E-14
8	TRIB1 *	rs2980879	125469233	A	T	0.2960950	0.0204609	0.0027658	4.4E-14
8	TRIB1 *	rs2980876	125469452	C	T	0.2963590	0.0206192	0.0027670	3.0E-14
8	TRIB1 *	rs2980875	125469505	A	G	0.4476630	0.0263446	0.0025425	2.2E-26
8	TRIB1 *	rs2954020	125469710	A	G	0.2964170	0.0208397	0.0027673	1.8E-14
8	TRIB1 *	rs2954021	125469835	A	G	0.4400020	0.0267464	0.0025438	3.7E-27
8	TRIB1 *	rs2954022	125470379	C	A	0.4464520	0.0264858	0.0025408	1.2E-26
8	TRIB1 *	rs79658059	125470680	T	TA	0.2965140	0.0207128	0.0027673	2.4E-14
8	TRIB1 *	rs28495284	125470681	G	A	0.3093020	0.0192220	0.0027859	1.6E-12
8	TRIB1 *	rs2954024	125470688	A	G	0.2965140	0.0207128	0.0027673	2.4E-14
8	TRIB1 *	rs2980870	125471598	A	G	0.3104800	0.0200227	0.0027678	1.5E-13
8	TRIB1 *	chr8:125471601_TAA_T	125471601	TAA	T	0.3017200	0.0200681	0.0027583	1.2E-13
8	TRIB1 *	rs4336630	125472034	T	G	0.3034660	0.0196596	0.0027479	2.9E-13
8	TRIB1 *	rs2954025	125472221	C	T	0.3034750	0.0196830	0.0027478	2.7E-13
8	TRIB1 *	rs2954026	125472284	T	G	0.2968800	0.0202708	0.0027652	6.9E-14
8	TRIB1 *	rs2980862	125472396	G	C	0.2968620	0.0203069	0.0027653	6.3E-14
8	TRIB1 *	rs13265432	125472467	A	G	0.1433980	0.0189085	0.0036044	4.9E-08
8	TRIB1 *	rs35575186	125472985	A	AT	0.3034780	0.0196836	0.0027478	2.7E-13
8	TRIB1 *	rs7828194	125473041	A	G	0.1433940	0.0189081	0.0036044	4.9E-08
8	TRIB1 *	rs2954027	125473052	T	A	0.4469220	0.0262199	0.0025407	3.0E-26
8	TRIB1 *	rs2954028	125473054	T	C	0.2968660	0.0203075	0.0027653	6.2E-14
8	TRIB1 *	rs2980860	125473095	A	G	0.4470110	0.0262120	0.0025410	3.2E-26
8	TRIB1 *	rs7828113	125473225	A	G	0.3035460	0.0198416	0.0027483	1.7E-13
8	TRIB1 *	rs7846466	125473289	T	C	0.2969910	0.0204278	0.0027661	4.8E-14
8	TRIB1 *	rs12545963	125473875	T	C	0.1434620	0.0188912	0.0036034	4.9E-08
8	TRIB1 *	chr8:125473988_G_GT	125473988	G	GT	0.3020550	0.0204691	0.0027711	4.4E-14
8	TRIB1 *	rs17321515	125474167	A	G	0.4470780	0.0262526	0.0025401	2.5E-26
8	TRIB1 *	rs12679184	125475269	T	C	0.1430040	0.0190869	0.0036093	3.7E-08
8	TRIB1 *	rs2980867	125475449	T	G	0.2969150	0.0203155	0.0027661	5.9E-14
8	TRIB1 *	rs2980868	125475993	C	T	0.4471930	0.0261239	0.0025412	5.3E-26
8	TRIB1 *	rs2980869	125476008	C	T	0.4473570	0.0261498	0.0025417	4.7E-26
8	TRIB1 *	rs59871348	125476465	ATTG	A	0.3041470	0.0198603	0.0027492	1.5E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	TRIB1 *	rs2980871	125476688	G	A	0.1264680	-0.0251178	0.0038140	1.0E-10
8	TRIB1 *	rs2954029	125478730	A	T	0.4469600	0.0264009	0.0025393	1.3E-26
8	TRIB1 *	rs5894757	125478769	T	TG	0.3037640	0.0196877	0.0027485	2.6E-13
8	TRIB1 *	rs2954030	125479062	T	C	0.3172590	0.0180317	0.0027178	2.0E-11
8	TRIB1 *	rs2954031	125479491	G	T	0.4610430	0.0251042	0.0025347	4.9E-24
8	TRIB1 *	rs56116731	125480684	C	CT	0.3009800	0.0204034	0.0027738	4.8E-14
8	TRIB1 *	rs2954032	125481150	A	G	0.2965580	0.0204100	0.0027685	4.1E-14
8	TRIB1 *	rs2954033	125481504	A	G	0.2972810	0.0203963	0.0027641	4.4E-14
8	TRIB1 *	rs4457349	125482075	G	A	0.4193970	-0.0148186	0.0025560	1.4E-09
8	TRIB1 *	rs12680798	125483251	G	C	0.0980129	-0.0265139	0.0042924	1.2E-09
8	TRIB1 *	rs10808546	125483576	T	C	0.1260700	-0.0247332	0.0038044	1.2E-10
8	TRIB1 *	rs35309034	125486023	A	C	0.1525680	0.0193258	0.0035112	1.1E-08
8	TRIB1 *	rs2980859	125487187	C	G	0.2823990	0.0221879	0.0028130	3.6E-16
8	TRIB1 *	rs4351435	125487636	G	A	0.2823960	0.0221616	0.0028131	3.9E-16
8	TRIB1 *	rs28601761	125487789	G	C	0.1513000	-0.0235498	0.0035329	5.9E-12
8	TRIB1 *	rs8180991	125488108	G	C	0.1549750	0.0186258	0.0034816	2.7E-08
8	TRIB1 *	rs2980858	125488935	T	C	0.2828540	0.0219699	0.0028115	6.7E-16
8	TRIB1 *	rs12677676	125490284	G	A	0.1547200	0.0186195	0.0034861	2.7E-08
8	TRIB1 *	rs55921265	125491673	A	G	0.1547210	0.0186099	0.0034861	2.7E-08
8	TRIB1 *	rs71940472	125492114	C	ACCACC	0.1532900	0.0186331	0.0035041	4.0E-08
8	TRIB1 *	rs13252684	125492119	A	G	0.1407360	0.0205486	0.0036706	8.7E-09
8	TRIB1 *	rs13252187	125492126	T	C	0.1371210	0.0216181	0.0037240	3.4E-09
8	TRIB1 *	rs13252202	125492129	T	C	0.1371210	0.0216181	0.0037240	3.4E-09
8	TRIB1 *	rs34087092	125492520	A	G	0.1547200	0.0186145	0.0034861	2.9E-08
8	TRIB1 *	rs75998532	125493463	C	T	0.4039680	-0.0153068	0.0025758	7.6E-10
8	TRIB1 *	rs112875651	125494452	A	G	0.1302820	-0.0230837	0.0037605	8.4E-10
8	TRIB1 *	rs2980888	125495066	T	C	0.2804970	0.0231049	0.0028128	2.4E-17
8	TRIB1 *	rs2954038	125495147	C	A	0.2806730	0.0232936	0.0028116	1.3E-17
8	TRIB1 *	rs6987904	125495783	T	C	0.4030060	-0.0149138	0.0025933	2.7E-09
9	ABCA1	rs2740488	104899461	C	A	0.2309550	-0.0183702	0.0029994	3.2E-10
9	ABCA1	rs1883025	104902020	T	C	0.2334780	-0.0186503	0.0029809	1.1E-10
9	ABCA1	rs2575876	104903458	A	G	0.2315460	-0.0189854	0.0029887	4.5E-11
9	PTPN3	rs149557654	109434560	A	G	0.2010320	-0.0175854	0.0031772	6.9E-09
9	PTPN3	rs61543659	109434691	G	A	0.2659220	-0.0155086	0.0028860	1.5E-08
9	PTPN3	rs17201500	109434773	A	G	0.2012170	-0.0177433	0.0031747	4.8E-09
9	PTPN3	rs75992442	109434977	G	A	0.2012180	-0.0177406	0.0031746	4.8E-09
9	PTPN3	rs16914135	109435232	C	A	0.2660910	-0.0155465	0.0028846	1.4E-08
9	PTPN3	rs75714696	109435291	C	G	0.2013070	-0.0176681	0.0031742	5.6E-09
9	PTPN3	rs7044766	109435739	T	C	0.2661350	-0.0155084	0.0028850	1.4E-08
9	PTPN3	rs56208012	109436498	T	A	0.2661450	-0.0155028	0.0028850	1.4E-08
9	PTPN3	rs112194983	109437194	T	C	0.2015640	-0.0174779	0.0031724	7.1E-09
9	PTPN3	rs17793718	109437226	A	G	0.2014990	-0.0175255	0.0031731	6.7E-09
9	PTPN3	rs17201542	109437914	C	T	0.2017450	-0.0175067	0.0031717	6.4E-09
9	PTPN3	rs1541090	109451227	T	A	0.3092650	-0.0140305	0.0027413	3.0E-08
9	PTPN3	rs1541091	109451408	A	G	0.3112150	-0.0141153	0.0027311	2.7E-08
9	PTPN3	rs74479508	109464472	C	G	0.3099500	-0.0146105	0.0027508	1.7E-08
9	PTPN3	rs111960097	109468618	A	G	0.3146770	-0.0148428	0.0027434	1.2E-08
9	PTPN3	rs57707037	109473833	C	T	0.2441980	-0.0180772	0.0029893	1.1E-10
9	PTPN3	rs60227798	109473873	T	C	0.2442300	-0.0181476	0.0029884	9.3E-11
9	PTPN3	rs76298084	109474452	T	G	0.2433020	-0.0181329	0.0029951	1.1E-10
9	PTPN3	rs7046039	109474599	C	T	0.2946710	-0.0151624	0.0028188	1.1E-08
9	PTPN3	rs58272963	109474628	A	G	0.2441840	-0.0182267	0.0029886	7.8E-11
9	PTPN3	rs59668107	109474718	A	G	0.2441810	-0.0182175	0.0029885	7.9E-11
9	PTPN3	rs78579422	109475873	T	C	0.2432930	-0.0184276	0.0029961	6.9E-11
9	PTPN3	rs75862441	109477363	T	C	0.2290230	-0.0182926	0.0030638	1.1E-10
9	PTPN3	rs41529151	109478114	G	C	0.2289020	-0.0187479	0.0030626	4.1E-11
9	PTPN3	rs56279802	109478850	T	C	0.2549820	-0.0173483	0.0029490	1.9E-10
9	PTPN3	rs77824033	109478856	C	T	0.2293690	-0.0186253	0.0030580	4.5E-11
9	PTPN3	rs796238584	109479010	TGTC	T	0.2557120	-0.0174077	0.0029522	1.8E-10
9	PTPN3	rs55727942	109479011	G	T	0.2546740	-0.0172214	0.0029605	3.1E-10
9	PTPN3	rs55824262	109479013	C	T	0.2547800	-0.0170978	0.0029594	4.0E-10
9	PTPN3	rs12376215	109479090	A	T	0.2547140	-0.0175325	0.0029505	1.2E-10
9	PTPN3	rs117969049	109480282	T	C	0.2295530	-0.0182903	0.0030545	9.8E-11
9	PTPN3	rs17793873	109482041	T	C	0.2299660	-0.0180246	0.0030514	1.7E-10
9	PTPN3	rs74928072	109482095	A	G	0.2299700	-0.0180778	0.0030511	1.6E-10
9	PTPN3	rs75024825	109482136	T	C	0.2297490	-0.0181233	0.0030499	1.5E-10
9	PTPN3	rs75113691	109483493	C	G	0.2308210	-0.0178885	0.0030419	2.2E-10
9	PTPN3	rs78919659	109483714	T	C	0.2305340	-0.0179464	0.0030424	2.0E-10
9	PTPN3	rs57906233	109485510	GA	G	0.2315030	-0.0170124	0.0030397	1.1E-09
9	PTPN3	rs78424787	109485849	A	C	0.2319910	-0.0170287	0.0030321	9.7E-10
9	PTPN3	rs59380239	109488319	T	C	0.2500170	-0.0160518	0.0029199	2.5E-09
9	PTPN3	rs139465238	109494073	A	AAGG	0.2500510	-0.0164549	0.0029181	1.1E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
9	PTPN3	rs75577555	109495675	T	C	0.2502460	-0.0165761	0.0029168	8.4E-10
9	PTPN3	rs184172568	109497966	T	C	0.2500140	-0.0161709	0.0029237	2.1E-09
9	PTPN3 *	rs117533884	109499788	G	C	0.2502600	-0.0165472	0.0029158	8.7E-10
9	PTPN3 *	rs78042633	109502844	T	C	0.2502370	-0.0163912	0.0029160	1.2E-09
9	PTPN3 *	rs17793891	109502949	G	A	0.2506270	-0.0164335	0.0029133	1.2E-09
9	MIR3927 *	rs140269699	109506584	C	CTCTT	0.2448320	-0.0173503	0.0029519	1.9E-10
9	MIR3927 *	rs10123707	109508041	C	G	0.2755620	-0.0159675	0.0028286	1.1E-09
9	MIR3927 *	rs61358126	109511453	G	A	0.2501100	-0.0163582	0.0029175	1.4E-09
9	MIR3927 *	rs2150260	109511914	G	A	0.2821230	-0.0153045	0.0028056	4.5E-09
9	MIR3927 *	rs79437785	109512085	C	T	0.2500620	-0.0163175	0.0029180	1.5E-09
9	MIR3927 *	rs6477708	109513462	G	A	0.2820390	-0.0152649	0.0028075	5.0E-09
9	MIR3927 *	rs7341726	109513495	G	C	0.2820300	-0.0152740	0.0028075	4.9E-09
9	MIR3927 *	rs1411682	109514077	T	C	0.2820400	-0.0152853	0.0028075	4.8E-09
9	MIR3927 *	rs10124300	109515460	C	A	0.2819590	-0.0150656	0.0028065	7.0E-09
9	MIR3927 *	rs77218860	109517046	A	G	0.2470440	-0.0160559	0.0029349	3.1E-09
9	MIR3927 *	rs76636909	109518424	T	C	0.2494350	-0.0157813	0.0029192	4.7E-09
9	MIR3927 *	rs139346903	109520059	A	T	0.2494380	-0.0157795	0.0029192	4.8E-09
9	MIR3927 *	rs80070092	109521917	T	C	0.2494380	-0.0157795	0.0029192	4.8E-09
9	MIR3927 *	rs117827315	109532784	G	T	0.2504930	-0.0156326	0.0029200	6.7E-09
9	MIR3927 *	rs117527665	109533559	A	C	0.2492670	-0.0159552	0.0029223	3.4E-09
9	MIR3927 *	chr9:109535507_C_CT	109535507	CT	C	0.2461470	-0.0150817	0.0029641	3.5E-08
9	MIR3927 *	rs77274786	109536366	G	A	0.2494470	-0.0161228	0.0029326	2.8E-09
9	MIR3927 *	rs17201835	109541578	G	A	0.2526080	-0.0160858	0.0029237	1.9E-09
9	MIR3927 *	chr9:109544207_GT_G	109544207	G	GT	0.2767830	-0.0154353	0.0028582	4.4E-09
9	MIR3927 *	rs1571642	109548492	A	G	0.2559410	-0.0159888	0.0029139	2.7E-09
9	MIR3927 *	rs75803161	109558741	A	T	0.2475220	-0.0164223	0.0029499	1.3E-09
9	MIR3927 *	rs139221760	109560788	CT	C	0.2497520	-0.0169390	0.0029455	5.6E-10
9	MIR3927 *	rs7858161	109562771	A	G	0.2547770	-0.0161103	0.0029219	2.0E-09
9	MIR3927 *	rs75001090	109565034	C	A	0.2502160	-0.0168863	0.0029455	5.7E-10
9	MIR3927 *	rs7849221	109567429	A	G	0.2483490	-0.0168657	0.0029529	5.3E-10
9	MIR3927 *	rs7861875	109570956	G	A	0.2175970	-0.0164839	0.0030863	4.1E-09
9	MIR3927 *	rs150040590	109573935	T	C	0.1915000	-0.0183900	0.0032324	4.8E-10
9	MIR3927 *	rs117103218	109574154	A	G	0.1889540	-0.0183078	0.0032458	6.8E-10
9	PALM2 *	rs200290358	109577536	A	AT	0.1912630	-0.0183747	0.0032293	7.5E-10
9	PALM2 *	rs200745414	109577539	C	A	0.1922760	-0.0183308	0.0032202	6.9E-10
9	PALM2 *	chr9:109578848_A_AT	109578848	AT	A	0.2208210	-0.0163620	0.0030560	7.7E-09
9	PALM2 *	rs76508340	109580420	T	C	0.1781620	-0.0174481	0.0033308	7.7E-09
9	PALM2 *	rs78815286	109582984	T	G	0.1927530	-0.0179134	0.0032117	1.3E-09
9	PALM2 *	rs78864591	109583284	T	C	0.1927510	-0.0179160	0.0032117	1.3E-09
9	PALM2 *	rs5899855	109586400	CTTAGCA	C	0.2208790	-0.0164085	0.0030512	5.5E-09
9	PALM2 *	rs10979952	109587348	C	A	0.2208560	-0.0165676	0.0030504	4.2E-09
9	PALM2 *	rs17202062	109591436	C	G	0.1907900	-0.0186351	0.0032252	3.4E-10
9	PALM2 *	rs17794184	109592937	C	A	0.1906420	-0.0186668	0.0032242	3.6E-10
9	PALM2 *	rs10125565	109593113	T	G	0.2179220	-0.0171406	0.0030634	1.6E-09
9	PALM2 *	rs58105812	109593130	A	T	0.1906390	-0.0186796	0.0032242	3.5E-10
9	PALM2 *	rs78927344	109593586	G	A	0.1906480	-0.0186578	0.0032244	3.7E-10
9	PALM2 *	rs10979958	109595732	A	G	0.1943150	-0.0175496	0.0032105	2.4E-09
9	PALM2 *	rs75235286	109596281	T	C	0.1955080	-0.0176811	0.0031980	1.8E-09
9	PALM2 *	rs137989413	109598306	A	C	0.1953200	-0.0177268	0.0031994	1.8E-09
10	AKR1C4	rs74827952	5203233	A	G	0.0888187	-0.0267267	0.0044878	1.4E-09
10	AKR1C4	rs76669111	5203817	T	G	0.1001890	-0.0234868	0.0042141	1.5E-08
10	AKR1C4	rs17134531	5204122	A	G	0.1003200	-0.0235140	0.0042089	1.3E-08
10	AKR1C4	rs77697233	5204162	T	C	0.1003190	-0.0235162	0.0042089	1.3E-08
10	AKR1C4	rs3039101	5204214	TGTA	T	0.1003600	-0.0235294	0.0042083	1.4E-08
10	AKR1C4	rs3039099	5204247	A	AAAAC	0.1003510	-0.0235947	0.0042088	1.2E-08
10	AKR1C4	rs10600924	5204790	C	CACAGAT	0.1002170	-0.0234276	0.0042110	1.5E-08
10	AKR1C4	rs17134533	5205135	A	G	0.1003600	-0.0236733	0.0042075	1.1E-08
10	AKR1C4	rs113775538	5205155	CT	C	0.1001890	-0.0235374	0.0042114	1.3E-08
10	AKR1C4	rs6601924	5205339	T	C	0.1003770	-0.0236203	0.0042068	1.2E-08
10	AKR1C4	rs3750572	5205413	C	T	0.1003770	-0.0236203	0.0042068	1.2E-08
10	AKR1C4	rs3750571	5205471	A	C	0.1003770	-0.0236203	0.0042068	1.2E-08
10	AKR1C4	rs3750569	5205567	G	A	0.1003770	-0.0236203	0.0042068	1.2E-08
10	AKR1C4	rs3750568	5205668	A	G	0.1003770	-0.0236203	0.0042068	1.2E-08
10	AKR1C4	rs3750567	5205671	A	G	0.1003770	-0.0236203	0.0042068	1.2E-08
10	AKR1C4	rs7921838	5205738	A	G	0.1003820	-0.0236278	0.0042067	1.2E-08
10	AKR1C4	rs3829125	5205821	G	C	0.1005110	-0.0238237	0.0042034	8.6E-09
10	AKR1C4	rs1931679	5208490	T	C	0.0990512	-0.0232100	0.0042347	2.4E-08
10	AKR1C4	rs7908297	5209739	A	G	0.1004080	-0.0236382	0.0042062	1.1E-08
10	AKR1C4	rs7909379	5209851	A	C	0.1003760	-0.0236896	0.0042067	1.0E-08
10	AKR1C4	rs7909380	5209852	T	C	0.1003760	-0.0236896	0.0042067	1.0E-08
10	AKR1C4	rs117310669	5210050	G	C	0.1003500	-0.0235829	0.0042074	1.3E-08
10	AKR1C4	rs4424574	5210114	T	G	0.1003500	-0.0235829	0.0042074	1.3E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	AKR1C4	rs7477230	5210768	T	C	0.1004920	-0.0236976	0.0042061	1.1E-08
10	AKR1C4	rs7477114	5210875	T	G	0.1003500	-0.0235829	0.0042074	1.3E-08
10	AKR1C4	rs7475279	5210903	C	A	0.1004080	-0.0236382	0.0042062	1.1E-08
10	AKR1C4	rs7475281	5210939	C	A	0.1004080	-0.0236382	0.0042062	1.1E-08
10	AKR1C4	rs117071142	5211396	G	T	0.1002450	-0.0236541	0.0042090	1.2E-08
10	AKR1C4	rs111481000	5211476	GTCA	G	0.1004120	-0.0236180	0.0042061	1.2E-08
10	AKR1C4	rs7078211	5211675	G	A	0.1004120	-0.0236180	0.0042061	1.2E-08
10	AKR1C4	rs6601927	5212183	G	A	0.1004290	-0.0235766	0.0042057	1.3E-08
10	AKR1C4	rs7897431	5212225	A	G	0.1004290	-0.0235766	0.0042057	1.3E-08
10	AKR1C4	rs4098025	5212857	C	A	0.0999887	-0.0235605	0.0042156	1.4E-08
10	AKR1C4	rs1831977	5212858	G	C	0.0999887	-0.0235605	0.0042156	1.4E-08
10	AKR1C4	rs1832007	5212884	G	A	0.1004180	-0.0231638	0.0042059	2.3E-08
10	AKR1C4	rs111648698	5213372	T	TCA	0.1004270	-0.0235820	0.0042058	1.2E-08
10	AKR1C4	rs148205663	5214017	A	ATATAT	0.1003370	-0.0236155	0.0042079	1.2E-08
10	AKR1C4	rs17134585	5214309	C	T	0.1017850	-0.0234993	0.0041875	1.1E-08
10	AKR1C4	rs59582332	5214373	TC	T	0.1006380	-0.0236338	0.0042078	9.7E-09
10	AKR1C4	rs17134588	5214534	A	G	0.1006140	-0.0236414	0.0042060	1.1E-08
10	AKR1C4	chr10:5214682_CTTT_C	5214682	C	CTTT	0.1005740	-0.0232281	0.0042049	2.1E-08
10	AKR1C4	rs148929884	5214779	TTC	T	0.1004320	-0.0235082	0.0042058	1.3E-08
10	AKR1C4	rs77503049	5214795	T	C	0.1005800	-0.0236333	0.0042056	1.1E-08
10	AKR1C4	rs76551580	5214871	C	T	0.1004320	-0.0235082	0.0042058	1.3E-08
10	AKR1C4	rs78585347	5215134	T	G	0.1003740	-0.0234528	0.0042070	1.5E-08
10	AKR1C4	rs75406471	5215684	A	G	0.1003780	-0.0235121	0.0042071	1.3E-08
10	AKR1C4	rs78686304	5215834	T	C	0.1003740	-0.0234528	0.0042070	1.5E-08
10	AKR1C4	rs7912751	5215978	T	C	0.1003740	-0.0234528	0.0042070	1.5E-08
10	AKR1C4	rs10586998	5216482	A	ATCTTT	0.1000240	-0.0234881	0.0042156	1.5E-08
10	AKR1C4	rs4881413	5216487	T	G	0.1000240	-0.0234881	0.0042156	1.5E-08
10	AKR1C4	rs17134589	5217078	C	G	0.1001860	-0.0234359	0.0042105	1.6E-08
10	AKR1C4	rs141745211	5218585	CAT	C	0.1003520	-0.0234055	0.0042075	1.6E-08
10	AKR1C4	rs17134592	5218719	G	C	0.1003520	-0.0234055	0.0042075	1.6E-08
10	AKR1C4	rs141695403	5218823	G	GTC	0.1003520	-0.0234055	0.0042075	1.6E-08
10	AKR1C4 *	rs75811842	5219138	G	A	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs76494948	5219148	T	C	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs11253048	5219196	G	A	0.1004620	-0.0235266	0.0042069	1.5E-08
10	AKR1C4 *	rs17134601	5219212	G	A	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs77353068	5219263	C	G	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs17134604	5219293	A	T	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs77896903	5219528	T	C	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs80264034	5219613	A	T	0.1003480	-0.0234419	0.0042076	1.6E-08
10	AKR1C4 *	rs74404998	5219720	G	A	0.1003490	-0.0234370	0.0042076	1.6E-08
10	AKR1C4 *	rs117849125	5219866	T	C	0.0999537	-0.0233753	0.0042155	1.7E-08
10	AKR1C4 *	rs117146235	5219867	G	A	0.0999537	-0.0233753	0.0042155	1.7E-08
10	AKR1C4 *	rs117488242	5219869	G	A	0.0999537	-0.0233753	0.0042155	1.7E-08
10	AKR1C4 *	rs17134607	5219947	A	G	0.1003510	-0.0234258	0.0042076	1.6E-08
10	AKR1C4 *	rs17134608	5220056	A	G	0.1003510	-0.0234258	0.0042076	1.6E-08
10	AKR1C4 *	rs79849481	5220133	A	G	0.1003510	-0.0234258	0.0042076	1.6E-08
10	AKR1C4 *	rs77355283	5220173	T	C	0.1003510	-0.0234258	0.0042076	1.6E-08
10	AKR1C4 *	rs79717793	5220304	A	G	0.1003520	-0.0234292	0.0042076	1.6E-08
10	AKR1C4 *	chr10:5220490_G_GT	5220490	GT	G	0.1001850	-0.0234651	0.0042105	1.6E-08
10	AKR1C4 *	rs78231592	5220527	C	G	0.1003520	-0.0234292	0.0042076	1.6E-08
10	AKR1C4 *	rs75529951	5220549	A	G	0.1003520	-0.0234292	0.0042076	1.6E-08
10	AKR1C4 *	rs140168704	5220815	T	C	0.1003540	-0.0234361	0.0042076	1.6E-08
10	AKR1C4 *	rs151163925	5220847	T	C	0.1003840	-0.0233993	0.0042070	1.7E-08
10	AKR1C4 *	rs143690051	5220859	T	C	0.1003840	-0.0233993	0.0042070	1.7E-08
10	AKR1C4 *	rs112455458	5220920	C	G	0.1003540	-0.0234361	0.0042076	1.6E-08
10	AKR1C4 *	rs111932715	5220978	C	G	0.1003540	-0.0234361	0.0042076	1.6E-08
10	AKR1C4 *	rs2151901	5221002	C	A	0.1003540	-0.0234361	0.0042076	1.6E-08
10	AKR1C4 *	rs17134610	5221060	T	G	0.1003550	-0.0234262	0.0042076	1.6E-08
10	AKR1C4 *	rs142122182	5221378	G	A	0.0970100	-0.0243869	0.0042822	7.6E-09
10	AKR1C4 *	rs75413156	5221531	A	C	0.0996966	-0.0235762	0.0042247	1.5E-08
10	AKR1C4 *	rs80011059	5221553	T	A	0.1003550	-0.0234262	0.0042076	1.6E-08
10	AKR1C4 *	rs17134617	5221739	A	C	0.1003550	-0.0234262	0.0042076	1.6E-08
10	AKR1C4 *	rs145211548	5221893	CA	C	0.1003510	-0.0234061	0.0042077	1.7E-08
10	AKR1C4 *	rs149977283	5223568	A	C	0.0998674	-0.0231983	0.0042242	2.3E-08
10	AKR1C4 *	rs138695384	5223859	G	A	0.1006060	-0.0232705	0.0042050	2.0E-08
10	AKR1C4 *	rs150754448	5224911	A	G	0.1003470	-0.0233733	0.0042078	1.8E-08
10	AKR1C4 *	rs140107293	5225228	G	A	0.1004060	-0.0234766	0.0042080	1.5E-08
10	AKR1C4 *	rs143431627	5228338	T	C	0.1004730	-0.0234179	0.0042087	1.7E-08
10	AKR1C4 *	rs7897822	5242594	A	G	0.1000720	-0.0235816	0.0042255	1.9E-08
10	NRBF2 *	rs67460150	63114009	G	GA	0.2434800	-0.0158483	0.0029884	1.8E-08
10	NRBF2 *	rs10995445	63114994	T	A	0.3161360	-0.0144264	0.0027363	1.9E-08
10	NRBF2 *	rs7903602	63115551	A	G	0.3862260	0.0223083	0.0026222	4.6E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	NRBF2 *	rs4414112	63115786	A	G	0.3858530	0.0227514	0.0026136	6.7E-20
10	NRBF2 *	rs4545434	63115985	C	T	0.3767950	0.0224902	0.0026230	1.9E-19
10	NRBF2 *	rs7084569	63116794	A	G	0.3151670	-0.0146968	0.0027347	1.0E-08
10	NRBF2 *	rs7084396	63116965	A	G	0.3856340	0.0227204	0.0026072	6.6E-20
10	NRBF2 *	rs35248047	63117160	A	AC	0.3890200	0.0225653	0.0026106	1.5E-19
10	NRBF2 *	rs10822138	63117400	G	A	0.3910620	0.0227665	0.0026226	7.8E-20
10	NRBF2 *	rs6479877	63118358	G	C	0.3160220	-0.0144888	0.0027123	1.5E-08
10	NRBF2 *	rs1396964	63118538	G	A	0.3887320	0.0231690	0.0025919	1.3E-20
10	NRBF2 *	rs6479878	63118657	A	G	0.3892290	0.0232232	0.0025937	1.0E-20
10	NRBF2 *	rs6479879	63118669	G	T	0.3892300	0.0232252	0.0025937	9.8E-21
10	NRBF2 *	rs6479880	63118671	A	T	0.3892300	0.0232252	0.0025937	9.8E-21
10	NRBF2 *	rs6479881	63118802	T	C	0.3886410	0.0231411	0.0025926	1.4E-20
10	NRBF2 *	rs10995447	63119761	A	G	0.3796060	0.0226096	0.0026075	1.1E-19
10	NRBF2 *	rs10761716	63122540	G	C	0.3172880	-0.0146814	0.0027144	9.5E-09
10	NRBF2 *	rs4746951	63123839	G	A	0.3796600	0.0226735	0.0026073	7.8E-20
10	NRBF2 *	rs61853335	63124977	T	C	0.3796480	0.0226477	0.0026073	8.6E-20
10	NRBF2 *	rs72824948	63126343	G	A	0.3796920	0.0226451	0.0026073	8.9E-20
10	NRBF2 *	rs10822143	63128096	T	C	0.3170870	-0.0146284	0.0027245	1.4E-08
10	NRBF2 *	rs4746974	63132292	T	G	0.3798450	0.0225079	0.0026041	1.3E-19
10	NRBF2	rs868798	63135250	G	A	0.3801850	0.0223156	0.0026016	2.2E-19
10	NRBF2	rs12416113	63136717	A	T	0.3800440	0.0223456	0.0026022	2.0E-19
10	NRBF2	rs61853336	63140115	A	G	0.3801900	0.0223708	0.0026015	1.8E-19
10	NRBF2	rs80082080	63142032	AT	A	0.2481700	-0.0169009	0.0029296	2.0E-09
10	NRBF2	rs7070052	63144054	A	G	0.3802260	0.0223032	0.0026009	2.3E-19
10	NRBF2	rs7073746	63144311	G	A	0.3149980	-0.0147544	0.0027183	9.0E-09
10	NRBF2	rs7916224	63144843	T	C	0.3893390	0.0226857	0.0025899	5.1E-20
10	NRBF2	rs4746994	63145564	A	T	0.3803330	0.0222500	0.0025990	2.5E-19
10	NRBF2	rs10733787	63147078	T	A	0.3894670	0.0226668	0.0025886	4.8E-20
10	NRBF2	chr10:63147321_AT_A	63147321	A	AT	0.3813380	0.0222005	0.0026161	4.4E-19
10	NRBF2	rs12240740	63147478	C	A	0.3894630	0.0226638	0.0025886	4.9E-20
10	NRBF2	rs11278263	63147821	T	GCTGTAG	0.3133070	-0.0145511	0.0027227	1.5E-08
10	NRBF2	rs12415984	63150528	A	G	0.3803620	0.0222255	0.0025984	2.7E-19
10	NRBF2	rs35751397	63154256	TA	T	0.3148060	-0.0146962	0.0027144	9.5E-09
10	NRBF2	rs13095	63154612	C	G	0.3148060	-0.0146962	0.0027144	9.5E-09
10	NRBF2	rs1160843	63154758	C	CATA	0.3147280	-0.0146074	0.0027155	1.2E-08
10	NRBF2 *	rs7897470	63156304	G	T	0.3669400	0.0213173	0.0026382	1.5E-17
10	NRBF2 *	rs1009984	63156709	T	G	0.3891040	0.0224254	0.0025890	1.2E-19
10	NRBF2 *	rs11814792	63157799	T	C	0.3790300	0.0223546	0.0026002	2.1E-19
10	NRBF2 *	rs10733788	63158105	T	C	0.3890680	0.0225557	0.0025891	7.5E-20
10	NRBF2 *	rs61853339	63158919	C	T	0.3794250	0.0222943	0.0025985	2.8E-19
10	NRBF2 *	rs12413415	63159751	C	T	0.3764650	0.0224266	0.0026042	2.0E-19
10	NRBF2 *	rs34132715	63160401	C	CTAAA	0.3786090	0.0222563	0.0026019	4.1E-19
10	JMJD1C *	rs11817689	63164457	C	T	0.3807920	0.0223792	0.0025976	2.1E-19
10	JMJD1C *	rs3072249	63165570	CCAT	C	0.3895080	0.0227861	0.0025881	3.9E-20
10	JMJD1C *	rs57618271	63165939	C	CTAAAG	0.3538450	-0.0147243	0.0026675	7.6E-09
10	JMJD1C *	rs4747045	63166722	T	C	0.3796400	0.0224962	0.0025984	1.4E-19
10	JMJD1C	rs1935	63168063	G	C	0.3114560	-0.0148802	0.0027233	5.3E-09
10	JMJD1C	rs57138498	63171287	G	GA	0.3297340	-0.0138595	0.0026822	4.4E-08
10	JMJD1C	rs1904296	63173019	C	G	0.3889630	0.0224100	0.0025932	1.3E-19
10	JMJD1C	rs4466712	63173508	C	G	0.3781050	0.0224378	0.0026002	1.7E-19
10	JMJD1C	chr10:63173739_G_GA	63173739	GA	G	0.3722590	0.0224546	0.0026246	3.8E-19
10	JMJD1C	rs35447916	63173832	CA	C	0.3137150	-0.0146535	0.0027175	7.9E-09
10	JMJD1C	rs10995453	63174571	T	C	0.3874240	0.0226517	0.0025914	6.4E-20
10	JMJD1C	rs10822145	63174788	T	C	0.3135080	-0.0146698	0.0027175	7.9E-09
10	JMJD1C	rs10995455	63176601	A	G	0.2436170	-0.0167866	0.0029432	1.8E-09
10	JMJD1C	rs907	63176919	A	G	0.3878550	0.0226304	0.0025944	6.8E-20
10	JMJD1C	rs10761721	63178644	T	G	0.3874240	0.0226355	0.0025910	6.8E-20
10	JMJD1C	rs72829170	63180529	G	A	0.3777510	0.0223665	0.0026004	2.7E-19
10	JMJD1C	rs10995459	63183050	A	G	0.3872690	0.0225920	0.0025915	9.3E-20
10	JMJD1C	rs56369591	63184054	A	AG	0.3865870	0.0224585	0.0025929	2.0E-19
10	JMJD1C	rs61853340	63184415	C	G	0.3730550	0.0225215	0.0026212	3.9E-19
10	JMJD1C	rs10740107	63184557	T	A	0.3776140	0.0219705	0.0026021	1.6E-18
10	JMJD1C	rs32111105	63185604	G	A	0.3875480	0.0226345	0.0025900	7.6E-20
10	JMJD1C	rs10733789	63188924	C	T	0.2439780	-0.0172280	0.0029429	9.2E-10
10	JMJD1C	rs10822146	63191707	A	G	0.3316730	-0.0138436	0.0026767	4.5E-08
10	JMJD1C	rs10761722	63195287	C	G	0.3874310	0.0226717	0.0025911	6.5E-20
10	JMJD1C	rs10761723	63195821	T	C	0.3133950	-0.0148083	0.0027183	6.1E-09
10	JMJD1C	rs61855465	63196847	T	A	0.3784040	0.0223631	0.0025970	2.5E-19
10	JMJD1C	rs10465990	63200776	A	G	0.3298470	-0.0140460	0.0026817	3.1E-08
10	JMJD1C	rs7099425	63200957	C	T	0.3787870	0.0222533	0.0025982	4.0E-19
10	JMJD1C	rs7895472	63201652	A	G	0.3115610	-0.0150416	0.0027241	4.0E-09
10	JMJD1C	rs7895610	63201899	T	C	0.3091390	-0.0150874	0.0027370	4.0E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs4379723	63203689	C	T	0.3129920	-0.0147499	0.0027205	7.3E-09
10	JMJD1C	rs12413730	63204388	T	C	0.3783760	0.0223484	0.0025965	2.8E-19
10	JMJD1C	rs1579045	63210688	G	A	0.3882260	0.0227221	0.0025863	5.2E-20
10	JMJD1C	chr10:63211997_TAAG_T	63211997	T	TAAG	0.3132970	-0.0149480	0.0027184	4.7E-09
10	JMJD1C	rs7920159	63212416	C	G	0.3882260	0.0227221	0.0025863	5.2E-20
10	JMJD1C	rs11819167	63216409	A	G	0.3784340	0.0224498	0.0025960	1.9E-19
10	JMJD1C	rs10822147	63216537	C	T	0.3881910	0.0227271	0.0025861	5.2E-20
10	JMJD1C	rs10822148	63219487	A	G	0.3883500	0.0226067	0.0025874	8.3E-20
10	JMJD1C	rs10761726	63220958	A	C	0.3881340	0.0226989	0.0025863	5.7E-20
10	JMJD1C	rs1904295	63223116	G	A	0.3885980	0.0214862	0.0026264	9.9E-18
10	JMJD1C	rs4335432	63226057	T	C	0.3316710	-0.0138896	0.0026770	3.9E-08
10	JMJD1C	rs6415875	63226657	A	G	0.3794480	0.0221805	0.0025954	4.9E-19
10	JMJD1C	rs10822149	63227652	A	G	0.3134060	-0.0148575	0.0027184	5.4E-09
10	JMJD1C	rs4281380	63227938	C	A	0.3784910	0.0224780	0.0025958	1.8E-19
10	JMJD1C	rs6479889	63228867	A	C	0.3308180	-0.0140247	0.0026819	3.4E-08
10	JMJD1C	rs7916868	63229171	A	T	0.3387560	0.0208186	0.0027168	2.1E-15
10	JMJD1C	rs10761727	63235733	T	C	0.3133580	-0.0148951	0.0027185	5.1E-09
10	JMJD1C	rs10761728	63235808	C	T	0.3881720	0.0227289	0.0025862	5.1E-20
10	JMJD1C	rs10761729	63235844	C	G	0.3133580	-0.0148951	0.0027185	5.1E-09
10	JMJD1C	chr10:63237348_T_TAAA	63237348	T	TAAA	0.3788620	0.0223729	0.0025969	2.8E-19
10	JMJD1C	rs4439410	63239012	C	G	0.3784150	0.0224514	0.0025961	1.9E-19
10	JMJD1C	rs7082066	63239211	A	G	0.3881150	0.0227007	0.0025864	5.5E-20
10	JMJD1C	rs7082090	63239252	A	G	0.3784150	0.0224514	0.0025961	1.9E-19
10	JMJD1C	rs4399232	63239730	T	C	0.3133860	-0.0149052	0.0027184	4.8E-09
10	JMJD1C	rs9414780	63241673	A	C	0.3784150	0.0224514	0.0025961	1.9E-19
10	JMJD1C	rs7902343	63245639	T	C	0.2847830	-0.0159327	0.0028006	2.1E-09
10	JMJD1C	rs6479891	63246696	T	C	0.3782050	0.0224749	0.0025962	1.8E-19
10	JMJD1C	chr10:63247839_TAAACAA	63247839	AAACAA	T	0.3929990	0.0222122	0.0025945	5.9E-19
10	JMJD1C	rs10995477	63250912	C	T	0.2852660	-0.0158274	0.0027942	2.1E-09
10	JMJD1C	rs7081614	63252088	C	T	0.3879020	0.0227218	0.0025880	5.9E-20
10	JMJD1C	rs4400684	63252927	G	A	0.2848240	-0.0157387	0.0027974	2.5E-09
10	JMJD1C	rs4454603	63252990	T	C	0.2852830	-0.0157735	0.0027941	2.4E-09
10	JMJD1C	rs4403688	63253156	G	A	0.3878950	0.0227274	0.0025880	5.8E-20
10	JMJD1C	rs4595427	63253184	C	A	0.2852740	-0.0157683	0.0027940	2.4E-09
10	JMJD1C	rs4450077	63253976	G	C	0.3036050	-0.0147034	0.0027427	1.9E-08
10	JMJD1C	rs4469770	63254152	G	A	0.3035020	-0.0146674	0.0027437	1.9E-08
10	JMJD1C	rs4405189	63254175	G	A	0.2850790	-0.0156680	0.0027946	2.8E-09
10	JMJD1C	rs1904297	63255428	G	A	0.3878240	0.0228270	0.0025884	4.3E-20
10	JMJD1C	rs7070693	63256402	A	G	0.3878280	0.0227673	0.0025884	5.3E-20
10	JMJD1C	rs7088799	63256414	G	T	0.2850850	-0.0158976	0.0027922	1.9E-09
10	JMJD1C	rs7896910	63256961	A	G	0.2453730	-0.0171797	0.0029318	8.1E-10
10	JMJD1C	rs10761730	63257293	C	T	0.3786220	0.0224293	0.0026018	2.6E-19
10	JMJD1C	rs10822150	63257736	G	A	0.3878100	0.0227377	0.0025883	6.0E-20
10	JMJD1C	rs11370668	63260747	G	GC	0.3834540	0.0215161	0.0026094	7.6E-18
10	JMJD1C	rs35843321	63260755	A	AT	0.3930590	0.0216584	0.0026006	3.5E-18
10	JMJD1C	rs9415680	63261130	A	G	0.3774840	0.0223861	0.0025995	2.3E-19
10	JMJD1C	chr10:63262822_AC_A	63262822	AC	A	0.3786140	0.0224234	0.0025986	2.2E-19
10	JMJD1C	rs7098181	63267383	T	G	0.2853750	-0.0156266	0.0027913	2.8E-09
10	JMJD1C	rs10761731	63267850	T	A	0.2853430	-0.0156240	0.0027916	2.9E-09
10	JMJD1C	rs10761732	63268497	C	T	0.3872710	0.0226717	0.0025891	6.2E-20
10	JMJD1C	rs7916282	63272051	A	T	0.3903020	0.0222843	0.0026441	1.6E-18
10	JMJD1C	rs7909555	63273348	T	C	0.3893200	0.0219781	0.0025868	7.1E-19
10	JMJD1C	rs9415682	63274057	G	T	0.3779950	0.0225164	0.0025987	1.9E-19
10	JMJD1C	rs10761733	63275024	T	C	0.4054390	0.0214989	0.0025935	6.8E-18
10	JMJD1C	rs10822151	63276907	G	C	0.3768860	0.0224449	0.0026001	2.1E-19
10	JMJD1C	rs9787438	63278270	C	G	0.2858550	-0.0157035	0.0027899	2.6E-09
10	JMJD1C	rs10740109	63280379	A	C	0.3015410	-0.0146369	0.0027525	2.4E-08
10	JMJD1C	rs10995489	63281085	A	G	0.3034330	-0.0153307	0.0027549	6.6E-09
10	JMJD1C	rs10761734	63281453	C	T	0.3866820	0.0227795	0.0025893	4.9E-20
10	JMJD1C	rs10740110	63283461	A	G	0.3769150	0.0224900	0.0025999	1.9E-19
10	JMJD1C	rs10761735	63284158	A	G	0.3805340	0.0222014	0.0026021	4.9E-19
10	JMJD1C	rs9414786	63284562	T	A	0.3769150	0.0224900	0.0025999	1.9E-19
10	JMJD1C	rs4417159	63285938	T	A	0.3866770	0.0227733	0.0025893	5.0E-20
10	JMJD1C	rs67907125	63286034	GA	G	0.3769150	0.0224900	0.0025999	1.9E-19
10	JMJD1C	rs10995493	63287266	C	T	0.3866800	0.0227742	0.0025893	5.0E-20
10	JMJD1C	rs10761736	63288009	A	T	0.3867150	0.0227880	0.0025894	4.8E-20
10	JMJD1C	rs7080386	63288546	A	C	0.2858550	-0.0157035	0.0027899	2.6E-09
10	JMJD1C	rs67135607	63289318	CAT	C	0.3867660	0.0227366	0.0025897	5.4E-20
10	JMJD1C	rs7074351	63290343	A	T	0.3769740	0.0224401	0.0026000	2.2E-19
10	JMJD1C	rs7075195	63290899	G	A	0.2863230	-0.0158853	0.0027878	1.8E-09
10	JMJD1C	rs4486510	63291134	C	G	0.3764150	0.0225742	0.0026007	1.5E-19
10	JMJD1C	rs10761737	63292445	C	T	0.2861860	-0.0159843	0.0027888	1.5E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs6479892	63292472	A	G	0.3769260	0.0224903	0.0025999	1.9E-19
10	JMJD1C	rs7084707	63292782	T	C	0.2863460	-0.0158883	0.0027878	1.8E-09
10	JMJD1C	rs11408050	63293789	A	AT	0.3876700	0.0225115	0.0025925	1.4E-19
10	JMJD1C	rs7913332	63293890	A	T	0.3866900	0.0227748	0.0025893	4.9E-20
10	JMJD1C	rs7093899	63294576	A	G	0.3866860	0.0227677	0.0025894	5.2E-20
10	JMJD1C	rs5785566	63295026	TA	T	0.2862480	-0.0158599	0.0027884	1.8E-09
10	JMJD1C	rs7907462	63295773	T	C	0.3872780	0.0229025	0.0025908	3.5E-20
10	JMJD1C	rs9414788	63296952	A	G	0.3769010	0.0225216	0.0026001	1.8E-19
10	JMJD1C	rs10822153	63297053	A	C	0.2864830	-0.0158596	0.0027871	1.9E-09
10	JMJD1C	rs12773283	63298464	C	T	0.3769080	0.0225036	0.0026001	1.9E-19
10	JMJD1C	rs10822154	63299284	C	T	0.3866890	0.0228072	0.0025893	4.7E-20
10	JMJD1C	rs7920768	63300754	C	T	0.3769260	0.0225144	0.0026000	1.8E-19
10	JMJD1C	chr10:63300891_C_CA	63300891	C	CA	0.3916460	0.0224827	0.0026026	2.5E-19
10	JMJD1C	rs10761739	63302248	C	G	0.2862230	-0.0157608	0.0027877	2.3E-09
10	JMJD1C	rs7073753	63303060	T	C	0.2862750	-0.0156941	0.0027877	2.6E-09
10	JMJD1C	rs10761740	63303503	G	A	0.3867110	0.0228213	0.0025894	4.4E-20
10	JMJD1C	rs74506613	63304076	A	ACTTTGCC	0.2861780	-0.0157983	0.0027900	2.3E-09
10	JMJD1C	rs61855497	63304084	A	T	0.2852280	-0.0157463	0.0027927	2.4E-09
10	JMJD1C	rs7100372	63304484	T	C	0.3769410	0.0225340	0.0026000	1.7E-19
10	JMJD1C	rs7896676	63305542	T	C	0.3589060	0.0222207	0.0026636	2.1E-18
10	JMJD1C	rs7896677	63305545	T	G	0.3596430	0.0221025	0.0026654	3.3E-18
10	JMJD1C	rs7897326	63306059	T	C	0.3866930	0.0228059	0.0025893	4.7E-20
10	JMJD1C	rs10761741	63306426	T	G	0.2861830	-0.0156663	0.0027878	2.7E-09
10	JMJD1C	rs7092139	63306540	A	C	0.3867180	0.0228290	0.0025894	4.3E-20
10	JMJD1C	rs7092539	63306749	C	T	0.3870820	0.0226000	0.0025914	1.2E-19
10	JMJD1C	rs7922587	63309854	C	T	0.2859490	-0.0155592	0.0027899	3.5E-09
10	JMJD1C	rs7085869	63310403	C	T	0.3769250	0.0225040	0.0026001	2.0E-19
10	JMJD1C	rs7070296	63310678	A	T	0.2864070	-0.0156736	0.0027874	2.7E-09
10	JMJD1C	rs10822155	63311455	A	C	0.2862210	-0.0156283	0.0027882	3.1E-09
10	JMJD1C	rs67173357	63312116	TG	T	0.4204500	0.0213094	0.0025670	5.4E-18
10	JMJD1C	rs9299455	63313841	A	G	0.3759700	0.0223243	0.0026026	3.7E-19
10	JMJD1C	chr10:63314548_A_AAC	63314548	AAC	A	0.2863400	-0.0155954	0.0027878	3.1E-09
10	JMJD1C	rs9733126	63314727	C	A	0.3864420	0.0226083	0.0025912	1.1E-19
10	JMJD1C	rs9414793	63315349	G	A	0.3769260	0.0225018	0.0026002	1.9E-19
10	JMJD1C	rs7090111	63318234	G	C	0.2862490	-0.0156582	0.0027880	2.9E-09
10	JMJD1C	rs7899715	63318695	T	C	0.3769740	0.0224538	0.0026002	2.3E-19
10	JMJD1C	rs4518976	63319017	C	T	0.3816050	0.0227217	0.0026064	9.1E-20
10	JMJD1C	rs7088045	63319637	A	T	0.3045270	-0.0146702	0.0027379	2.0E-08
10	JMJD1C	rs10822156	63320967	C	T	0.2863940	-0.0156701	0.0027875	2.7E-09
10	JMJD1C	rs10740112	63322315	G	A	0.3867060	0.0227595	0.0025896	5.6E-20
10	JMJD1C	rs10740113	63322516	T	C	0.3867060	0.0227595	0.0025896	5.6E-20
10	JMJD1C	rs10740114	63322659	A	G	0.3867060	0.0227595	0.0025896	5.6E-20
10	JMJD1C	rs34979184	63323439	GA	G	0.3867020	0.0227632	0.0025896	5.6E-20
10	JMJD1C	rs10761742	63325288	G	A	0.2864940	-0.0157631	0.0027872	2.3E-09
10	JMJD1C	rs4525102	63326513	C	T	0.3769090	0.0225489	0.0026003	1.7E-19
10	JMJD1C	rs7899503	63327708	C	G	0.3769020	0.0225416	0.0026003	1.7E-19
10	JMJD1C	rs12767177	63327882	C	G	0.3875580	0.0227316	0.0025921	7.6E-20
10	JMJD1C	chr10:63329478_GA_G	63329478	GA	G	0.3788590	0.0218157	0.0026245	6.0E-18
10	JMJD1C	rs7092504	63329679	A	G	0.3769060	0.0225227	0.0026004	1.8E-19
10	JMJD1C	rs10822157	63329720	A	G	0.3866860	0.0227797	0.0025898	5.1E-20
10	JMJD1C	rs10995505	63331399	G	A	0.3046330	-0.0147064	0.0027380	1.8E-08
10	JMJD1C	rs4133250	63332645	G	A	0.3769080	0.0225190	0.0026004	1.8E-19
10	JMJD1C	rs7918743	63333302	T	C	0.3866790	0.0228034	0.0025897	4.7E-20
10	JMJD1C	rs7902187	63333375	C	T	0.3866790	0.0228034	0.0025897	4.7E-20
10	JMJD1C	rs10822158	63334623	G	A	0.2862920	-0.0156618	0.0027885	2.8E-09
10	JMJD1C	rs10995506	63334706	A	G	0.3769080	0.0225190	0.0026004	1.8E-19
10	JMJD1C	rs10740115	63335230	A	G	0.2859310	-0.0158926	0.0027908	1.9E-09
10	JMJD1C	rs10740116	63335232	C	T	0.2859310	-0.0158926	0.0027908	1.9E-09
10	JMJD1C	rs12219332	63335932	G	C	0.3769280	0.0224816	0.0026005	2.0E-19
10	JMJD1C	rs10761743	63336258	C	T	0.3867800	0.0226816	0.0025901	7.1E-20
10	JMJD1C	rs10822159	63336490	T	C	0.2861820	-0.0156655	0.0027887	2.9E-09
10	JMJD1C	rs10740117	63338517	G	A	0.3768950	0.0225086	0.0026004	1.9E-19
10	JMJD1C	rs6479894	63338981	T	C	0.3768950	0.0225086	0.0026004	1.9E-19
10	JMJD1C	rs56674933	63339623	T	TAA	0.3858790	0.0225868	0.0025915	9.3E-20
10	JMJD1C	rs71025161	63340059	C	CAATA	0.3837160	0.0227108	0.0026057	1.5E-19
10	JMJD1C	rs10733790	63340574	G	C	0.3731740	0.0223655	0.0026107	5.1E-19
10	JMJD1C	rs10761744	63341266	C	G	0.3768940	0.0225173	0.0026003	1.8E-19
10	JMJD1C	rs10761745	63341311	G	C	0.3770360	0.0220331	0.0026035	1.2E-18
10	JMJD1C	rs10740118	63341447	C	G	0.2863730	-0.0155614	0.0027882	3.7E-09
10	JMJD1C	rs7091664	63342040	G	A	0.3768940	0.0225173	0.0026003	1.8E-19
10	JMJD1C	rs7896518	63344740	G	A	0.2862090	-0.0157144	0.0027885	2.6E-09
10	JMJD1C	rs10761746	63345134	A	G	0.3866710	0.0228129	0.0025896	4.6E-20

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs7081275	63346791	G	T	0.3769660	0.0224749	0.0026004	2.1E-19
10	JMJD1C	chr10:63348205_CAA_C	63348205	CAA	C	0.3735130	0.0225045	0.0026097	4.1E-19
10	JMJD1C	rs10761747	63348396	C	G	0.3046140	-0.0147662	0.0027381	1.6E-08
10	JMJD1C	rs7895348	63349781	C	A	0.3769180	0.0225650	0.0026002	1.6E-19
10	JMJD1C	rs7073932	63350160	C	T	0.3866870	0.0228497	0.0025896	4.1E-20
10	JMJD1C	rs10761748	63350216	T	G	0.3866870	0.0228497	0.0025896	4.1E-20
10	JMJD1C	rs10822160	63353036	G	T	0.2814040	-0.0158019	0.0028152	4.2E-09
10	JMJD1C	rs7912797	63353620	G	A	0.3046250	-0.0147433	0.0027380	1.7E-08
10	JMJD1C	rs7913278	63353774	G	A	0.3875760	0.0228377	0.0025895	4.5E-20
10	JMJD1C	rs10761749	63354049	C	T	0.4195230	0.0209234	0.0025742	5.4E-17
10	JMJD1C	rs200427687	63354672	G	GCTT	0.3766180	0.0225662	0.0026047	1.7E-19
10	JMJD1C	rs149520237	63354674	T	TTTGTG	0.3864130	0.0228417	0.0025940	4.5E-20
10	JMJD1C	rs9415692	63355392	A	G	0.3758460	0.0225170	0.0026026	1.7E-19
10	JMJD1C	rs7098614	63355667	T	C	0.3043950	-0.0147658	0.0027394	1.6E-08
10	JMJD1C	rs7082926	63355771	T	G	0.3859720	0.0229462	0.0025918	3.0E-20
10	JMJD1C	rs7083356	63356028	T	A	0.3857900	0.0229748	0.0025910	2.5E-20
10	JMJD1C	rs35971912	63357004	C	CA	0.3858430	0.0227422	0.0025933	5.8E-20
10	JMJD1C	rs10822161	63358443	A	G	0.2863090	-0.0156741	0.0027884	2.8E-09
10	JMJD1C	rs9415693	63360127	C	T	0.3771510	0.0226181	0.0026009	1.4E-19
10	JMJD1C	rs144958118	63362473	TTATATA	T	0.3874440	0.0227037	0.0025928	7.6E-20
10	JMJD1C	rs9629895	63363027	A	C	0.3867310	0.0227724	0.0025895	5.2E-20
10	JMJD1C	rs10822162	63364320	A	G	0.3867310	0.0227724	0.0025895	5.2E-20
10	JMJD1C	rs10822163	63364338	G	C	0.2866630	-0.0155928	0.0027879	3.6E-09
10	JMJD1C	rs10740119	63365477	T	G	0.3858730	0.0229527	0.0025908	2.7E-20
10	JMJD1C	rs6479896	63367072	C	T	0.2863020	-0.0157959	0.0027886	2.3E-09
10	JMJD1C	rs10822164	63367498	A	G	0.2863020	-0.0157959	0.0027886	2.3E-09
10	JMJD1C	rs7909692	63368517	T	A	0.3860790	0.0230759	0.0025915	1.7E-20
10	JMJD1C	rs10761750	63368859	A	G	0.2863070	-0.0157762	0.0027885	2.3E-09
10	JMJD1C	rs9414799	63369842	C	T	0.3749770	0.0231103	0.0026060	2.4E-20
10	JMJD1C	rs4746119	63370157	C	T	0.3769520	0.0224918	0.0026001	1.9E-19
10	JMJD1C	rs9414800	63371522	A	T	0.3761080	0.0226936	0.0026014	9.0E-20
10	JMJD1C	rs10546984	63371680	C	CATA	0.2863260	-0.0158129	0.0027884	2.1E-09
10	JMJD1C	rs2393967	63373396	C	A	0.2473400	-0.0170326	0.0029193	8.8E-10
10	JMJD1C	rs7923609	63374062	G	A	0.2867610	-0.0156590	0.0027868	2.9E-09
10	JMJD1C	rs9415696	63374588	T	A	0.3761100	0.0227160	0.0026012	8.1E-20
10	JMJD1C	rs2893919	63375018	A	G	0.2864240	-0.0157539	0.0027876	2.3E-09
10	JMJD1C	rs2393966	63375054	G	T	0.2864240	-0.0157539	0.0027876	2.3E-09
10	JMJD1C	rs9415697	63375377	C	T	0.3761220	0.0226803	0.0026011	9.1E-20
10	JMJD1C	rs7076310	63375912	A	C	0.2864240	-0.0157539	0.0027876	2.3E-09
10	JMJD1C	rs6479897	63376868	C	T	0.3858900	0.0229771	0.0025904	2.2E-20
10	JMJD1C	rs4310508	63378813	G	A	0.2864240	-0.0157539	0.0027876	2.3E-09
10	JMJD1C	rs7910927	63379150	G	T	0.2871170	-0.0160929	0.0027879	1.0E-09
10	JMJD1C	rs6479899	63379287	T	A	0.3770350	0.0224287	0.0026050	2.6E-19
10	JMJD1C	rs724553	63380624	C	G	0.3761220	0.0226803	0.0026011	9.1E-20
10	JMJD1C	rs2393969	63380680	C	A	0.2864870	-0.0157785	0.0027878	2.2E-09
10	JMJD1C	rs9415699	63383798	C	T	0.3769640	0.0225136	0.0025999	1.7E-19
10	JMJD1C	rs9415700	63385805	T	C	0.3047650	0.0200385	0.0027428	2.5E-15
10	JMJD1C	rs10822165	63387199	T	C	0.3867370	0.0227891	0.0025892	4.4E-20
10	JMJD1C	rs71025168	63387563	GA	G	0.3876550	0.0226095	0.0025900	7.4E-20
10	JMJD1C	rs10995527	63387659	A	G	0.2941650	-0.0162331	0.0027796	9.0E-10
10	JMJD1C	chr10:63390573_TACA_T	63390573	TACA	T	0.3879690	0.0224397	0.0025971	2.4E-19
10	JMJD1C	rs9414802	63391622	C	T	0.3137000	0.0204417	0.0027222	4.4E-16
10	JMJD1C	rs9415701	63391749	C	T	0.3039310	0.0202109	0.0027448	1.4E-15
10	JMJD1C	rs4746125	63393125	A	G	0.3070230	0.0204961	0.0027415	5.2E-16
10	JMJD1C	rs10740122	63395451	C	A	0.3854920	0.0229348	0.0025922	2.6E-20
10	JMJD1C	rs10822167	63398991	C	T	0.3872180	0.0227791	0.0025908	4.8E-20
10	JMJD1C	rs67434572	63399012	A	AAAG	0.2864290	-0.0156157	0.0027883	3.3E-09
10	JMJD1C	rs4745706	63399820	C	T	0.3721360	0.0226412	0.0026228	2.7E-19
10	JMJD1C	rs12415038	63401098	G	A	0.3775310	0.0224362	0.0026006	2.4E-19
10	JMJD1C	rs9415705	63401790	G	T	0.3764830	0.0226212	0.0025990	1.1E-19
10	JMJD1C	rs10740123	63404755	A	G	0.3147930	0.0205515	0.0027177	2.9E-16
10	JMJD1C	rs10822168	63405424	A	G	0.2856640	-0.0157584	0.0027916	2.3E-09
10	JMJD1C	chr10:63407820_CA_C	63407820	C	CA	0.3071220	0.0201890	0.0027479	1.3E-15
10	JMJD1C	rs10822170	63411395	G	T	0.3880000	0.0227092	0.0025942	9.0E-20
10	JMJD1C	rs10761755	63412212	G	A	0.3875300	0.0227375	0.0025884	5.7E-20
10	JMJD1C	rs10761756	63412568	T	C	0.2862770	-0.0156013	0.0027883	3.3E-09
10	JMJD1C	rs10761757	63412790	C	G	0.3875280	0.0227396	0.0025884	5.6E-20
10	JMJD1C	rs10761758	63412987	T	A	0.2855370	-0.0158560	0.0027927	2.1E-09
10	JMJD1C	rs71837985	63413039	A	AAAC	0.2865340	-0.0156294	0.0027885	3.5E-09
10	JMJD1C	rs10761759	63414032	G	T	0.3153100	0.0204899	0.0027227	4.1E-16
10	JMJD1C	rs61853587	63414817	C	G	0.3047100	0.0205027	0.0027415	5.7E-16
10	JMJD1C	rs7909269	63418006	A	G	0.2862710	-0.0157047	0.0027881	2.7E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	JMJD1C	rs35999426	63418722	T	TG	0.3768200	0.0225888	0.0026000	1.5E-19
10	JMJD1C	rs10761760	63419392	C	A	0.2833930	-0.0153919	0.0028081	6.3E-09
10	JMJD1C	rs10761761	63419398	T	A	0.3910700	0.0223707	0.0025940	2.7E-19
10	JMJD1C	rs10995530	63419654	G	A	0.3145100	0.0206455	0.0027198	2.1E-16
10	JMJD1C	rs11818194	63420692	A	G	0.3657240	0.0231836	0.0026794	1.9E-19
10	JMJD1C	rs6479901	63421016	C	A	0.3867290	0.0228748	0.0025895	3.4E-20
10	JMJD1C	rs7077580	63421125	A	G	0.2862710	-0.0157047	0.0027881	2.7E-09
10	JMJD1C	rs35654741	63425460	CAT	C	0.3046390	0.0204509	0.0027422	6.7E-16
10	JMJD1C	rs10740124	63426034	C	T	0.3144400	0.0207000	0.0027196	1.9E-16
10	JMJD1C	rs9415706	63426587	T	C	0.3047260	0.0204888	0.0027415	6.0E-16
10	JMJD1C	rs72837019	63427258	C	T	0.3144400	0.0207000	0.0027196	1.9E-16
10	JMJD1C	rs61853589	63427351	A	T	0.3053330	0.0205478	0.0027424	4.2E-16
10	JMJD1C	rs9414803	63428309	A	G	0.3047230	0.0204834	0.0027415	6.1E-16
10	JMJD1C	rs9415707	63428530	C	T	0.3055510	0.0203265	0.0027396	9.9E-16
10	JMJD1C	rs10761764	63429143	C	G	0.3146030	0.0205507	0.0027200	3.0E-16
10	JMJD1C	rs10761765	63429213	A	G	0.3144360	0.0206946	0.0027196	1.9E-16
10	JMJD1C	rs12413029	63429366	C	T	0.3047230	0.0204834	0.0027415	6.1E-16
10	JMJD1C	rs9415708	63430282	C	G	0.3047230	0.0204834	0.0027415	6.1E-16
10	JMJD1C	rs7924036	63431885	G	T	0.3339430	0.0205460	0.0026812	7.7E-17
10	JMJD1C	rs10761767	63432671	T	C	0.3139760	0.0207920	0.0027194	1.4E-16
10	JMJD1C	rs7917169	63433181	T	C	0.3149520	0.0205891	0.0027183	2.5E-16
10	JMJD1C	rs10761768	63434369	C	A	0.3149900	0.0206969	0.0027170	2.0E-16
10	JMJD1C	rs72837025	63434731	C	A	0.3055970	0.0203451	0.0027397	9.6E-16
10	JMJD1C	rs12784772	63435695	A	T	0.3055460	0.0204098	0.0027395	7.7E-16
10	JMJD1C	rs77494594	63437549	C	A	0.3047270	0.0206151	0.0027413	4.1E-16
10	JMJD1C	rs10437345	63443186	C	T	0.3047260	0.0205992	0.0027414	4.2E-16
10	JMJD1C	rs2616631	63448154	A	T	0.3042830	0.0206257	0.0027415	3.8E-16
10	JMJD1C	rs2466128	63448561	C	T	0.3042830	0.0206257	0.0027415	3.8E-16
10	JMJD1C	rs2719815	63450534	C	G	0.3042830	0.0206257	0.0027415	3.8E-16
10	JMJD1C	rs2616630	63453579	C	A	0.3042830	0.0206257	0.0027415	3.8E-16
10	JMJD1C	rs2616629	63454056	C	T	0.3042830	0.0206257	0.0027415	3.8E-16
10	JMJD1C	rs10822172	63455478	T	C	0.3142800	0.0208572	0.0027202	1.1E-16
10	JMJD1C	rs12573212	63458665	A	C	0.3139190	0.0207719	0.0027199	1.5E-16
10	JMJD1C	rs7074735	63459519	T	A	0.3141430	0.0208200	0.0027193	1.3E-16
10	JMJD1C	rs7075205	63459834	T	C	0.3139730	0.0208450	0.0027196	1.2E-16
10	JMJD1C	rs10995540	63460170	C	G	0.3139730	0.0208450	0.0027196	1.2E-16
10	JMJD1C	rs2616628	63460197	C	G	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C	rs10159609	63461168	C	T	0.3139730	0.0208450	0.0027196	1.2E-16
10	JMJD1C	chr10:63464698_CA_C	63464698	CA	C	0.3319500	0.0208664	0.0026915	2.8E-17
10	JMJD1C	rs2393980	63464750	G	C	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C, JMJD1C-AS1	rs1061259	63465484	G	C	0.3143210	0.0208929	0.0027208	1.0E-16
10	JMJD1C *	rs58806797	63466790	A	AT	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C *	rs10995541	63473575	G	T	0.3137070	0.0208308	0.0027208	1.2E-16
10	JMJD1C *	rs59215788	63474074	G	A	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C *	chr10:63474104_TAATA_T	63474104	T	TAATA	0.3332410	0.0163387	0.0026829	2.6E-11
10	JMJD1C *	rs59246603	63474182	C	T	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C *	chr10:63474856_T_TA	63474856	TA	T	0.3141390	0.0207503	0.0027206	1.6E-16
10	JMJD1C *	rs12414159	63479017	T	A	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C *	rs10995543	63479787	C	T	0.3042660	0.0206528	0.0027416	3.5E-16
10	JMJD1C *	rs10761773	63480322	G	C	0.3239750	0.0205530	0.0027357	3.6E-16
10	JMJD1C *	rs4746138	63481981	G	A	0.3040930	0.0206481	0.0027427	3.3E-16
10	JMJD1C *	rs2393978	63482050	C	A	0.3148730	0.0207944	0.0027185	1.4E-16
10	JMJD1C *	rs10822173	63483842	A	T	0.3139680	0.0208456	0.0027196	1.2E-16
10	JMJD1C *	rs7915680	63484544	C	T	0.3139680	0.0208456	0.0027196	1.2E-16
10	JMJD1C *	rs7085862	63486687	T	G	0.3139680	0.0208456	0.0027196	1.2E-16
10	JMJD1C *	rs2893922	63487259	G	T	0.3042830	0.0206746	0.0027418	3.3E-16
10	JMJD1C *	chr10:63488541_TA_T	63488541	TA	T	0.3143470	0.0208335	0.0027203	1.2E-16
10	JMJD1C *	rs9919452	63488812	T	C	0.3139610	0.0208529	0.0027195	1.1E-16
10	JMJD1C *	rs10740128	63490783	A	G	0.3123600	0.0211076	0.0027270	6.9E-17
10	JMJD1C *	rs10761776	63491217	C	T	0.3138880	0.0208494	0.0027200	1.2E-16
10	JMJD1C *	rs2393976	63493679	C	G	0.3053840	0.0206438	0.0027401	3.4E-16
10	REEP3 *	rs7910662	63493940	C	T	0.3136960	0.0209086	0.0027209	9.9E-17
10	REEP3 *	chr10:63495406_TA_T	63495406	T	TA	0.3042020	0.0207114	0.0027418	2.8E-16
10	REEP3 *	rs10822175	63495414	A	T	0.3090190	0.0203985	0.0027438	7.0E-16
10	REEP3 *	rs4746149	63497633	C	T	0.3042800	0.0206967	0.0027415	3.1E-16
10	REEP3 *	rs72837056	63500718	G	T	0.3038430	0.0206749	0.0027438	3.8E-16
10	REEP3 *	rs2893924	63501594	A	G	0.3139890	0.0208495	0.0027194	1.2E-16
10	REEP3 *	rs2393981	63501605	A	G	0.3139890	0.0208495	0.0027194	1.2E-16
10	REEP3 *	rs9971294	63503108	A	G	0.3139890	0.0208495	0.0027194	1.2E-16
10	REEP3 *	rs76677248	63503505	C	CAT	0.3042900	0.0206505	0.0027414	3.6E-16
10	REEP3 *	rs80026135	63505240	G	C	0.3038360	0.0206442	0.0027460	4.5E-16
10	REEP3 *	rs11815969	63506095	T	C	0.3042900	0.0206505	0.0027414	3.6E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	REEP3 *	rs7078456	63509719	C	T	0.3044700	0.0206080	0.0027411	4.0E-16
10	REEP3 *	rs7083823	63510912	G	C	0.3146340	0.0204834	0.0027208	3.4E-16
10	REEP3 *	chr10:63512289_C_CT	63512289	CT	C	0.2961820	0.0205902	0.0027862	2.1E-15
10	REEP3 *	rs7097698	63513635	G	A	0.3140670	0.0209021	0.0027208	1.1E-16
10	REEP3 *	rs7068144	63514500	C	G	0.3140640	0.0208996	0.0027208	1.1E-16
10	REEP3 *	rs72837070	63514919	C	T	0.3043640	0.0206861	0.0027428	3.5E-16
10	REEP3 *	chr10:63514949_A_AT	63514949	AT	A	0.3017830	0.0205790	0.0027575	7.2E-16
10	REEP3 *	rs35605123	63516140	GA	G	0.3144240	0.0207127	0.0027213	2.1E-16
10	REEP3 *	rs61853635	63516750	G	T	0.3043690	0.0206799	0.0027428	3.6E-16
10	REEP3 *	rs7082076	63517185	C	G	0.3155100	0.0209534	0.0027234	1.1E-16
10	REEP3 *	rs4745729	63517323	G	A	0.3043510	0.0206606	0.0027430	3.8E-16
10	REEP3 *	rs10740133	63517676	C	T	0.3140460	0.0208679	0.0027210	1.2E-16
10	REEP3 *	rs12416349	63517783	T	C	0.3014090	0.0216052	0.0027685	5.7E-17
10	REEP3 *	rs7358191	63519028	A	C	0.3140460	0.0208679	0.0027210	1.2E-16
10	REEP3 *	rs7358152	63519138	T	C	0.3140460	0.0208679	0.0027210	1.2E-16
10	REEP3 *	rs10822179	63520404	T	C	0.3140460	0.0208679	0.0027210	1.2E-16
10	REEP3	rs10761780	63524272	C	T	0.3044280	0.0207366	0.0027429	3.0E-16
10	REEP3	rs10761781	63524843	T	C	0.3043290	0.0207128	0.0027432	3.3E-16
10	REEP3	rs12412946	63529792	G	T	0.2965690	0.0199787	0.0027862	6.3E-15
10	REEP3	rs12414188	63529854	G	A	0.3036450	0.0206802	0.0027473	4.2E-16
10	REEP3	rs11375382	63530178	A	AC	0.3042930	0.0206464	0.0027432	4.0E-16
10	REEP3	rs5785580	63530494	AT	A	0.3325550	0.0206000	0.0026838	6.6E-17
10	REEP3	rs7087279	63532176	T	A	0.3043480	0.0206144	0.0027428	4.2E-16
10	REEP3	rs59035163	63532283	G	C	0.3043480	0.0206144	0.0027428	4.2E-16
10	REEP3	rs12413081	63533959	T	C	0.3043480	0.0206144	0.0027428	4.2E-16
10	REEP3	rs16918567	63534910	C	A	0.3041610	0.0204855	0.0027438	5.9E-16
10	REEP3	rs16918573	63541045	A	T	0.3018870	0.0205261	0.0027481	5.5E-16
10	REEP3	rs16918575	63541565	G	A	0.3018880	0.0205207	0.0027481	5.7E-16
10	REEP3	rs147232123	63541637	G	GT	0.3018880	0.0205207	0.0027481	5.7E-16
10	REEP3	rs12414796	63543327	A	G	0.3018460	0.0205523	0.0027483	5.2E-16
10	REEP3	rs61853639	63545353	T	G	0.3024380	0.0206758	0.0027469	3.7E-16
10	REEP3	rs4746195	63547893	G	A	0.3024580	0.0206387	0.0027464	4.1E-16
10	REEP3	rs4469774	63550017	T	G	0.3035290	0.0204221	0.0027473	1.1E-15
10	REEP3	rs61853642	63554019	A	G	0.2864620	0.0204006	0.0027906	2.9E-15
10	REEP3	rs9919429	63554059	G	A	0.3146340	0.0202628	0.0027223	5.9E-16
10	REEP3	rs2163188	63554951	C	G	0.3148000	0.0201491	0.0027226	7.7E-16
10	REEP3	rs2393984	63555211	G	A	0.3146360	0.0202576	0.0027223	6.0E-16
10	REEP3	rs6479905	63555471	G	A	0.3131120	0.0201654	0.0027275	1.2E-15
10	REEP3	rs12411988	63555637	C	G	0.2866360	0.0204061	0.0027903	2.8E-15
10	REEP3	rs12412012	63556003	T	C	0.2865800	0.0203717	0.0027903	3.1E-15
10	REEP3	rs7919685	63556040	T	G	0.3147620	0.0202246	0.0027220	6.4E-16
10	REEP3	rs61117531	63556475	T	TACTC	0.3142440	0.0205916	0.0027296	2.4E-16
10	REEP3	rs12247907	63557285	C	G	0.3147660	0.0202249	0.0027220	6.4E-16
10	REEP3	rs7070761	63557296	T	A	0.3147660	0.0202249	0.0027220	6.4E-16
10	REEP3	rs10761785	63559006	G	T	0.3163610	0.0199812	0.0027198	1.2E-15
10	REEP3	rs61579729	63559553	G	A	0.2865840	0.0203646	0.0027903	3.1E-15
10	REEP3	rs7898861	63559918	C	T	0.3136290	0.0202871	0.0027287	6.0E-16
10	REEP3	rs16918599	63560319	C	T	0.2865600	0.0203434	0.0027905	3.4E-15
10	REEP3	rs16918600	63560690	A	C	0.2865600	0.0203434	0.0027905	3.4E-15
10	REEP3	rs11812934	63560970	A	G	0.2865600	0.0203434	0.0027905	3.4E-15
10	REEP3	rs16918601	63561291	A	C	0.2865910	0.0203779	0.0027916	3.0E-15
10	REEP3	rs12245149	63561387	A	C	0.3147610	0.0202203	0.0027231	6.8E-16
10	REEP3	rs12245367	63561704	T	C	0.3143000	0.0203237	0.0027307	6.1E-16
10	REEP3	rs16918603	63561712	G	A	0.2861200	0.0205880	0.0027995	2.0E-15
10	REEP3	rs4746201	63562621	T	G	0.2861960	0.0206158	0.0028010	1.8E-15
10	REEP3	rs10666196	63562704	ATCAG	A	0.3143940	0.0203532	0.0027323	5.0E-16
10	REEP3	rs7899657	63563505	A	G	0.3144120	0.0202748	0.0027326	6.4E-16
10	REEP3	rs4746203	63564237	T	G	0.3138520	0.0202874	0.0027358	6.4E-16
10	REEP3	rs10822181	63565366	A	G	0.3147250	0.0201171	0.0027347	1.0E-15
10	REEP3	rs4746204	63568758	T	C	0.3145890	0.0203063	0.0027360	6.6E-16
10	REEP3	rs7907451	63568980	A	T	0.3146000	0.0203216	0.0027361	6.5E-16
10	REEP3	rs4746205	63569758	G	A	0.3146080	0.0203508	0.0027366	5.9E-16
10	REEP3	rs7100409	63570435	A	T	0.3145870	0.0203984	0.0027368	5.3E-16
10	REEP3	rs7100413	63570448	C	T	0.3145870	0.0203984	0.0027368	5.3E-16
10	REEP3	rs61853655	63570645	G	A	0.2860440	0.0206116	0.0028081	2.1E-15
10	REEP3	rs3847325	63571751	C	G	0.3149540	0.0204046	0.0027365	5.6E-16
10	REEP3	rs3847326	63572099	G	A	0.3168170	0.0204722	0.0027341	4.9E-16
10	REEP3	chr10:63572305_C_CT	63572305	CT	C	0.3005560	0.0200190	0.0027842	6.8E-15
10	REEP3	rs6479908	63573888	G	C	0.3069400	0.0201818	0.0027549	1.9E-15
10	REEP3	rs7090758	63575555	C	T	0.3069530	0.0201785	0.0027550	1.9E-15
10	REEP3	rs7077256	63576425	G	A	0.3069890	0.0202333	0.0027551	1.6E-15
10	REEP3	rs7902616	63576613	A	G	0.3069890	0.0202333	0.0027551	1.6E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	REEP3	rs10822183	63577381	C	T	0.3068560	0.0203242	0.0027558	1.2E-15
10	REEP3	rs7910951	63578544	G	A	0.3069890	0.0202333	0.0027551	1.6E-15
10	REEP3	rs7911761	63578993	G	A	0.3070120	0.0202083	0.0027553	1.7E-15
10	REEP3	rs11817901	63580123	A	G	0.2880290	0.0207162	0.0028051	1.7E-15
10	REEP3	rs12768534	63581137	A	G	0.3069900	0.0202272	0.0027552	1.6E-15
10	REEP3	rs16918638	63583371	C	T	0.2891490	0.0207661	0.0028028	1.6E-15
10	REEP3	rs61853658	63590037	T	C	0.2831430	0.0199162	0.0028261	2.9E-14
10	REEP3	chr10:63590519_AT_A	63590519	AT	A	0.3112560	0.0197085	0.0027581	8.2E-15
10	REEP3	rs11817169	63596549	G	A	0.2845320	0.0201122	0.0028277	2.0E-14
10	REEP3	rs4746244	63599941	T	C	0.2826930	0.0198390	0.0028375	5.0E-14
10	REEP3	rs11818738	63604971	C	A	0.2863830	0.0204354	0.0028426	9.6E-15
10	REEP3 *	rs2565187	63632093	C	T	0.2333650	0.0178458	0.0030011	3.1E-10
10	REEP3 *	rs2565186	63632270	A	G	0.2333410	0.0178619	0.0030011	3.0E-10
10	REEP3 *	rs1268639	63632720	A	G	0.2334730	0.0178658	0.0029995	3.1E-10
10	REEP3 *	rs1255495	63634690	G	A	0.2336620	0.0177895	0.0029936	3.6E-10
10	CYP26A1 *	rs2068888	93079885	G	A	0.1905280	0.0192813	0.0032212	4.8E-10
10	CYP26A1 *	rs4418728	93079967	G	T	0.1904830	0.0189097	0.0032229	1.0E-09
10	WDR11 *	rs2246958	121129610	C	T	0.3790410	-0.0156383	0.0026156	4.0E-09
10	WDR11 *	rs2246730	121131141	C	T	0.3776640	-0.0161508	0.0026207	1.6E-09
10	WDR11 *	rs1873446	121131995	C	T	0.3772260	-0.0160270	0.0026172	1.7E-09
10	WDR11 *	rs1907239	121135315	A	C	0.3667040	0.0167868	0.0026174	1.5E-10
10	WDR11 *	rs2250266	121138399	A	G	0.3654890	0.0165809	0.0026226	2.5E-10
10	WDR11 *	rs1907240	121138445	G	A	0.4159480	-0.0172349	0.0025577	1.7E-11
10	WDR11 *	rs1907241	121138470	G	T	0.4154220	-0.0173981	0.0025578	1.0E-11
10	WDR11 *	rs2257129	121139183	T	C	0.4130540	-0.0180883	0.0025605	1.4E-12
10	WDR11 *	rs2263985	121143992	C	T	0.4130440	-0.0182341	0.0025618	8.7E-13
10	WDR11 *	rs2451876	121144368	T	C	0.4129690	-0.0182416	0.0025614	8.4E-13
10	WDR11 *	rs2263983	121145186	T	C	0.4129660	-0.0182289	0.0025613	8.8E-13
10	WDR11 *	rs2220607	121146746	C	A	0.4144340	-0.0182539	0.0025598	9.7E-13
10	WDR11 *	rs2172073	121150111	C	A	0.4146050	-0.0182730	0.0025597	8.4E-13
10	WDR11 *	rs1907256	121150416	A	G	0.3703320	0.0172973	0.0026133	2.6E-11
10	WDR11 *	rs2263997	121151174	A	C	0.3670210	0.0170806	0.0026299	6.9E-11
10	WDR11 *	rs7098433	121153961	C	T	0.4147790	-0.0184349	0.0025587	5.2E-13
10	WDR11 *	rs17101518	121155455	G	A	0.3673800	-0.0166643	0.0026168	2.2E-10
10	WDR11 *	rs72631105	121155831	A	G	0.3518470	0.0175372	0.0026397	2.6E-11
10	WDR11 *	rs56351107	121155983	G	C	0.3671810	-0.0166462	0.0026157	2.1E-10
10	WDR11 *	rs17101521	121156039	C	T	0.3662130	-0.0164876	0.0026199	3.4E-10
10	WDR11 *	rs59313277	121156141	T	G	0.3670230	-0.0166020	0.0026165	2.3E-10
10	WDR11 *	chr10:121156208_T_TA	121156208	TA	T	0.3594130	-0.0164330	0.0026574	5.9E-10
10	WDR11 *	rs73366917	121156240	A	G	0.3666800	-0.0166045	0.0026170	2.4E-10
10	WDR11 *	rs17101524	121156265	A	C	0.3671810	-0.0166462	0.0026157	2.1E-10
10	WDR11 *	rs59082214	121156440	A	CACACAC	0.3610460	-0.0154467	0.0026468	4.3E-09
10	WDR11 *	rs4752500	121156448	T	A	0.3695020	-0.0162908	0.0026197	5.1E-10
10	WDR11 *	rs1907266	121156628	T	C	0.4145090	-0.0183060	0.0025584	7.2E-13
10	WDR11 *	rs7920116	121156957	C	T	0.3671810	-0.0166462	0.0026157	2.1E-10
10	WDR11 *	rs7903585	121157114	G	A	0.3655790	-0.0165126	0.0026210	3.6E-10
10	WDR11 *	rs7903948	121157125	A	G	0.3670430	-0.0166795	0.0026162	2.0E-10
10	WDR11 *	rs10710843	121157294	C	CA	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs7904102	121157377	G	C	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs59754371	121157811	C	T	0.3664150	-0.0165163	0.0026193	3.1E-10
10	WDR11 *	rs57615383	121157842	A	G	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs112209982	121158067	A	G	0.3631490	-0.0164237	0.0026316	4.8E-10
10	WDR11 *	rs58324269	121158215	G	A	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs60089052	121158221	C	T	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs58217496	121158313	C	T	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs60711290	121158469	T	G	0.3671710	-0.0166671	0.0026155	2.0E-10
10	WDR11 *	rs57142282	121158561	T	C	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs17101530	121158601	C	T	0.3672160	-0.0166337	0.0026157	2.2E-10
10	WDR11 *	rs71945618	121158703	AG	A	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs73366943	121158995	G	A	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs17101534	121159361	C	T	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs11199803	121159565	G	A	0.3671760	-0.0166563	0.0026155	2.0E-10
10	WDR11 *	rs11199804	121159660	G	C	0.3671750	-0.0166566	0.0026155	2.0E-10
10	WDR11 *	rs11199805	121159692	T	C	0.3671750	-0.0166566	0.0026155	2.0E-10
10	WDR11 *	rs11199806	121159795	A	G	0.3671810	-0.0166514	0.0026155	2.1E-10
10	WDR11 *	rs7917346	121160328	G	A	0.3673460	-0.0166328	0.0026160	2.1E-10
10	WDR11 *	rs7902919	121160588	C	T	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs7917833	121160641	A	C	0.3671830	-0.0166535	0.0026156	2.0E-10
10	WDR11 *	rs7917847	121160676	A	C	0.3183380	-0.0146813	0.0027069	4.8E-08
10	WDR11 *	rs2130786	121161069	C	T	0.4145310	-0.0183298	0.0025582	6.8E-13
10	WDR11 *	rs1907267	121161442	T	C	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs1907268	121161733	C	T	0.3671810	-0.0166459	0.0026155	2.1E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
10	WDR11 *	rs1907269	121161835	C	A	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs6585696	121162049	G	A	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs6585697	121162083	T	C	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs6585698	121162088	G	T	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs6585699	121162146	C	T	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs6585700	121162243	C	G	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs6585701	121162277	C	T	0.3671810	-0.0166459	0.0026155	2.1E-10
10	WDR11 *	rs7920041	121162857	C	T	0.3671850	-0.0166592	0.0026155	2.0E-10
10	WDR11 *	rs7906567	121162944	C	A	0.3671850	-0.0166592	0.0026155	2.0E-10
10	WDR11 *	rs59296617	121163320	A	T	0.3671850	-0.0166592	0.0026155	2.0E-10
10	WDR11 *	rs11199810	121164064	C	T	0.3671850	-0.0166592	0.0026155	2.0E-10
10	WDR11 *	rs60590589	121164227	AAAAC	A	0.3672180	-0.0166733	0.0026157	2.0E-10
10	WDR11 *	rs7087606	121164303	T	C	0.3671460	-0.0166981	0.0026155	1.8E-10
10	WDR11 *	rs6585702	121164396	T	G	0.3671460	-0.0166981	0.0026155	1.8E-10
10	WDR11 *	rs6585703	121164626	A	G	0.3671830	-0.0166568	0.0026155	2.0E-10
10	WDR11 *	rs7915733	121165125	A	C	0.3671960	-0.0166715	0.0026156	2.0E-10
10	WDR11 *	rs10788141	121165340	G	T	0.4145780	-0.0183456	0.0025582	6.5E-13
10	WDR11 *	rs1907274	121165824	T	G	0.3671720	-0.0166622	0.0026157	2.0E-10
10	WDR11 *	rs6585708	121167429	T	C	0.3671540	-0.0166451	0.0026162	2.2E-10
10	WDR11 *	rs7897890	121168240	T	C	0.3177710	-0.0147318	0.0027087	4.6E-08
10	WDR11 *	rs11199811	121169559	A	C	0.3180390	-0.0147801	0.0027085	4.2E-08
10	WDR11 *	rs10886862	121169894	C	T	0.4143270	-0.0185185	0.0025600	3.9E-13
10	WDR11 *	rs35326857	121169898	G	T	0.3697460	0.0175944	0.0026140	1.1E-11
10	WDR11 *	rs10886863	121169979	T	C	0.4143270	-0.0185185	0.0025600	3.9E-13
10	WDR11 *	rs10886864	121170023	C	T	0.4143270	-0.0185185	0.0025600	3.9E-13
10	WDR11 *	rs7071036	121171054	C	T	0.3669890	-0.0168091	0.0026172	1.5E-10
10	WDR11 *	rs7071062	121171098	C	T	0.3669890	-0.0168091	0.0026172	1.5E-10
10	WDR11 *	rs11199812	121171431	A	G	0.3176900	-0.0150006	0.0027104	2.9E-08
10	WDR11 *	rs1873449	121172138	T	G	0.3635500	-0.0168120	0.0026277	1.8E-10
10	WDR11 *	rs754227	121172490	C	T	0.3700550	-0.0160941	0.0026191	7.3E-10
10	WDR11 *	rs3962120	121177844	A	C	0.3641760	-0.0166174	0.0026568	2.7E-10
10	WDR11 *	rs191959515	121178085	T	C	0.3256750	-0.0167829	0.0027290	4.1E-10
10	WDR11 *	rs200553592	121178117	A	ATAGATA	0.3252460	-0.0166962	0.0027282	4.8E-10
10	WDR11 *	rs10788142	121181315	C	T	0.3775700	0.0142100	0.0026086	4.6E-08
10	WDR11 *	rs1907282	121182017	A	G	0.3854720	0.0143775	0.0025932	2.6E-08
10	WDR11 *	rs1907284	121182265	G	T	0.3859820	0.0143098	0.0025942	3.4E-08
10	WDR11 *	rs7088428	121185738	G	T	0.3858460	0.0143393	0.0025956	3.4E-08
10	FGFR2 *	rs10788149	121207656	G	A	0.3197600	0.0149568	0.0027029	5.5E-09
10	FGFR2 *	rs10749408	121208012	C	T	0.3192290	0.0152236	0.0027066	3.1E-09
10	FGFR2 *	rs2172071	121208516	C	T	0.3181350	0.0150605	0.0027113	4.9E-09
10	FGFR2 *	rs11592107	121209450	A	G	0.3181460	0.0150474	0.0027114	5.2E-09
10	FGFR2 *	rs1907218	121210702	T	C	0.3181040	0.0150732	0.0027111	4.9E-09
10	FGFR2 *	rs1907220	121211409	A	G	0.3179770	0.0150308	0.0027121	5.3E-09
10	FGFR2 *	rs1994655	121211732	T	G	0.3179910	0.0150224	0.0027120	5.5E-09
10	FGFR2 *	rs1907221	121212913	C	T	0.3190520	0.0148318	0.0027047	7.3E-09
10	FGFR2 *	rs1907225	121216119	C	T	0.3185780	0.0148640	0.0027105	8.0E-09
10	FGFR2 *	rs10749409	121217052	C	G	0.3185410	0.0148625	0.0027104	8.1E-09
10	FGFR2 *	rs11199835	121217643	G	A	0.3185860	0.0148652	0.0027103	8.1E-09
10	FGFR2 *	rs1907228	121219430	G	A	0.4980870	-0.0139968	0.0025278	6.4E-09
10	FGFR2 *	rs7093348	121221734	C	T	0.4958340	-0.0137429	0.0025316	1.0E-08
10	FGFR2 *	rs1907231	121221742	T	A	0.4958340	-0.0137429	0.0025316	1.0E-08
10	FGFR2 *	rs2420922	121223863	G	A	0.4979600	-0.0136710	0.0025221	1.4E-08
10	FGFR2 *	rs7920546	121224230	G	A	0.4979600	-0.0136710	0.0025221	1.4E-08
10	FGFR2 *	rs7098079	121224699	G	C	0.4943770	-0.0136480	0.0025242	1.3E-08
10	FGFR2 *	rs11199837	121227134	A	T	0.4979940	-0.0137519	0.0025227	1.2E-08
10	FGFR2 *	rs1907232	121227612	A	G	0.4966180	-0.0135725	0.0025224	1.7E-08
10	FGFR2 *	rs11597855	121229534	T	C	0.4979650	-0.0137859	0.0025228	1.1E-08
10	FGFR2 *	rs60834189	121233878	A	AT	0.4834910	-0.0134181	0.0025409	2.6E-08
10	FGFR2 *	rs878409	121240036	A	G	0.4971500	-0.0136990	0.0025277	1.3E-08
10	FGFR2 *	rs12245393	121240386	T	C	0.4971660	-0.0136920	0.0025280	1.3E-08
10	FGFR2 *	rs145325908	121241120	TG	T	0.4953370	-0.0142050	0.0025692	6.0E-09
10	FGFR2 *	rs5016035	121241124	G	T	0.4947100	-0.0140587	0.0025665	8.7E-09
11	ARNTL	rs7947951	13334483	G	A	0.3642910	0.0148279	0.0026190	2.9E-08
11	ARNTL	rs2896635	13338198	A	T	0.3634820	0.0149887	0.0026225	2.2E-08
11	ARNTL	rs6486122	13339977	T	C	0.3669650	0.0152401	0.0026098	1.0E-08
11	DAGLA *	rs7925523	61675020	A	G	0.2542750	-0.0163251	0.0028945	1.3E-08
11	DAGLA *	rs60399071	61675683	A	G	0.2544200	-0.0163783	0.0028947	1.1E-08
11	DAGLA *	rs151242175	61679851	T	C	0.2539140	-0.0167029	0.0029006	6.6E-09
11	DAGLA *	rs115702847	61679884	A	T	0.2539190	-0.0167032	0.0029006	6.6E-09
11	DAGLA	rs59200224	61682665	G	A	0.2543490	-0.0165211	0.0028980	9.1E-09
11	DAGLA	rs59371352	61682823	A	G	0.2545140	-0.0163694	0.0029030	1.3E-08
11	DAGLA	rs72918042	61684076	G	C	0.2543670	-0.0165086	0.0028980	9.3E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	DAGLA	rs35404524	61687658	C	CTT	0.2543640	-0.0164667	0.0028983	1.0E-08
11	DAGLA	rs4963308	61688954	A	G	0.2543650	-0.0165290	0.0028986	8.8E-09
11	DAGLA	rs883724	61690385	T	C	0.2539400	-0.0163037	0.0029009	1.2E-08
11	DAGLA	rs11827215	61691123	A	G	0.2547370	-0.0163535	0.0028962	1.1E-08
11	DAGLA	rs72315101	61695289	C	CTCTG	0.2543400	-0.0163701	0.0028993	1.2E-08
11	DAGLA	rs60507107	61696297	T	C	0.2542960	-0.0163901	0.0028995	1.1E-08
11	DAGLA	rs2097853	61698795	T	G	0.2544410	-0.0163105	0.0028996	1.4E-08
11	DAGLA	rs58217294	61702031	A	T	0.2544730	-0.0163246	0.0028999	1.4E-08
11	DAGLA	rs12274157	61710175	C	A	0.2546000	-0.0163823	0.0029011	1.3E-08
11	DAGLA	rs731842	61712719	C	T	0.2547200	-0.0163707	0.0029007	1.3E-08
11	DAGLA	rs2107617	61714167	G	C	0.3046150	-0.0152359	0.0027632	2.0E-08
11	DAGLA	rs17156244	61714923	G	T	0.2547920	-0.0163115	0.0029001	1.4E-08
11	DAGLA	rs198435	61715852	C	G	0.2516400	-0.0165025	0.0029157	1.1E-08
11	DAGLA	rs2903825	61721496	T	C	0.2619980	-0.0164661	0.0028758	8.7E-09
11	DAGLA	rs9735635	61723408	A	C	0.2613710	-0.0165547	0.0028781	7.3E-09
11	DAGLA	rs4963243	61726855	A	G	0.2624040	-0.0164847	0.0028730	7.4E-09
11	DAGLA	rs2240287	61738111	A	G	0.2648620	-0.0167049	0.0028692	5.9E-09
11	DAGLA	rs2240286	61738982	C	T	0.2649010	-0.0167563	0.0028696	5.3E-09
11	DAGLA	rs4963255	61740134	A	G	0.2649200	-0.0167516	0.0028701	5.6E-09
11	DAGLA	rs3741252	61744026	T	C	0.2620500	-0.0165267	0.0028873	1.1E-08
11	MYRF	rs174528	61776027	T	C	0.4031080	-0.0212292	0.0025836	1.4E-16
11	MYRF	rs174529	61776489	T	C	0.4033610	-0.0212804	0.0025845	1.4E-16
11	MYRF	rs174530	61779120	A	G	0.4125100	-0.0217544	0.0025726	1.7E-17
11	MYRF	rs108499	61779765	C	T	0.4158300	-0.0218621	0.0025677	1.0E-17
11	MYRF	rs509360	61781087	A	G	0.4030620	-0.0203391	0.0025848	3.2E-15
11	MYRF	rs174533	61781553	G	A	0.4154860	-0.0213733	0.0025707	5.5E-17
11	MYRF	rs174534	61781986	A	G	0.4122280	-0.0218486	0.0025746	1.1E-17
11	MYRF	rs174535	61783884	T	C	0.4114250	-0.0217934	0.0025729	1.6E-17
11	MYRF	rs174536	61784455	A	C	0.4139830	-0.0221564	0.0025707	4.3E-18
11	MYRF	rs174537	61785208	G	T	0.4148580	-0.0221069	0.0025682	5.3E-18
11	TMEM258	rs102275	61790331	T	C	0.4143890	-0.0221428	0.0025683	4.5E-18
11	TMEM258	rs102274	61790354	T	C	0.4145630	-0.0220540	0.0025687	5.9E-18
11	TMEM258	rs174538	61792609	G	A	0.4169190	-0.0217958	0.0025660	1.4E-17
11	FEN1	rs4246215	61796827	G	T	0.4148240	-0.0219870	0.0025676	7.9E-18
11	FADS1 *	rs174541	61798436	T	C	0.4146490	-0.0221632	0.0025693	4.9E-18
11	FADS1	rs174544	61800281	C	A	0.4236390	-0.0222018	0.0025684	3.0E-18
11	FADS1	rs174545	61801834	C	G	0.4150840	-0.0221167	0.0025674	5.4E-18
11	FADS1	rs174546	61802358	C	T	0.4151230	-0.0221739	0.0025676	4.5E-18
11	FADS1	rs174547	61803311	T	C	0.4150270	-0.0219698	0.0025687	9.1E-18
11	FADS1	rs174548	61803876	C	G	0.4227410	-0.0226409	0.0025627	6.2E-19
11	FADS1	rs174549	61803910	G	A	0.4231320	-0.0224887	0.0025633	1.1E-18
11	FADS1	rs174550	61804006	T	C	0.4150670	-0.0221640	0.0025674	4.6E-18
11	FADS1	rs174553	61807686	A	G	0.4154030	-0.0224064	0.0025676	2.2E-18
11	FADS1	rs72643557	61811955	T	C	0.4120330	-0.0220248	0.0025784	1.2E-17
11	FADS1	rs174554	61811991	A	G	0.4154320	-0.0224332	0.0025674	1.9E-18
11	FADS1	rs174555	61812288	T	C	0.4226460	-0.0229201	0.0025628	2.6E-19
11	FADS1	rs174556	61813163	C	T	0.4227000	-0.0229339	0.0025629	2.5E-19
11	FADS1	rs174559	61814184	G	A	0.4243780	-0.0226811	0.0025618	6.3E-19
11	FADS1	rs174560	61814292	T	C	0.4226860	-0.0229342	0.0025629	2.5E-19
11	FADS1, MIR1908	rs174561	61815236	T	C	0.4226640	-0.0228968	0.0025635	2.8E-19
11	FADS2	rs174562	61817672	A	G	0.4146210	-0.0224594	0.0025705	1.9E-18
11	FADS2	rs35473591	61818856	C	CT	0.4148300	-0.0222055	0.0025700	4.6E-18
11	FADS2	rs174564	61820833	A	G	0.4137180	-0.0220813	0.0025735	7.8E-18
11	FADS2	rs28456	61822009	A	G	0.4213710	-0.0225896	0.0025707	1.2E-18
11	FADS2	rs174565	61824164	C	G	0.4156200	-0.0219277	0.0025722	1.2E-17
11	FADS2	chr11:61824525_A_AAG	61824525	A	AAG	0.4179530	-0.0216398	0.0025794	4.0E-17
11	FADS2	rs174566	61824890	A	G	0.4137140	-0.0220920	0.0025735	7.7E-18
11	FADS2	rs174567	61825533	A	G	0.4166290	-0.0225937	0.0025697	1.4E-18
11	FADS2	rs174568	61826344	C	T	0.4156640	-0.0223909	0.0025692	2.3E-18
11	FADS2	rs3834458	61827448	CT	C	0.4148220	-0.0223871	0.0025713	2.7E-18
11	FADS2	rs5792235	61828850	CA	C	0.4138080	-0.0223175	0.0025696	3.3E-18
11	FADS2	rs99780	61829161	C	T	0.4138160	-0.0223108	0.0025696	3.4E-18
11	FADS2	rs174570	61829740	C	T	0.4157440	-0.0221709	0.0025677	5.2E-18
11	FADS2	rs1535	61830500	A	G	0.4136890	-0.0224019	0.0025692	2.5E-18
11	FADS2	rs174574	61832870	C	A	0.4138550	-0.0221938	0.0025708	5.1E-18
11	FADS2	rs2524296	61833906	T	C	0.4381790	0.0204135	0.0025498	1.2E-15
11	FADS2	rs2845574	61834400	T	C	0.4429520	0.0207275	0.0025384	2.5E-16
11	FADS2	rs2845573	61834436	G	A	0.4483260	0.0201806	0.0025386	1.9E-15
11	FADS2	rs199649489	61834989	A	C	0.4320890	-0.0206825	0.0026087	2.8E-15
11	FADS2	rs2727270	61835765	T	C	0.4451490	0.0213045	0.0025374	3.0E-17
11	FADS2	rs2727271	61835886	T	A	0.4452060	0.0210271	0.0025376	7.8E-17
11	FADS2	rs174576	61836038	C	A	0.4133600	-0.0222922	0.0025707	3.8E-18

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	FADS2	rs2524299	61837310	T	A	0.4455620	0.0211526	0.0025365	4.6E-17
11	FADS2	rs174577	61837342	C	A	0.4135020	-0.0223679	0.0025701	2.9E-18
11	FADS2	rs2072113	61837495	T	C	0.4451780	0.0213563	0.0025378	2.4E-17
11	FADS2	rs2072114	61837743	G	A	0.4451530	0.0210078	0.0025374	8.0E-17
11	FADS2	rs174578	61838027	T	A	0.4137190	-0.0222215	0.0025715	5.1E-18
11	FADS2	rs174580	61839170	A	G	0.4130960	-0.0222594	0.0025725	4.2E-18
11	FADS2	rs174581	61839211	G	A	0.4132350	-0.0221743	0.0025729	5.4E-18
11	FADS2	rs2727265	61841532	A	C	0.4457240	0.0214317	0.0025518	2.4E-17
11	FADS2	rs174583	61842278	C	T	0.4127230	-0.0223169	0.0025714	3.9E-18
11	FADS2	rs174584	61843278	G	A	0.4124460	-0.0223312	0.0025728	3.4E-18
11	FADS2	rs2526680	61843744	T	C	0.4475350	0.0214345	0.0025421	1.9E-17
11	FADS2	rs2845572	61847123	A	G	0.4441330	0.0216039	0.0025428	1.2E-17
11	FADS2	rs2851682	61848540	G	A	0.4445770	0.0214959	0.0025392	1.6E-17
11	FADS2	rs2727263	61850540	T	C	0.4456130	0.0214096	0.0025498	3.2E-17
11	FADS2	rs174592	61851136	A	G	0.4094820	-0.0225643	0.0025725	1.5E-18
11	FADS2	rs174594	61852357	A	C	0.4094540	-0.0228625	0.0025762	5.6E-19
11	FADS2	rs72643559	61852802	C	T	0.4059130	-0.0227622	0.0025894	1.2E-18
11	FADS2	chr11:61853156_AAACAA	61853156 AAACAA	A	A	0.4094940	-0.0222854	0.0025867	5.2E-18
11	FADS2	rs174598	61853722	G	A	0.4107890	-0.0225498	0.0025720	1.7E-18
11	FADS2	rs174599	61854084	G	C	0.4085340	-0.0228711	0.0025756	5.3E-19
11	FADS2	rs174600	61854755	T	C	0.4100280	-0.0226491	0.0025773	1.3E-18
11	FADS2	rs174601	61855668	C	T	0.4048290	-0.0224986	0.0025773	2.0E-18
11	GRM5	rs142722149	88593788 TCTCTTT	C	C	0.4254660	0.0145086	0.0025893	3.0E-08
11	BUD13 *	rs191081678	116505105	T	G	0.0118530	0.0703953	0.0116999	4.2E-10
11	BUD13 *	rs140673349	116525979	A	G	0.0158544	0.0722029	0.0101475	6.2E-13
11	BUD13 *	rs74954439	116567025	A	G	0.0566308	-0.0302285	0.0054234	2.4E-08
11	BUD13 *	rs11605293	116567039	T	C	0.0566628	-0.0299408	0.0054246	3.3E-08
11	BUD13 *	rs144641996	116579022	T	A	0.0360229	0.0411556	0.0068189	3.0E-09
11	BUD13 *	rs114594921	116602565	C	T	0.0500632	0.0389421	0.0058843	3.8E-11
11	BUD13 *	rs74733106	116608826	T	G	0.0557648	0.0381177	0.0054778	1.8E-11
11	BUD13 *	rs116585768	116615113	A	G	0.0582308	0.0442485	0.0054195	1.8E-15
11	BUD13 *	rs10891999	116618165	T	A	0.1455700	0.0328435	0.0036060	6.1E-20
11	BUD13 *	rs11216043	116619262	C	T	0.1444370	0.0321769	0.0036159	5.8E-19
11	BUD13 *	rs148093284	116620192	C	T	0.0296686	0.0458878	0.0075200	1.4E-10
11	BUD13 *	rs182744169	116620615	C	T	0.0128312	0.0748079	0.0112388	2.0E-11
11	BUD13 *	rs11216045	116621694	C	T	0.1454870	0.0316764	0.0036042	1.4E-18
11	BUD13 *	rs79801428	116623547	A	G	0.0832233	-0.0338497	0.0046491	2.8E-14
11	BUD13 *	rs11216048	116624342	G	A	0.0873803	-0.0325654	0.0045177	6.7E-14
11	BUD13 *	rs11216049	116624458	C	T	0.0876393	-0.0322164	0.0045105	1.1E-13
11	BUD13 *	rs11216050	116624597	T	C	0.0881135	-0.0324449	0.0044963	6.2E-14
11	BUD13 *	rs112305884	116625067	T	C	0.0895161	-0.0308733	0.0044521	5.2E-13
11	BUD13 *	rs112494128	116625184	T	C	0.0896132	-0.0306184	0.0044473	7.7E-13
11	BUD13 *	rs7114844	116625470	A	G	0.1431100	0.0363185	0.0035954	3.2E-23
11	BUD13 *	rs4340085	116625592	T	C	0.0900872	-0.0310017	0.0044332	3.5E-13
11	BUD13 *	rs7114993	116625593	T	G	0.1427250	0.0364374	0.0035999	3.0E-23
11	BUD13 *	rs2156122	116625906	A	C	0.1435670	0.0371403	0.0035865	2.3E-24
11	BUD13 *	rs77984767	116626027	G	A	0.0909680	-0.0298048	0.0044092	1.9E-12
11	BUD13 *	rs77623050	116626231	T	C	0.0890323	-0.0303425	0.0044594	1.3E-12
11	BUD13 *	rs78485217	116626244	A	T	0.0881701	-0.0304363	0.0044863	1.6E-12
11	BUD13 *	rs147788053	116626296	CAT	C	0.0775710	-0.0287796	0.0047934	5.8E-10
11	BUD13 *	rs77966841	116627973	AC	A	0.0926895	-0.0308996	0.0043535	1.3E-13
11	BUD13 *	rs10892000	116628145	G	T	0.1485090	0.0350417	0.0035479	2.9E-22
11	BUD13 *	rs11216054	116628234	C	T	0.1485160	0.0350743	0.0035480	2.7E-22
11	BUD13 *	rs11216055	116629871	T	C	0.0936478	-0.0306574	0.0043239	1.7E-13
11	BUD13 *	rs11216056	116629912	A	C	0.0936939	-0.0306203	0.0043227	1.8E-13
11	BUD13 *	rs11216057	116630051	T	C	0.0936384	-0.0304391	0.0043208	2.4E-13
11	BUD13 *	rs77649044	116630336	C	T	0.0936612	-0.0302546	0.0043186	3.2E-13
11	BUD13 *	rs76055915	116630355	T	C	0.0936704	-0.0302430	0.0043185	3.2E-13
11	BUD13 *	rs74424292	116630372	T	A	0.0936704	-0.0302430	0.0043185	3.2E-13
11	BUD13 *	rs76267862	116630652	C	CCTT	0.0938359	-0.0306516	0.0043144	1.5E-13
11	BUD13 *	rs11216059	116631270	A	C	0.0940127	-0.0313663	0.0043094	4.0E-14
11	BUD13 *	rs11216060	116631550	A	G	0.0946398	-0.0316925	0.0042988	2.7E-14
11	BUD13 *	rs58675830	116631757	TATTG	T	0.0939892	-0.0319483	0.0043085	1.4E-14
11	BUD13 *	rs11216061	116632035	C	T	0.0939436	-0.0319899	0.0043093	1.4E-14
11	BUD13 *	rs11216062	116632051	A	C	0.0939574	-0.0319883	0.0043091	1.3E-14
11	BUD13 *	rs11216063	116632059	A	T	0.0939574	-0.0319883	0.0043091	1.3E-14
11	BUD13 *	rs11216064	116632106	C	G	0.0939620	-0.0319595	0.0043090	1.4E-14
11	BUD13 *	rs4502019	116632117	G	C	0.1440830	0.0354823	0.0036089	6.2E-22
11	BUD13 *	rs60952109	116632129	CT	C	0.0941480	-0.0316180	0.0043052	2.4E-14
11	BUD13 *	rs7946423	116632686	T	A	0.1458120	0.0350189	0.0036016	2.4E-21
11	BUD13 *	rs2096961	116632927	A	G	0.0919036	-0.0316930	0.0043617	4.0E-14
11	BUD13 *	rs11216067	116633660	G	A	0.0934892	-0.0319434	0.0043255	1.8E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs76801336	116634037	C	T	0.0927764	-0.0321387	0.0043462	1.7E-14
11	BUD13 *	rs59232710	116634267	G	A	0.0917011	-0.0321885	0.0043826	2.2E-14
11	BUD13 *	rs11216068	116634522	T	C	0.1368630	0.0394219	0.0037298	2.5E-25
11	BUD13 *	rs10892001	116634723	A	G	0.1405370	0.0416081	0.0036954	1.3E-28
11	BUD13 *	rs10892002	116634775	C	G	0.1404130	0.0415730	0.0036972	1.6E-28
11	BUD13 *	rs2077334	116635693	A	C	0.0897286	-0.0339511	0.0044586	2.0E-15
11	BUD13 *	rs77983701	116636339	C	T	0.0900533	-0.0341897	0.0044566	1.1E-15
11	BUD13 *	rs74948313	116636865	G	A	0.0956095	-0.0378144	0.0043755	2.2E-19
11	BUD13 *	rs76747451	116638116	G	T	0.0831297	-0.0400916	0.0046154	1.5E-19
11	BUD13 *	rs725524	116639652	A	G	0.0833884	-0.0405645	0.0046026	4.2E-20
11	BUD13 *	rs79315770	116639825	A	T	0.0834860	-0.0403202	0.0045997	6.2E-20
11	BUD13 *	rs184616707	116639841	G	C	0.0297478	0.0899234	0.0074833	2.1E-34
11	BUD13 *	rs117437529	116641735	T	C	0.0873934	-0.0401585	0.0044750	1.0E-20
11	BUD13 *	rs116892227	116642030	A	G	0.0887913	-0.0399838	0.0044305	1.3E-20
11	BUD13 *	rs1145184	116642465	A	G	0.1375090	0.0361496	0.0037029	3.7E-23
11	BUD13 *	rs117239953	116642471	C	T	0.0924010	-0.0386299	0.0043416	3.8E-20
11	BUD13 *	rs116859831	116642711	C	T	0.0925808	-0.0388986	0.0043373	2.0E-20
11	BUD13 *	rs78642155	116643375	C	G	0.0919784	-0.0387530	0.0043534	3.8E-20
11	BUD13 *	rs116948654	116643602	C	T	0.0920777	-0.0389908	0.0043545	2.4E-20
11	BUD13 *	rs117689643	116643612	T	G	0.0920773	-0.0389590	0.0043546	2.6E-20
11	BUD13 *	rs191049803	116643878	A	G	0.0203490	-0.0539426	0.0088691	2.0E-09
11	BUD13 *	rs1145185	116643982	A	G	0.1374610	0.0366388	0.0036711	1.8E-24
11	BUD13 *	rs78221557	116644811	A	G	0.2128750	0.0254377	0.0031260	3.0E-17
11	BUD13 *	rs71480306	116644840	C	T	0.1423960	0.0374557	0.0035998	2.0E-26
11	BUD13 *	rs11216072	116645635	C	T	0.0263851	-0.0489803	0.0078685	4.3E-10
11	BUD13 *	chr11:116645661_CA_C	116645661	C	CA	0.0982242	-0.0377240	0.0043061	1.5E-19
11	BUD13 *	rs139668970	116645673	T	TAAAAC	0.1418520	0.0375729	0.0036014	1.2E-26
11	BUD13 *	rs869271932	116645674	A	AAAAC	0.1426420	0.0374267	0.0035921	1.9E-26
11	BUD13 *	rs2212428	116645870	T	C	0.0918718	-0.0411117	0.0043732	2.3E-22
11	BUD13 *	rs1002037	116646019	C	G	0.0963080	-0.0416420	0.0042994	5.5E-24
11	BUD13 *	rs71480307	116646156	A	G	0.1421380	0.0376880	0.0035981	1.0E-26
11	BUD13 *	rs35165288	116646608	C	T	0.1427660	0.0373109	0.0035903	2.6E-26
11	BUD13 *	rs1124874	116647291	A	G	0.0893516	-0.0410608	0.0044285	1.1E-21
11	BUD13 *	rs117338034	116648026	G	T	0.0893199	-0.0411444	0.0044303	8.9E-22
11	BUD13 *	rs1240771	116648172	G	A	0.2288380	0.0239977	0.0029899	1.6E-16
11	BUD13 *	rs73580632	116648184	T	C	0.0893021	-0.0411495	0.0044310	9.1E-22
11	BUD13 *	rs1261672	116648243	G	A	0.2284430	0.0241574	0.0029907	1.0E-16
11	BUD13 *	rs1240772	116648412	C	G	0.3201310	0.0257308	0.0027349	8.4E-22
11	BUD13 *	rs513533	116648641	G	A	0.1155190	0.0483751	0.0039441	2.1E-35
11	BUD13 *	rs516043	116648867	G	C	0.1155660	0.0480869	0.0039432	5.1E-35
11	BUD13 *	rs499790	116649022	T	C	0.1155410	0.0481192	0.0039432	4.5E-35
11	BUD13 *	rs504268	116649487	T	C	0.1155430	0.0481562	0.0039431	4.1E-35
11	BUD13 *	rs544479	116649681	C	T	0.1155530	0.0480877	0.0039428	5.1E-35
11	BUD13 *	rs506222	116649717	C	A	0.1155540	0.0480950	0.0039428	5.0E-35
11	BUD13 *	rs1240773	116649810	T	G	0.2291350	0.0240998	0.0029835	9.5E-17
11	BUD13 *	rs549125	116650209	G	C	0.1193300	0.0503451	0.0038872	2.1E-39
11	BUD13 *	rs533668	116650418	G	T	0.1193290	0.0503454	0.0038872	2.1E-39
11	BUD13 *	rs573985	116650599	A	G	0.1191800	0.0505373	0.0038889	1.3E-39
11	BUD13 *	rs575906	116650841	G	A	0.1194970	0.0504456	0.0038852	1.5E-39
11	BUD13 *	rs143762798	116650954	A	G	0.0204627	-0.0536994	0.0088882	3.7E-09
11	BUD13 *	rs562756	116651258	C	G	0.1192530	0.0497605	0.0038887	1.5E-38
11	BUD13 *	rs491022	116651271	C	T	0.1369870	0.0390065	0.0037148	2.7E-26
11	BUD13 *	rs563796	116651394	G	A	0.1202060	0.0504313	0.0038722	1.1E-39
11	BUD13 *	rs563917	116651439	T	C	0.1202290	0.0504771	0.0038717	9.0E-40
11	BUD13 *	rs492182	116651447	A	G	0.1202590	0.0506008	0.0038710	5.5E-40
11	BUD13 *	rs5795043	116651516	T	TC	0.1111000	0.0490159	0.0040335	1.4E-35
11	BUD13 *	rs565607	116651613	T	C	0.1202280	0.0506795	0.0038710	3.7E-40
11	BUD13 *	rs567576	116651842	G	A	0.1201390	0.0509111	0.0038681	1.6E-40
11	BUD13 *	rs567599	116651848	T	G	0.1201590	0.0509804	0.0038677	1.3E-40
11	BUD13 *	rs3017237	116651908	C	G	0.1203040	0.0508200	0.0038646	1.9E-40
11	BUD13 *	rs480028	116652053	G	C	0.1203340	0.0508329	0.0038632	1.9E-40
11	BUD13 *	rs480878	116652137	A	G	0.1208040	0.0504632	0.0038588	5.4E-40
11	BUD13 *	rs499563	116652244	T	C	0.1205180	0.0508689	0.0038604	1.3E-40
11	BUD13 *	rs138535309	116652253	C	CTT	0.1202560	0.0507950	0.0038638	2.0E-40
11	BUD13 *	rs202191031	116652259	A	AAGTGG	0.1202560	0.0507950	0.0038638	2.0E-40
11	BUD13 *	rs79770434	116652448	T	C	0.0860100	-0.0422057	0.0045133	5.9E-22
11	BUD13 *	rs483747	116652450	C	T	0.1203620	0.0508155	0.0038627	2.0E-40
11	BUD13 *	rs141584077	116652587	T	A	0.1127110	0.0492113	0.0040084	2.4E-35
11	BUD13 *	rs523980	116652589	T	A	0.1074760	0.0489761	0.0041101	2.8E-33
11	BUD13 *	rs485638	116652656	C	G	0.1203580	0.0508223	0.0038628	1.9E-40
11	BUD13 *	rs117742492	116652940	A	G	0.0858233	-0.0424085	0.0045210	4.7E-22
11	BUD13 *	rs528647	116653104	T	C	0.1203620	0.0508441	0.0038624	1.8E-40

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs528732	116653127	A	G	0.1203620	0.0508441	0.0038624	1.8E-40
11	BUD13 *	rs3017778	116653214	T	C	0.1203310	0.0508615	0.0038631	1.7E-40
11	BUD13 *	rs3017779	116653271	T	C	0.1202970	0.0509002	0.0038634	1.5E-40
11	BUD13 *	rs76860051	116654589	C	A	0.0854292	-0.0431955	0.0045364	9.5E-23
11	BUD13 *	rs79862998	116654602	A	G	0.0852459	-0.0437193	0.0045424	3.3E-23
11	BUD13 *	rs480823	116655013	C	T	0.1152070	0.0553667	0.0039793	6.8E-45
11	BUD13 *	rs481843	116655150	T	C	0.1144180	0.0553582	0.0039965	2.1E-44
11	BUD13 *	rs116857027	116655278	T	C	0.0852285	-0.0438436	0.0045447	2.9E-23
11	BUD13 *	rs34485603	116655315	C	CCT	0.1143810	0.0551456	0.0039997	4.6E-44
11	BUD13 *	rs486394	116655605	C	A	0.1177800	0.0565633	0.0039574	4.1E-47
11	BUD13 *	rs78347813	116658413	T	C	0.0845359	-0.0466274	0.0045435	5.5E-26
11	BUD13 *	rs117935983	116658471	G	T	0.1823780	0.0276572	0.0033113	2.1E-17
11	BUD13 *	rs1892947	116659344	A	G	0.0868277	-0.0469905	0.0044696	3.0E-27
11	BUD13 *	rs116905034	116659391	C	G	0.0641886	0.0342520	0.0052243	9.4E-12
11	BUD13 *	rs146893332	116660321	AGGGGGG	T	0.0644477	0.0343119	0.0052128	9.0E-12
11	BUD13 *	rs117889066	116660333	C	G	0.0876076	-0.0472851	0.0044431	8.3E-28
11	BUD13 *	rs117293980	116660758	G	T	0.0876076	-0.0472925	0.0044431	7.8E-28
11	BUD13 *	rs2155216	116661022	T	C	0.1926120	0.0241796	0.0031912	4.8E-15
11	BUD13 *	rs2186670	116661233	T	C	0.1926260	0.0242001	0.0031909	4.5E-15
11	BUD13 *	rs7117145	116661252	T	A	0.0877919	-0.0469900	0.0044377	1.7E-27
11	BUD13 *	rs1944153	116661504	C	T	0.1926360	0.0241878	0.0031907	4.6E-15
11	BUD13 *	rs78198334	116661566	C	G	0.0877919	-0.0469900	0.0044377	1.7E-27
11	BUD13 *	rs118175510	116661831	C	T	0.0817688	0.0676352	0.0046265	1.1E-48
11	BUD13 *	rs79291519	116662593	T	C	0.0865802	-0.0474385	0.0044642	1.3E-27
11	BUD13 *	rs75942205	116662878	C	T	0.0867660	-0.0471393	0.0044588	2.8E-27
11	BUD13 *	rs61659529	116662911	G	A	0.0867738	-0.0471848	0.0044589	2.2E-27
11	BUD13 *	rs486915	116663571	T	A	0.3674020	-0.0473919	0.0026688	3.3E-73
11	BUD13 *	rs146134775	116663577	C	CT	0.0867206	-0.0465434	0.0044636	1.2E-26
11	BUD13 *	rs76547220	116663833	G	T	0.0868038	-0.0471038	0.0044588	2.7E-27
11	BUD13 *	rs567209	116664111	T	C	0.1678840	0.0251037	0.0033933	1.7E-14
11	BUD13 *	rs2105609	116664370	A	G	0.0868030	-0.0471077	0.0044589	2.6E-27
11	BUD13 *	rs2105610	116664409	C	T	0.0863474	-0.0469058	0.0044714	5.2E-27
11	BUD13 *	rs77226464	116664718	T	C	0.0869312	-0.0469854	0.0044574	2.7E-27
11	BUD13 *	rs190069353	116664907	A	C	0.0867737	-0.0470362	0.0044603	3.2E-27
11	BUD13 *	rs117014628	116664914	T	C	0.0867934	-0.0469710	0.0044595	3.7E-27
11	BUD13 *	rs1240776	116665564	T	C	0.3738460	-0.0477144	0.0026058	2.0E-78
11	BUD13 *	rs12803249	116665701	G	A	0.1679230	0.0250710	0.0033925	1.8E-14
11	BUD13 *	rs1240777	116665759	C	T	0.2009560	0.0245639	0.0031365	7.0E-16
11	BUD13 *	rs1240778	116665773	C	A	0.3718850	0.0327692	0.0026365	6.8E-38
11	BUD13 *	rs10892010	116665939	C	A	0.2476160	0.0190883	0.0029534	7.9E-11
11	BUD13 *	rs79063991	116666103	T	C	0.0867919	-0.0469386	0.0044598	4.0E-27
11	BUD13 *	rs61906081	116666342	A	G	0.1679440	0.0250073	0.0033922	2.0E-14
11	BUD13 *	rs118103820	116666399	G	A	0.0867919	-0.0469386	0.0044598	4.0E-27
11	BUD13 *	rs6589557	116667044	T	C	0.4240730	0.0294762	0.0025464	2.8E-32
11	BUD13 *	rs140973748	116667081	C	T	0.0868005	-0.0469401	0.0044597	4.0E-27
11	BUD13 *	rs35933073	116667129	A	C	0.1679730	0.0249994	0.0033917	2.0E-14
11	BUD13 *	rs6589558	116667225	A	G	0.4240730	0.0294782	0.0025464	2.8E-32
11	BUD13 *	rs1784125	116667245	C	G	0.2009470	0.0246149	0.0031363	6.1E-16
11	BUD13 *	rs12787592	116667257	C	G	0.1679810	0.0250022	0.0033916	2.0E-14
11	BUD13 *	rs143380339	116667386	A	C	0.0868005	-0.0469401	0.0044597	4.0E-27
11	BUD13 *	rs1784126	116667498	T	G	0.3718140	-0.0474429	0.0026066	1.3E-77
11	BUD13 *	rs1784127	116667859	A	G	0.3721480	-0.0474615	0.0026062	1.2E-77
11	BUD13 *	rs1784128	116667972	A	G	0.3721590	-0.0474920	0.0026062	1.0E-77
11	BUD13 *	rs1632755	116668134	C	A	0.2009870	0.0246306	0.0031367	5.9E-16
11	BUD13 *	rs1787682	116668486	G	C	0.2009470	0.0246058	0.0031363	6.3E-16
11	BUD13 *	rs150937658	116668605	G	A	0.0998024	-0.0357583	0.0042485	9.0E-17
11	BUD13 *	rs9681206	116668801	T	C	0.2495550	0.0185699	0.0029438	2.3E-10
11	BUD13 *	rs1784131	116669151	C	T	0.2006800	0.0245881	0.0031385	6.9E-16
11	BUD13 *	rs11216085	116669432	C	T	0.2495950	0.0186077	0.0029438	2.1E-10
11	BUD13 *	rs2846015	116669722	T	C	0.2009450	0.0246146	0.0031363	6.1E-16
11	BUD13 *	rs3016354	116670075	C	T	0.2009540	0.0245832	0.0031362	6.5E-16
11	BUD13 *	rs3017337	116670090	T	C	0.2011310	0.0247818	0.0031366	3.8E-16
11	BUD13 *	rs7925553	116670267	G	A	0.1682000	0.0249147	0.0033885	2.2E-14
11	BUD13 *	rs144188664	116670317	T	A	0.0868024	-0.0469643	0.0044602	3.9E-27
11	BUD13 *	rs1784133	116670700	T	C	0.2009520	0.0245756	0.0031362	6.6E-16
11	BUD13 *	rs1787686	116670755	A	G	0.2849870	-0.0362697	0.0027935	2.5E-40
11	BUD13 *	rs2846016	116670822	T	C	0.2006730	0.0246689	0.0031384	5.6E-16
11	BUD13 *	rs36195057	116671530	A	G	0.2497440	0.0186299	0.0029427	2.0E-10
11	BUD13 *	rs1787692	116671779	G	T	0.4604230	0.0156860	0.0025562	1.5E-10
11	BUD13 *	rs148462279	116672020	G	A	0.0868171	-0.0469706	0.0044603	3.8E-27
11	BUD13 *	rs75930640	116672095	T	G	0.2009490	0.0245717	0.0031362	6.7E-16
11	BUD13 *	rs144256947	116672308	C	T	0.0867428	-0.0469848	0.0044626	4.3E-27

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs111446876	116672353	T	TA	0.2496940	0.0187646	0.0029431	1.6E-10
11	BUD13 *	rs113264811	116672394	T	C	0.2027640	0.0249057	0.0031277	2.8E-16
11	BUD13 *	rs12294322	116672835	G	A	0.2009430	0.0245815	0.0031361	6.5E-16
11	BUD13 *	chr11:116672851_TA_T	116672851	TA	T	0.2849870	-0.0362749	0.0027936	2.4E-40
11	BUD13 *	chr11:116673046_T_TA	116673046	TA	T	0.0917805	0.0243237	0.0043828	2.0E-08
11	BUD13 *	rs74724948	116673298	T	A	0.1982980	0.0233997	0.0031576	1.7E-14
11	BUD13 *	chr11:116674066_A_ATAT	116674066	ATATT	A	0.0864374	-0.0472969	0.0044727	2.4E-27
11	BUD13 *	rs180815846	116674155	G	T	0.2437660	0.0189832	0.0029754	1.3E-10
11	BUD13 *	rs117179746	116674534	A	G	0.0865633	-0.0472186	0.0044691	3.2E-27
11	BUD13 *	rs3016355	116674778	T	A	0.2009380	0.0245914	0.0031361	6.4E-16
11	BUD13 *	rs11530558	116674881	C	A	0.0252591	0.0548522	0.0080526	1.9E-12
11	BUD13 *	rs1787688	116675006	C	T	0.2845100	-0.0362019	0.0027966	4.6E-40
11	BUD13 *	rs78106248	116675263	CA	C	0.1721680	0.0238342	0.0033669	2.1E-13
11	BUD13 *	rs61906102	116675786	C	T	0.1724290	0.0237092	0.0033640	2.6E-13
11	BUD13 *	rs116944258	116675916	A	C	0.0869292	-0.0473719	0.0044618	1.9E-27
11	BUD13 *	rs58672319	116676219	T	TG	0.2840790	-0.0360610	0.0027977	9.9E-40
11	BUD13 *	rs1960036	116676692	A	C	0.1724240	0.0236621	0.0033637	3.0E-13
11	BUD13 *	rs1614444	116676831	G	A	0.2012030	0.0244302	0.0031379	9.5E-16
11	BUD13 *	rs372407480	116677221	A	C	0.0139471	0.0728576	0.0107932	2.7E-12
11	BUD13 *	rs868329903	116677410	C	A	0.0674538	-0.0508437	0.0050863	8.3E-25
11	BUD13 *	rs12801136	116677632	A	G	0.1724490	0.0236550	0.0033635	3.0E-13
11	BUD13 *	rs79678269	116678255	C	G	0.0870218	-0.0474593	0.0044616	1.5E-27
11	BUD13 *	rs1005705	116678399	C	A	0.0869088	-0.0474899	0.0044632	1.4E-27
11	BUD13 *	rs74792494	116678691	C	A	0.1983260	0.0237899	0.0031538	6.0E-15
11	BUD13 *	chr11:116678728_T_TGA	116678728	TGA	T	0.0869164	-0.0474515	0.0044631	1.5E-27
11	BUD13 *	chr11:116678738_A_AGAA	116678738	AGAAT	A	0.1988850	0.0249345	0.0031571	4.5E-16
11	BUD13 *	rs58060512	116678740	A	AAT	0.1712040	0.0235264	0.0033944	6.7E-13
11	BUD13 *	rs1787687	116679179	G	A	0.2009810	0.0245635	0.0031351	6.8E-16
11	BUD13 *	rs35963862	116679180	C	T	0.1685270	0.0246029	0.0033850	4.7E-14
11	BUD13 *	rs117830617	116679254	A	G	0.0869186	-0.0474467	0.0044633	1.6E-27
11	BUD13 *	rs61906104	116679398	G	A	0.1724870	0.0235014	0.0033630	4.1E-13
11	BUD13 *	rs11216091	116679966	G	A	0.0215433	-0.0556061	0.0086771	3.6E-11
11	BUD13 *	rs12417015	116680059	G	A	0.1980560	0.0235533	0.0031554	1.1E-14
11	BUD13 *	chr11:116681564_G_GA	116681564	GA	G	0.1725620	0.0234356	0.0033617	4.9E-13
11	BUD13 *	rs1787717	116682049	T	C	0.3693920	-0.0480230	0.0026152	8.8E-79
11	BUD13 *	rs12806224	116682098	C	T	0.1723730	0.0234124	0.0033644	5.4E-13
11	BUD13 *	rs113194822	116682143	A	G	0.0921971	0.0256316	0.0043785	3.4E-09
11	BUD13 *	rs12805061	116682308	G	A	0.1726260	0.0234760	0.0033612	4.5E-13
11	BUD13 *	rs5795046	116682757	T	TG	0.3694090	-0.0478138	0.0026152	4.0E-78
11	BUD13 *	rs11826999	116683062	A	G	0.1727240	0.0233324	0.0033613	6.7E-13
11	BUD13 *	rs71480312	116683372	T	C	0.0984891	0.0234884	0.0042471	2.3E-08
11	BUD13 *	rs66560466	116683783	T	TG	0.2832340	-0.0360051	0.0027945	9.8E-40
11	BUD13 *	rs35310854	116684317	TA	T	0.1727700	0.0234512	0.0033612	5.0E-13
11	BUD13 *	rs117341026	116684410	A	G	0.0856720	-0.0491212	0.0045039	8.9E-29
11	BUD13 *	rs7932330	116684491	G	A	0.2468090	0.0191604	0.0029607	5.9E-11
11	BUD13 *	rs35681250	116684670	T	A	0.1729890	0.0232644	0.0033631	7.6E-13
11	BUD13 *	rs3016357	116684699	T	C	0.2910390	-0.0374679	0.0028087	6.9E-43
11	BUD13 *	rs1145213	116684706	G	A	0.2944200	-0.0356867	0.0028074	4.8E-39
11	BUD13 *	rs77835865	116684713	G	A	0.1727630	0.0233916	0.0033613	5.7E-13
11	BUD13 *	rs956832572	116684717	T	A	0.0142068	0.0729376	0.0106921	1.7E-12
11	BUD13 *	rs71037408	116684780	C	CTG	0.0914223	0.0256507	0.0043978	3.4E-09
11	BUD13 *	rs61906112	116685049	A	T	0.1726930	0.0235316	0.0033620	4.3E-13
11	BUD13 *	rs17092638	116685520	G	C	0.1727060	0.0238164	0.0033628	2.5E-13
11	BUD13 *	rs1145212	116686149	A	G	0.4528140	0.0313588	0.0025665	1.9E-35
11	BUD13 *	rs2156120	116686439	G	A	0.2495620	0.0192412	0.0029490	4.5E-11
11	BUD13 *	rs1145211	116686500	A	C	0.2828430	-0.0364352	0.0028093	2.1E-40
11	BUD13 *	rs17092642	116686532	C	T	0.1725990	0.0240094	0.0033665	1.7E-13
11	BUD13 *	rs947990	116686598	T	G	0.0622334	-0.0472825	0.0052302	1.1E-18
11	BUD13 *	rs11216093	116687166	C	A	0.2502930	0.0193437	0.0029491	3.7E-11
11	BUD13 *	rs61906115	116687529	A	T	0.1684350	0.0252143	0.0033919	1.5E-14
11	BUD13 *	rs12799766	116687711	A	G	0.1684360	0.0252695	0.0033921	1.3E-14
11	BUD13 *	rs12799441	116687799	T	A	0.1685580	0.0253059	0.0033914	1.2E-14
11	BUD13 *	rs12799449	116687809	G	A	0.1685900	0.0253966	0.0033920	1.0E-14
11	BUD13 *	rs80134543	116688524	C	CTT	0.0805289	0.0319688	0.0046894	1.5E-11
11	BUD13 *	rs77277788	116688720	T	C	0.0924672	0.0240662	0.0043597	3.0E-08
11	BUD13 *	rs11824135	116688837	T	G	0.2022740	0.0186108	0.0031893	1.0E-09
11	BUD13 *	rs11828763	116688947	G	A	0.2129230	0.0207418	0.0031070	7.6E-12
11	BUD13 *	rs3016360	116689027	C	T	0.2134720	0.0205883	0.0031021	1.2E-11
11	BUD13 *	rs1787716	116689458	A	G	0.1997010	0.0257494	0.0031527	8.9E-17
11	BUD13 *	rs1787715	116689609	T	C	0.1996990	0.0257314	0.0031527	9.4E-17
11	BUD13 *	rs1623797	116689731	T	C	0.4313340	-0.0428857	0.0025687	5.5E-66
11	BUD13 *	rs34937367	116689808	C	T	0.1998410	0.0256530	0.0031528	1.1E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs74330350	116689812	G	A	0.1998410	0.0256530	0.0031528	1.1E-16
11	BUD13 *	rs79280888	116689813	G	A	0.1998410	0.0256530	0.0031528	1.1E-16
11	BUD13 *	rs1787714	116689894	A	G	0.2458000	-0.0483777	0.0029637	1.3E-62
11	BUD13 *	rs1787713	116689895	G	C	0.2458000	-0.0483777	0.0029637	1.3E-62
11	BUD13 *	rs12291024	116689951	G	T	0.3660430	0.0273450	0.0026294	7.1E-27
11	BUD13 *	rs1787711	116690062	G	A	0.1997240	0.0256513	0.0031523	1.1E-16
11	BUD13 *	rs3017232	116690167	T	C	0.2000490	0.0257791	0.0031504	7.8E-17
11	BUD13 *	rs3017231	116690232	A	G	0.1997280	0.0256249	0.0031522	1.2E-16
11	BUD13 *	rs3017230	116690245	C	G	0.1997260	0.0256208	0.0031522	1.2E-16
11	BUD13 *	rs3017229	116690251	A	G	0.2475020	-0.0488154	0.0029533	6.4E-64
11	BUD13 *	rs3017228	116690276	G	A	0.1997260	0.0256208	0.0031522	1.2E-16
11	BUD13 *	rs1787710	116690486	A	G	0.1997330	0.0255551	0.0031521	1.4E-16
11	BUD13 *	rs76483212	116690550	A	G	0.0922849	0.0254938	0.0043528	3.9E-09
11	BUD13 *	rs1787709	116690612	G	C	0.1997240	0.0255397	0.0031520	1.5E-16
11	BUD13 *	rs1784123	116690665	C	T	0.1997170	0.0255450	0.0031519	1.5E-16
11	BUD13 *	rs1787708	116690677	A	G	0.1997490	0.0255447	0.0031516	1.5E-16
11	BUD13 *	rs116505113	116690754	A	C	0.1991760	0.0245849	0.0031576	2.0E-15
11	BUD13 *	rs116116656	116690755	A	T	0.1991760	0.0245849	0.0031576	2.0E-15
11	BUD13 *	rs116365797	116690756	A	C	0.1991760	0.0245849	0.0031576	2.0E-15
11	BUD13 *	rs118013839	116690798	A	G	0.0834678	-0.0500681	0.0045741	2.6E-29
11	BUD13 *	rs1784122	116690985	A	T	0.1997750	0.0255905	0.0031511	1.3E-16
11	BUD13 *	rs1784121	116691074	T	G	0.4305400	-0.0427181	0.0025719	1.8E-65
11	BUD13 *	rs1784120	116691143	G	C	0.1997780	0.0256149	0.0031511	1.3E-16
11	BUD13 *	rs1787706	116691212	A	G	0.1997780	0.0256149	0.0031511	1.3E-16
11	BUD13 *	rs1787705	116691222	A	G	0.1997810	0.0256015	0.0031511	1.3E-16
11	BUD13 *	rs1787704	116691280	T	C	0.4320130	-0.0431272	0.0025687	1.1E-66
11	BUD13 *	rs1787703	116691550	T	C	0.1997750	0.0255717	0.0031511	1.4E-16
11	BUD13 *	rs1787702	116691572	A	G	0.1997750	0.0255717	0.0031511	1.4E-16
11	BUD13 *	rs11216096	116691864	A	C	0.3661120	0.0274458	0.0026270	4.4E-27
11	BUD13 *	rs117393825	116691971	T	C	0.1003710	-0.0375006	0.0042331	7.3E-19
11	BUD13 *	rs35256265	116691985	ACC	A	0.1997800	0.0256568	0.0031512	1.1E-16
11	BUD13 *	rs1784119	116692089	T	C	0.2474350	-0.0490091	0.0029533	2.0E-64
11	BUD13 *	rs12785772	116692892	A	G	0.3661590	0.0274054	0.0026281	5.0E-27
11	BUD13 *	rs12785990	116692990	A	G	0.3643440	0.0282472	0.0026311	1.4E-28
11	BUD13 *	rs79962987	116693078	T	G	0.0391056	-0.0504189	0.0064828	4.8E-15
11	BUD13 *	rs12420888	116693106	G	C	0.3645850	0.0282522	0.0026298	1.3E-28
11	BUD13 *	rs1787701	116693276	C	G	0.3349830	-0.0593795	0.0027041	1.1E-111
11	BUD13 *	chr11:116693645_G_GCA	116693645	GCA	G	0.1871240	0.0248411	0.0032611	1.3E-14
11	BUD13 *	rs117889337	116693777	T	C	0.0827880	-0.0506926	0.0045914	8.6E-30
11	BUD13 *	rs1787699	116693837	G	A	0.2465530	-0.0495633	0.0029600	1.2E-65
11	BUD13 *	rs1787698	116693846	T	C	0.2465500	-0.0495531	0.0029600	1.2E-65
11	BUD13 *	rs1784118	116694339	T	C	0.2493910	-0.0495545	0.0029460	3.4E-66
11	BUD13 *	rs12293222	116694593	A	G	0.2869950	0.0308802	0.0028022	1.3E-28
11	BUD13 *	rs111226221	116694718	T	C	0.0920153	0.0251738	0.0043614	5.5E-09
11	BUD13 *	rs117607796	116694887	A	C	0.0832332	-0.0502998	0.0045805	1.7E-29
11	BUD13 *	rs111218525	116695822	T	C	0.2062820	0.0270213	0.0031383	5.2E-19
11	BUD13 *	rs59854309	116696047	T	C	0.2548490	-0.0505516	0.0029548	2.4E-68
11	BUD13 *	rs60954647	116696217	T	C	0.4084530	-0.0307220	0.0026102	5.7E-33
11	BUD13 *	rs1784106	116696733	A	C	0.2515400	-0.0503435	0.0029405	4.8E-68
11	BUD13 *	rs78888567	116696897	A	G	0.0958563	0.0244261	0.0042856	8.1E-09
11	BUD13 *	rs4938300	116696903	T	C	0.2031120	0.0306713	0.0031425	1.3E-23
11	BUD13 *	rs10892017	116697165	C	G	0.3600340	0.0314473	0.0026212	6.6E-35
11	BUD13 *	rs66473272	116697382	G	GT	0.3525420	0.0319961	0.0026551	5.6E-35
11	BUD13 *	rs11605568	116697452	A	G	0.3599870	0.0314456	0.0026212	7.2E-35
11	BUD13 *	rs11606013	116697509	T	G	0.3600440	0.0313933	0.0026209	8.8E-35
11	BUD13 *	rs140078194	116697574	A	C	0.0865335	-0.0489829	0.0044995	1.2E-28
11	BUD13 *	rs11608173	116697648	A	T	0.3600480	0.0313746	0.0026208	9.4E-35
11	BUD13 *	rs1787689	116697666	G	A	0.4419190	-0.0438598	0.0025493	5.0E-69
11	BUD13 *	rs1787690	116697800	T	G	0.2513970	-0.0498434	0.0029337	4.4E-67
11	BUD13 *	rs1787691	116697997	A	G	0.4413080	-0.0438998	0.0025488	3.5E-69
11	BUD13 *	rs947986	116698488	A	G	0.2500230	-0.0497432	0.0029401	1.7E-66
11	BUD13 *	rs3017338	116698629	A	G	0.4412970	-0.0430171	0.0025527	3.0E-66
11	BUD13 *	rs71037412	116699941	CA	C	0.4438910	-0.0431923	0.0025439	3.4E-67
11	BUD13 *	rs1145191	116700002	G	C	0.4438910	-0.0431923	0.0025439	3.4E-67
11	BUD13 *	rs200445365	116700100	A	AAAAAAAA	0.0863865	-0.0486866	0.0045041	2.6E-28
11	BUD13 *	rs150808564	116700125	T	C	0.0415643	-0.0563671	0.0063197	1.5E-19
11	BUD13 *	rs1145193	116700226	G	A	0.4452450	-0.0434953	0.0025431	3.3E-68
11	BUD13 *	rs1145194	116700252	A	C	0.2490890	-0.0505755	0.0029480	3.8E-68
11	BUD13 *	rs11601168	116700422	A	T	0.0785915	-0.0484854	0.0046686	1.5E-24
11	BUD13 *	rs1145195	116700534	A	G	0.4439870	-0.0432799	0.0025438	1.7E-67
11	BUD13 *	rs11601584	116700568	C	T	0.3489430	0.0330833	0.0026286	2.4E-38
11	BUD13 *	rs61905066	116700892	G	A	0.2075390	0.0183658	0.0031218	4.4E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs1892948	116701373	T	C	0.2067830	0.0183819	0.0031262	4.8E-09
11	BUD13 *	rs1145196	116701489	T	C	0.4443100	-0.0431773	0.0025440	3.7E-67
11	BUD13 *	rs1240783	116701809	C	T	0.4442780	-0.0432231	0.0025443	2.6E-67
11	BUD13 *	rs11216100	116701814	G	C	0.3446590	0.0335164	0.0026406	9.4E-39
11	BUD13 *	rs879858	116702404	A	G	0.2066620	0.0186810	0.0031302	2.7E-09
11	BUD13 *	rs947989	116702805	A	C	0.4510460	-0.0430898	0.0025854	2.6E-65
11	BUD13 *	rs882398	116703122	C	T	0.2074170	0.0184512	0.0031292	3.8E-09
11	BUD13 *	rs77206548	116703747	A	G	0.0865899	-0.0492029	0.0045006	8.4E-29
11	BUD13 *	rs11216103	116703772	A	G	0.2038700	0.0183737	0.0031521	6.0E-09
11	BUD13 *	rs1240782	116703868	A	G	0.3514990	-0.0298033	0.0026686	4.1E-30
11	BUD13 *	rs10617144	116703898	CTG	C	0.3513190	-0.0296862	0.0026693	7.7E-30
11	BUD13 *	rs1240781	116704101	T	C	0.2440510	-0.0495996	0.0029736	1.6E-64
11	BUD13 *	rs1268832	116704513	T	G	0.3047340	-0.0238083	0.0027721	1.2E-18
11	BUD13 *	rs4938301	116704757	A	G	0.2060590	0.0282165	0.0031306	3.4E-20
11	BUD13 *	rs1263058	116704839	A	G	0.3065260	-0.0225089	0.0027646	6.4E-17
11	BUD13 *	rs76124005	116704898	G	T	0.0871145	-0.0487479	0.0044888	1.8E-28
11	BUD13 *	rs12574790	116704971	T	C	0.0162472	-0.0604437	0.0100697	2.2E-10
11	BUD13 *	rs74939223	116705164	G	A	0.0871093	-0.0487151	0.0044897	2.0E-28
11	BUD13 *	rs59873384	116705494	T	C	0.0870340	-0.0487938	0.0044913	1.7E-28
11	BUD13 *	rs12802944	116705684	C	T	0.2045520	0.0299275	0.0031385	1.5E-22
11	BUD13 *	rs1263056	116705699	A	G	0.3425840	-0.0590236	0.0026932	6.8E-110
11	BUD13 *	rs1263055	116706327	A	G	0.2516310	-0.0500905	0.0029448	9.0E-67
11	BUD13 *	rs11216105	116706725	A	G	0.2516650	-0.0501217	0.0029458	1.1E-66
11	BUD13 *	rs117684324	116707255	T	A	0.0871103	-0.0487041	0.0044892	1.9E-28
11	BUD13 *	rs12221682	116707501	G	C	0.3085300	-0.0231392	0.0027723	6.4E-17
11	BUD13 *	rs11216107	116708947	C	T	0.4968920	0.0335593	0.0025343	7.9E-41
11	BUD13 *	rs148075162	116709936	C	G	0.0157659	0.0809272	0.0101453	8.8E-17
11	BUD13 *	rs61346349	116710082	G	A	0.1784820	-0.0528901	0.0032971	1.2E-59
11	BUD13 *	rs11216109	116710099	G	C	0.3106380	0.0759284	0.0027188	5.6E-177
11	BUD13 *	rs75476300	116710153	C	G	0.0545145	0.0872679	0.0055575	9.0E-57
11	BUD13 *	rs59620302	116710443	G	C	0.0861510	-0.0502804	0.0045012	4.6E-30
11	BUD13 *	rs2367970	116710925	A	G	0.3107840	0.0760033	0.0027189	2.3E-177
11	BUD13 *	rs77574778	116711084	T	C	0.0862108	-0.0501673	0.0044987	5.6E-30
11	BUD13 *	rs77646493	116711464	A	C	0.0861802	-0.0500655	0.0044991	7.6E-30
11	BUD13 *	rs74360954	116711826	T	C	0.0862212	-0.0500293	0.0044975	8.4E-30
11	BUD13 *	rs7480302	116712301	G	A	0.4951350	0.0332687	0.0025151	1.0E-40
11	BUD13 *	rs6589562	116712723	A	G	0.3113560	0.0756225	0.0027182	2.7E-175
11	BUD13 *	rs886022	116712797	A	C	0.2344910	-0.0600009	0.0029921	4.2E-92
11	BUD13 *	rs117450838	116712972	A	G	0.0680621	-0.0494402	0.0049998	8.4E-24
11	BUD13 *	rs151007118	116713148	T	G	0.0993218	0.0836259	0.0042468	3.2E-87
11	BUD13 *	rs1144035	116713601	C	T	0.2354920	-0.0601300	0.0029873	9.0E-93
11	BUD13 *	rs117837319	116713731	C	A	0.0847089	-0.0502409	0.0045379	1.6E-29
11	BUD13 *	rs4938302	116713788	C	T	0.4952170	0.0331676	0.0025131	1.7E-40
11	BUD13 *	rs4938303	116714271	C	T	0.4951830	0.0334131	0.0025113	3.9E-41
11	BUD13 *	rs79886324	116714728	A	G	0.0865497	-0.0506650	0.0044916	1.7E-30
11	BUD13 *	rs2000571	116714817	A	G	0.3102040	0.0767519	0.0027241	3.4E-180
11	BUD13 *	rs17119918	116714897	A	G	0.1084840	-0.0454816	0.0040706	3.6E-30
11	BUD13 *	rs34100096	116714909	A	G	0.1027890	0.0227364	0.0041368	1.7E-08
11	BUD13 *	rs117785509	116715515	A	G	0.0865879	-0.0505916	0.0044925	2.2E-30
11	BUD13 *	rs7350481	116715567	T	C	0.2356180	0.1148310	0.0029620	2.6E-335
11	BUD13 *	rs7926828	116715707	C	T	0.3136180	0.0800961	0.0027145	3.5E-197
11	BUD13 *	rs5795050	116716065	T	TC	0.1011700	0.0221235	0.0041626	4.4E-08
11	BUD13 *	rs151061355	116716138	A	G	0.0872563	-0.0512064	0.0044765	2.0E-31
11	BUD13 *	rs555105607	116716397	CT	C	0.0874885	-0.0506409	0.0044652	7.2E-31
11	BUD13 *	rs373804009	116716399	T	TG	0.0870418	-0.0506301	0.0044789	1.2E-30
11	BUD13 *	rs142290703	116716430	A	G	0.0874885	-0.0506409	0.0044652	7.2E-31
11	BUD13 *	rs4938304	116717709	T	C	0.0793315	-0.0502458	0.0046353	1.1E-26
11	BUD13 *	rs79408961	116717877	T	C	0.0543222	0.0913635	0.0055562	8.8E-63
11	BUD13 *	rs4938305	116717913	T	C	0.3122370	0.0820405	0.0027262	2.4E-205
11	BUD13 *	rs180378	116718193	A	G	0.3131460	0.0817745	0.0027234	1.5E-204
11	BUD13 *	rs10711344	116718401	TA	T	0.3124450	0.0819556	0.0027261	4.9E-205
11	BUD13 *	rs180377	116718411	T	C	0.3130810	0.0818815	0.0027236	5.5E-205
11	BUD13 *	rs10892020	116718936	G	C	0.3120330	0.0819737	0.0027274	8.3E-205
11	BUD13 *	rs180376	116719323	C	G	0.3280560	-0.0353947	0.0026979	1.6E-40
11	BUD13 *	rs118046012	116719812	A	G	0.0858068	-0.0512723	0.0045048	3.6E-31
11	BUD13 *	rs180375	116720324	T	C	0.3281400	-0.0353673	0.0026973	2.0E-40
11	BUD13 *	rs116962103	116720402	A	G	0.0216147	-0.0660393	0.0086897	1.1E-14
11	BUD13 *	rs180373	116720837	A	C	0.1662500	-0.0570597	0.0033922	6.4E-66
11	BUD13 *	rs147232672	116721147	A	C	0.0117001	0.1049870	0.0117263	1.6E-18
11	BUD13 *	rs180372	116721218	A	G	0.3272730	-0.0352730	0.0026989	5.2E-40
11	BUD13 *	rs180371	116721487	A	G	0.4163620	-0.0483276	0.0025617	6.8E-82
11	BUD13 *	rs143315658	116721532	C	T	0.0862539	-0.0510443	0.0044928	4.4E-31

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs180370	116721649	T	C	0.3272730	-0.0352730	0.0026989	5.2E-40
11	BUD13 *	rs74680844	116721744	C	G	0.1646870	-0.0570580	0.0034045	2.2E-65
11	BUD13 *	rs79100692	116722391	A	G	0.1643930	-0.0568461	0.0034073	6.8E-65
11	BUD13 *	rs12420920	116723315	A	G	0.1643990	-0.0568475	0.0034072	6.6E-65
11	BUD13 *	rs12421191	116723578	T	C	0.1643990	-0.0568475	0.0034072	6.6E-65
11	BUD13 *	rs180365	116725458	T	C	0.2932280	-0.0662755	0.0027969	7.8E-128
11	BUD13 *	rs61905078	116725593	C	A	0.1637350	-0.0569232	0.0034152	9.5E-65
11	BUD13 *	rs11216118	116725679	T	C	0.0771565	0.1234630	0.0047363	2.0E-153
11	BUD13 *	rs180364	116726036	G	A	0.2554690	-0.0627122	0.0029138	1.1E-106
11	BUD13 *	rs78347254	116726040	A	G	0.1009420	0.0223634	0.0041597	2.8E-08
11	BUD13 *	rs146714678	116726114	G	T	0.0925269	-0.0532470	0.0043689	1.3E-35
11	BUD13 *	rs75662937	116726178	T	C	0.0349301	0.1717570	0.0068542	4.7E-143
11	BUD13 *	rs144027752	116726289	A	G	0.0101097	0.0930995	0.0125309	2.7E-14
11	BUD13 *	rs180363	116727173	C	T	0.2538230	-0.0636288	0.0029139	1.1E-109
11	BUD13 *	rs78484485	116727349	A	G	0.2521560	-0.0634700	0.0029201	1.3E-108
11	BUD13 *	rs10892023	116727532	T	C	0.3095620	0.0839094	0.0027342	2.5E-213
11	BUD13 *	rs180361	116727933	T	C	0.3278250	-0.0351080	0.0026993	1.3E-39
11	BUD13 *	rs139283556	116728079	T	C	0.0133785	0.0797411	0.0109240	8.4E-14
11	BUD13 *	rs180360	116728272	G	A	0.2530470	-0.0635091	0.0029171	6.4E-109
11	BUD13 *	rs76240380	116728819	A	G	0.0351329	0.1711500	0.0068342	4.7E-143
11	BUD13 *	rs7123583	116729305	C	T	0.4336060	-0.0240927	0.0025591	2.8E-21
11	BUD13 *	rs141882698	116730622	C	A	0.0919532	-0.0533658	0.0043809	1.3E-35
11	BUD13 *	rs108533	116730995	T	A	0.3300490	-0.0354296	0.0026935	1.4E-40
11	BUD13 *	rs3212282	116731229	A	G	0.3107440	0.0836241	0.0027276	6.9E-213
11	BUD13 *	rs75387300	116731683	A	G	0.1639600	-0.0572194	0.0034097	1.7E-65
11	BUD13 *	rs2008915	116732418	C	G	0.3094450	0.0843074	0.0027300	3.0E-216
11	BUD13 *	rs1893460	116732961	A	G	0.3336820	-0.0708145	0.0026857	6.7E-157
11	BUD13 *	rs4938307	116733798	A	G	0.2436440	-0.0627576	0.0029377	3.9E-103
11	BUD13 *	rs117170971	116734549	A	G	0.0878181	-0.0501473	0.0044530	1.7E-30
11	BUD13 *	chr11:116735204_C_CT	116735204	CT	C	0.0135480	0.0762573	0.0109459	5.8E-13
11	BUD13 *	rs1974718	116736050	G	A	0.2043090	0.1063960	0.0031160	1.9E-260
11	BUD13 *	rs68149171	116736335	T	TTCTG	0.2419370	-0.0624524	0.0029456	1.5E-101
11	BUD13 *	rs1558860	116736652	A	C	0.2040650	0.1068070	0.0031163	2.7E-262
11	BUD13 *	rs1558861	116736721	C	T	0.2040580	0.1065030	0.0031160	5.6E-261
11	BUD13 *	rs180351	116736925	T	C	0.3528940	-0.0145545	0.0026449	3.0E-08
11	BUD13 *	rs114554198	116736935	T	C	0.0104666	0.0748001	0.0124116	3.3E-10
11	BUD13 *	rs180350	116739332	T	C	0.2784320	-0.0716244	0.0028213	8.0E-146
11	BUD13 *	rs61905084	116739578	C	T	0.3407150	-0.0706375	0.0026681	2.3E-158
11	BUD13 *	rs9326246	116741017	C	G	0.2039240	0.1071950	0.0031195	6.2E-264
11	BUD13 *	rs180349	116741111	A	T	0.2043820	0.1071580	0.0031171	4.1E-264
11	BUD13 *	rs180348	116741279	A	G	0.0677708	-0.0473104	0.0050179	2.1E-20
11	BUD13 *	rs11216125	116741558	A	G	0.2595110	-0.0607152	0.0028663	8.2E-102
11	BUD13 *	chr11:116741689_AACACA	116741689	A	ACACACA	0.0715971	0.1573400	0.0048992	3.9E-232
11	BUD13 *	rs180346	116741943	C	A	0.2778030	-0.0712453	0.0028166	8.4E-145
11	BUD13 *	rs117788500	116742318	C	G	0.0839131	-0.0494569	0.0045485	1.7E-28
11	BUD13 *	rs180344	116742468	C	T	0.3556000	-0.0148993	0.0026347	1.1E-08
11	BUD13 *	rs17518841	116744528	A	G	0.0842164	-0.0493731	0.0045394	1.7E-28
11	BUD13 *	rs180340	116745686	C	T	0.3571930	-0.0155080	0.0026342	2.2E-09
11	BUD13 *	rs11216126	116746524	C	A	0.2565220	-0.0635541	0.0028724	1.2E-110
11	BUD13 *	rs180339	116747066	T	C	0.4410450	-0.0582993	0.0025427	2.4E-118
11	BUD13 *	rs45539536	116747179	T	C	0.0842991	-0.0494204	0.0045381	1.6E-28
11	BUD13	rs34637368	116748889	A	G	0.2499420	-0.0625081	0.0029246	1.0E-103
11	BUD13	rs141923916	116749021	GA	G	0.0843883	-0.0493704	0.0045348	1.8E-28
11	BUD13	rs11216129	116749540	A	C	0.2515210	-0.0638559	0.0029035	2.3E-109
11	BUD13	rs57950207	116749954	C	T	0.0844903	-0.0492508	0.0045351	2.4E-28
11	BUD13	rs2849179	116750080	T	C	0.3531850	-0.0153908	0.0026361	3.0E-09
11	BUD13	rs17440396	116751054	A	G	0.0831822	-0.0485871	0.0045690	2.4E-27
11	BUD13	rs74368849	116751583	A	G	0.0669416	0.1586410	0.0050589	6.4E-223
11	BUD13	rs180329	116752242	A	G	0.3549040	-0.0156045	0.0026348	2.0E-09
11	BUD13	chr11:116752497_TA_T	116752497	TA	T	0.3040600	0.0920911	0.0027421	1.5E-253
11	BUD13	rs180327	116752943	C	T	0.3052690	0.0916551	0.0027374	2.8E-252
11	BUD13	rs6589564	116753437	C	G	0.2019100	0.1103180	0.0031302	1.2E-277
11	BUD13	rs180326	116753987	G	T	0.2037700	0.1089430	0.0031182	7.2E-273
11	BUD13	rs7930786	116754011	C	G	0.2021230	0.1103460	0.0031308	1.4E-277
11	BUD13	rs12421652	116755159	T	G	0.2529780	-0.0639257	0.0028958	2.3E-110
11	BUD13	rs77112220	116755510	T	C	0.0842438	-0.0494157	0.0045385	1.6E-28
11	BUD13	rs182500870	116755846	A	T	0.0113695	0.1693460	0.0118855	1.6E-48
11	BUD13	rs180322	116756019	C	T	0.3582500	-0.0456879	0.0026196	6.8E-69
11	BUD13	rs4938309	116756339	T	C	0.2531720	-0.0641691	0.0028960	5.0E-111
11	BUD13	rs117685786	116756907	C	T	0.0434102	-0.0554943	0.0061789	1.2E-19
11	BUD13	rs2075295	116757685	C	T	0.4411710	-0.0581584	0.0025423	4.5E-118
11	BUD13	rs17519093	116759189	A	G	0.0844250	-0.0487400	0.0045332	7.9E-28

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13	rs75955612	116759802	T	A	0.0428002	0.0913773	0.0062338	3.6E-51
11	BUD13	rs918143	116759884	T	C	0.3544090	-0.0146507	0.0026337	1.7E-08
11	BUD13	rs3741301	116760675	C	T	0.2805820	-0.0714744	0.0028062	8.4E-147
11	BUD13	rs3741300	116760974	A	G	0.3568800	-0.0147465	0.0026285	1.4E-08
11	BUD13	rs3825041	116760991	T	C	0.2004210	0.1105320	0.0031388	5.5E-277
11	BUD13	rs139872819	116761196	C	T	0.0842160	-0.0492615	0.0045372	2.9E-28
11	BUD13	rs11602240	116762082	C	T	0.2571870	-0.0640290	0.0028797	5.6E-112
11	BUD13	rs918144	116763109	T	C	0.4415990	-0.0586329	0.0025438	1.0E-119
11	BUD13	rs10488698	116763231	A	G	0.0835409	-0.0491533	0.0045534	5.0E-28
11	BUD13	rs17440824	116763457	T	C	0.0862244	-0.0457342	0.0044917	3.3E-25
11	BUD13	rs116877083	116763581	C	A	0.0861653	-0.0456703	0.0044926	3.6E-25
11	BUD13	rs17119975	116763841	C	T	0.2545340	-0.0638599	0.0028961	4.3E-110
11	BUD13	rs2187126	116765068	G	A	0.0409187	-0.0380478	0.0063478	9.0E-10
11	BUD13	rs75542782	116766286	A	G	0.0409006	-0.0383533	0.0063493	6.8E-10
11	BUD13	rs1145208	116767269	C	A	0.3429410	-0.0165533	0.0026518	3.6E-10
11	BUD13	rs532088210	116767607	G	A	0.0144881	-0.0613493	0.0106198	4.0E-09
11	BUD13	rs57643109	116768035	A	G	0.0409318	-0.0383273	0.0063474	7.2E-10
11	BUD13	rs10790162	116768388	A	G	0.2008560	0.1109930	0.0031416	7.1E-279
11	BUD13	rs1268353	116768976	T	C	0.3002180	-0.0687594	0.0027522	6.9E-141
11	BUD13	rs1263149	116769225	G	A	0.4543950	-0.0570387	0.0025291	2.8E-115
11	BUD13	rs622604	116769346	C	T	0.3034270	-0.0693763	0.0027375	4.0E-145
11	BUD13	rs610675	116769378	A	T	0.3034330	-0.0693746	0.0027375	4.0E-145
11	BUD13	rs6589565	116769521	A	G	0.2015490	0.1113050	0.0031357	1.7E-281
11	BUD13	rs623908	116769652	G	A	0.3035680	-0.0694841	0.0027370	1.2E-145
11	BUD13	rs1263151	116770312	T	C	0.3847790	-0.0220497	0.0025883	8.1E-18
11	BUD13	rs181315084	116770469	C	T	0.0132532	0.0826249	0.0109774	1.6E-14
11	BUD13	rs117579298	116771384	G	A	0.0409559	-0.0378775	0.0063446	1.0E-09
11	BUD13	rs79110162	116772295	G	A	0.0409512	-0.0378101	0.0063450	1.1E-09
11	BUD13	rs656417	116772720	T	G	0.4911870	-0.0139768	0.0025217	2.7E-08
11	BUD13 *	rs12422076	116773572	G	A	0.0696909	-0.0509832	0.0049494	1.2E-25
11	BUD13 *	rs141740837	116774378	T	TCA	0.0409593	-0.0378379	0.0063442	1.0E-09
11	BUD13 *	rs2041967	116774433	G	A	0.4104800	-0.0527513	0.0025609	2.0E-96
11	BUD13 *	rs7118999	116774559	T	C	0.3854370	-0.0224174	0.0025854	2.4E-18
11	BUD13 *	rs11216135	116775346	G	C	0.3011760	-0.0688930	0.0027443	2.3E-142
11	ZPR1 *	rs11602073	116776142	T	C	0.3006960	-0.0684037	0.0027449	2.1E-140
11	ZPR1 *	rs11216136	116776404	G	T	0.3033380	-0.0691162	0.0027375	3.4E-144
11	ZPR1 *	rs2160669	116776891	C	T	0.2027360	0.1115850	0.0031265	5.3E-285
11	ZPR1 *	rs78296522	116778060	A	C	0.0409527	-0.0378941	0.0063446	9.9E-10
11	ZPR1 *	rs964184	116778201	G	C	0.2031830	0.1115100	0.0031240	4.6E-285
11	ZPR1	rs75198898	116779090	A	G	0.0668810	0.1720010	0.0050323	9.1E-265
11	ZPR1	rs113932726	116779922	T	C	0.0660530	0.1723490	0.0050649	3.8E-262
11	ZPR1	rs34248274	116779950	C	CTAGT	0.3008620	-0.0684939	0.0027423	7.8E-141
11	ZPR1	rs11604424	116780399	C	T	0.3535780	0.0806956	0.0026275	2.1E-211
11	ZPR1	rs200405951	116780493	G	C	0.0111872	0.1596980	0.0119856	6.9E-43
11	ZPR1	rs1942478	116780747	G	T	0.3028190	-0.0687109	0.0027384	3.7E-142
11	ZPR1	rs9633942	116781154	C	T	0.0256407	-0.0581420	0.0079953	2.0E-12
11	ZPR1	rs4417316	116781585	T	C	0.3006290	-0.0686932	0.0027400	7.3E-142
11	ZPR1	rs6589566	116781707	G	A	0.2031130	0.1116450	0.0031248	1.3E-285
11	ZPR1	rs7483863	116781775	A	G	0.2031130	0.1116450	0.0031248	1.3E-285
11	ZPR1	rs2075290	116782580	C	T	0.2212470	0.1008400	0.0030273	6.3E-248
11	ZPR1	rs76836072	116783046	T	C	0.0410113	-0.0382728	0.0063395	7.4E-10
11	ZPR1	rs603446	116783719	T	C	0.2784430	-0.0725190	0.0027975	1.6E-152
11	ZPR1	rs139678706	116784368	A	G	0.0185989	-0.0747846	0.0093526	4.2E-16
11	ZPR1	rs10750096	116786072	C	A	0.2031420	0.1116460	0.0031248	1.3E-285
11	ZPR1	rs3741298	116786845	C	T	0.3629360	0.0781860	0.0026099	6.8E-201
11	ZPR1	rs3741297	116786951	T	C	0.0656860	0.1759970	0.0050737	4.1E-273
11	APOA5	rs2266788	116789970	G	A	0.2030640	0.1119780	0.0031264	6.2E-287
11	APOA5	rs2075291	116790676	A	C	0.0657363	0.1763060	0.0050677	1.4E-274
11	APOA5	rs2072560	116791110	T	C	0.2021110	0.1121670	0.0031368	2.9E-286
11	APOA5	rs651821	116791863	C	T	0.2716320	0.1457010	0.0028265	5.1E-595
11	APOA5 *	rs34003087	116792880	T	C	0.0406172	-0.0359928	0.0063861	9.8E-09
11	APOA5 *	rs662799	116792991	G	A	0.2718250	0.1453100	0.0028243	2.6E-592
11	APOA5 *	rs17120035	116793135	T	C	0.0818070	-0.0485583	0.0046109	7.5E-26
11	APOA5 *	rs7103224	116793250	A	G	0.0817925	-0.0486462	0.0046114	6.3E-26
11	APOA5 *	rs10750097	116793324	G	A	0.4346590	0.0278977	0.0025691	8.6E-28
11	APOA5 *	rs1787680	116794060	A	T	0.2648210	-0.0736677	0.0028959	1.2E-146
11	APOA5 *	rs9804646	116794363	T	C	0.2191270	-0.0641548	0.0030987	1.3E-97
11	APOA5 *	rs35904674	116795383	T	C	0.0540651	-0.0409535	0.0055868	1.4E-13
11	APOA5 *	chr11:116795401_C_CA	116795401	CA	C	0.0532661	-0.0419760	0.0056347	6.9E-14
11	APOA5 *	rs117730008	116795625	A	G	0.0462576	0.0326614	0.0060514	2.2E-08
11	APOA5 *	rs7123666	116796367	A	G	0.1573200	0.1020660	0.0035050	4.9E-190
11	APOA5 *	rs75919952	116796829	T	C	0.0414421	-0.0372316	0.0063312	2.8E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	APOA5 *	rs35606865	116798127	C	T	0.0536555	-0.0402961	0.0056093	4.6E-13
11	APOA5 *	rs11216137	116799112	A	G	0.0505350	-0.0416890	0.0057799	4.5E-13
11	APOA5 *	rs11600380	116799466	C	T	0.0537032	-0.0405561	0.0056076	3.3E-13
11	APOA5 *	rs12294065	116800824	C	G	0.0501181	-0.0418591	0.0058072	4.2E-13
11	APOA5 *	rs116852373	116800861	A	G	0.0228239	-0.0623371	0.0084076	2.4E-14
11	APOA5 *	rs188651594	116802375	A	G	0.0270295	0.0910674	0.0077945	2.6E-32
11	APOA5 *	rs12791103	116802599	T	G	0.0500209	-0.0420049	0.0058149	4.1E-13
11	APOA5 *	rs1263164	116804575	A	C	0.3016140	-0.0353533	0.0027981	4.5E-37
11	APOA4 *	rs1729407	116806654	G	C	0.3041580	-0.0353446	0.0027746	1.0E-37
11	APOA4 *	rs1263168	116807283	T	C	0.3047250	-0.0340395	0.0027424	1.2E-35
11	APOA4 *	rs139154032	116807284	A	G	0.0132308	-0.0784270	0.0110159	1.7E-13
11	APOA4 *	rs1263169	116807423	T	A	0.3069650	-0.0348758	0.0027439	2.1E-37
11	APOA4 *	rs11398704	116807533	CA	C	0.3516850	-0.0374337	0.0026781	7.2E-45
11	APOA4 *	rs1263170	116807697	C	T	0.3082380	-0.0346570	0.0027318	2.9E-37
11	APOA4 *	rs1729405	116808044	T	C	0.3078220	-0.0345784	0.0027314	4.3E-37
11	APOA4 *	rs75542613	116808439	A	G	0.0401829	-0.0821796	0.0064245	3.6E-39
11	APOA4 *	rs1263171	116809614	A	G	0.3048270	-0.0333579	0.0027245	1.6E-34
11	APOA4 *	rs6589571	116809702	T	C	0.1941030	0.0640430	0.0032303	3.5E-89
11	APOA4 *	rs1263172	116810202	A	G	0.3576680	-0.0373752	0.0026276	4.2E-46
11	APOA4 *	rs1263173	116810292	A	G	0.3049660	-0.0333002	0.0027228	2.1E-34
11	APOA4 *	rs1263174	116810527	T	G	0.3086800	-0.0331955	0.0027191	2.4E-34
11	APOA4 *	rs6589572	116810847	G	A	0.3057170	0.0731934	0.0027320	1.2E-161
11	APOA4 *	rs79538491	116811203	G	A	0.0613268	0.0510578	0.0052798	2.8E-23
11	APOA4 *	rs7927820	116811440	G	A	0.3045660	0.0734790	0.0027303	5.8E-163
11	APOA4 *	rs35180165	116811633	C	CAG	0.3036660	-0.0332470	0.0027316	3.7E-34
11	APOA4 *	rs76636922	116812279	A	G	0.3358230	-0.0310079	0.0026731	2.9E-32
11	APOA4 *	rs2727793	116812658	T	C	0.3037440	-0.0324415	0.0027361	1.7E-32
11	APOA4 *	rs75318540	116813146	T	C	0.2201150	-0.0224709	0.0030607	4.9E-14
11	APOA4 *	rs7396835	116813312	T	C	0.3051520	0.0729866	0.0027242	1.5E-161
11	APOA4 *	rs7396851	116813448	T	C	0.3048100	0.0733288	0.0027264	9.0E-163
11	APOA4 *	rs79841374	116813844	T	C	0.3349060	-0.0310119	0.0026741	3.7E-32
11	APOA4 *	rs2727791	116813846	G	C	0.3062050	-0.0333753	0.0027311	1.4E-34
11	APOA4 *	rs2849167	116814028	A	G	0.3060940	-0.0334517	0.0027324	1.1E-34
11	APOA4 *	rs2542063	116814051	A	G	0.3065360	-0.0334456	0.0027310	1.1E-34
11	APOA4 *	rs77535577	116814675	A	G	0.3338310	-0.0314572	0.0026852	1.3E-32
11	APOA4 *	rs6589573	116815050	C	G	0.3073620	0.0733799	0.0027513	5.6E-160
11	APOA4 *	rs7107757	116815572	T	C	0.3565530	0.0619824	0.0026458	4.6E-124
11	APOA4 *	chr11:116816190_CT_C	116816190	C	CT	0.3145270	-0.0295097	0.0027558	2.4E-27
11	APOA4 *	rs9735326	116818049	C	A	0.3262100	0.0683323	0.0027112	2.4E-142
11	APOA4 *	rs1263176	116819407	T	C	0.3682330	0.0595629	0.0026285	1.3E-115
11	APOA4 *	rs1268354	116819862	C	T	0.3685430	0.0594843	0.0026279	2.0E-115
11	APOA4 *	rs1263177	116819996	C	T	0.3670560	0.0598553	0.0026324	1.3E-116
11	APOA4	rs2234669	116820795	G	GGACA	0.3031020	-0.0335238	0.0027662	4.1E-34
11	APOA4	rs5104	116821618	C	T	0.3198470	0.0707431	0.0027130	3.0E-152
11	APOA4	rs6413456	116821733	A	G	0.0331185	-0.0869705	0.0070229	5.1E-37
11	APOA4	rs5100	116821978	G	A	0.3724070	0.0597177	0.0026242	1.5E-116
11	APOA4	rs5096	116822379	G	A	0.3724070	0.0596983	0.0026241	1.8E-116
11	APOA4	rs2239013	116822637	T	C	0.0405659	-0.0814472	0.0063888	8.4E-39
11	APOA4	rs5093	116822638	A	G	0.2183010	-0.0229742	0.0030858	2.9E-14
11	APOA4	rs5092	116822748	C	T	0.3719840	0.0595409	0.0026262	1.2E-115
11	APOA4 *	rs1268833	116824150	G	A	0.3723250	0.0596296	0.0026238	2.6E-116
11	APOA4 *	rs10892035	116824222	A	G	0.3717620	0.0596548	0.0026247	2.8E-116
11	APOA4 *	rs182352602	116824894	A	G	0.2124650	-0.0223223	0.0031173	2.4E-13
11	APOA4 *	rs7111242	116825064	A	G	0.3207970	0.0702425	0.0027214	2.5E-149
11	APOA4 *	rs2216311	116825327	G	A	0.3723170	0.0597240	0.0026233	1.2E-116
11	APOA4 *	rs2098453	116825964	C	T	0.3718100	0.0599284	0.0026250	2.9E-117
11	APOA4 *	rs2727789	116826171	G	T	0.3733710	0.0596678	0.0026239	2.0E-116
11	APOA4 *	rs2849176	116826205	T	C	0.3724190	0.0598060	0.0026246	7.7E-117
11	APOA4 *	rs2542050	116826401	C	A	0.3718390	0.0600014	0.0026243	1.2E-117
11	APOC3 *	rs2849173	116826605	G	C	0.3718600	0.0599274	0.0026242	2.5E-117
11	APOC3 *	rs2071523	116826628	C	T	0.3718960	0.0599300	0.0026240	2.3E-117
11	APOC3 *	rs2071522	116826822	T	C	0.3718930	0.0599002	0.0026242	3.3E-117
11	APOC3 *	rs2542051	116827022	C	A	0.3720180	0.0598993	0.0026240	3.1E-117
11	APOC3 *	rs2071521	116827132	G	A	0.3719950	0.0599179	0.0026237	2.4E-117
11	APOC3 *	rs595049	116828729	C	A	0.3735850	0.0600215	0.0026147	3.4E-118
11	APOC3	rs734104	116830144	C	T	0.2931050	0.0563380	0.0027834	9.2E-92
11	APOC3	rs5128	116832924	G	C	0.2910580	0.0573516	0.0027685	4.0E-96
11	APOA1 *	rs10750098	116834852	G	T	0.2905010	0.0567841	0.0027777	2.0E-93
11	APOA1 *	rs12718462	116835003	C	T	0.0440359	-0.0774620	0.0061293	1.0E-37
11	APOA1 *	rs12721025	116835331	A	G	0.0472989	-0.0753149	0.0059674	8.5E-38
11	APOA1 *	rs12721026	116835452	G	T	0.0427797	-0.0772223	0.0062169	2.2E-36
11	APOA1	rs12718464	116836685	A	G	0.0426883	-0.0769827	0.0062210	3.1E-36

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	APOA1 *	rs368405969	116839577	T	C	0.0118410	-0.0795495	0.0116356	1.4E-12
11	APOA1 *	rs613808	116840252	G	A	0.2761950	-0.0478989	0.0028519	3.6E-64
11	APOA1 *	rs2727784	116840425	T	C	0.2573750	-0.0511746	0.0029214	8.9E-70
11	SIK3 *	rs480009	116841258	T	C	0.2490340	-0.0179983	0.0029295	6.5E-10
11	SIK3 *	rs370143719	116841590	C	T	0.0134624	-0.0751187	0.0109205	6.5E-13
11	SIK3 *	rs591592	116842850	T	C	0.2216180	-0.0363525	0.0030690	2.8E-32
11	SIK3 *	rs200408997	116842862	A	ACCC	0.0496064	0.0536786	0.0057848	6.1E-21
11	SIK3 *	rs579163	116842914	G	C	0.2220720	-0.0365595	0.0030673	1.2E-32
11	SIK3	rs371090973	116844640	T	TTA	0.0497933	0.0518556	0.0057828	1.1E-19
11	SIK3	rs201579941	116844674	A	ATAT	0.0486704	0.0538423	0.0058399	9.3E-21
11	SIK3	rs142174850	116845068	A	G	0.0811955	-0.0610500	0.0046016	2.0E-41
11	SIK3	rs143120617	116846722	T	C	0.0365740	-0.0493301	0.0067042	1.7E-13
11	SIK3	rs61905145	116847699	A	G	0.0503464	0.0520386	0.0057378	4.8E-20
11	SIK3	rs7127590	116848086	G	T	0.4045710	-0.0220556	0.0025695	1.2E-17
11	SIK3	rs532815	116848142	A	G	0.2344280	-0.0360929	0.0029774	5.6E-34
11	SIK3	rs112030791	116848208	ATT	A	0.4036900	-0.0220406	0.0025730	1.4E-17
11	SIK3	rs145730196	116848209	A	G	0.4036900	-0.0220406	0.0025730	1.4E-17
11	SIK3	rs61905155	116848213	T	G	0.0501905	0.0520429	0.0057473	7.0E-20
11	SIK3	rs2289893	116849373	C	T	0.3495290	-0.0336560	0.0026428	3.2E-37
11	SIK3	rs660083	116850113	G	C	0.2312760	-0.0353076	0.0029831	1.3E-32
11	SIK3	rs11216161	116850485	C	T	0.4004920	-0.0214544	0.0025669	6.3E-17
11	SIK3	rs10047459	116851110	T	C	0.4000390	-0.0213201	0.0025645	1.0E-16
11	SIK3	rs10047462	116851325	T	G	0.4822240	-0.0384100	0.0025120	2.2E-53
11	SIK3	rs689243	116851977	C	G	0.2307300	-0.0347109	0.0029857	1.8E-31
11	SIK3	rs139952838	116852044	T	C	0.0279027	0.0813074	0.0076264	1.7E-27
11	SIK3	rs888245	116853021	G	C	0.0503305	0.0520087	0.0057357	6.1E-20
11	SIK3	rs888246	116853516	T	C	0.0503203	0.0525973	0.0057357	2.6E-20
11	SIK3	rs12099358	116855332	A	C	0.0504558	0.0518530	0.0057285	6.9E-20
11	SIK3	rs112618266	116855993	T	C	0.0785402	-0.0606097	0.0046539	9.2E-40
11	SIK3	rs640621	116856053	G	C	0.2345380	-0.0362348	0.0029655	1.8E-34
11	SIK3	rs78857232	116856749	T	C	0.0502717	0.0517180	0.0057374	1.1E-19
11	SIK3	rs1035237	116857134	C	G	0.4833410	-0.0388564	0.0025216	3.5E-54
11	SIK3	rs6589574	116859922	A	G	0.3120560	0.0481956	0.0027400	2.4E-70
11	SIK3	rs567312	116860022	A	G	0.2332350	-0.0357787	0.0029728	1.7E-33
11	SIK3	rs4938315	116860489	A	G	0.4819380	-0.0385966	0.0025225	1.9E-53
11	SIK3	rs2075292	116861796	T	G	0.4813110	-0.0391671	0.0025254	7.5E-55
11	SIK3	rs484646	116862140	G	A	0.2346350	-0.0361971	0.0029651	2.1E-34
11	SIK3	rs6589575	116862594	T	C	0.4826670	-0.0388580	0.0025209	3.4E-54
11	SIK3	rs2080586	116862600	C	T	0.0501118	0.0527646	0.0057474	2.1E-20
11	SIK3	rs476399	116863012	C	T	0.2345810	-0.0362392	0.0029649	1.8E-34
11	SIK3	rs718847	116863430	T	C	0.4820930	-0.0389249	0.0025215	1.9E-54
11	SIK3	rs17120099	116864744	C	A	0.0786115	-0.0603116	0.0046521	2.4E-39
11	SIK3	rs6589576	116865072	G	C	0.4825690	-0.0388564	0.0025206	3.2E-54
11	SIK3	rs573549	116865963	G	A	0.2351800	-0.0363926	0.0029658	8.3E-35
11	SIK3	chr11:116866441_C_CTTT/	116866441	CTTTA	C	0.0399441	0.0535726	0.0064536	5.0E-17
11	SIK3	rs17120101	116867872	T	C	0.0323179	-0.0464385	0.0071203	6.3E-11
11	SIK3	rs11216168	116870837	A	G	0.0502943	0.0518856	0.0057367	8.6E-20
11	SIK3	rs533556	116870856	C	A	0.2355500	-0.0357284	0.0029586	1.1E-33
11	SIK3	rs17120111	116873302	T	C	0.0497806	0.0535940	0.0057687	9.2E-21
11	SIK3	rs11216169	116873673	C	T	0.0497964	0.0530765	0.0057696	2.0E-20
11	SIK3	rs9919599	116874768	G	C	0.4820050	-0.0383439	0.0025269	2.4E-52
11	SIK3	rs17120119	116876566	G	C	0.0766221	-0.0582285	0.0047097	7.8E-36
11	SIK3	rs77682889	116876596	T	C	0.0301898	0.0721360	0.0073261	7.9E-24
11	SIK3	rs12278117	116877453	A	G	0.0766221	-0.0582285	0.0047097	7.8E-36
11	SIK3	rs12279433	116877505	T	G	0.0779921	-0.0597249	0.0046684	2.4E-38
11	SIK3	rs12279464	116877766	T	C	0.0766221	-0.0582285	0.0047097	7.8E-36
11	SIK3	rs112867178	116877768	CTCTATT	C	0.4807030	-0.0378710	0.0025297	4.9E-51
11	SIK3	rs12292614	116877799	G	A	0.0766221	-0.0582285	0.0047097	7.8E-36
11	SIK3	rs12286581	116878028	C	T	0.0766221	-0.0582285	0.0047097	7.8E-36
11	SIK3	rs61907566	116878189	G	C	0.2329640	-0.0357869	0.0029816	4.3E-33
11	SIK3	rs75294699	116878356	A	C	0.0766221	-0.0582285	0.0047097	7.8E-36
11	SIK3	rs76523703	116878793	G	T	0.0498150	0.0523118	0.0057688	7.0E-20
11	SIK3	rs11216172	116879162	A	G	0.3596620	-0.0187843	0.0026318	2.9E-12
11	SIK3	rs6589577	116879261	T	C	0.4819720	-0.0383769	0.0025277	1.9E-52
11	SIK3	rs543819	116879357	G	A	0.0826689	-0.0602320	0.0045537	6.1E-41
11	SIK3	rs7396061	116880158	C	A	0.3161350	-0.0331458	0.0027231	2.7E-33
11	SIK3	rs74341458	116880833	A	G	0.0496775	0.0529160	0.0057768	2.8E-20
11	SIK3	rs482371	116881447	C	T	0.2286170	-0.0346570	0.0030001	1.1E-30
11	SIK3	rs7124741	116881503	T	A	0.4815770	-0.0383912	0.0025251	1.4E-52
11	SIK3	rs12275565	116882836	G	A	0.0814927	-0.0584328	0.0045862	4.8E-38
11	SIK3	rs12416987	116883549	C	T	0.0780158	-0.0597400	0.0046674	2.0E-38
11	SIK3	rs1269329	116884325	C	T	0.2344210	-0.0354860	0.0029760	1.3E-32

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs139733873	116884844	G	A	0.0124671	0.1051810	0.0113483	1.8E-19
11	SIK3	rs11827828	116884868	A	G	0.0498241	0.0522123	0.0057682	8.3E-20
11	SIK3	rs2044426	116885467	A	G	0.0759563	-0.0585056	0.0047308	6.2E-36
11	SIK3	rs35378097	116886122	G	GT	0.0338376	-0.0481962	0.0069465	3.9E-12
11	SIK3	rs10892040	116886270	A	G	0.0762455	-0.0585038	0.0047193	3.8E-36
11	SIK3	rs11216174	116886532	G	A	0.0762455	-0.0585038	0.0047193	3.8E-36
11	SIK3	rs11216175	116886682	T	C	0.0762455	-0.0585038	0.0047193	3.8E-36
11	SIK3	chr11:116886752_T_TA	116886752	TA	T	0.2337400	-0.0354263	0.0029784	1.7E-32
11	SIK3	rs12284346	116887077	C	T	0.0771590	-0.0605522	0.0046923	4.0E-39
11	SIK3	rs7106641	116887385	A	G	0.2847690	-0.0188939	0.0027921	1.9E-11
11	SIK3	rs12292278	116887977	C	A	0.0825142	-0.0600569	0.0045559	8.7E-41
11	SIK3	rs1473177	116888616	C	T	0.0497007	0.0528130	0.0057743	3.2E-20
11	SIK3	rs17174502	116888939	G	A	0.4821470	-0.0384050	0.0025281	1.8E-52
11	SIK3	rs12294191	116889108	G	A	0.0826654	-0.0602674	0.0045521	3.5E-41
11	SIK3	rs10892042	116889829	A	G	0.0497007	0.0528130	0.0057743	3.2E-20
11	SIK3	rs660443	116889977	C	T	0.2288090	-0.0346462	0.0029995	1.1E-30
11	SIK3	rs12285074	116891312	G	A	0.4817930	-0.0387569	0.0025341	2.5E-53
11	SIK3	rs72645459	116891441	C	A	0.4810230	-0.0386319	0.0025307	4.9E-53
11	SIK3	chr11:116891662_AAG_A	116891662	AAG	A	0.4801930	-0.0387263	0.0025280	2.2E-53
11	SIK3	rs144010715	116891837	AG	A	0.0826181	-0.0602481	0.0045536	3.9E-41
11	SIK3	rs75158858	116892113	A	G	0.0497007	0.0528130	0.0057743	3.2E-20
11	SIK3	rs499910	116892318	A	G	0.2789380	-0.0178843	0.0028104	3.1E-10
11	SIK3	rs672058	116893305	T	C	0.3989870	-0.0364829	0.0025753	1.9E-46
11	SIK3	rs77349713	116894760	C	T	0.0831862	-0.0603675	0.0045358	1.4E-41
11	SIK3	rs11820814	116894984	C	T	0.0496711	0.0527961	0.0057786	3.5E-20
11	SIK3	rs74881320	116895209	C	A	0.0831825	-0.0603810	0.0045351	1.3E-41
11	SIK3	rs149874218	116895594	TTG	T	0.0833890	-0.0605326	0.0045340	8.1E-42
11	SIK3	rs11216178	116895674	T	G	0.0496360	0.0528388	0.0057819	3.5E-20
11	SIK3	rs10892044	116896183	C	T	0.0496586	0.0527889	0.0057794	3.7E-20
11	SIK3	rs2270392	116896972	C	T	0.1206790	-0.0500102	0.0038562	3.7E-40
11	SIK3	chr11:116897883_CA_C	116897883	C	CA	0.0737597	-0.0617105	0.0048118	2.6E-38
11	SIK3	rs111884008	116898027	C	G	0.1159500	-0.0493635	0.0039208	5.8E-38
11	SIK3	rs190051172	116898198	G	C	0.0831910	-0.0603305	0.0045349	1.5E-41
11	SIK3	rs609177	116899801	G	A	0.2351030	-0.0351782	0.0029768	3.2E-32
11	SIK3	rs72645460	116900659	A	G	0.4791470	-0.0383347	0.0025319	4.0E-52
11	SIK3	rs1076485	116901725	C	T	0.4419670	-0.0366665	0.0025445	6.3E-47
11	SIK3	rs17120131	116901770	C	T	0.0834815	-0.0606086	0.0045309	5.0E-42
11	SIK3	rs518181	116902071	A	C	0.2277270	-0.0346500	0.0030073	1.3E-30
11	SIK3	rs17120132	116902602	A	T	0.0835909	-0.0607065	0.0045275	3.1E-42
11	SIK3	rs11216180	116902662	T	A	0.0496858	0.0529130	0.0057770	2.9E-20
11	SIK3	rs17120136	116903045	G	T	0.0814289	-0.0589513	0.0045887	6.6E-39
11	SIK3	rs17120139	116903485	G	A	0.4787170	-0.0387965	0.0025330	3.3E-53
11	SIK3	rs78694306	116903528	T	G	0.0772992	-0.0590274	0.0046879	2.3E-37
11	SIK3	rs11216181	116903758	T	A	0.0462251	0.0536407	0.0059939	1.7E-19
11	SIK3	rs78832854	116903759	A	T	0.0802621	-0.0536616	0.0046175	6.8E-32
11	SIK3	rs115971514	116903783	C	G	0.0772992	-0.0590274	0.0046879	2.3E-37
11	SIK3	rs12280030	116904480	A	T	0.0833748	-0.0604562	0.0045289	6.6E-42
11	SIK3	rs7111854	116906110	T	A	0.1208800	-0.0501235	0.0038521	1.7E-40
11	SIK3	rs12273762	116906347	A	T	0.0833748	-0.0604562	0.0045289	6.6E-42
11	SIK3	rs9651681	116907349	C	T	0.0835890	-0.0607068	0.0045275	3.1E-42
11	SIK3	rs4938317	116907559	C	T	0.0496807	0.0529615	0.0057772	2.7E-20
11	SIK3	rs35184536	116908097	G	A	0.0834475	-0.0604768	0.0045310	7.7E-42
11	SIK3	rs10790166	116908783	G	A	0.2450170	-0.0183314	0.0029262	2.0E-10
11	SIK3	rs200905431	116909318	G	GA	0.0938638	-0.0518920	0.0043973	7.9E-33
11	SIK3	rs75920871	116909379	T	A	0.0497995	0.0552574	0.0057808	4.6E-22
11	SIK3	rs11216183	116910829	A	C	0.0746538	-0.0618123	0.0047566	1.1E-39
11	SIK3	rs7123336	116912103	C	T	0.1623250	-0.0182352	0.0034006	2.3E-08
11	SIK3	rs11216185	116912258	G	T	0.0787613	-0.0602984	0.0046448	1.1E-39
11	SIK3	rs983567	116912884	C	T	0.1623410	-0.0183070	0.0034016	2.1E-08
11	SIK3	rs142195028	116913525	A	AG	0.0745856	-0.0619343	0.0047597	8.8E-40
11	SIK3	rs11357208	116913587	C	CT	0.0496575	0.0529966	0.0057797	2.7E-20
11	SIK3	rs7115583	116913660	T	G	0.1162520	-0.0496511	0.0039173	1.5E-38
11	SIK3	rs149566815	116913905	T	TAAAC	0.0746019	-0.0619830	0.0047600	7.5E-40
11	SIK3	rs11216186	116913976	C	T	0.0982254	-0.0581255	0.0042081	3.3E-44
11	SIK3	rs10892045	116914108	A	C	0.0465681	0.0540416	0.0059673	8.3E-20
11	SIK3	rs79711490	116914625	T	C	0.0982243	-0.0581286	0.0042081	3.3E-44
11	SIK3	rs11216187	116916432	T	C	0.0496433	0.0530681	0.0057806	2.4E-20
11	SIK3	rs12277181	116916604	A	G	0.0982840	-0.0581202	0.0042100	4.5E-44
11	SIK3	rs12277092	116916611	T	C	0.0982243	-0.0581286	0.0042081	3.3E-44
11	SIK3	rs7928298	116916811	T	A	0.0731821	-0.0357127	0.0048840	7.7E-14
11	SIK3	rs12418208	116916917	T	C	0.0955340	-0.0594127	0.0042673	9.9E-45
11	SIK3	rs12418209	116916925	T	C	0.0955340	-0.0594127	0.0042673	9.9E-45

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs1006176	116917417	C	T	0.0984072	-0.0581941	0.0042035	2.2E-44
11	SIK3	chr11:116917733_AAGAG_	116917733	A	AAGAG	0.0955618	-0.0562362	0.0042714	3.9E-40
11	SIK3	rs76136280	116917775	T	C	0.0496654	0.0530918	0.0057792	2.4E-20
11	SIK3	rs1135663	116918121	T	C	0.0847096	-0.0542502	0.0045485	2.0E-33
11	SIK3	rs79530380	116918472	A	T	0.0411670	0.0627110	0.0063758	2.8E-23
11	SIK3	rs78692246	116920591	A	G	0.0990248	-0.0575688	0.0041907	1.0E-43
11	SIK3	rs141203891	116921220	C	T	0.0101635	-0.0920760	0.0125179	1.1E-14
11	SIK3	rs7934763	116921641	G	T	0.0499196	0.0509505	0.0057649	5.4E-19
11	SIK3	rs7948838	116922245	G	A	0.1360220	-0.0492805	0.0036601	9.8E-43
11	SIK3	rs12225187	116922515	A	G	0.2027880	-0.0311201	0.0031317	2.5E-23
11	SIK3	rs12288386	116922907	T	C	0.0986498	-0.0574573	0.0041969	1.9E-43
11	SIK3	rs10892047	116922977	T	C	0.0985374	-0.0578175	0.0042012	6.6E-44
11	SIK3	rs117287138	116924163	A	G	0.0498358	0.0511740	0.0057698	3.9E-19
11	SIK3	rs56314469	116924187	A	G	0.0498358	0.0511740	0.0057698	3.9E-19
11	SIK3	rs12292371	116925232	C	G	0.0987684	-0.0573036	0.0041950	3.1E-43
11	SIK3	rs12292434	116925349	A	G	0.0986759	-0.0574720	0.0041964	1.9E-43
11	SIK3	rs7121898	116926130	T	A	0.2030990	-0.0311363	0.0031295	2.4E-23
11	SIK3	rs61907591	116926139	A	T	0.0499196	0.0509505	0.0057649	5.4E-19
11	SIK3	rs12285956	116926759	A	G	0.0986804	-0.0574902	0.0041963	1.8E-43
11	SIK3	rs11216190	116926968	C	T	0.1352290	-0.0492377	0.0036721	2.3E-42
11	SIK3	chr11:116927081_AT_A	116927081	A	AT	0.0960976	-0.0565463	0.0042651	1.0E-40
11	SIK3	rs1446105	116927828	T	C	0.2030860	-0.0311810	0.0031282	1.8E-23
11	SIK3	rs579890	116928247	G	A	0.4701180	-0.0372323	0.0025319	3.3E-49
11	SIK3	rs79157715	116929554	A	G	0.0987778	-0.0573873	0.0041943	2.4E-43
11	SIK3	rs10790167	116930227	C	T	0.2029540	-0.0310453	0.0031289	2.9E-23
11	SIK3	rs75776964	116930345	G	C	0.0987518	-0.0573608	0.0041947	2.6E-43
11	SIK3	rs645258	116930485	A	C	0.3138050	0.0423044	0.0027217	3.2E-55
11	SIK3	rs76690043	116930813	G	C	0.0499236	0.0509658	0.0057646	5.2E-19
11	SIK3	rs61907594	116931095	T	C	0.0499236	0.0509658	0.0057646	5.2E-19
11	SIK3	rs79974099	116931865	A	T	0.0499236	0.0509658	0.0057646	5.2E-19
11	SIK3	rs74615346	116932256	C	A	0.0988578	-0.0572009	0.0041930	4.6E-43
11	SIK3	rs12270974	116933289	T	C	0.0987473	-0.0573624	0.0041948	2.7E-43
11	SIK3	rs7107702	116933428	C	T	0.1862760	-0.0222272	0.0032183	1.4E-12
11	SIK3	rs12272491	116933654	T	C	0.0987473	-0.0573624	0.0041948	2.7E-43
11	SIK3	rs12418735	116934046	G	T	0.0987518	-0.0573448	0.0041947	2.8E-43
11	SIK3	rs77204473	116934348	G	T	0.0644784	-0.0574719	0.0051043	4.5E-30
11	SIK3	rs562179	116934488	C	T	0.4354380	-0.0308808	0.0025490	6.4E-34
11	SIK3	rs79207844	116934725	A	G	0.0639864	-0.0583757	0.0051219	9.2E-31
11	SIK3	rs12274590	116934980	A	G	0.0639864	-0.0583757	0.0051219	9.2E-31
11	SIK3	rs144015791	116935158	T	G	0.0499236	0.0509658	0.0057646	5.2E-19
11	SIK3	rs2513095	116935553	C	T	0.4705200	-0.0371205	0.0025321	6.8E-49
11	SIK3	rs2513094	116935696	C	T	0.2650190	-0.0216868	0.0028489	1.7E-14
11	SIK3	rs2513093	116935971	G	A	0.4702900	-0.0372225	0.0025313	3.5E-49
11	SIK3	rs12273769	116936457	G	T	0.0987520	-0.0573721	0.0041945	2.5E-43
11	SIK3	rs12294657	116936652	C	G	0.0987520	-0.0573721	0.0041945	2.5E-43
11	SIK3	rs77920516	116936711	C	T	0.0884803	0.0317883	0.0044548	8.2E-13
11	SIK3	rs473172	116937254	G	A	0.4702900	-0.0372237	0.0025313	3.4E-49
11	SIK3	rs77136879	116937737	T	C	0.0987565	-0.0574096	0.0041944	2.2E-43
11	SIK3	chr11:116938204_AGAGGC	116938204	A	GGAGGGG	0.1140130	-0.0387961	0.0039723	8.8E-23
11	SIK3	rs142440762	116938378	A	G	0.1427080	-0.0247725	0.0036172	3.3E-12
11	SIK3	rs61907600	116938632	G	A	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs7480278	116939073	G	T	0.0987599	-0.0574449	0.0041943	2.0E-43
11	SIK3	rs61624438	116939229	A	C	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs80015203	116940190	G	A	0.0987599	-0.0574449	0.0041943	2.0E-43
11	SIK3	rs117877581	116940238	G	T	0.0988830	-0.0575157	0.0041944	1.5E-43
11	SIK3	rs116597701	116940771	G	C	0.0971804	-0.0570690	0.0042271	4.9E-42
11	SIK3	rs145705809	116940967	A	C	0.0131297	0.1282630	0.0110508	9.1E-33
11	SIK3	rs139127609	116940986	T	TTTTG	0.0987599	-0.0574449	0.0041943	2.0E-43
11	SIK3	rs473188	116941313	G	C	0.4700320	-0.0372020	0.0025305	3.1E-49
11	SIK3	rs78066444	116941342	C	A	0.0976898	-0.0574963	0.0042196	4.6E-43
11	SIK3	chr11:116941408_TA_T	116941408	T	TA	0.4789830	-0.0387135	0.0025589	4.3E-52
11	SIK3	rs17120157	116941912	C	T	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs75410648	116942722	T	C	0.0987679	-0.0572986	0.0041938	3.1E-43
11	SIK3	rs510988	116943088	T	C	0.4699990	-0.0372255	0.0025305	2.7E-49
11	SIK3	rs12292858	116943263	C	A	0.1358860	-0.0492244	0.0036602	1.1E-42
11	SIK3	rs10892048	116943880	G	A	0.2010680	-0.0308578	0.0031429	9.5E-23
11	SIK3	rs12421902	116943930	G	A	0.0969760	-0.0572250	0.0042342	2.8E-42
11	SIK3	chr11:116944465_GCAAT_	116944465	G	GCAAT	0.4699930	-0.0372185	0.0025306	2.8E-49
11	SIK3	rs11216193	116944883	T	C	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	chr11:116944965_C_CTT	116944965	CTT	C	0.0786944	-0.0553718	0.0047504	6.4E-32
11	SIK3	rs11216194	116945022	C	G	0.0984024	-0.0565869	0.0042091	7.3E-42
11	SIK3	rs11216195	116945175	A	G	0.0966169	-0.0579949	0.0042436	3.7E-43

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs11216196	116945176	G	T	0.0966169	-0.0579949	0.0042436	3.7E-43
11	SIK3	rs35485516	116945411	C	CAG	0.0987711	-0.0574468	0.0041942	2.0E-43
11	SIK3	rs10892049	116945500	C	G	0.1358800	-0.0492087	0.0036604	1.2E-42
11	SIK3	rs10892050	116945678	A	C	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs7924318	116945914	G	C	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs11216197	116946062	G	A	0.0990320	-0.0570121	0.0041910	6.7E-43
11	SIK3	rs191655881	116946939	C	A	0.1358800	-0.0492087	0.0036604	1.2E-42
11	SIK3	rs111327557	116947068	T	C	0.0496009	0.0495203	0.0057907	6.1E-18
11	SIK3	rs1565486994	116947173	TATATTA	T	0.0118733	-0.0647550	0.0117510	1.0E-08
11	SIK3	rs146056222	116947627	G	A	0.1358800	-0.0492087	0.0036604	1.2E-42
11	SIK3	rs61907604	116947691	G	A	0.1865340	-0.0223451	0.0032171	1.0E-12
11	SIK3	rs112704540	116947811	G	A	0.1862890	-0.0222941	0.0032179	1.2E-12
11	SIK3	rs146503809	116948352	G	A	0.0271988	0.0688036	0.0077304	1.2E-19
11	SIK3	rs4316540	116948525	T	C	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs12293755	116948548	T	A	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs1241658	116948901	A	G	0.4693520	-0.0366006	0.0025326	1.6E-47
11	SIK3	rs139552563	116949016	CAAAT	C	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs112297132	116949116	GA	G	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs6589580	116949157	A	G	0.1862890	-0.0222941	0.0032179	1.2E-12
11	SIK3	rs12419047	116949190	A	G	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs12421834	116949307	C	A	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs61907605	116949355	A	T	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs12420518	116949372	C	T	0.1358800	-0.0492087	0.0036604	1.2E-42
11	SIK3	rs142344418	116949918	C	CAG	0.0856599	0.0340060	0.0045233	3.0E-14
11	SIK3	rs12419437	116949974	A	G	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs1473324	116951202	G	T	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs1473325	116951318	T	C	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs76538122	116951618	G	A	0.0316737	-0.0506509	0.0071800	1.5E-12
11	SIK3	rs12286405	116951812	T	C	0.1358770	-0.0491483	0.0036604	1.5E-42
11	SIK3	rs11605327	116952346	A	G	0.2025090	-0.0312738	0.0031327	1.6E-23
11	SIK3	rs77467134	116952391	C	T	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs76654964	116952805	A	G	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs76146269	116952901	G	A	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs1473326	116952956	C	T	0.0499287	0.0509322	0.0057644	5.5E-19
11	SIK3	rs143550340	116953197	G	T	0.0652517	0.0288871	0.0051552	3.7E-08
11	SIK3	rs1473327	116953280	T	A	0.0499677	0.0509138	0.0057628	5.5E-19
11	SIK3	rs12275355	116953446	G	A	0.0987746	-0.0574398	0.0041940	1.9E-43
11	SIK3	rs12289974	116953570	T	C	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs2289890	116953904	A	G	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs511676	116954168	G	T	0.4703840	-0.0372854	0.0025318	2.4E-49
11	SIK3	rs2289892	116954524	A	G	0.0986750	-0.0575567	0.0041961	1.5E-43
11	SIK3	rs12291040	116955901	C	T	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs12270837	116955927	C	A	0.0987577	-0.0574372	0.0041943	2.0E-43
11	SIK3	rs10502221	116956154	T	C	0.2023420	-0.0312539	0.0031323	1.5E-23
11	SIK3	rs17120177	116956653	C	T	0.0987768	-0.0575494	0.0041959	1.4E-43
11	SIK3	rs1940626	116957405	C	T	0.1862430	-0.0222659	0.0032187	1.3E-12
11	SIK3	rs682048	116957604	G	T	0.2649550	-0.0216951	0.0028497	1.7E-14
11	SIK3	rs193291566	116957830	G	T	0.0101967	-0.0936143	0.0124977	4.0E-15
11	SIK3	rs878692	116958223	A	C	0.0986835	-0.0575360	0.0041991	1.9E-43
11	SIK3	rs6589582	116958484	C	A	0.2042550	-0.0314519	0.0031219	6.7E-24
11	SIK3	rs12420857	116958726	T	G	0.0986744	-0.0575368	0.0041993	2.0E-43
11	SIK3	rs7120706	116959371	C	T	0.2042510	-0.0314431	0.0031219	6.8E-24
11	SIK3	rs7120963	116959545	C	T	0.2042510	-0.0314431	0.0031219	6.8E-24
11	SIK3	rs11216199	116960300	T	C	0.0986484	-0.0575046	0.0041999	2.2E-43
11	SIK3	rs145400227	116960788	CAGTAAA	C	0.0986484	-0.0575046	0.0041999	2.2E-43
11	SIK3	rs11216200	116961127	T	C	0.1358360	-0.0492611	0.0036620	1.2E-42
11	SIK3	rs7112967	116961196	T	C	0.0499321	0.0507997	0.0057641	6.7E-19
11	SIK3	rs10892051	116962002	A	C	0.0986348	-0.0575615	0.0042001	1.9E-43
11	SIK3	rs117157737	116962297	T	G	0.0172214	-0.0558053	0.0096938	4.1E-09
11	SIK3	rs56134734	116962339	A	G	0.0499417	0.0506356	0.0057635	8.4E-19
11	SIK3	rs61905677	116962939	G	T	0.0499417	0.0506356	0.0057635	8.4E-19
11	SIK3	rs493134	116962963	T	C	0.4697780	-0.0373664	0.0025310	1.1E-49
11	SIK3	rs10502222	116963014	T	C	0.1847660	-0.0346219	0.0032475	1.0E-26
11	SIK3	rs10892052	116963597	A	G	0.1847530	-0.0346211	0.0032477	1.0E-26
11	SIK3	rs61905678	116964069	T	C	0.0499468	0.0505511	0.0057632	9.5E-19
11	SIK3	rs61905679	116964071	T	C	0.0499468	0.0505511	0.0057632	9.5E-19
11	SIK3	rs1815789	116964237	C	T	0.1860430	-0.0221519	0.0032216	2.0E-12
11	SIK3	rs1815788	116964255	C	T	0.1860150	-0.0221247	0.0032213	2.1E-12
11	SIK3	rs201165469	116964853	G	GC	0.0987603	-0.0577218	0.0041973	8.7E-44
11	SIK3	rs61905680	116965315	A	G	0.0499468	0.0505511	0.0057632	9.5E-19
11	SIK3	rs76930628	116965385	T	A	0.0203650	-0.0541594	0.0089314	1.3E-09
11	SIK3	rs61905681	116965493	C	A	0.0499468	0.0505511	0.0057632	9.5E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs2513097	116965496	G	A	0.2643210	-0.0218970	0.0028537	9.7E-15
11	SIK3	rs77320801	116965633	T	C	0.0499366	0.0506332	0.0057638	8.6E-19
11	SIK3	rs761823852	116965753	A	AT	0.0423249	0.0535567	0.0063205	1.4E-17
11	SIK3	rs78044162	116966373	T	C	0.1357220	-0.0491182	0.0036643	2.4E-42
11	SIK3	rs9971422	116966657	C	T	0.1351570	-0.0488534	0.0036733	7.6E-42
11	SIK3	rs113224863	116966687	G	GT	0.1855610	-0.0219185	0.0032264	3.1E-12
11	SIK3	rs1241655	116967092	T	G	0.2649470	-0.0216542	0.0028525	2.0E-14
11	SIK3	rs12281729	116967414	C	A	0.0986419	-0.0575239	0.0042011	2.3E-43
11	SIK3	rs7941927	116968188	G	A	0.1860950	-0.0221707	0.0032211	1.7E-12
11	SIK3	rs149144614	116968288	A	G	0.0450244	0.0522379	0.0060747	3.5E-18
11	SIK3	rs12417152	116968577	C	G	0.0984451	-0.0575003	0.0042062	3.0E-43
11	SIK3	rs11823013	116968819	C	T	0.0499547	0.0504064	0.0057633	1.2E-18
11	SIK3	rs11216204	116968898	A	G	0.0984235	-0.0575735	0.0042067	2.3E-43
11	SIK3	rs1241657	116969045	T	C	0.3124150	0.0423990	0.0027271	2.2E-55
11	SIK3	rs12272305	116969222	A	G	0.0951185	-0.0583888	0.0042823	6.0E-43
11	SIK3	rs12279266	116969317	C	T	0.0978350	-0.0571516	0.0042217	1.8E-42
11	SIK3	rs201227770	116969542	T	GCATTG	0.0360561	0.0542395	0.0068161	9.1E-16
11	SIK3	rs59294170	116970730	T	A	0.0499451	0.0505960	0.0057636	8.8E-19
11	SIK3	rs12418324	116971960	T	C	0.0983716	-0.0573658	0.0042072	4.7E-43
11	SIK3	rs11216206	116972709	G	C	0.3134790	-0.0241283	0.0027131	1.4E-19
11	SIK3	rs17120197	116974388	C	T	0.0501454	0.0507819	0.0057502	5.6E-19
11	SIK3	chr11:116974556_C_CTGT	116974556	CTGTT	C	0.0985648	-0.0576374	0.0042030	1.6E-43
11	SIK3	rs74927399	116975550	C	T	0.0985784	-0.0576886	0.0042028	1.4E-43
11	SIK3	rs76949321	116975627	A	G	0.0985784	-0.0576886	0.0042028	1.4E-43
11	SIK3	rs11216209	116977470	C	T	0.0985875	-0.0577215	0.0042026	1.2E-43
11	SIK3	rs11216210	116977613	T	G	0.1359820	-0.0487794	0.0036580	6.5E-42
11	SIK3	rs7109876	116977932	A	C	0.0501709	0.0508281	0.0057488	5.0E-19
11	SIK3	rs509171	116978141	T	C	0.2651710	-0.0212927	0.0028436	5.0E-14
11	SIK3	chr11:116978213_C_CA	116978213	CA	C	0.1688330	-0.0391284	0.0033980	2.7E-30
11	SIK3	rs11216212	116979635	A	T	0.0985875	-0.0577215	0.0042026	1.2E-43
11	SIK3	rs146178826	116980651	G	A	0.0985875	-0.0577215	0.0042026	1.2E-43
11	SIK3	rs7358350	116980892	C	T	0.1359820	-0.0487794	0.0036580	6.5E-42
11	SIK3	rs4938321	116981791	T	C	0.1864990	-0.0218572	0.0032144	3.3E-12
11	SIK3	rs11216215	116981971	A	T	0.0985875	-0.0577215	0.0042026	1.2E-43
11	SIK3	rs3863304	116982407	A	G	0.2010840	-0.0327511	0.0031466	2.2E-25
11	SIK3	rs3863305	116982408	T	C	0.2010840	-0.0327511	0.0031466	2.2E-25
11	SIK3	rs3863306	116982497	T	C	0.2026240	-0.0312888	0.0031331	1.6E-23
11	SIK3	rs7131351	116982890	A	G	0.2020520	-0.0305648	0.0031370	2.2E-22
11	SIK3	rs7117123	116982970	A	T	0.1924420	-0.0296672	0.0032108	1.9E-20
11	SIK3	rs10128690	116983206	A	G	0.0928329	-0.0568502	0.0043440	8.5E-40
11	SIK3	rs10128570	116983305	G	A	0.0985875	-0.0577215	0.0042026	1.2E-43
11	SIK3	rs10128571	116983465	G	A	0.0985875	-0.0577215	0.0042026	1.2E-43
11	SIK3	rs113184611	116984048	A	C	0.0501714	0.0508620	0.0057485	4.8E-19
11	SIK3	rs374519262	116984705	A	AC	0.1175690	-0.0510433	0.0039465	9.7E-40
11	SIK3	rs146725667	116985530	A	G	0.0334808	-0.0506138	0.0069921	4.7E-13
11	SIK3	rs12287768	116985606	C	A	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs588918	116985926	C	T	0.4703050	-0.0369728	0.0025261	8.4E-49
11	SIK3	rs12274771	116985982	G	C	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs12274773	116985993	T	C	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs75212922	116986276	A	T	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs10892053	116986287	T	C	0.2033620	-0.0307545	0.0031225	6.5E-23
11	SIK3	rs11216217	116986936	A	G	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	chr11:116987321_TAA_T	116987321	T	TAA	0.1004030	-0.0553657	0.0041801	1.0E-40
11	SIK3	rs201445271	116987332	AC	A	0.0499362	0.0497057	0.0057741	2.2E-18
11	SIK3	rs10160754	116988278	C	A	0.1359660	-0.0487294	0.0036585	8.2E-42
11	SIK3	rs10160755	116988287	G	A	0.1359660	-0.0487294	0.0036585	8.2E-42
11	SIK3	rs11406946	116988385	CA	C	0.2061690	-0.0318709	0.0031162	1.7E-24
11	SIK3	rs519794	116988737	C	T	0.4708670	-0.0370227	0.0025275	7.7E-49
11	SIK3	rs10706688	116989575	T	TA	0.2026320	-0.0305779	0.0031320	1.8E-22
11	SIK3	rs7939934	116990552	T	A	0.1876200	-0.0222933	0.0032135	1.3E-12
11	SIK3	rs61905687	116991428	C	T	0.0501878	0.0508838	0.0057474	4.6E-19
11	SIK3	rs80242245	116991529	G	C	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs11216218	116991945	T	C	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs11216219	116992039	T	C	0.0985794	-0.0576600	0.0042029	1.5E-43
11	SIK3	rs607273	116992102	A	T	0.3117440	0.0431057	0.0027170	1.8E-57
11	SIK3	rs12272973	116992331	C	A	0.0991652	-0.0581070	0.0042049	3.8E-44
11	SIK3	rs10128682	116992742	T	C	0.0987202	-0.0579213	0.0041993	4.7E-44
11	SIK3	rs6589583	116993050	T	C	0.2654040	-0.0212512	0.0028413	5.1E-14
11	SIK3	rs7130531	116993117	T	C	0.0501878	0.0508838	0.0057474	4.6E-19
11	SIK3	rs11216220	116993272	C	T	0.1359650	-0.0486840	0.0036583	9.3E-42
11	SIK3	rs11375002	116993436	CA	C	0.4713680	-0.0371353	0.0025250	3.4E-49
11	SIK3	rs75826529	116994384	A	T	0.0987202	-0.0579213	0.0041993	4.7E-44

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs74460214	116994491	C	T	0.0987202	-0.0579213	0.0041993	4.7E-44
11	SIK3	rs79349393	116994651	G	A	0.0987202	-0.0579213	0.0041993	4.7E-44
11	SIK3	rs7931665	116995524	G	A	0.1361030	-0.0489246	0.0036562	3.1E-42
11	SIK3	rs7931770	116995574	T	C	0.4700540	-0.0369249	0.0025243	9.7E-49
11	SIK3	rs7121347	116996493	T	G	0.4700540	-0.0369249	0.0025243	9.7E-49
11	SIK3	rs11604866	116996798	T	C	0.0987202	-0.0579213	0.0041993	4.7E-44
11	SIK3	rs10892054	116997505	T	C	0.1865260	-0.0218537	0.0032141	3.3E-12
11	SIK3	rs10892055	116997655	A	G	0.1865260	-0.0218537	0.0032141	3.3E-12
11	SIK3	rs7950213	116997938	A	C	0.0502031	0.0508859	0.0057465	4.6E-19
11	SIK3	chr11:116999579_G_GTTT	116999579	GTTTTC	G	0.0502031	0.0508859	0.0057465	4.6E-19
11	SIK3	rs10892056	116999695	C	G	0.0987202	-0.0579213	0.0041993	4.7E-44
11	SIK3	rs10502224	116999764	G	A	0.1361150	-0.0488695	0.0036567	3.8E-42
11	SIK3	rs7930264	117000050	A	G	0.2654620	-0.0212816	0.0028408	4.7E-14
11	SIK3	rs17120233	117000507	G	A	0.0502031	0.0508859	0.0057465	4.6E-19
11	SIK3	rs10892057	117001318	C	A	0.1367440	-0.0489809	0.0036552	2.2E-42
11	SIK3	chr11:117001505_C_CA	117001505	CA	C	0.2805950	-0.0286978	0.0028179	6.3E-24
11	SIK3	rs75858236	117001547	G	A	0.0502031	0.0508859	0.0057465	4.6E-19
11	SIK3	rs12278943	117003642	C	T	0.0985840	-0.0576946	0.0042028	1.3E-43
11	SIK3	rs7946390	117004436	G	A	0.1361030	-0.0488868	0.0036561	3.5E-42
11	SIK3	rs6589587	117004622	G	T	0.1865280	-0.0218226	0.0032140	3.5E-12
11	SIK3	rs11216224	117005208	C	T	0.1349470	-0.0488245	0.0036717	9.5E-42
11	SIK3	rs7114963	117005267	C	T	0.4658920	-0.0365971	0.0025361	1.0E-47
11	SIK3	rs1940625	117005726	G	A	0.1361010	-0.0488824	0.0036561	3.6E-42
11	SIK3	rs10892058	117005905	T	C	0.2027950	-0.0306941	0.0031244	8.1E-23
11	SIK3	rs10790169	117006443	C	A	0.4702680	-0.0369918	0.0025235	5.4E-49
11	SIK3	rs77250716	117006637	C	T	0.0496654	0.0508117	0.0057794	8.6E-19
11	SIK3	rs11216225	117007298	G	A	0.1361010	-0.0488824	0.0036561	3.6E-42
11	SIK3	rs11216226	117007350	G	C	0.0987202	-0.0579213	0.0041993	4.7E-44
11	SIK3	rs11216227	117007881	G	C	0.2029350	-0.0307439	0.0031254	6.8E-23
11	SIK3	rs12276805	117008043	C	T	0.0965589	-0.0599264	0.0042491	8.2E-46
11	SIK3	rs57278884	117008464	'AAAAGA'	C	0.1865880	-0.0219421	0.0032133	2.7E-12
11	SIK3	chr11:117008471_G_GAAA	117008471	iAAAAGA	G	0.1864370	-0.0223779	0.0032169	1.1E-12
11	SIK3	rs12271319	117008508	T	C	0.1361050	-0.0488849	0.0036561	3.5E-42
11	SIK3	rs12284696	117008803	G	A	0.1352450	-0.0485827	0.0036700	2.4E-41
11	SIK3	rs7931398	117008960	C	T	0.2660270	-0.0213910	0.0028390	3.5E-14
11	SIK3	rs117901629	117008963	A	G	0.0985849	-0.0576391	0.0042031	1.6E-43
11	SIK3	rs138181556	117009007	A	G	0.0985840	-0.0576946	0.0042028	1.3E-43
11	SIK3	rs7112937	117009740	C	T	0.1361190	-0.0489121	0.0036560	3.3E-42
11	SIK3	rs61905691	117009987	G	A	0.0502031	0.0508859	0.0057465	4.6E-19
11	SIK3	rs7127881	117010082	A	G	0.2067530	-0.0305027	0.0031237	1.8E-22
11	SIK3	rs58176010	117010731	A	G	0.0193906	0.0769355	0.0091516	7.9E-18
11	SIK3	rs10892059	117010929	A	G	0.2029220	-0.0307247	0.0031226	6.8E-23
11	SIK3	rs10892060	117010946	A	C	0.2025910	-0.0305475	0.0031258	1.2E-22
11	SIK3	rs4245168	117011922	A	C	0.4698990	-0.0370008	0.0025217	4.7E-49
11	SIK3	rs35123861	117012098	CA	C	0.2035930	-0.0308613	0.0031201	4.3E-23
11	SIK3	rs7125788	117012680	C	T	0.0501980	0.0508477	0.0057468	4.9E-19
11	SIK3	rs1442498591	117012824	AG	A	0.1646070	-0.0307034	0.0034504	1.7E-19
11	SIK3	chr11:117012827_G_GTT	117012827	GTT	G	0.0986795	-0.0579786	0.0042003	3.9E-44
11	SIK3	rs10790170	117012828	G	T	0.2039460	-0.0316702	0.0031287	4.1E-24
11	SIK3	rs61905705	117013060	T	A	0.0501985	0.0508502	0.0057468	4.9E-19
11	SIK3	rs61905706	117013061	T	G	0.0501985	0.0508502	0.0057468	4.9E-19
11	SIK3	rs140947361	117013808	A	AC	0.0501985	0.0508502	0.0057468	4.9E-19
11	SIK3	rs374772197	117013968	C	T	0.0501205	0.0507433	0.0057509	5.6E-19
11	SIK3	rs11216230	117014073	A	G	0.1737870	-0.0285912	0.0033429	1.6E-17
11	SIK3	rs35190172	117014597	T	TC	0.0501985	0.0508502	0.0057468	4.9E-19
11	SIK3	rs7119185	117015380	T	C	0.1865550	-0.0219719	0.0032137	2.4E-12
11	SIK3	rs10892061	117015398	T	C	0.2034660	-0.0308822	0.0031216	4.4E-23
11	SIK3	chr11:117015578_AT_A	117015578	A	AT	0.2655260	-0.0214188	0.0028400	3.3E-14
11	SIK3	rs79870586	117016005	A	G	0.0986786	-0.0579186	0.0042001	4.4E-44
11	SIK3	rs66751419	117017528	T	TG	0.2036970	-0.0310508	0.0031226	2.5E-23
11	SIK3	rs7128772	117018695	A	T	0.2609870	-0.0215490	0.0028702	5.6E-14
11	SIK3	rs80054374	117019951	G	A	0.0986831	-0.0579460	0.0042000	3.9E-44
11	SIK3	rs12808524	117020277	C	T	0.2036070	-0.0307835	0.0031218	6.5E-23
11	SIK3	rs17120237	117020330	C	T	0.0502036	0.0508024	0.0057466	5.3E-19
11	SIK3	rs77955134	117021652	A	G	0.0985469	-0.0577193	0.0042035	1.1E-43
11	SIK3	rs77594377	117021730	A	G	0.0985378	-0.0577276	0.0042037	1.1E-43
11	SIK3	rs112619870	117021940	C	A	0.0271361	0.0545439	0.0078535	4.3E-12
11	SIK3	rs142310263	117022278	C	AATCTCA	0.0976732	-0.0573604	0.0042245	1.0E-42
11	SIK3	rs4936359	117023008	A	T	0.0502031	0.0508050	0.0057465	5.3E-19
11	SIK3	rs4936360	117023053	C	G	0.0502025	0.0508069	0.0057465	5.3E-19
11	SIK3	rs10466590	117023697	G	C	0.2594100	-0.0220715	0.0028775	1.1E-14
11	SIK3	rs143791312	117024639	T	C	0.0625858	-0.0564240	0.0051863	2.8E-28

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs11216239	117024796	G	C	0.2655120	-0.0214365	0.0028397	3.2E-14
11	SIK3	rs10892063	117025439	C	A	0.2041590	-0.0307126	0.0031175	8.0E-23
11	SIK3	rs111860754	117025569	C	CA	0.0501967	0.0510263	0.0057456	3.5E-19
11	SIK3	rs10892064	117025837	C	G	0.2036600	-0.0307373	0.0031171	6.5E-23
11	SIK3	rs145746824	117025856	G	A	0.0211719	-0.0489133	0.0087289	3.6E-08
11	SIK3	rs2186844	117026197	T	C	0.0985560	-0.0577132	0.0042033	1.2E-43
11	SIK3	rs10892065	117026308	C	T	0.2036600	-0.0307373	0.0031171	6.5E-23
11	SIK3	rs61905709	117027118	T	C	0.0502013	0.0510444	0.0057453	3.5E-19
11	SIK3	rs4936361	117027438	C	T	0.1806980	-0.0209747	0.0032729	5.3E-11
11	SIK3	rs4938325	117027763	A	G	0.0502097	0.0511607	0.0057448	2.9E-19
11	SIK3	rs7950364	117028170	G	C	0.4697800	-0.0371557	0.0025219	2.2E-49
11	SIK3	rs11216240	117028532	T	A	0.2654890	-0.0214107	0.0028389	3.4E-14
11	SIK3	rs11216241	117028533	C	A	0.2655160	-0.0214384	0.0028387	3.1E-14
11	SIK3	rs1228864	117028864	T	C	0.0985605	-0.0577569	0.0042032	9.9E-44
11	SIK3	rs141750997	117028962	GCTGGAT	A	0.1856280	-0.0218470	0.0032224	3.7E-12
11	SIK3	rs7926104	117029066	A	G	0.2034510	-0.0308431	0.0031192	5.1E-23
11	SIK3	rs112120205	117029070	A	G	0.0502097	0.0511607	0.0057448	2.9E-19
11	SIK3	rs146943088	117029109	C	A	0.0985605	-0.0577569	0.0042032	9.9E-44
11	SIK3	rs11600552	117030231	C	T	0.2655160	-0.0214496	0.0028387	3.0E-14
11	SIK3	rs11216242	117030833	A	G	0.2034590	-0.0308622	0.0031191	4.6E-23
11	SIK3	rs7112191	117031340	A	G	0.0502080	0.0511835	0.0057447	2.8E-19
11	SIK3	chr11:117031495_C_CATT	117031495	CATTTT	C	0.4697760	-0.0371794	0.0025218	1.9E-49
11	SIK3	rs199986368	117031627	C	T	0.0153533	0.1339200	0.0102611	5.2E-40
11	SIK3	rs7481286	117031656	T	G	0.0986650	-0.0580962	0.0042008	2.2E-44
11	SIK3	rs12804122	117031900	G	C	0.2033590	-0.0305789	0.0031198	1.2E-22
11	SIK3	rs4548653	117032600	A	G	0.1865280	-0.0219045	0.0032129	2.9E-12
11	SIK3	rs7941428	117032668	G	C	0.2638250	-0.0204012	0.0028503	7.3E-13
11	SIK3	chr11:117032674_CTT_C	117032674	C	CTT	0.1047950	-0.0563336	0.0041090	1.1E-43
11	SIK3	rs4575311	117033641	A	G	0.2035020	-0.0308888	0.0031184	3.9E-23
11	SIK3	rs4938326	117034748	C	G	0.0502080	0.0511835	0.0057447	2.8E-19
11	SIK3	rs187437651	117034813	A	G	0.0187862	0.0793286	0.0093238	4.0E-18
11	SIK3	rs147518949	117035258	A	G	0.0187862	0.0793286	0.0093238	4.0E-18
11	SIK3	rs4938327	117036012	C	T	0.1865940	-0.0219462	0.0032117	2.5E-12
11	SIK3	rs3181	117036327	A	G	0.1866150	-0.0219266	0.0032115	2.6E-12
11	SIK3	rs10732856	117036397	C	T	0.4701100	-0.0371212	0.0025206	2.4E-49
11	SIK3	rs721783	117036733	T	C	0.1866590	-0.0220539	0.0032114	2.0E-12
11	SIK3	rs75216569	117036999	G	A	0.0986922	-0.0579174	0.0042000	4.8E-44
11	SIK3	rs7115242	117037567	A	G	0.3130920	0.0428589	0.0027044	1.8E-57
11	SIK3	rs7118591	117037741	A	C	0.1866250	-0.0219855	0.0032115	2.3E-12
11	SIK3	chr11:117037793_AAC_A	117037793	A	AAC	0.1866250	-0.0219855	0.0032115	2.3E-12
11	SIK3	rs80273401	117037990	C	T	0.0986922	-0.0579174	0.0042000	4.8E-44
11	SIK3	rs61905712	117038577	A	G	0.0502635	0.0510854	0.0057426	3.3E-19
11	SIK3	rs112870705	117038708	T	TCAC	0.0499853	0.0502959	0.0057600	1.1E-18
11	SIK3	rs61905713	117038713	T	C	0.0499853	0.0502959	0.0057600	1.1E-18
11	SIK3	rs147501797	117038982	A	G	0.0343337	-0.0468333	0.0069188	1.2E-11
11	SIK3	rs12273536	117040255	T	C	0.0959553	-0.0566840	0.0042530	6.1E-41
11	SIK3	rs12273545	117040296	T	C	0.0959553	-0.0566840	0.0042530	6.1E-41
11	SIK3	rs77999164	117041401	T	C	0.0959599	-0.0566594	0.0042532	6.8E-41
11	SIK3	rs58194633	117041909	C	CT	0.2622250	-0.0206925	0.0028516	4.4E-13
11	SIK3	rs11216244	117042014	T	C	0.2628020	-0.0203425	0.0028476	9.1E-13
11	SIK3	rs11216245	117042486	T	C	0.2628020	-0.0203425	0.0028476	9.1E-13
11	SIK3	rs80143284	117042854	A	C	0.0960999	-0.0569201	0.0042492	2.2E-41
11	SIK3	rs12279066	117043193	G	C	0.2626870	-0.0203408	0.0028483	9.3E-13
11	SIK3	rs17120241	117044304	C	T	0.0502419	0.0509607	0.0057428	3.9E-19
11	SIK3	rs11351498	117044488	T	TA	0.2624640	-0.0202048	0.0028506	1.5E-12
11	SIK3	rs2155583	117044501	G	A	0.4699150	-0.0372307	0.0025217	1.2E-49
11	SIK3	chr11:117044615_GA_G	117044615	G	GA	0.2198430	-0.0302190	0.0030938	8.9E-23
11	SIK3	rs2000614	117045026	T	C	0.4698400	-0.0372300	0.0025214	1.3E-49
11	SIK3	rs2000615	117045103	T	C	0.4698400	-0.0372300	0.0025214	1.3E-49
11	SIK3	rs2000616	117045813	T	C	0.4698350	-0.0372298	0.0025214	1.3E-49
11	SIK3	rs76972960	117045962	C	T	0.0502419	0.0509607	0.0057428	3.9E-19
11	SIK3	rs10750100	117046528	C	T	0.4698350	-0.0372298	0.0025214	1.3E-49
11	SIK3	rs61905716	117048351	T	C	0.0502419	0.0509607	0.0057428	3.9E-19
11	SIK3	rs12280172	117048557	A	G	0.0966510	-0.0564228	0.0042423	1.3E-40
11	SIK3	rs112151056	117048652	A	G	0.0502419	0.0509607	0.0057428	3.9E-19
11	SIK3	rs61905718	117048961	T	C	0.0502419	0.0509607	0.0057428	3.9E-19
11	SIK3	rs75890305	117049253	G	A	0.0959723	-0.0567422	0.0042527	5.3E-41
11	SIK3	chr11:117049961_T_TA	117049961	TA	T	0.4717190	-0.0374746	0.0025326	9.6E-50
11	SIK3	rs11826651	117049977	A	T	0.0502521	0.0508977	0.0057416	4.2E-19
11	SIK3	rs10892066	117050211	T	C	0.2627990	-0.0202851	0.0028476	1.0E-12
11	SIK3	rs4938328	117050503	T	G	0.2065790	-0.0321465	0.0031022	2.1E-25
11	SIK3	rs1815786	117050674	T	C	0.3130240	0.0431595	0.0027122	8.6E-58

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs1815787	117050681	C	T	0.4700760	-0.0372174	0.0025214	1.4E-49
11	SIK3	rs138470332	117051591	T	C	0.0188696	-0.0650683	0.0092453	7.0E-13
11	SIK3	rs111530588	117051870	A	G	0.0959723	-0.0567422	0.0042527	5.3E-41
11	SIK3	rs61905719	117051998	T	C	0.0502521	0.0508977	0.0057416	4.2E-19
11	SIK3	rs564325746	117052134	TG	T	0.0921304	0.0276341	0.0044585	4.0E-10
11	SIK3	rs7130297	117053154	T	C	0.4684550	-0.0382139	0.0025225	2.8E-52
11	SIK3	rs11216250	117053284	T	C	0.0952470	-0.0560950	0.0042697	7.4E-40
11	SIK3	rs80259223	117053602	A	G	0.0511142	0.0492879	0.0057012	3.1E-18
11	SIK3	rs3886960	117054274	T	G	0.2627560	-0.0202825	0.0028477	1.0E-12
11	SIK3	rs723955	117054326	A	G	0.2627560	-0.0202825	0.0028477	1.0E-12
11	SIK3	rs7108912	117055280	A	G	0.2627590	-0.0202842	0.0028477	1.0E-12
11	SIK3	rs201829635	117056603	T	TC	0.0496035	0.0500432	0.0057782	1.9E-18
11	SIK3	rs117091722	117056884	A	G	0.0634866	-0.0513525	0.0051586	4.5E-24
11	SIK3	rs10790172	117057024	T	G	0.4713950	-0.0375602	0.0025316	4.2E-50
11	SIK3	rs10892067	117057046	C	G	0.0960851	-0.0569947	0.0042498	1.8E-41
11	SIK3	rs7124872	117057235	G	A	0.2628860	-0.0202647	0.0028473	1.1E-12
11	SIK3	rs7124996	117057290	T	C	0.2628860	-0.0202647	0.0028473	1.1E-12
11	SIK3	rs4938329	117057396	T	C	0.2628800	-0.0202355	0.0028474	1.2E-12
11	SIK3	rs11216252	117057507	A	G	0.0959621	-0.0567851	0.0042532	4.8E-41
11	SIK3	rs11216253	117057509	C	A	0.0959621	-0.0567851	0.0042532	4.8E-41
11	SIK3	rs4938330	117057798	G	C	0.2256560	-0.0192061	0.0030007	3.2E-10
11	SIK3	rs10892068	117057830	T	C	0.0960830	-0.0569805	0.0042497	1.9E-41
11	SIK3	rs9943680	117058538	C	T	0.1873070	-0.0294563	0.0032845	2.5E-19
11	SIK3	rs11216255	117059279	G	A	0.2629470	-0.0202675	0.0028477	1.1E-12
11	SIK3	rs34992009	117059421	G	GC	0.2060960	-0.0322283	0.0031084	1.7E-25
11	SIK3	rs4938331	117059966	A	C	0.2060160	-0.0322007	0.0031086	1.9E-25
11	SIK3	rs4938332	117060082	G	A	0.2060990	-0.0322363	0.0031084	1.7E-25
11	SIK3	rs4938333	117060172	G	A	0.0502583	0.0508728	0.0057413	4.3E-19
11	SIK3	rs4938334	117060326	C	G	0.2062370	-0.0323520	0.0031091	1.2E-25
11	SIK3	rs61903394	117061182	A	G	0.0502583	0.0508728	0.0057413	4.3E-19
11	SIK3	rs11216257	117061845	T	C	0.3720300	-0.0186185	0.0026069	9.1E-13
11	SIK3	rs6589590	117065365	C	A	0.2068760	-0.0321627	0.0031031	1.9E-25
11	SIK3	rs56751865	117066155	T	C	0.1148430	-0.0505552	0.0039587	2.8E-38
11	SIK3	rs112895963	117066443	T	A	0.0496236	0.0511379	0.0057798	5.0E-19
11	SIK3	rs79955870	117066645	T	C	0.0967687	-0.0568501	0.0042462	2.3E-41
11	SIK3	rs35187263	117067811	AC	A	0.2051320	-0.0337234	0.0031113	8.7E-28
11	SIK3	rs368388328	117069182	T	TTTG	0.0409253	0.0495646	0.0063659	3.0E-15
11	SIK3	rs11216261	117069494	C	T	0.0958584	-0.0567829	0.0042562	5.2E-41
11	SIK3	rs12280210	117069733	C	T	0.1333820	-0.0475096	0.0036882	4.3E-39
11	SIK3	rs9971421	117070824	T	C	0.0946446	-0.0569701	0.0042871	9.4E-41
11	SIK3	rs61903398	117070897	T	C	0.0500865	0.0509883	0.0057520	3.7E-19
11	SIK3	rs144942164	117071184	C	T	0.0392251	0.0527427	0.0065083	1.4E-16
11	SIK3	rs202154722	117071196	AT	A	0.0958921	-0.0566897	0.0042575	5.9E-41
11	SIK3	rs7101763	117071269	T	G	0.1834860	-0.0204665	0.0032356	1.1E-10
11	SIK3	rs17120280	117071416	A	G	0.0514591	0.0496184	0.0056847	1.5E-18
11	SIK3	rs77182215	117071650	A	C	0.0852490	0.0359981	0.0045290	1.1E-15
11	SIK3	rs61903399	117071759	T	A	0.0496145	0.0504374	0.0057817	9.8E-19
11	SIK3	chr11:117071926_G_GTGT	117071926	GTGTT	G	0.2004500	-0.0340399	0.0031526	1.9E-27
11	SIK3	rs116582417	117072350	A	G	0.0957506	-0.0566685	0.0042587	7.5E-41
11	SIK3	rs1351452	117072638	C	A	0.4702230	-0.0372434	0.0025244	1.5E-49
11	SIK3	rs7109649	117072828	T	C	0.2626370	-0.0201121	0.0028510	1.7E-12
11	SIK3	rs1531706	117073236	A	C	0.2626370	-0.0201121	0.0028510	1.7E-12
11	SIK3	rs77400241	117073331	T	C	0.0173245	-0.0526296	0.0096572	2.4E-08
11	SIK3	rs7935913	117073632	A	G	0.2626370	-0.0201121	0.0028510	1.7E-12
11	SIK3	rs7935834	117073721	G	C	0.2626370	-0.0201121	0.0028510	1.7E-12
11	SIK3	rs1531707	117073996	A	G	0.2626310	-0.0201029	0.0028510	1.7E-12
11	SIK3	rs17120293	117074130	C	T	0.0957643	-0.0566123	0.0042585	8.7E-41
11	SIK3	rs4620758	117075002	A	G	0.1832730	-0.0202262	0.0032379	1.9E-10
11	SIK3	rs12274388	117075522	T	C	0.2603860	-0.0193016	0.0028657	1.7E-11
11	SIK3	rs7130213	117075936	A	C	0.1829300	-0.0206346	0.0032401	7.9E-11
11	SIK3	rs12274725	117076137	T	C	0.0957403	-0.0566946	0.0042592	7.0E-41
11	SIK3	rs7484045	117076174	T	C	0.2626420	-0.0201492	0.0028509	1.6E-12
11	SIK3	rs11216265	117076464	C	T	0.0957403	-0.0566946	0.0042592	7.0E-41
11	SIK3	rs12418036	117076590	A	G	0.0957403	-0.0566946	0.0042592	7.0E-41
11	SIK3	rs4938335	117076645	C	A	0.4698770	-0.0373645	0.0025252	8.6E-50
11	SIK3	rs4938336	117077726	G	A	0.0500792	0.0508142	0.0057528	4.9E-19
11	SIK3	rs10082609	117078358	T	C	0.2549000	-0.0194345	0.0028877	1.9E-11
11	SIK3	chr11:117078990_TA_T	117078990	T	TA	0.2611890	-0.0163261	0.0029039	7.8E-09
11	SIK3	rs11216266	117079434	C	T	0.2626310	-0.0201151	0.0028510	1.7E-12
11	SIK3	rs10736487	117079516	G	A	0.4711460	-0.0367958	0.0025244	2.0E-48
11	SIK3	rs56777911	117080329	C	CT	0.2626340	-0.0201173	0.0028510	1.7E-12
11	SIK3	rs7106662	117080669	C	T	0.2626340	-0.0201173	0.0028510	1.7E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs10892070	117080817	A	G	0.2198200	-0.0313005	0.0030512	5.4E-25
11	SIK3	rs10082561	117080868	C	A	0.0908370	-0.0561788	0.0043600	1.9E-38
11	SIK3	rs4936362	117081484	T	C	0.0500854	0.0507596	0.0057535	5.3E-19
11	SIK3	rs11216267	117081676	T	C	0.2075630	-0.0313377	0.0030986	2.5E-24
11	SIK3	rs144977225	117082379	C	CCCA	0.2626340	-0.0201094	0.0028510	1.7E-12
11	SIK3	rs11216270	117082928	A	C	0.0957334	-0.0567626	0.0042594	5.9E-41
11	SIK3	rs1871756	117082929	A	G	0.1834230	-0.0204078	0.0032361	1.2E-10
11	SIK3	rs10892071	117083849	T	C	0.2626320	-0.0201033	0.0028510	1.7E-12
11	SIK3	rs61903416	117084333	C	T	0.2658580	-0.0204797	0.0028431	5.0E-13
11	SIK3	rs2368149	117085218	A	G	0.0956224	-0.0565638	0.0042627	1.4E-40
11	SIK3	rs61903417	117085441	G	T	0.0500803	0.0507898	0.0057531	5.2E-19
11	SIK3	rs61903418	117085949	A	G	0.0500803	0.0507898	0.0057531	5.2E-19
11	SIK3	rs12281358	117086274	C	T	0.0956179	-0.0565590	0.0042627	1.4E-40
11	SIK3	rs12274465	117086473	T	C	0.2623080	-0.0204077	0.0028536	8.3E-13
11	SIK3	rs6589592	117087191	C	G	0.3090540	0.0431033	0.0027362	9.0E-57
11	SIK3	rs12277910	117087817	A	C	0.1641920	-0.0238068	0.0034181	3.6E-12
11	SIK3	rs111901638	117089132	A	G	0.0501346	0.0506689	0.0057498	6.0E-19
11	SIK3	rs10892072	117089597	A	G	0.2072750	-0.0313741	0.0031016	2.6E-24
11	SIK3	rs11823918	117089781	C	G	0.0501341	0.0506660	0.0057498	6.0E-19
11	SIK3	rs77431162	117090820	T	C	0.0687835	0.0401326	0.0049540	9.9E-17
11	SIK3	rs61903421	117091086	T	A	0.0501335	0.0506626	0.0057498	6.1E-19
11	SIK3	rs116861530	117091945	A	G	0.0943364	-0.0563260	0.0042896	1.1E-39
11	SIK3	rs74420345	117092561	A	C	0.0943329	-0.0563980	0.0042897	8.8E-40
11	SIK3	rs7950093	117092803	T	G	0.2614340	-0.0199999	0.0028565	2.6E-12
11	SIK3	rs7950381	117093181	A	C	0.0501307	0.0506168	0.0057503	6.6E-19
11	SIK3	rs7950501	117093249	T	C	0.0501307	0.0506168	0.0057503	6.6E-19
11	SIK3	rs57383565	117093678	AG	A	0.0505278	0.0499578	0.0057392	1.5E-18
11	SIK3	rs900012	117095719	A	G	0.4668500	-0.0365476	0.0025292	1.8E-47
11	SIK3	rs1320668	117096950	T	C	0.4717900	-0.0353328	0.0025280	7.8E-45
11	SIK3	rs61903426	117097552	T	C	0.0543431	0.0516605	0.0055382	8.4E-21
11	SIK3	rs7128071	117098082	A	G	0.0528996	0.0505189	0.0056139	2.0E-19
11	SIK3 *	rs10892073	117098674	T	C	0.2026940	-0.0308930	0.0031328	3.6E-23
11	SIK3 *	rs76567973	117100045	G	C	0.0955944	-0.0565245	0.0042611	1.3E-40
11	SIK3 *	chr11:117100110_GT_G	117100110	G	GT	0.4743390	-0.0345996	0.0025302	3.3E-43
11	SIK3 *	rs78135964	117100961	T	G	0.0956199	-0.0564126	0.0042600	1.7E-40
11	SIK3 *	rs148233183	117101511	A	G	0.0956347	-0.0564634	0.0042594	1.3E-40
11	SIK3 *	rs4938338	117102178	A	C	0.0544813	0.0516947	0.0055283	8.0E-21
11	SIK3 *	rs4936363	117102219	T	C	0.0544819	0.0516954	0.0055283	8.0E-21
11	SIK3 *	rs76942203	117102531	A	G	0.0956737	-0.0565343	0.0042583	1.0E-40
11	SIK3 *	rs796725952	117102596	G	GA	0.0184845	-0.0565351	0.0093272	2.2E-09
11	SIK3 *	chr11:117103138_A_AAAT	117103138	AAAT	A	0.0956145	-0.0566866	0.0042631	7.9E-41
11	SIK3 *	rs12269901	117103213	C	G	0.2677760	-0.0183780	0.0028307	5.6E-11
11	SIK3 *	rs149576335	117104420	A	G	0.0956619	-0.0565337	0.0042587	9.8E-41
11	SIK3 *	rs11216275	117104988	G	T	0.0917084	0.0262490	0.0043406	3.7E-09
11	SIK3 *	rs142395187	117105293	G	A	0.0951008	-0.0570368	0.0042703	2.4E-41
11	SIK3 *	chr11:117105573_A_AT	117105573	AT	A	0.2019350	-0.0348230	0.0031784	4.1E-28
11	SIK3 *	rs4388921	117106062	C	T	0.1876950	-0.0190435	0.0032108	9.5E-10
11	SIK3 *	rs145671645	117106195	A	G	0.0287758	-0.0525773	0.0075236	1.5E-12
11	SIK3 *	rs10160799	117107172	A	G	0.4717630	-0.0353105	0.0025313	1.4E-44
11	SIK3 *	rs181104223	117107559	C	A	0.0291236	0.0686628	0.0074900	3.9E-21
11	SIK3 *	rs12416941	117108647	A	G	0.0962718	-0.0559468	0.0042490	4.6E-40
11	SIK3 *	rs113784559	117108649	G	C	0.0567680	0.0457932	0.0054216	2.2E-17
11	SIK3 *	rs10750101	117108973	C	T	0.4719000	-0.0352039	0.0025294	2.2E-44
11	SIK3 *	rs12271169	117109305	G	C	0.1770590	-0.0183187	0.0032904	1.0E-08
11	SIK3 *	rs4938339	117109878	T	C	0.0567800	0.0458271	0.0054212	2.1E-17
11	SIK3 *	rs4938340	117109906	A	G	0.0571141	0.0448963	0.0054199	8.4E-17
11	SIK3 *	rs10892074	117109925	T	G	0.2023080	-0.0295100	0.0031366	3.1E-21
11	SIK3 *	rs114221654	117109963	T	C	0.0962718	-0.0559468	0.0042490	4.6E-40
11	SIK3 *	rs35172278	117110063	CCTG	C	0.4837680	-0.0371520	0.0025346	3.5E-49
11	SIK3 *	rs61903427	117110070	C	G	0.0567800	0.0458271	0.0054212	2.1E-17
11	SIK3 *	rs7112111	117110142	G	T	0.1902390	-0.0210830	0.0031982	1.7E-11
11	SIK3 *	rs4635117	117110285	A	G	0.2989250	0.0416623	0.0027747	5.4E-52
11	SIK3 *	rs148910068	117110595	T	C	0.0184628	-0.0578549	0.0093499	2.1E-10
11	SIK3 *	rs6589595	117110619	A	G	0.0567800	0.0458271	0.0054212	2.1E-17
11	SIK3 *	rs116770907	117110799	T	C	0.0962718	-0.0559468	0.0042490	4.6E-40
11	SIK3 *	rs2127907	117110864	G	A	0.4866400	-0.0370264	0.0025305	6.7E-49
11	SIK3 *	rs111677878	117111718	T	C	0.0962520	-0.0559664	0.0042498	4.5E-40
11	SIK3 *	rs7104023	117111886	T	A	0.1902010	-0.0209490	0.0031986	2.2E-11
11	SIK3 *	rs59700451	117112212	A	G	0.0567869	0.0458053	0.0054210	2.1E-17
11	SIK3 *	rs113979111	117112300	A	G	0.0567863	0.0457985	0.0054210	2.1E-17
11	SIK3 *	rs111560312	117112840	A	G	0.0567856	0.0457989	0.0054210	2.1E-17
11	SIK3 *	rs55703909	117114150	A	G	0.0567863	0.0457806	0.0054210	2.2E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3 *	rs74882651	117114475	A	G	0.0962537	-0.0559637	0.0042501	4.7E-40
11	SIK3 *	rs60834024	117115141	A	C	0.0962629	-0.0559202	0.0042499	5.2E-40
11	SIK3 *	chr11:117115776_AG_A	117115776	A	AG	0.0139201	-0.0590482	0.0108998	9.8E-09
11	SIK3 *	rs61903429	117115968	A	C	0.0568060	0.0457675	0.0054206	2.2E-17
11	SIK3 *	rs11216277	117116330	A	G	0.2927410	-0.0286163	0.0027755	1.1E-24
11	SIK3 *	rs145335872	117116511	A	C	0.0550261	-0.0562111	0.0055048	4.8E-25
11	SIK3 *	rs61903430	117116626	C	G	0.0568060	0.0457811	0.0054206	2.2E-17
11	SIK3 *	rs75904569	117117597	G	A	0.0568066	0.0457835	0.0054206	2.2E-17
11	SIK3 *	rs80197460	117118074	G	C	0.0962755	-0.0557519	0.0042499	9.4E-40
11	SIK3 *	rs10892076	117118220	A	G	0.2914970	-0.0286087	0.0027803	1.1E-24
11	SIK3 *	rs74428560	117119266	T	C	0.0568123	0.0458173	0.0054204	2.0E-17
11	SIK3 *	rs117300172	117119795	C	A	0.0156746	0.0696437	0.0100953	9.6E-13
11	SIK3 *	chr11:117120044_G_GAAA	117120044	GAAAC	G	0.4277340	-0.0478717	0.0025557	8.0E-79
11	SIK3 *	rs200802441	117120056	C	A	0.4138070	-0.0469694	0.0025979	1.0E-73
11	SIK3 *	rs12366015	117120135	G	A	0.4274480	-0.0478426	0.0025548	9.6E-79
11	SIK3 *	rs138720977	117120356	ATAAG	A	0.2879210	-0.0276042	0.0027987	9.0E-23
11	SIK3 *	rs142756367	117120357	TAAGA	T	0.2924670	-0.0287686	0.0027759	6.7E-25
11	PAFAH1B2 *	rs74955808	117121969	A	G	0.0965262	-0.0552666	0.0042447	3.7E-39
11	PAFAH1B2 *	rs71037454	117122203	AGAAAAG	G	0.4851710	-0.0367667	0.0025243	2.1E-48
11	PAFAH1B2 *	rs6589596	117122465	C	T	0.4853500	-0.0366213	0.0025238	5.0E-48
11	PAFAH1B2 *	rs76868258	117122576	T	C	0.0568560	0.0461075	0.0054176	1.2E-17
11	PAFAH1B2 *	rs12420361	117123072	A	G	0.0963328	-0.0558254	0.0042473	7.2E-40
11	PAFAH1B2 *	rs10892078	117123213	T	A	0.2029600	-0.0300071	0.0031275	5.8E-22
11	PAFAH1B2 *	rs11344600	117123743	C	CA	0.4852510	-0.0366976	0.0025217	3.0E-48
11	PAFAH1B2 *	rs35722128	117124277	C	CA	0.0568787	0.0459002	0.0054167	1.7E-17
11	PAFAH1B2 *	chr11:117125062_TAA_T	117125062	T	TAA	0.4855640	-0.0366429	0.0025180	2.5E-48
11	PAFAH1B2 *	rs17120344	117125629	A	G	0.0965463	-0.0553844	0.0042413	1.9E-39
11	PAFAH1B2 *	rs17120347	117125823	A	G	0.0569446	0.0459318	0.0054128	1.5E-17
11	PAFAH1B2 *	rs12419454	117125915	T	C	0.0965645	-0.0554672	0.0042410	1.5E-39
11	PAFAH1B2 *	rs12419459	117125995	T	C	0.0976806	-0.0530405	0.0042215	1.4E-36
11	PAFAH1B2 *	rs12416691	117126067	T	A	0.0966056	-0.0553442	0.0042402	2.0E-39
11	PAFAH1B2 *	rs6589597	117127082	T	C	0.4862230	-0.0364064	0.0025151	6.7E-48
11	PAFAH1B2 *	rs78302396	117127400	G	A	0.0843369	0.0318945	0.0045324	6.6E-13
11	PAFAH1B2 *	rs12420200	117127590	A	G	0.0966193	-0.0553898	0.0042399	1.8E-39
11	PAFAH1B2 *	rs182980806	117127672	T	G	0.0156243	0.0713516	0.0101170	1.3E-13
11	PAFAH1B2 *	rs145802214	117128196	C	A	0.0966193	-0.0553898	0.0042399	1.8E-39
11	PAFAH1B2 *	rs141250514	117128309	C	T	0.0966193	-0.0553898	0.0042399	1.8E-39
11	PAFAH1B2 *	rs4516002	117128343	G	A	0.4862000	-0.0364297	0.0025152	6.0E-48
11	PAFAH1B2 *	rs9326248	117128509	G	T	0.3518280	-0.0152337	0.0026285	1.1E-08
11	PAFAH1B2 *	rs7131536	117128730	T	C	0.4863700	-0.0363722	0.0025156	9.3E-48
11	PAFAH1B2 *	rs7131686	117128843	T	C	0.4862070	-0.0363898	0.0025151	7.4E-48
11	PAFAH1B2 *	rs138039720	117128884	T	C	0.0966363	-0.0553991	0.0042403	1.7E-39
11	PAFAH1B2 *	chr11:117129006_TA_T	117129006	T	TA	0.4426350	-0.0341660	0.0025540	1.3E-40
11	PAFAH1B2 *	rs146067038	117129463	G	A	0.0966348	-0.0552772	0.0042403	2.5E-39
11	PAFAH1B2 *	rs10400366	117130239	A	G	0.2926010	-0.0286724	0.0027642	8.1E-25
11	PAFAH1B2 *	rs199498085	117130739	G	A	0.0897176	-0.0553050	0.0044096	9.9E-37
11	PAFAH1B2 *	rs12421425	117131244	T	C	0.0966759	-0.0552410	0.0042395	2.8E-39
11	PAFAH1B2 *	chr11:117131317_A_AT	117131317	AT	A	0.4401500	-0.0318424	0.0025694	3.2E-35
11	PAFAH1B2 *	rs142848583	117131334	AC	A	0.0115532	0.1012930	0.0117616	7.5E-17
11	PAFAH1B2 *	rs191044888	117131336	T	G	0.0115529	0.1012890	0.0117616	7.5E-17
11	PAFAH1B2 *	rs6589598	117131687	G	A	0.3888550	-0.0178913	0.0025772	3.4E-12
11	PAFAH1B2 *	rs4938341	117131880	A	G	0.0571437	0.0458565	0.0054007	2.1E-17
11	PAFAH1B2 *	rs17120367	117132112	T	C	0.0966953	-0.0553055	0.0042388	2.2E-39
11	PAFAH1B2 *	rs11216284	117132344	T	C	0.3510000	-0.0152870	0.0026309	8.4E-09
11	PAFAH1B2 *	chr11:117132474_CA_C	117132474	C	CA	0.4863510	-0.0362590	0.0025189	1.9E-47
11	PAFAH1B2 *	rs17120370	117132672	C	T	0.0966953	-0.0553055	0.0042388	2.2E-39
11	PAFAH1B2 *	rs74735277	117132702	T	C	0.0966920	-0.0553101	0.0042388	2.2E-39
11	PAFAH1B2 *	rs4938342	117132704	G	C	0.0572555	0.0455705	0.0053874	2.8E-17
11	PAFAH1B2 *	rs17120373	117132743	G	A	0.1346480	-0.0477070	0.0036700	1.3E-39
11	PAFAH1B2 *	rs4938343	117132812	C	G	0.4483470	-0.0335691	0.0025282	3.1E-40
11	PAFAH1B2 *	rs75208249	117132907	C	G	0.0968801	-0.0547832	0.0042345	9.8E-39
11	PAFAH1B2 *	rs4938344	117133033	A	G	0.3496770	-0.0162270	0.0026317	8.7E-10
11	PAFAH1B2 *	rs11216285	117133242	T	C	0.3498140	-0.0150542	0.0026340	1.4E-08
11	PAFAH1B2 *	rs11216286	117133371	A	G	0.3489840	-0.0153868	0.0026411	8.4E-09
11	PAFAH1B2 *	rs114945429	117133485	T	G	0.0968118	-0.0546943	0.0042359	1.4E-38
11	PAFAH1B2 *	rs12792314	117133694	A	T	0.3514690	-0.0156045	0.0026313	4.3E-09
11	PAFAH1B2 *	rs12417098	117134137	A	G	0.0961467	-0.0541369	0.0042491	1.5E-37
11	PAFAH1B2 *	rs141936239	117134911	C	T	0.1009830	-0.0545159	0.0041918	5.3E-39
11	PAFAH1B2 *	rs143261386	117135035	C	T	0.1009830	-0.0545159	0.0041918	5.3E-39
11	PAFAH1B2 *	rs2735181	117139073	T	C	0.2800850	-0.0297515	0.0028416	1.1E-25
11	PAFAH1B2 *	rs115991973	117139375	A	G	0.0961410	-0.0536991	0.0042492	5.3E-37
11	PAFAH1B2 *	rs116384608	117139407	G	A	0.0961410	-0.0536991	0.0042492	5.3E-37

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PAFAH1B2 *	rs2471884	117139604	C	T	0.4858630	-0.0364881	0.0025184	5.4E-48
11	PAFAH1B2 *	rs77661993	117139758	C	A	0.0961445	-0.0537476	0.0042492	4.6E-37
11	PAFAH1B2 *	rs2622935	117140042	G	A	0.3893570	-0.0186042	0.0025798	4.7E-13
11	PAFAH1B2 *	rs4277146	117140263	A	G	0.3515440	-0.0160095	0.0026338	1.6E-09
11	PAFAH1B2 *	rs7934690	117140583	A	T	0.0569299	0.0458181	0.0054141	2.5E-17
11	PAFAH1B2 *	rs7951095	117140724	A	C	0.3515420	-0.0160090	0.0026338	1.6E-09
11	PAFAH1B2 *	rs2735182	117141494	T	A	0.3515350	-0.0160081	0.0026338	1.7E-09
11	PAFAH1B2 *	rs1555026168	117143445	AAG	A	0.4831730	-0.0336994	0.0025310	1.1E-40
11	PAFAH1B2 *	rs2622934	117144146	T	G	0.2937440	-0.0294353	0.0027637	2.8E-26
11	PAFAH1B2 *	rs76904522	117144147	A	G	0.0575496	0.0454391	0.0053863	2.2E-17
11	PAFAH1B2	rs113560866	117144473	C	G	0.0579146	0.0441408	0.0053744	1.1E-16
11	PAFAH1B2	rs2735183	117144479	T	C	0.2949840	-0.0286409	0.0027680	7.2E-25
11	PAFAH1B2	rs12419227	117144522	A	C	0.0989530	-0.0457640	0.0041980	5.3E-28
11	PAFAH1B2	rs149188200	117144559	T	G	0.0374973	0.0522629	0.0066649	1.5E-15
11	PAFAH1B2	rs11420191	117145447	CG	C	0.4940790	-0.0350277	0.0025174	2.4E-44
11	PAFAH1B2	rs2306471	117145734	T	C	0.1003850	-0.0458335	0.0041698	2.3E-28
11	PAFAH1B2	rs10892079	117146108	G	T	0.3514960	-0.0173926	0.0026512	8.3E-11
11	PAFAH1B2	rs78270178	117146132	G	T	0.3151440	-0.0291696	0.0027709	3.1E-26
11	PAFAH1B2	rs4936365	117146281	T	C	0.3567390	-0.0170826	0.0026300	1.1E-10
11	PAFAH1B2	rs12419436	117146739	G	T	0.1001790	-0.0455617	0.0041730	4.7E-28
11	PAFAH1B2	rs12420725	117146814	G	A	0.1005260	-0.0452635	0.0041667	9.1E-28
11	PAFAH1B2	rs117592676	117146994	T	C	0.0194152	0.1173520	0.0091528	5.4E-39
11	PAFAH1B2	rs12417984	117146998	A	G	0.1003990	-0.0456988	0.0041692	3.1E-28
11	PAFAH1B2	rs139864910	117147046	C	A	0.1003990	-0.0456988	0.0041692	3.1E-28
11	PAFAH1B2	rs2008908	117148294	T	C	0.3562590	-0.0168115	0.0026256	2.3E-10
11	PAFAH1B2	rs139146464	117149151	G	A	0.0994507	-0.0446635	0.0041915	9.1E-27
11	PAFAH1B2	rs71037463	117149256	A	AT	0.4929270	-0.0350397	0.0025164	2.7E-44
11	PAFAH1B2	rs1461576929	117149430	T	G	0.0212185	0.0690655	0.0088172	3.3E-15
11	PAFAH1B2	rs7115562	117149754	G	A	0.4568940	-0.0323837	0.0025238	1.5E-37
11	PAFAH1B2	rs7116454	117150418	T	A	0.4568890	-0.0323954	0.0025238	1.5E-37
11	PAFAH1B2	rs45625638	117150710	C	G	0.0577528	0.0449629	0.0053763	4.0E-17
11	PAFAH1B2	chr11:117150989_GAA_G	117150989	G	GAA	0.1004960	-0.0451419	0.0041845	3.2E-27
11	PAFAH1B2	rs4938347	117151043	A	T	0.4556520	-0.0319923	0.0025366	2.2E-36
11	PAFAH1B2	rs4938348	117151161	C	G	0.4540510	-0.0313793	0.0025316	3.7E-35
11	PAFAH1B2	rs4938349	117151207	T	C	0.3522970	-0.0159109	0.0026352	2.4E-09
11	PAFAH1B2	rs4938350	117151560	G	A	0.4539830	-0.0313238	0.0025320	4.9E-35
11	PAFAH1B2	rs79831695	117151612	G	A	0.0304621	-0.0524403	0.0073371	5.6E-13
11	PAFAH1B2	rs4938351	117151636	C	A	0.2956610	-0.0288457	0.0027603	2.0E-25
11	PAFAH1B2	rs146629336	117152290	C	G	0.0199948	-0.0492126	0.0089896	4.5E-08
11	PAFAH1B2	rs7128382	117152271	C	A	0.4539690	-0.0313348	0.0025298	3.9E-35
11	PAFAH1B2	rs143494314	117152990	T	C	0.1004040	-0.0457183	0.0041691	3.0E-28
11	PAFAH1B2	rs10790174	117153548	A	G	0.3538650	-0.0158630	0.0026297	2.3E-09
11	PAFAH1B2	rs7950633	117153586	T	C	0.4929220	-0.0338556	0.0025198	1.6E-41
11	PAFAH1B2	rs7940310	117153765	C	T	0.4918830	-0.0343196	0.0025176	1.2E-42
11	PAFAH1B2	chr11:117154119_G_GA	117154119	GA	G	0.4524090	-0.0317093	0.0025347	4.9E-36
11	PAFAH1B2	rs78123099	117154123	G	A	0.0182621	0.0595880	0.0094210	1.4E-10
11	PAFAH1B2	rs35500922	117154603	AT	A	0.0970290	-0.0470518	0.0042443	1.3E-28
11	PAFAH1B2	rs68137714	117154641	G	A	0.0577528	0.0449629	0.0053763	4.0E-17
11	PAFAH1B2	rs12418349	117155216	G	A	0.1004040	-0.0457183	0.0041691	3.0E-28
11	PAFAH1B2	rs2127905	117155658	C	A	0.4972660	-0.0352965	0.0025138	3.2E-45
11	PAFAH1B2	rs4936366	117156169	A	G	0.4569030	-0.0323819	0.0025237	1.5E-37
11	PAFAH1B2	rs4938352	117156765	A	G	0.4569030	-0.0323819	0.0025237	1.5E-37
11	PAFAH1B2	rs199763004	117157038	A	AG	0.4984280	-0.0334940	0.0025274	1.7E-40
11	PAFAH1B2	rs7123517	117157039	A	G	0.4986910	-0.0334910	0.0025271	1.7E-40
11	PAFAH1B2	rs117588325	117157577	T	A	0.0277317	0.0699939	0.0076773	3.7E-21
11	PAFAH1B2	rs12420250	117158011	A	G	0.1001090	-0.0452800	0.0041751	1.1E-27
11	PAFAH1B2	rs78166985	117159069	T	A	0.1001910	-0.0457804	0.0041743	2.8E-28
11	PAFAH1B2	rs1871757	117159865	A	T	0.4567390	-0.0323845	0.0025243	1.5E-37
11	PAFAH1B2	chr11:117159908_AT_A	117159908	A	AT	0.3553100	-0.0169236	0.0026272	1.6E-10
11	PAFAH1B2	rs200545029	117159917	C	T	0.1003310	-0.0455503	0.0041701	4.8E-28
11	PAFAH1B2	rs142017584	117160647	A	G	0.1004040	-0.0457183	0.0041691	3.0E-28
11	PAFAH1B2	rs3736120	117161409	T	G	0.3296550	-0.0250598	0.0026764	1.2E-20
11	PAFAH1B2	rs12281009	117162243	G	A	0.1004040	-0.0457183	0.0041691	3.0E-28
11	PAFAH1B2	chr11:117162461_TC_T	117162461	T	TC	0.0116979	-0.0751314	0.0118758	7.3E-11
11	PAFAH1B2	rs71037468	117163187	3CTGAGTC	C	0.4542580	-0.0320956	0.0025331	1.3E-36
11	PAFAH1B2	rs7122944	117163903	T	G	0.4932300	-0.0357742	0.0025151	2.8E-46
11	PAFAH1B2	rs10790175	117164013	C	T	0.3563090	-0.0169362	0.0026217	1.6E-10
11	PAFAH1B2	rs150984554	117164300	A	G	0.0995587	-0.0464745	0.0041877	6.6E-29
11	PAFAH1B2	rs12420127	117164603	G	A	0.1004040	-0.0457183	0.0041691	3.0E-28
11	PAFAH1B2	rs10892080	117164786	G	A	0.2968510	-0.0297068	0.0027551	7.6E-27
11	PAFAH1B2	rs149378955	117164863	A	G	0.0459082	0.0507720	0.0060123	1.1E-17
11	PAFAH1B2	chr11:117164958_C_CT	117164958	CT	C	0.3559460	-0.0156879	0.0026473	5.9E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PAFAH1B2	rs7931335	117166089	T	C	0.4569140	-0.0323585	0.0025237	1.7E-37
11	PAFAH1B2	rs6589602	117166349	C	T	0.2978980	-0.0301093	0.0027501	1.2E-27
11	PAFAH1B2	rs7112513	117166645	G	A	0.4940930	-0.0352648	0.0025131	4.9E-45
11	PAFAH1B2	rs77171490	117168025	A	T	0.1004040	-0.0457183	0.0041691	3.0E-28
11	PAFAH1B2	rs190482111	117168438	A	G	0.1003990	-0.0457295	0.0041692	2.9E-28
11	PAFAH1B2	rs10892082	117168609	G	T	0.4939070	-0.0356421	0.0025140	5.7E-46
11	PAFAH1B2	rs116773440	117168745	C	A	0.1000570	-0.0455937	0.0041773	5.3E-28
11	PAFAH1B2	rs1060211	117169081	A	G	0.4568790	-0.0324127	0.0025239	1.4E-37
11	PAFAH1B2	rs45628435	117169482	GT	G	0.2978780	-0.0301991	0.0027503	8.1E-28
11	PAFAH1B2	rs77678768	117169789	C	G	0.1003990	-0.0457295	0.0041692	2.9E-28
11	PAFAH1B2	rs10750103	117171522	T	C	0.2972370	-0.0300991	0.0027533	1.5E-27
11	PAFAH1B2	rs4936367	117171661	A	G	0.4941100	-0.0353127	0.0025132	3.7E-45
11	PAFAH1B2	rs10892083	117171864	C	G	0.2078680	-0.0316951	0.0030972	8.0E-25
11	PAFAH1B2	rs7120309	117172100	A	T	0.4569170	-0.0323965	0.0025238	1.5E-37
11	PAFAH1B2	rs7120449	117172183	C	T	0.4566590	-0.0324083	0.0025244	1.4E-37
11	PAFAH1B2	rs7120565	117172233	C	T	0.2978790	-0.0301967	0.0027503	8.2E-28
11	PAFAH1B2	rs56371319	117172251	A	C	0.0577591	0.0449231	0.0053761	4.3E-17
11	PAFAH1B2	rs4604928	117173487	A	C	0.4941100	-0.0353128	0.0025132	3.7E-45
11	PAFAH1B2	chr11:117174484_A_AT	117174484	AT	A	0.0949194	-0.0467407	0.0042921	6.3E-28
11	PAFAH1B2	chr11:117174494_CT_C	117174494	C	CT	0.2961680	-0.0301417	0.0027637	2.0E-27
11	PAFAH1B2	rs7925256	117174619	T	C	0.2861900	0.0407297	0.0027983	9.5E-49
11	PAFAH1B2	rs146228126	117175016	T	G	0.0155501	0.0794281	0.0101915	3.2E-14
11	PAFAH1B2	rs10535646	117175444	T	TTGC	0.2980610	-0.0301132	0.0027508	1.1E-27
11	PAFAH1B2	rs4938353	117175481	A	G	0.4569020	-0.0323883	0.0025239	1.5E-37
11	PAFAH1B2	rs10790176	117177136	T	G	0.4569280	-0.0323707	0.0025239	1.6E-37
11	PAFAH1B2	rs80353869	117177406	A	G	0.1001650	-0.0461326	0.0041746	1.1E-28
11	PAFAH1B2	rs10790177	117177701	G	A	0.3564200	-0.0168055	0.0026222	2.2E-10
11	SIDT2	rs12419178	117180202	T	C	0.1000580	-0.0460568	0.0041769	1.5E-28
11	SIDT2	rs34783152	117180423	A	AG	0.1000640	-0.0460185	0.0041767	1.7E-28
11	SIDT2	rs76883864	117181009	T	C	0.1000630	-0.0460165	0.0041767	1.7E-28
11	SIDT2	rs35248926	117181353	G	GTCTCT	0.4570250	-0.0324820	0.0025274	9.0E-38
11	SIDT2	rs7946257	117182449	G	A	0.3561990	-0.0169172	0.0026229	1.6E-10
11	SIDT2	rs2046150	117182717	A	C	0.1022000	-0.0450370	0.0041394	7.1E-28
11	SIDT2	rs4938355	117182959	G	A	0.0564153	0.0453117	0.0054383	5.4E-17
11	SIDT2	rs34033077	117183654	CT	C	0.0949348	-0.0423100	0.0042960	4.9E-23
11	SIDT2	rs2046149	117183993	G	C	0.1022000	-0.0450370	0.0041394	7.1E-28
11	SIDT2	rs10892085	117185065	C	T	0.3375630	-0.0158055	0.0027014	7.5E-09
11	SIDT2	rs6589603	117185123	C	T	0.4936990	-0.0356523	0.0025228	9.1E-46
11	SIDT2	rs11606672	117185343	T	C	0.1019500	-0.0449666	0.0041456	9.6E-28
11	SIDT2	rs7107152	117185364	G	A	0.3563560	-0.0170434	0.0026233	1.2E-10
11	SIDT2	rs2306472	117187346	T	C	0.1000280	-0.0455332	0.0041776	6.3E-28
11	SIDT2	rs546506427	117188416	C	T	0.1019520	-0.0449042	0.0041452	1.1E-27
11	SIDT2	rs775148500	117188417	TCA	T	0.1002780	-0.0456223	0.0041711	4.3E-28
11	SIDT2	rs90192	117188631	T	C	0.4593610	-0.0310358	0.0025254	1.5E-34
11	SIDT2	rs474339	117188836	A	G	0.3561910	-0.0168461	0.0026233	1.9E-10
11	SIDT2	rs7933134	117189078	C	G	0.1022010	-0.0449944	0.0041389	7.9E-28
11	SIDT2	rs12419470	117191059	T	C	0.1019500	-0.0449071	0.0041452	1.1E-27
11	SIDT2	rs61703672	117191109	T	C	0.1019500	-0.0449071	0.0041452	1.1E-27
11	SIDT2	rs140056851	117191110	G	T	0.0459492	0.0502488	0.0060128	2.2E-17
11	SIDT2	rs499713	117191245	C	T	0.4566710	-0.0323086	0.0025309	3.5E-37
11	SIDT2	rs1242230	117191467	C	T	0.4958590	-0.0354700	0.0025134	1.3E-45
11	SIDT2	rs1242229	117191654	C	T	0.4961870	-0.0354190	0.0025131	1.5E-45
11	SIDT2	rs3213459	117191773	C	T	0.1021990	-0.0449974	0.0041388	7.8E-28
11	SIDT2	rs2301174	117192993	G	C	0.1019520	-0.0448982	0.0041452	1.2E-27
11	SIDT2	rs521171	117193977	G	C	0.3568760	-0.0171307	0.0026242	9.5E-11
11	SIDT2	rs11605883	117194060	G	C	0.1002760	-0.0456253	0.0041711	4.3E-28
11	SIDT2	rs73008568	117194291	G	C	0.0563580	0.0453931	0.0054412	5.3E-17
11	SIDT2	rs3781985	117194350	C	G	0.1002760	-0.0456253	0.0041711	4.3E-28
11	SIDT2	rs80183569	117194437	A	G	0.1002760	-0.0456253	0.0041711	4.3E-28
11	SIDT2	rs1784042	117194760	A	G	0.2089960	-0.0314724	0.0030918	1.5E-24
11	SIDT2	rs11606480	117194817	A	G	0.1002760	-0.0456253	0.0041711	4.3E-28
11	SIDT2	rs112712475	117195056	A	C	0.0990704	-0.0460579	0.0042002	3.5E-28
11	SIDT2	rs1794116	117195063	C	T	0.3560790	-0.0170202	0.0026230	1.2E-10
11	LOC100652768, SIDT2	rs2269399	117195637	C	G	0.1002750	-0.0456313	0.0041711	4.2E-28
11	LOC100652768, SIDT2	rs8521	117196983	T	C	0.3560620	-0.0169817	0.0026229	1.3E-10
11	LOC100652768	rs74385934	117197728	A	G	0.1002740	-0.0456358	0.0041711	4.2E-28
11	LOC100652768	rs588534	117197788	G	A	0.4565750	-0.0324791	0.0025244	7.6E-38
11	LOC100652768	rs2075547	117197818	A	C	0.0563417	0.0452575	0.0054424	6.6E-17
11	LOC100652768	rs147581841	117197929	T	C	0.0248084	0.0659881	0.0080753	1.2E-16
11	LOC100652768	rs474488	117198261	G	A	0.4565670	-0.0324256	0.0025245	9.7E-38
11	LOC100652768	rs7112573	117198307	C	T	0.1021820	-0.0449454	0.0041393	9.0E-28
11	LOC100652768	rs585849	117198345	G	A	0.3554930	-0.0170553	0.0026262	1.1E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	LOC100652768	rs2269398	117199072	T	C	0.1002230	-0.0455966	0.0041736	4.9E-28
11	LOC100652768	rs17523113	117199185	A	G	0.0442805	0.0502416	0.0061174	6.3E-17
11	LOC100652768, TAGLN	rs3833897	117199831	T	TGAG	0.3554850	-0.0173213	0.0026313	6.9E-11
11	LOC100652768, TAGLN	rs2239678	117199880	T	C	0.1002160	-0.0456781	0.0041733	4.1E-28
11	LOC100652768, TAGLN	rs2170317	117200024	C	A	0.1002730	-0.0457231	0.0041733	3.8E-28
11	LOC100652768, TAGLN	rs664971	117200141	A	G	0.3562340	-0.0170599	0.0026289	1.3E-10
11	LOC100652768, TAGLN	rs664922	117200179	A	C	0.3560750	-0.0171664	0.0026284	9.5E-11
11	LOC100652768, TAGLN	rs664082	117200354	G	C	0.3553720	-0.0170299	0.0026324	1.3E-10
11	LOC100652768, TAGLN	rs494356	117201254	C	T	0.4682480	-0.0324871	0.0025409	4.7E-37
11	LOC100652768, TAGLN	rs488962	117201809	C	T	0.3562870	-0.0171672	0.0026284	9.3E-11
11	TAGLN	rs634960	117202247	T	C	0.3562960	-0.0171419	0.0026283	9.9E-11
11	TAGLN	rs145613978	117202393	A	G	0.0291067	0.0661189	0.0075183	1.0E-19
11	TAGLN	rs12970	117203393	A	G	0.1005640	-0.0451402	0.0041647	1.2E-27
11	TAGLN	rs641620	117203513	T	C	0.4363250	-0.0294407	0.0025567	2.7E-30
11	TAGLN	rs2269397	117203583	C	T	0.1066700	-0.0419470	0.0040628	1.8E-25
11	PCSK7	rs28590104	117206318	A	G	0.3309860	-0.0170200	0.0027316	5.5E-10
11	PCSK7	rs659955	117209663	T	A	0.4972670	-0.0342518	0.0025256	2.2E-42
11	PCSK7	rs11216315	117209924	G	C	0.1023430	-0.0444702	0.0041343	2.4E-27
11	PCSK7	rs11216316	117210784	A	C	0.4952490	-0.0342512	0.0025211	1.2E-42
11	PCSK7	rs171052	117211047	C	G	0.3548970	-0.0161214	0.0026310	1.1E-09
11	PCSK7	rs236910	117211258	A	G	0.3548970	-0.0161214	0.0026310	1.1E-09
11	PCSK7	rs12417682	117211393	A	G	0.1026070	-0.0442176	0.0041299	3.9E-27
11	PCSK7	rs76169968	117212250	A	G	0.1027300	-0.0443552	0.0041260	2.2E-27
11	PCSK7	rs67201490	117212288	G	T	0.0551847	0.0426281	0.0054961	6.4E-15
11	PCSK7	rs4938357	117213324	A	G	0.0551790	0.0427090	0.0054963	5.6E-15
11	PCSK7	rs12418705	117213680	T	C	0.1006750	-0.0447271	0.0041623	3.1E-27
11	PCSK7	rs139694434	117213935	TTTTTC	T	0.4940870	-0.0346219	0.0025230	1.9E-43
11	PCSK7	rs77683187	117214494	C	A	0.1026460	-0.0441593	0.0041278	4.3E-27
11	PCSK7	rs236911	117214554	A	C	0.4945870	-0.0349093	0.0025205	3.9E-44
11	PCSK7	rs56081989	117214589	A	G	0.0553305	0.0422521	0.0054903	9.2E-15
11	PCSK7	rs36028244	117215198	C	CTTA	0.1024290	-0.0442092	0.0041335	5.4E-27
11	PCSK7	rs56061158	117216402	C	G	0.0553191	0.0424494	0.0054911	8.5E-15
11	PCSK7	rs150159690	117217269	GTCACCTC	A	0.1023470	-0.0442176	0.0041356	4.5E-27
11	PCSK7	rs2238005	117217366	T	C	0.1026060	-0.0441696	0.0041294	4.5E-27
11	PCSK7	rs236915	117217734	A	G	0.2977120	-0.0280942	0.0027569	2.6E-24
11	PCSK7	rs236916	117218912	G	A	0.4589930	-0.0308047	0.0025294	3.4E-34
11	PCSK7	rs2239009	117219006	C	G	0.1022640	-0.0443260	0.0041386	3.1E-27
11	PCSK7	rs74830	117219842	C	T	0.3025600	-0.0275515	0.0027469	1.4E-23
11	PCSK7	rs35590772	117220535	TG	T	0.4615970	-0.0306692	0.0025290	6.0E-34
11	PCSK7	rs236918	117220893	G	C	0.4969560	-0.0340710	0.0025146	2.6E-42
11	PCSK7	rs7941150	117221105	A	G	0.0553890	0.0421167	0.0054863	1.3E-14
11	PCSK7	rs78628783	117221335	T	C	0.1023240	-0.0442341	0.0041381	3.9E-27
11	PCSK7	rs80351364	117221678	T	A	0.1027700	-0.0442009	0.0041282	3.5E-27
11	PCSK7	rs6589606	117222170	T	C	0.1023280	-0.0442411	0.0041381	3.8E-27
11	PCSK7	rs17120523	117223875	G	A	0.0732842	-0.0415607	0.0048481	6.9E-18
11	PCSK7	rs236919	117224645	C	T	0.3082600	-0.0220109	0.0027505	2.3E-15
11	PCSK7	rs146871029	117225450	T	C	0.0117271	0.0998304	0.0116708	1.7E-16
11	PCSK7	rs75519898	117226533	A	G	0.0252837	0.0512903	0.0080303	6.0E-11
11	PCSK7	chr11:117226836_T_TGGG	117226836	GGGAGCT	T	0.4961280	0.0298620	0.0025264	9.8E-33
11	PCSK7	rs2306473	117227236	T	C	0.0597956	0.0361684	0.0052920	8.1E-12
11	PCSK7	rs111809212	117228821	C	T	0.0550818	0.0336584	0.0055340	1.1E-09
11	PCSK7	rs4938361	117229225	C	G	0.0587750	0.0356365	0.0053484	3.3E-11
11	PCSK7	rs4938362	117229313	A	G	0.0594503	0.0368588	0.0053174	4.1E-12
11	PCSK7	rs11542139	117229541	T	C	0.0436429	0.0354259	0.0062100	1.3E-08
11	RNF214	rs200694867	117244658	C	CTTTA	0.0245772	0.0723128	0.0081802	1.8E-19
11	RNF214	rs145918995	117256488	T	C	0.0150924	0.0606965	0.0104063	1.4E-09
11	BACE1 *	rs1038851424	117317566	C	T	0.0145373	0.0651330	0.0106091	4.1E-10
11	CEP164	rs515756	117330449	G	T	0.1573920	0.0202636	0.0035088	3.7E-09
11	CEP164	rs193196748	117330506	A	G	0.0182955	-0.0517701	0.0095931	2.1E-08
11	CEP164	chr11:117330649_CA_C	117330649	C	CA	0.1361610	0.0261952	0.0036814	8.4E-13
11	CEP164	rs609663	117331033	G	C	0.1517050	0.0197606	0.0035178	1.1E-08
11	CEP164	rs144584200	117332064	G	A	0.0324097	0.0635687	0.0071775	1.2E-18
11	CEP164	rs371259597	117332128	T	C	0.0149833	0.0658764	0.0104507	1.2E-10
11	CEP164	rs527347	117332917	G	A	0.1517100	0.0244282	0.0035123	2.5E-12
11	CEP164	rs576190	117335050	C	T	0.1516720	0.0243565	0.0035126	2.9E-12
11	CEP164	rs487298	117335128	T	G	0.1516720	0.0243565	0.0035126	2.9E-12
11	CEP164	rs520315	117336910	C	T	0.1552440	0.0240057	0.0034991	4.9E-12
11	CEP164	rs620848	117336912	G	C	0.1552440	0.0240057	0.0034991	4.9E-12
11	CEP164	rs875209	117337554	A	G	0.1525910	0.0247696	0.0035030	1.4E-12
11	CEP164	rs645305	117338031	C	T	0.1530690	0.0247355	0.0034963	1.1E-12
11	CEP164	rs948181	117338233	T	C	0.1530690	0.0247355	0.0034963	1.1E-12
11	CEP164	rs573801	117338552	T	C	0.1530640	0.0247122	0.0034963	1.2E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	CEP164	rs578781	117339991	A	G	0.1520910	0.0250407	0.0035080	7.1E-13
11	CEP164	rs536021	117340185	C	T	0.1530900	0.0246981	0.0034960	1.2E-12
11	CEP164	rs610749	117340524	T	G	0.1536350	0.0248555	0.0034870	7.4E-13
11	CEP164	rs474891	117341621	T	G	0.1730580	0.0201194	0.0033659	2.2E-09
11	CEP164	rs561473	117341924	C	T	0.1503230	0.0256020	0.0035340	3.1E-13
11	CEP164	rs475385	117342176	T	C	0.1527770	0.0245518	0.0035009	1.9E-12
11	CEP164	rs495473	117342192	G	A	0.1367060	0.0230714	0.0036633	2.0E-10
11	CEP164	rs493516	117342444	A	G	0.1527500	0.0245756	0.0035013	1.8E-12
11	CEP164	rs573827	117343375	A	G	0.1529290	0.0247801	0.0034988	1.2E-12
11	CEP164	rs580119	117345497	G	T	0.1528300	0.0248372	0.0035027	1.1E-12
11	CEP164	rs652346	117345883	T	C	0.1367690	0.0233099	0.0036648	1.4E-10
11	CEP164	rs494722	117345887	T	A	0.1367690	0.0233099	0.0036648	1.4E-10
11	CEP164	rs138869088	117346455	T	C	0.0110485	0.1022540	0.0121168	1.5E-17
11	CEP164	rs1261744	117347744	C	T	0.1506150	0.0239352	0.0035249	9.4E-12
11	CEP164	rs592828	117348589	C	G	0.1515000	0.0244749	0.0035144	2.9E-12
11	CEP164	rs508871	117349054	A	G	0.1503810	0.0232191	0.0035282	4.1E-11
11	CEP164	rs688207	117351423	T	C	0.1511950	0.0247799	0.0035194	1.4E-12
11	CEP164	rs490262	117351876	A	G	0.1376450	0.0301242	0.0037010	1.6E-16
11	CEP164	rs514806	117352226	T	G	0.1512030	0.0247600	0.0035192	1.5E-12
11	CEP164	rs657666	117353644	A	G	0.1512030	0.0247600	0.0035192	1.5E-12
11	CEP164	rs67060142	117353997	T	TCTTCTC	0.1449780	0.0240924	0.0035968	2.8E-11
11	CEP164	rs553303	117354102	T	C	0.1493160	0.0234233	0.0035446	2.9E-11
11	CEP164	rs655389	117354162	A	G	0.1512030	0.0247600	0.0035192	1.5E-12
11	CEP164	rs553506	117354171	T	C	0.1497890	0.0244533	0.0035374	3.3E-12
11	CEP164	rs654479	117354418	A	G	0.1512030	0.0247600	0.0035192	1.5E-12
11	CEP164	rs542176	117354725	T	G	0.1509710	0.0247725	0.0035225	1.6E-12
11	CEP164	rs542869	117354739	A	T	0.1339050	0.0240225	0.0037018	5.4E-11
11	CEP164	rs542900	117354751	A	T	0.1500020	0.0256077	0.0035341	3.1E-13
11	CEP164	rs535366	117355900	C	T	0.1512080	0.0247527	0.0035192	1.5E-12
11	CEP164	rs11216364	117355903	T	C	0.0863779	0.0443349	0.0045534	9.4E-23
11	CEP164	chr11:117355999_G_GAGC	117355999	GCGAGCA	G	0.1489180	0.0230273	0.0035491	5.3E-11
11	CEP164	rs537323	117356133	T	C	0.1512080	0.0247527	0.0035192	1.5E-12
11	CEP164	rs528720	117356970	A	G	0.1509100	0.0251242	0.0035233	7.9E-13
11	CEP164	rs595367	117356978	C	T	0.1348270	0.0235760	0.0036894	1.1E-10
11	CEP164	rs534296	117357579	G	A	0.1512030	0.0247264	0.0035199	1.5E-12
11	CEP164	rs558854	117357948	A	G	0.1511680	0.0248468	0.0035200	1.2E-12
11	CEP164	rs486366	117357993	G	A	0.1511700	0.0248394	0.0035200	1.2E-12
11	CEP164	rs4018864	117358402	AAT	A	0.1511520	0.0248420	0.0035203	1.2E-12
11	CEP164	rs2508664	117359175	T	C	0.1351220	0.0232673	0.0036855	1.7E-10
11	CEP164	rs2510450	117359186	T	C	0.1511920	0.0248267	0.0035205	1.3E-12
11	CEP164	rs512730	117360341	A	T	0.1528710	0.0238344	0.0035127	7.8E-12
11	CEP164	rs11216366	117360895	T	G	0.1354710	0.0228850	0.0036869	3.2E-10
11	CEP164	rs12421205	117361440	G	C	0.1515580	0.0245330	0.0035222	2.2E-12
11	CEP164	rs12421494	117361517	A	G	0.1515580	0.0245330	0.0035222	2.2E-12
11	CEP164	rs12418678	117361544	G	A	0.1354610	0.0228799	0.0036869	3.2E-10
11	CEP164	rs17500548	117361675	G	A	0.1354610	0.0228799	0.0036869	3.2E-10
11	CEP164	rs2305825	117361776	T	C	0.1512010	0.0245692	0.0035275	2.1E-12
11	CEP164	rs7934067	117362238	G	A	0.1515580	0.0245330	0.0035222	2.2E-12
11	CEP164	rs11828506	117362711	T	C	0.1511920	0.0248267	0.0035205	1.3E-12
11	CEP164	rs7945704	117364652	A	G	0.1084420	-0.0240318	0.0040541	1.7E-09
11	CEP164	rs7124084	117364696	T	C	0.1511790	0.0247944	0.0035208	1.4E-12
11	CEP164	rs10892097	117365344	T	C	0.1351180	0.0232645	0.0036856	1.7E-10
11	CEP164	chr11:117365567_A_ATTTC	117365567	ATTTC	A	0.1324130	0.0245732	0.0037260	3.1E-11
11	CEP164	rs10790179	117365603	T	G	0.1351180	0.0232645	0.0036856	1.7E-10
11	CEP164	rs7109923	117366771	G	A	0.1506070	0.0245618	0.0035297	2.4E-12
11	CEP164	rs10892098	117367775	T	C	0.1505410	0.0243918	0.0035307	3.4E-12
11	CEP164	rs7115177	117368457	C	A	0.1510360	0.0234266	0.0035263	2.2E-11
11	CEP164	rs7115526	117368474	T	G	0.1510360	0.0234266	0.0035263	2.2E-11
11	CEP164	rs9651682	117369641	A	G	0.1515170	0.0238440	0.0035215	8.4E-12
11	CEP164	rs12417440	117370713	T	C	0.1336620	0.0230006	0.0037087	3.2E-10
11	CEP164	rs10790180	117375434	C	T	0.3465240	0.0161371	0.0026545	1.4E-09
11	CEP164	rs7952470	117377552	A	G	0.1342740	0.0229520	0.0036994	3.3E-10
11	CEP164	rs2305828	117380427	G	A	0.3423100	0.0165389	0.0026660	5.9E-10
11	CEP164	rs897837	117390772	G	C	0.1387900	0.0201623	0.0036616	2.5E-08
11	CEP164	rs9163	117413092	T	C	0.1540120	0.0191675	0.0035175	2.7E-08
11	CEP164 *	rs10736488	117414341	G	A	0.1545250	0.0188660	0.0035123	4.6E-08
11	CEP164 *	rs59114541	117419236	A	G	0.0116949	0.0720037	0.0116577	8.4E-10
11	DSCAML1 *	rs75493192	117422143	G	A	0.0118937	0.0673892	0.0115831	6.4E-09
11	DSCAML1 *	rs11607141	117423306	G	T	0.0331765	-0.0382432	0.0070567	4.4E-08
11	DSCAML1 *	chr11:117423756_AAAAC_	117423756	AAAAC	A	0.0116683	0.1115190	0.0118084	1.2E-21
11	DSCAML1 *	rs7115491	117424434	G	T	0.0317205	-0.0398526	0.0072290	2.3E-08
12	FAM222A *	rs79339138	109776127	A	G	0.0502551	0.0315417	0.0058635	3.9E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
12	IFT81	rs141965732	110144533	T	C	0.0794002	0.0286060	0.0047104	5.1E-09
12	IFT81	rs117624317	110194076	T	C	0.0971651	0.0254514	0.0043159	6.1E-09
12	IFT81 *	rs144825998	110237558	T	C	0.0799705	0.0288288	0.0046937	3.7E-09
12	ATP2A2 *	rs117121174	110259525	A	G	0.0794579	0.0297676	0.0047076	1.1E-09
14	C14orf166 *	rs36016197	51987660	C	A	0.1470460	-0.0207804	0.0035962	4.6E-09
14	C14orf166	rs56877201	51992899	A	G	0.1467990	-0.0197260	0.0035958	1.6E-08
14	C14orf166	rs57358451	51993112	C	CAGTA	0.1468180	-0.0196850	0.0035958	1.7E-08
14	C14orf166	rs61971506	51996807	A	AG	0.1478740	-0.0199870	0.0035931	8.9E-09
14	C14orf166	rs144834676	52001241	A	AGT	0.1485810	-0.0198157	0.0035739	1.2E-08
14	NID2	rs2029984	52007011	G	A	0.1582890	-0.0196316	0.0034911	5.5E-09
14	NID2	rs61971551	52013257	G	C	0.1561510	-0.0187835	0.0034929	3.1E-08
14	NID2	rs61971552	52014806	T	G	0.1559810	-0.0186259	0.0034885	3.5E-08
14	NID2	rs71422049	52016737	G	A	0.1559890	-0.0190923	0.0034862	1.5E-08
14	NID2	rs77091361	52020243	T	C	0.1548340	-0.0189903	0.0034997	1.9E-08
14	NID2	rs61971553	52020797	G	A	0.1617660	-0.0180198	0.0034447	4.7E-08
14	NID2	rs3783632	52031393	A	C	0.1625490	-0.0186881	0.0034602	1.5E-08
14	NID2	rs2073620	52033610	C	T	0.1617850	-0.0186297	0.0034678	1.7E-08
14	NID2	rs11415769	52035018	C	CA	0.1565950	-0.0192591	0.0035212	1.1E-08
14	NID2	rs2645750	52036074	C	A	0.1529110	-0.0222538	0.0035360	8.3E-11
14	NID2	rs2645749	52036077	C	A	0.1529120	-0.0222757	0.0035360	7.9E-11
14	NID2	rs2516593	52036651	T	C	0.1677860	-0.0212840	0.0033976	1.4E-10
14	NID2	rs2749875	52036678	G	A	0.1678020	-0.0212771	0.0033974	1.4E-10
14	NID2	rs2516592	52036827	T	C	0.1533950	-0.0226434	0.0035254	3.4E-11
14	NID2	rs71121678	52036872	A	AG	0.1535490	-0.0226010	0.0035264	3.8E-11
14	NID2	rs2749876	52037679	T	G	0.1538990	-0.0221118	0.0035160	7.6E-11
14	NID2	rs904061	52037906	T	C	0.1539160	-0.0221423	0.0035154	7.1E-11
14	NID2	rs753051	52038642	A	G	0.1540140	-0.0219604	0.0035136	9.8E-11
14	NID2	rs753050	52038657	A	G	0.1540430	-0.0220085	0.0035140	9.0E-11
14	NID2	rs2029976	52039093	C	T	0.1540850	-0.0219240	0.0035122	1.0E-10
14	NID2	rs2029975	52039352	C	T	0.1541500	-0.0219380	0.0035111	9.7E-11
14	NID2	rs10139288	52039768	T	C	0.1543730	-0.0218173	0.0035063	1.1E-10
14	NID2	rs3742536	52040711	A	G	0.1544580	-0.0218692	0.0035046	9.5E-11
14	NID2	rs1982963	52042383	G	A	0.1546130	-0.0224447	0.0034987	3.2E-11
14	NID2	rs3841694	52042541	TA	T	0.1546070	-0.0223907	0.0034989	3.5E-11
14	NID2	rs4898729	52042765	T	C	0.1542550	-0.0225124	0.0035033	2.9E-11
14	NID2	rs4901186	52042766	G	A	0.1546200	-0.0224532	0.0034996	3.3E-11
14	NID2	rs3818187	52043070	G	A	0.1544810	-0.0224328	0.0035012	3.5E-11
14	NID2	rs61973203	52043849	G	A	0.1510410	-0.0230818	0.0035418	1.4E-11
14	NID2	chr14:52044610_CT_C	52044610	CT	C	0.1544050	-0.0229597	0.0035061	1.3E-11
14	NID2	rs1566132	52045118	C	T	0.1544210	-0.0228334	0.0035029	1.6E-11
14	NID2	rs75766425	52045193	C	G	0.1182980	-0.0288129	0.0039160	1.8E-14
14	NID2	rs79823890	52045251	T	G	0.1186070	-0.0286558	0.0039118	2.7E-14
14	NID2	rs2516589	52045892	A	G	0.1520570	-0.0219510	0.0035305	1.5E-10
14	NID2	rs33921845	52045899	C	CTG	0.1543240	-0.0228441	0.0035059	1.5E-11
14	NID2	rs2749880	52046151	G	A	0.1539530	-0.0230436	0.0035083	1.1E-11
14	NID2	rs2645738	52046484	G	A	0.1539460	-0.0229940	0.0035082	1.2E-11
14	NID2	rs1566131	52047966	G	A	0.1539360	-0.0230928	0.0035089	9.5E-12
15	AQP9 *	rs71478659	58281964	G	C	0.4705210	0.0129667	0.0025701	4.3E-08
15	AQP9 *	rs1711037	58284151	T	A	0.4695210	0.0140847	0.0025420	2.6E-09
15	AQP9 *	rs12903590	58285578	T	A	0.4670550	0.0139612	0.0025405	3.7E-09
15	AQP9 *	rs72294268	58287170	T	TATCAC	0.4617350	0.0136429	0.0025360	1.0E-08
15	AQP9 *	rs12910051	58288326	G	A	0.4627540	0.0135003	0.0025303	1.3E-08
15	AQP9 *	rs7179728	58289227	C	G	0.4575870	0.0143880	0.0025379	1.8E-09
15	AQP9 *	rs938507	58289835	A	G	0.4609740	0.0133079	0.0025327	2.1E-08
15	LIPC *	rs1601934	58379522	G	A	0.2566590	0.0235014	0.0029588	1.8E-15
15	LIPC *	rs1601935	58379566	G	T	0.3168210	0.0220019	0.0027759	4.7E-16
15	LIPC *	rs11071376	58379635	C	T	0.1408310	0.0218810	0.0036568	5.0E-10
15	LIPC *	rs74248028	58380169	A	G	0.3709890	-0.0259584	0.0026699	3.8E-23
15	LIPC *	chr15:58381250_GA_G	58381250	G	GA	0.3265540	0.0286473	0.0027206	2.8E-27
15	LIPC *	rs62001736	58381852	A	G	0.1872130	0.0237389	0.0032432	5.6E-14
15	LIPC *	rs2043082	58382109	A	G	0.3257240	0.0287729	0.0027139	7.6E-28
15	LIPC *	rs4775041	58382496	C	G	0.1884220	0.0237493	0.0032306	3.8E-14
15	LIPC *	rs4775042	58382531	C	G	0.4843000	-0.0194872	0.0025589	5.0E-15
15	LIPC *	rs116543766	58382658	C	A	0.0899874	0.0325770	0.0044565	1.8E-13
15	LIPC *	rs75525508	58383286	A	G	0.3695540	-0.0260941	0.0026543	9.1E-24
15	LIPC *	rs80123226	58383833	T	A	0.1911100	0.0235882	0.0032158	5.6E-14
15	LIPC *	rs16940147	58383920	A	G	0.1345110	0.0230523	0.0037221	1.6E-10
15	LIPC *	rs11858759	58384622	A	G	0.1879260	0.0237038	0.0032368	5.2E-14
15	LIPC *	rs10468017	58386313	T	C	0.1819000	0.0223589	0.0032755	2.1E-12
15	LIPC *	rs261290	58386521	T	C	0.3225080	0.0280646	0.0027115	1.6E-26
15	LIPC *	rs7350789	58387469	A	G	0.3224700	0.0281138	0.0027106	1.2E-26
15	LIPC *	rs58719229	58387608	C	CAGA	0.3225410	0.0281904	0.0027109	9.3E-27

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	LIPC *	rs261291	58387979	C	T	0.4151720	0.0317066	0.0025738	2.2E-36
15	LIPC *	rs7177289	58387985	T	C	0.3227710	0.0278170	0.0027101	4.2E-26
15	LIPC *	rs261292	58388705	A	G	0.4666340	-0.0181119	0.0025429	2.7E-13
15	LIPC *	rs2043085	58388755	T	C	0.4422730	0.0308312	0.0025510	3.8E-35
15	LIPC *	rs80328086	58388800	G	A	0.3784760	-0.0262429	0.0026129	1.1E-24
15	LIPC *	rs75437656	58388929	C	A	0.2240300	0.0194924	0.0030486	2.9E-11
15	LIPC *	rs79745310	58388956	C	T	0.3801870	-0.0262833	0.0026112	9.1E-25
15	LIPC *	chr15:58389334_G_GT	58389334	G	GT	0.3591740	0.0255370	0.0026988	8.8E-23
15	LIPC *	rs261293	58389573	C	T	0.2518420	0.0176309	0.0029361	3.2E-10
15	LIPC *	rs76262110	58389830	T	TGAA	0.2227890	0.0196811	0.0030599	2.2E-11
15	LIPC *	rs2043084	58390297	C	G	0.1145230	0.0309917	0.0040197	1.3E-14
15	LIPC *	rs1825955	58390584	A	C	0.2476470	0.0173916	0.0029591	7.9E-10
15	LIPC *	rs12185071	58391028	T	C	0.2234380	0.0192365	0.0030536	4.5E-11
15	LIPC *	rs1532085	58391167	A	G	0.4416070	0.0316360	0.0025513	4.8E-37
15	LIPC *	rs12185072	58391211	T	C	0.2515600	0.0174626	0.0029338	4.0E-10
15	LIPC *	rs12905732	58391343	C	G	0.1120600	0.0313738	0.0040422	1.1E-14
15	LIPC *	rs11853674	58391858	G	A	0.1121630	0.0311738	0.0040404	1.6E-14
15	LIPC *	rs16940168	58391955	T	A	0.2452480	0.0160590	0.0029624	1.1E-08
15	LIPC *	rs16940170	58392083	A	G	0.2446640	0.0163011	0.0029643	6.8E-09
15	LIPC *	rs28495863	58392182	A	G	0.2454000	0.0158704	0.0029617	1.5E-08
15	LIPC *	rs12185093	58392477	A	G	0.2439500	0.0163466	0.0029694	7.0E-09
15	LIPC *	rs72475921	58392838	G	T	0.3791440	-0.0267984	0.0026249	9.4E-26
15	LIPC *	rs199962452	58393355	A	T	0.3734960	-0.0269039	0.0026480	1.8E-25
15	LIPC *	rs28703614	58393361	T	C	0.2451810	0.0163449	0.0029633	6.7E-09
15	LIPC *	rs7497636	58393432	T	C	0.2453240	0.0163520	0.0029623	6.4E-09
15	LIPC *	rs1444942	58393614	C	G	0.2452650	0.0163631	0.0029631	6.7E-09
15	LIPC *	rs8042174	58393771	C	T	0.3808890	-0.0268000	0.0026240	1.0E-25
15	LIPC *	rs447794	58394439	G	C	0.2455920	0.0163774	0.0029628	6.3E-09
15	LIPC *	rs76679589	58394492	T	C	0.2455950	0.0164246	0.0029627	5.8E-09
15	LIPC *	rs7164909	58394555	T	C	0.3623750	-0.0261235	0.0026472	8.3E-24
15	LIPC *	rs7165077	58394610	T	C	0.3876370	-0.0256709	0.0026109	1.3E-23
15	LIPC *	rs261301	58394740	T	C	0.2456560	0.0164743	0.0029617	5.2E-09
15	LIPC *	rs75663614	58394841	C	T	0.3636510	-0.0258451	0.0026435	2.2E-23
15	LIPC *	rs5812934	58395053	G	GA	0.1093610	0.0322636	0.0040839	5.1E-15
15	LIPC *	rs17240832	58395171	G	A	0.2458120	0.0166725	0.0029591	3.6E-09
15	LIPC *	rs74019425	58395266	T	G	0.2455910	0.0165751	0.0029578	4.0E-09
15	LIPC *	rs16940181	58395325	C	A	0.2457250	0.0165724	0.0029565	4.0E-09
15	LIPC *	rs71711102	58395331	A	G	0.1092950	0.0321872	0.0040852	6.2E-15
15	LIPC *	rs174418	58395404	T	C	0.3933110	0.0253372	0.0026060	1.4E-23
15	LIPC *	rs166359	58395410	G	T	0.2467320	0.0160496	0.0029548	1.2E-08
15	LIPC *	rs495348	58395591	C	G	0.2461410	0.0166243	0.0029556	3.2E-09
15	LIPC *	rs8032310	58395663	A	G	0.2473620	0.0164458	0.0029563	5.6E-09
15	LIPC *	rs493987	58395707	T	C	0.2457400	0.0166246	0.0029561	3.5E-09
15	LIPC *	rs76438892	58395733	G	A	0.3626310	-0.0260783	0.0026442	9.7E-24
15	LIPC *	rs4238329	58395987	C	A	0.3609550	-0.0265529	0.0026481	1.6E-24
15	LIPC *	rs920917	58396279	C	A	0.2449900	0.0167685	0.0029614	2.5E-09
15	LIPC *	rs11855284	58396988	C	T	0.1111370	0.0320533	0.0040589	4.9E-15
15	LIPC *	rs11858481	58396998	T	C	0.1089990	0.0321686	0.0040937	8.3E-15
15	LIPC *	rs76898656	58399003	A	G	0.3584250	-0.0262713	0.0026685	1.2E-23
15	LIPC *	rs74019428	58399009	T	C	0.3584280	-0.0262718	0.0026686	1.2E-23
15	LIPC *	rs490098	58399026	C	A	0.2523310	0.0158515	0.0029423	9.9E-09
15	LIPC *	rs2082149	58399190	A	G	0.2587190	0.0166625	0.0029189	1.3E-09
15	LIPC *	rs8024755	58399670	A	G	0.4164350	-0.0262160	0.0026036	3.1E-24
15	LIPC *	rs397923	58399919	A	T	0.3687230	0.0275082	0.0026636	4.3E-26
15	LIPC *	rs35128881	58399949	T	G	0.1076070	0.0327483	0.0041394	3.4E-15
15	LIPC *	rs414671	58400280	C	T	0.2540610	0.0164897	0.0029324	2.7E-09
15	LIPC *	rs60900172	58400418	C	G	0.3577320	-0.0264399	0.0026947	1.6E-23
15	LIPC *	rs12906722	58400516	T	C	0.1052060	0.0326766	0.0041757	6.1E-15
15	LIPC *	rs16940204	58400737	T	C	0.1026370	0.0317873	0.0042302	6.5E-14
15	LIPC *	rs487766	58401661	C	T	0.1076050	0.0325191	0.0041526	7.6E-15
15	LIPC *	rs16940212	58401821	T	G	0.2738410	0.0185617	0.0028375	7.1E-12
15	LIPC *	rs76686550	58402458	G	C	0.2901490	0.0178790	0.0028394	4.5E-11
15	LIPC *	rs16940213	58403138	T	C	0.2724040	0.0191953	0.0028792	4.3E-12
15	LIPC *	rs79111033	58403393	A	G	0.2709200	0.0193612	0.0028920	3.8E-12
15	LIPC *	rs35980001	58430391	GC	G	0.3420250	0.0327100	0.0026978	5.2E-37
15	LIPC *	rs1077835	58431227	G	A	0.3844940	0.0328120	0.0025934	3.4E-40
15	LIPC *	rs1077834	58431280	C	T	0.3838230	0.0321927	0.0025930	7.0E-39
15	LIPC *	rs1800588	58431476	T	C	0.3592820	0.0325894	0.0026268	6.0E-39
15	LIPC *	rs2070895	58431740	A	G	0.3824960	0.0330341	0.0025937	9.2E-41
15	LIPC	rs6494005	58432325	G	A	0.2424220	-0.0161775	0.0029496	4.1E-10
15	LIPC	rs8034802	58432593	T	A	0.3579910	-0.0168177	0.0026343	4.1E-13
15	LIPC	rs8033940	58432643	G	A	0.3029840	-0.0201748	0.0027491	1.3E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	LIPC	rs633695	58433640	A	G	0.3553810	-0.0161980	0.0026485	4.1E-12
15	LIPC	rs261334	58434545	G	C	0.3421100	0.0309633	0.0026579	1.8E-34
15	LIPC	rs71116564	58434769	C	CCAAAG _L	0.3435910	0.0306762	0.0026674	1.7E-33
15	LIPC, LOC101928694	rs261333	58435080	C	T	0.2385040	-0.0179658	0.0030067	2.5E-11
15	LIPC, LOC101928694	rs17190517	58436945	T	C	0.2220530	-0.0162776	0.0030652	2.7E-09
15	LIPC, LOC101928694	rs588136	58438299	C	T	0.3641410	0.0278435	0.0026308	4.7E-29
15	LIPC, LOC101928694	rs261342	58438954	C	G	0.4257450	-0.0147040	0.0025635	2.6E-10
15	LIPC, LOC101928694	rs17301746	58439196	T	C	0.2581060	0.0220109	0.0029332	5.7E-16
15	LIPC, LOC101928694	rs261341	58439368	G	A	0.3400950	-0.0146300	0.0026810	4.5E-10
15	LIPC, LOC101928694	rs8043310	58439619	A	C	0.2323480	0.0255975	0.0030455	4.1E-19
15	LIPC, LOC101928694	rs12594375	58440269	A	G	0.2534530	0.0228526	0.0029658	9.1E-17
15	LIPC, LOC101928694	rs6494007	58442446	T	C	0.2586480	0.0236541	0.0029474	3.9E-18
15	TLE3 *	rs12593720	69868843	T	C	0.2373740	-0.0154889	0.0029951	3.7E-08
15	TLE3 *	rs10162636	69875502	T	G	0.2412610	-0.0158363	0.0030006	1.9E-08
15	TLE3 *	rs78943073	69876104	A	G	0.2380910	-0.0154554	0.0030063	4.0E-08
15	TLE3 *	rs7166273	69881625	C	T	0.2393500	-0.0154506	0.0029885	2.9E-08
15	TLE3 *	rs304948	69884491	A	G	0.3479050	-0.0140958	0.0026751	2.9E-08
15	TLE3 *	rs304941	69887624	T	C	0.3468150	-0.0144076	0.0026735	1.7E-08
15	TLE3 *	rs80287865	69889112	T	G	0.2301560	-0.0174908	0.0030224	8.1E-10
15	TLE3 *	rs77648222	69890512	G	A	0.2351570	-0.0171988	0.0029884	1.2E-09
15	TLE3 *	rs17756181	69891852	G	A	0.2445790	-0.0172725	0.0029463	8.5E-10
15	TLE3 *	rs28521935	69892800	C	A	0.2394440	-0.0171937	0.0029794	1.4E-09
15	TLE3 *	rs881053	69894413	A	G	0.3741180	-0.0140621	0.0026240	4.7E-08
15	TLE3 *	rs8041139	69896404	G	T	0.3470140	-0.0144701	0.0026729	1.3E-08
15	TLE3 *	rs1155996	69897006	C	T	0.3469030	-0.0145112	0.0026706	1.1E-08
15	TLE3 *	rs12591142	69897251	C	A	0.2306390	-0.0171180	0.0030181	1.7E-09
15	TLE3 *	rs12440731	69899052	A	G	0.3567750	-0.0144698	0.0026580	1.3E-08
15	TLE3 *	rs80039904	69901814	T	C	0.2291440	-0.0166527	0.0030467	6.5E-09
15	TLE3 *	rs2601883	69903678	C	G	0.2369070	-0.0171509	0.0030231	4.1E-09
16	CMIP	rs2925979	81501185	T	C	0.4281730	0.0180521	0.0025509	2.4E-13
17	PTRH2	rs58742647	59701700	TG	T	0.4345550	0.0144999	0.0025725	1.5E-08
17	PTRH2	rs7226149	59702871	C	T	0.4355470	0.0143155	0.0025674	2.1E-08
17	VMP1	rs111723017	59710070	C	G	0.4354800	0.0142730	0.0025664	2.4E-08
17	VMP1	chr17:59711135_C_CA	59711135	CA	C	0.4352670	0.0143693	0.0025781	2.2E-08
17	VMP1	rs9903626	59713266	G	A	0.4356770	0.0143703	0.0025658	1.9E-08
17	VMP1	rs60451858	59749244	G	A	0.4348260	0.0139051	0.0025556	4.7E-08
17	VMP1	rs72838857	59759406	G	A	0.4333890	0.0139233	0.0025598	4.9E-08
17	VMP1	rs201444735	59774421	A	AAAGAA _A	0.4294880	0.0147810	0.0025799	1.3E-08
17	VMP1	rs2777900	59795133	A	G	0.4328600	0.0144123	0.0025551	1.8E-08
17	VMP1	rs2645492	59798193	A	G	0.4328220	0.0144305	0.0025549	1.7E-08
17	VMP1	rs2102507	59798546	G	A	0.4327100	0.0143869	0.0025551	1.8E-08
17	VMP1	rs2645491	59799688	T	C	0.4328580	0.0143936	0.0025549	1.8E-08
17	VMP1	rs2665400	59802840	A	G	0.4361690	0.0147053	0.0025549	8.6E-09
17	VMP1	rs34890976	59803949	AT	A	0.3991640	-0.0145826	0.0026016	1.3E-08
17	VMP1	rs2645489	59806010	G	T	0.4312300	0.0146668	0.0025614	1.1E-08
17	VMP1	rs2645486	59808540	A	T	0.4328930	0.0144437	0.0025549	1.6E-08
17	VMP1	rs2645487	59808764	G	T	0.4328920	0.0144456	0.0025549	1.6E-08
17	VMP1	rs11079389	59810591	A	G	0.4328960	0.0144605	0.0025550	1.5E-08
17	VMP1	rs2063353	59811831	G	T	0.4043100	-0.0139174	0.0025795	4.6E-08
17	VMP1	rs2665403	59812624	A	G	0.4332980	0.0144675	0.0025536	1.6E-08
17	VMP1	rs2173120	59815279	T	A	0.4332570	0.0143993	0.0025537	1.9E-08
17	VMP1	chr17:59815464_ATTT_A	59815464	A	ATTT	0.4316990	0.0147846	0.0025611	8.9E-09
17	VMP1	rs115869798	59815468	A	T	0.4316990	0.0147846	0.0025611	8.9E-09
17	VMP1	rs71145576	59815855	C	AAAAAA _A	0.4345210	0.0143236	0.0025576	2.2E-08
17	VMP1	rs147970496	59817246	CTGGGCA	C	0.4332770	0.0144750	0.0025538	1.5E-08
17	VMP1	rs7223793	59818661	G	T	0.4332820	0.0144739	0.0025537	1.5E-08
17	VMP1	rs2526352	59827462	A	G	0.4312450	0.0140338	0.0025599	4.7E-08
17	VMP1	rs34385574	59829215	T	TC	0.4041000	-0.0139023	0.0025791	4.6E-08
17	VMP1	rs1292063	59830407	T	A	0.4345270	0.0144347	0.0025583	1.8E-08
17	VMP1	rs1295926	59832012	G	A	0.4041200	-0.0139572	0.0025789	4.0E-08
17	VMP1	rs1296280	59832068	T	A	0.4039740	-0.0139836	0.0025795	3.8E-08
17	VMP1	rs1292061	59833869	G	A	0.4042550	-0.0138857	0.0025794	4.7E-08
17	MIR21 *	rs1292037	59841547	C	T	0.4332500	0.0145092	0.0025536	1.3E-08
17	MIR21 *	rs13137	59841670	T	A	0.4332500	0.0145092	0.0025536	1.3E-08
17	MIR21 *	rs2645479	59843171	A	G	0.4040700	-0.0139653	0.0025801	3.9E-08
17	MIR21 *	rs1292072	59848288	G	A	0.4330100	0.0143689	0.0025615	2.0E-08
17	RPS6KB1	rs1358683643	59915799	TA	T	0.4418480	-0.0145159	0.0025679	3.0E-08
17	BPTF *	rs74949631	67809515	T	C	0.4177360	0.0135290	0.0025763	3.4E-08
17	BPTF *	rs3936134	67818266	C	G	0.3754820	-0.0151175	0.0026670	7.2E-09
17	BPTF *	rs72631329	67822258	T	C	0.3750340	-0.0152887	0.0026688	5.7E-09
17	BPTF	rs3833111	67826457	CAG	C	0.3408200	-0.0174868	0.0027268	6.0E-11
17	BPTF	chr17:67829112_TTTG_T	67829112	TTTG	T	0.3453290	-0.0178146	0.0027113	2.6E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	BPTF	rs12603589	67829132	T	C	0.3445240	-0.0179335	0.0027046	1.5E-11
17	BPTF	rs12601921	67829238	C	T	0.3435860	-0.0183988	0.0027214	6.3E-12
17	BPTF	rs12601919	67829258	A	G	0.3449620	-0.0179982	0.0027029	1.3E-11
17	BPTF	rs9915591	67829974	C	G	0.3450700	-0.0178014	0.0027040	2.0E-11
17	BPTF	rs12602556	67830745	A	G	0.3443660	-0.0178965	0.0027007	1.4E-11
17	BPTF	rs62084208	67831327	C	T	0.3448220	-0.0177811	0.0026982	2.1E-11
17	BPTF	rs2080090	67832255	T	A	0.3480320	-0.0182506	0.0027180	6.4E-12
17	BPTF	rs62084210	67832594	A	G	0.3444960	-0.0180750	0.0026976	9.4E-12
17	BPTF	rs12449312	67833242	A	C	0.3508860	-0.0171387	0.0027096	7.8E-11
17	BPTF	rs7223643	67834166	A	G	0.3453250	-0.0176591	0.0026826	2.0E-11
17	BPTF	rs1976052	67834462	C	T	0.3454500	-0.0177004	0.0026798	1.9E-11
17	BPTF	rs7209675	67835142	A	T	0.3453080	-0.0175828	0.0026658	2.0E-11
17	BPTF	chr17:67835212_T_TA	67835212	T	TA	0.3467080	-0.0177718	0.0026679	1.3E-11
17	BPTF	rs75873575	67835625	GT	G	0.3454070	-0.0177034	0.0026615	1.4E-11
17	BPTF	rs142633440	67835663	TTTTTTT	A	0.3451920	-0.0176202	0.0026645	1.7E-11
17	BPTF	rs7218014	67835900	T	C	0.3444300	-0.0178870	0.0026679	8.2E-12
17	BPTF	rs7221651	67836274	G	A	0.3453920	-0.0176450	0.0026612	1.6E-11
17	BPTF	rs12452511	67836460	A	G	0.3453920	-0.0176450	0.0026612	1.6E-11
17	BPTF	rs1976053	67836886	C	G	0.3381230	-0.0176530	0.0026826	1.8E-11
17	BPTF	rs1976054	67837108	T	G	0.3453920	-0.0176450	0.0026612	1.6E-11
17	BPTF	rs7208909	67837430	T	C	0.3482580	-0.0177955	0.0026666	1.0E-11
17	BPTF	rs2052187	67838621	T	C	0.3453920	-0.0176450	0.0026612	1.6E-11
17	BPTF	rs11079705	67839336	A	T	0.3490680	-0.0169482	0.0026668	8.3E-11
17	BPTF	rs11079706	67839354	G	T	0.3456270	-0.0175737	0.0026668	2.0E-11
17	BPTF	rs11079707	67839501	G	A	0.3456440	-0.0176012	0.0026620	1.8E-11
17	BPTF	rs80135947	67839885	A	C	0.3453880	-0.0176553	0.0026612	1.5E-11
17	BPTF	chr17:67840458_CTTG_C	67840458	CTTG	C	0.3467580	-0.0178429	0.0026667	1.2E-11
17	BPTF	rs59252707	67840471	T	C	0.3579860	-0.0169298	0.0026857	1.0E-10
17	BPTF	rs6504542	67840526	T	C	0.3453730	-0.0176247	0.0026613	1.7E-11
17	BPTF	rs8082512	67840943	T	C	0.3453730	-0.0176247	0.0026613	1.7E-11
17	BPTF	rs1599859	67841077	C	G	0.3452190	-0.0175873	0.0026621	1.9E-11
17	BPTF	rs1966410	67841099	T	C	0.3452190	-0.0175873	0.0026621	1.9E-11
17	BPTF	rs58551145	67841119	A	G	0.3453420	-0.0174873	0.0026623	2.5E-11
17	BPTF	rs6504543	67841543	T	C	0.3395630	-0.0176741	0.0026742	1.5E-11
17	BPTF	rs8067892	67841867	A	G	0.3453730	-0.0176247	0.0026613	1.7E-11
17	BPTF	rs8074078	67842627	T	G	0.3453730	-0.0176247	0.0026613	1.7E-11
17	BPTF	rs8073510	67843094	A	G	0.3465920	-0.0176236	0.0026624	1.9E-11
17	BPTF	rs12450363	67843992	T	C	0.3459970	-0.0173235	0.0026648	3.5E-11
17	BPTF	rs62084212	67844128	G	A	0.3559610	-0.0170521	0.0026979	1.2E-10
17	BPTF	rs112222385	67844408	T	C	0.3447540	-0.0175271	0.0026646	2.0E-11
17	BPTF	rs11871285	67844693	G	T	0.3471270	-0.0176428	0.0026613	1.9E-11
17	BPTF	rs11868959	67844694	T	C	0.3471270	-0.0176428	0.0026613	1.9E-11
17	BPTF	rs2365466	67845013	G	A	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs3029927	67845167	A	AAGT	0.3406370	-0.0176267	0.0026755	2.2E-11
17	BPTF	rs2365467	67845169	A	T	0.3406370	-0.0176267	0.0026755	2.2E-11
17	BPTF	rs2365468	67845202	C	T	0.3400160	-0.0177483	0.0026723	1.2E-11
17	BPTF	rs62084213	67845900	A	G	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs7223930	67846070	G	A	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs7224923	67846149	T	G	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs62084214	67847209	C	G	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	chr17:67848171_CT_C	67848171	CT	C	0.3343710	-0.0184943	0.0027121	3.3E-12
17	BPTF	rs8081517	67849581	A	T	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs8081856	67849802	A	G	0.3457560	-0.0179446	0.0026630	8.4E-12
17	BPTF	rs62084234	67850944	A	G	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs7212293	67851209	A	G	0.3402550	-0.0177359	0.0026728	1.2E-11
17	BPTF	chr17:67851919_CT_C	67851919	CT	C	0.3279190	-0.0174592	0.0027282	4.9E-11
17	BPTF	rs34733047	67852002	T	TA	0.3468060	-0.0175959	0.0026631	1.7E-11
17	BPTF	rs78452260	67852406	G	T	0.3459010	-0.0177306	0.0026597	1.2E-11
17	BPTF	rs79993364	67852461	C	CCT	0.3400160	-0.0177483	0.0026723	1.2E-11
17	BPTF	rs4791048	67852878	G	A	0.3400160	-0.0177483	0.0026723	1.2E-11
17	BPTF	rs2086744	67853159	C	G	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs2046323	67853811	T	G	0.3458280	-0.0177036	0.0026596	1.3E-11
17	BPTF	rs4791046	67855857	G	A	0.3465420	-0.0176610	0.0026616	1.2E-11
17	BPTF	rs4790908	67856791	T	G	0.3458220	-0.0176987	0.0026595	1.3E-11
17	BPTF	rs11079709	67857247	C	T	0.3453940	-0.0179170	0.0026677	1.1E-11
17	BPTF	rs62084235	67857321	C	T	0.3436210	-0.0175148	0.0026706	2.9E-11
17	BPTF	rs12450072	67857401	C	G	0.3459260	-0.0177119	0.0026597	1.3E-11
17	BPTF	rs74541577	67857535	C	T	0.3467990	-0.0175587	0.0026637	1.7E-11
17	BPTF	rs74561219	67857643	T	A	0.3458850	-0.0177225	0.0026595	1.2E-11
17	BPTF	rs28609796	67858988	T	A	0.3432830	-0.0177633	0.0026798	2.0E-11
17	BPTF	rs62084238	67860457	T	A	0.3461680	-0.0176590	0.0026613	1.6E-11
17	BPTF	rs2128792	67861061	C	T	0.3458470	-0.0176641	0.0026596	1.4E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	BPTF	rs2365764	67861598	G	A	0.3458180	-0.0176933	0.0026595	1.3E-11
17	BPTF	rs62084240	67863117	C	A	0.3458100	-0.0177056	0.0026595	1.3E-11
17	BPTF	rs75352663	67863943	AT	A	0.3457200	-0.0176094	0.0026600	1.6E-11
17	BPTF	rs60432293	67864291	T	C	0.3458400	-0.0176620	0.0026596	1.4E-11
17	BPTF	rs59950564	67864743	A	G	0.3458100	-0.0177056	0.0026595	1.3E-11
17	BPTF	rs8077872	67864943	G	T	0.3400020	-0.0177373	0.0026722	1.2E-11
17	BPTF	rs34739687	67865998	TA	T	0.3400020	-0.0177373	0.0026722	1.2E-11
17	BPTF	rs4790905	67867234	C	A	0.3458110	-0.0177007	0.0026594	1.3E-11
17	BPTF	rs34872586	67867350	T	C	0.3460310	-0.0176777	0.0026605	1.4E-11
17	BPTF	rs58141639	67868786	C	T	0.3458400	-0.0176914	0.0026598	1.3E-11
17	BPTF	rs61067468	67869919	G	A	0.3496180	-0.0177796	0.0026693	1.2E-11
17	BPTF	rs62084246	67871795	G	C	0.3457830	-0.0176609	0.0026595	1.4E-11
17	BPTF	rs9912084	67871919	A	C	0.3458050	-0.0176929	0.0026594	1.3E-11
17	BPTF	rs9912770	67872117	C	T	0.3458050	-0.0176929	0.0026594	1.3E-11
17	BPTF	rs11869819	67872553	A	C	0.3457840	-0.0176621	0.0026595	1.4E-11
17	BPTF	rs55939964	67873181	G	A	0.3463880	-0.0179241	0.0026601	7.8E-12
17	BPTF	rs12602912	67873957	C	T	0.3460070	-0.0177302	0.0026578	1.1E-11
17	BPTF	rs12450907	67874528	T	G	0.3457840	-0.0176621	0.0026595	1.4E-11
17	BPTF	rs9890629	67875443	G	A	0.3457840	-0.0176621	0.0026595	1.4E-11
17	BPTF	rs12451707	67875482	G	A	0.3457840	-0.0176621	0.0026595	1.4E-11
17	BPTF	rs4569324	67876634	C	T	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs62084247	67876787	C	T	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs112651248	67876819	AAG	A	0.3400020	-0.0177442	0.0026722	1.2E-11
17	BPTF	rs9915108	67878347	T	C	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs9913471	67878379	C	T	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs62084248	67878425	C	T	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs12451511	67878745	T	G	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs62084249	67878882	A	G	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs73352808	67879041	G	A	0.3597490	-0.0159785	0.0026905	1.1E-09
17	BPTF	rs11867517	67879210	C	T	0.3465550	-0.0176371	0.0026656	1.7E-11
17	BPTF	rs11867537	67879376	A	G	0.3468170	-0.0177039	0.0026599	1.4E-11
17	BPTF	rs11867618	67879471	G	A	0.3471390	-0.0175467	0.0026595	1.9E-11
17	BPTF	rs35243555	67880361	G	C	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs58122682	67880799	T	C	0.3465170	-0.0177948	0.0026619	9.3E-12
17	BPTF	rs8074644	67882101	G	C	0.3458740	-0.0177014	0.0026594	1.3E-11
17	BPTF	rs62084251	67882620	G	A	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs9892803	67883127	T	G	0.3458070	-0.0176940	0.0026594	1.3E-11
17	BPTF	rs140912776	67883456	TA	T	0.3475320	-0.0174187	0.0026608	3.3E-11
17	BPTF	rs62084252	67883462	G	C	0.3475320	-0.0174187	0.0026608	3.3E-11
17	BPTF	rs9897982	67883476	G	T	0.3410790	-0.0177293	0.0026745	1.4E-11
17	BPTF	rs6504545	67884251	A	G	0.3464340	-0.0175928	0.0026628	1.6E-11
17	BPTF	rs6504546	67884269	A	C	0.3466510	-0.0178853	0.0026601	7.3E-12
17	BPTF	rs7213292	67884327	A	G	0.3464370	-0.0175543	0.0026597	1.8E-11
17	BPTF	rs115210018	67884423	T	C	0.3588380	-0.0158786	0.0026934	1.5E-09
17	BPTF	rs3935969	67885843	A	G	0.3457890	-0.0177250	0.0026595	1.2E-11
17	BPTF	rs4318247	67886056	A	G	0.3457890	-0.0177250	0.0026595	1.2E-11
17	BPTF	rs75360723	67886426	A	AT	0.3455590	-0.0179348	0.0026615	8.6E-12
17	BPTF	rs8082661	67888585	G	A	0.3462340	-0.0174334	0.0026989	4.6E-11
17	BPTF	rs7208663	67889055	T	C	0.3457890	-0.0177250	0.0026595	1.2E-11
17	BPTF	rs75231441	67889369	A	G	0.3457890	-0.0177250	0.0026595	1.2E-11
17	BPTF	rs12452823	67889667	G	A	0.3457870	-0.0177202	0.0026595	1.2E-11
17	BPTF	rs11079710	67889795	C	T	0.3149690	-0.0159456	0.0027256	1.8E-09
17	BPTF	rs6504548	67889932	T	C	0.3399510	-0.0177468	0.0026724	1.2E-11
17	BPTF	rs8079291	67891506	A	G	0.3447610	-0.0176932	0.0026639	1.6E-11
17	BPTF	rs8079754	67891780	A	G	0.3457690	-0.0176998	0.0026597	1.3E-11
17	BPTF	rs6504549	67892668	A	G	0.3399210	-0.0177262	0.0026726	1.2E-11
17	BPTF	rs61676547	67896391	G	C	0.3349180	-0.0174312	0.0027032	4.5E-11
17	BPTF	rs56148300	67896636	T	C	0.3274260	-0.0182184	0.0026978	5.8E-12
17	BPTF	rs3206817	67896718	A	G	0.3334770	-0.0182034	0.0026840	5.8E-12
17	BPTF	rs56404791	67896903	T	G	0.3279740	-0.0182788	0.0026962	5.2E-12
17	BPTF	rs145606454	67897173	AC	A	0.3325120	-0.0183327	0.0026862	4.6E-12
17	BPTF	rs60477798	67897174	C	A	0.3561840	-0.0189272	0.0026967	1.8E-12
17	BPTF	rs6504550	67898426	A	G	0.2950310	-0.0169548	0.0027767	3.5E-10
17	BPTF	chr17:67898661_CT_C	67898661	CT	C	0.3311250	-0.0175055	0.0027186	5.9E-11
17	BPTF	rs7216064	67902693	G	A	0.3346280	-0.0178189	0.0026806	1.6E-11
17	BPTF	rs8065906	67906529	G	A	0.3465040	-0.0178205	0.0026608	8.3E-12
17	BPTF	rs6504551	67907210	T	G	0.2951240	-0.0167406	0.0027763	5.4E-10
17	BPTF	rs12602655	67913326	A	G	0.3453340	-0.0176562	0.0026649	1.3E-11
17	BPTF	rs8072225	67916844	A	G	0.3267790	-0.0181349	0.0027006	7.4E-12
17	BPTF	rs55896768	67917242	T	C	0.3272580	-0.0181342	0.0027013	7.0E-12
17	BPTF	rs12600941	67922691	A	G	0.3458980	-0.0176863	0.0026632	1.2E-11
17	BPTF	rs62085991	67924392	G	A	0.3465120	-0.0177383	0.0026614	9.6E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	BPTF	rs62085992	67926967	T	A	0.3469030	-0.0178922	0.0026617	7.2E-12
17	BPTF	rs62085993	67927036	T	C	0.3336460	-0.0181900	0.0026820	5.9E-12
17	BPTF	rs73338706	67930488	T	C	0.3323480	-0.0181531	0.0026887	8.5E-12
17	BPTF	rs4271626	67934017	G	A	0.3334180	-0.0182414	0.0026827	5.2E-12
17	BPTF	rs4791300	67934656	A	G	0.3283100	-0.0187943	0.0027096	1.8E-12
17	BPTF	rs4791299	67934821	A	G	0.3274390	-0.0187624	0.0027111	1.7E-12
17	BPTF	rs56393562	67937802	C	T	0.3328030	-0.0183936	0.0026869	4.0E-12
17	BPTF	rs5821447	67940063	TATTA	T	0.3335070	-0.0185734	0.0026876	3.0E-12
17	BPTF	rs8071463	67942539	A	G	0.3323250	-0.0182103	0.0026865	5.4E-12
17	BPTF	rs12451721	67942959	G	A	0.3463290	-0.0177924	0.0026615	8.6E-12
17	BPTF	rs6504555	67944611	G	A	0.3298140	-0.0182637	0.0027100	8.4E-12
17	BPTF	rs11870068	67948399	A	C	0.3324290	-0.0180497	0.0026858	9.3E-12
17	BPTF	rs7223357	67949420	C	G	0.3332090	-0.0180128	0.0026837	9.9E-12
17	BPTF	rs7223813	67949724	A	G	0.3332090	-0.0180128	0.0026837	9.9E-12
17	BPTF	rs12449442	67951524	G	A	0.3437770	-0.0181895	0.0026803	5.8E-12
17	BPTF	rs11867401	67951854	A	G	0.3274410	-0.0182917	0.0026982	5.6E-12
17	BPTF	rs9907491	67953877	A	G	0.3274140	-0.0182858	0.0026979	5.8E-12
17	BPTF	rs71142114	67954174	G	GT	0.3248650	-0.0179325	0.0027138	1.7E-11
17	BPTF	rs4790974	67954991	T	A	0.3274780	-0.0182947	0.0026982	5.8E-12
17	BPTF	rs4790973	67955017	C	T	0.3334560	-0.0181232	0.0026826	7.9E-12
17	BPTF	rs77706698	67957232	G	A	0.3464550	-0.0177553	0.0026637	1.1E-11
17	BPTF	rs12601759	67959168	A	G	0.3330220	-0.0182374	0.0026849	6.0E-12
17	BPTF	rs9899520	67961452	G	A	0.3233490	-0.0183832	0.0027186	7.2E-12
17	BPTF	rs146879804	67961470	C	CT	0.3477450	-0.0179341	0.0026713	8.6E-12
17	BPTF	chr17:67961971_CA_C	67961971	CA	C	0.2946430	-0.0171045	0.0027803	3.0E-10
17	BPTF	rs148803332	67962134	C	AAAAGAA	0.3145080	-0.0190052	0.0027739	3.8E-12
17	BPTF	rs60626066	67965117	G	A	0.3525840	-0.0196816	0.0026841	1.4E-13
17	BPTF	rs10445361	67966122	T	G	0.3341010	-0.0196431	0.0026853	1.6E-13
17	BPTF	rs5821446	67966422	AT	A	0.3327810	-0.0194021	0.0026855	3.2E-13
17	BPTF	rs77596502	67968054	TAGG	T	0.3417260	-0.0182259	0.0026752	3.3E-12
17	BPTF	rs62086042	67971327	T	C	0.2872360	-0.0171069	0.0028003	3.6E-10
17	BPTF	rs62086043	67971887	A	G	0.3288150	-0.0182450	0.0027060	7.5E-12
17	BPTF	rs62086044	67974721	G	T	0.3289150	-0.0183046	0.0026995	5.5E-12
17	BPTF	rs62086045	67977615	G	A	0.3277920	-0.0184224	0.0027025	4.7E-12
17	BPTF	rs4791212	67979269	C	T	0.3401830	-0.0181794	0.0026833	4.7E-12
17	BPTF	rs7210027	67980937	T	C	0.3273410	-0.0184707	0.0027054	4.2E-12
17	BPTF	rs4790941	67981016	G	A	0.3277060	-0.0184281	0.0027033	4.5E-12
17	BPTF	rs11656743	67984173	A	G	0.3260240	-0.0182852	0.0027094	7.2E-12
17	BPTF *	rs62086046	67986827	C	T	0.3286210	-0.0184581	0.0027034	4.3E-12
17	C17orf58 *	rs75772932	67988421	G	A	0.3435390	-0.0177421	0.0026798	1.5E-11
17	C17orf58	rs5821444	67991393	T	TTAA	0.3241570	-0.0185717	0.0027378	5.3E-12
17	C17orf58	rs9891146	67991933	C	T	0.2858400	-0.0174786	0.0028308	1.8E-10
17	C17orf58 *	rs7502307	67993845	C	G	0.3434390	-0.0181688	0.0027193	7.3E-12
17	C17orf58 *	rs113985803	67993855	A	G	0.3272560	-0.0186342	0.0027454	3.9E-12
17	C17orf58 *	rs56305452	67994384	A	C	0.3256390	-0.0185536	0.0027456	5.4E-12
17	C17orf58 *	rs56315139	67994455	G	C	0.2844090	-0.0169849	0.0028503	7.0E-10
17	C17orf58 *	rs62086884	67998284	G	C	0.3463190	-0.0168246	0.0026966	1.8E-10
17	C17orf58 *	rs4791295	68001201	G	A	0.3378730	-0.0178371	0.0026898	2.1E-11
17	C17orf58 *	rs28855509	68002051	T	C	0.3381520	-0.0175784	0.0026876	4.7E-11
17	C17orf58 *	rs74564337	68003451	C	T	0.3378020	-0.0178417	0.0026956	2.5E-11
17	C17orf58 *	rs6504568	68003532	T	C	0.3374540	-0.0179113	0.0026915	1.9E-11
17	C17orf58 *	rs75756093	68004462	TAGTC	T	0.3402600	-0.0174692	0.0026964	6.7E-11
17	C17orf58 *	rs62086889	68004487	C	T	0.3392570	-0.0176606	0.0026945	4.3E-11
17	C17orf58 *	rs8081714	68005014	G	A	0.3381890	-0.0176658	0.0026904	4.2E-11
17	C17orf58 *	chr17:68007425_G_GT	68007425	G	GT	0.3095790	-0.0157601	0.0028004	2.7E-08
17	C17orf58 *	rs28437386	68008555	T	A	0.3501600	-0.0171440	0.0027097	1.6E-10
17	C17orf58 *	rs78186330	68008599	G	A	0.3433350	-0.0167548	0.0027031	4.7E-10
17	C17orf58 *	chr17:68011432_TTTTG_T	68011432	TTTTG	T	0.3398580	-0.0173257	0.0026956	8.2E-11
17	C17orf58 *	rs62086897	68011928	A	C	0.3351260	-0.0162877	0.0026915	1.1E-09
17	C17orf58 *	rs62086898	68013004	A	G	0.3351260	-0.0162877	0.0026915	1.1E-09
17	C17orf58 *	rs62086899	68013018	C	T	0.3351260	-0.0162877	0.0026915	1.1E-09
17	KPNA2 *	rs7225959	68018993	T	A	0.3395500	-0.0163766	0.0026862	7.4E-10
17	KPNA2 *	rs62086903	68019890	T	C	0.3234040	-0.0158509	0.0027112	4.1E-09
17	KPNA2 *	rs62086904	68019980	C	T	0.3376040	-0.0159026	0.0026819	1.9E-09
17	KPNA2 *	rs8182243	68022389	C	T	0.2989380	-0.0157521	0.0027571	7.0E-09
17	KPNA2 *	rs8065296	68022446	A	T	0.2989910	-0.0156861	0.0027571	8.0E-09
17	KPNA2 *	rs62086906	68023810	T	C	0.3365850	-0.0162141	0.0026827	9.9E-10
17	KPNA2 *	rs145520076	68024495	G	A	0.3433160	-0.0159215	0.0027012	2.7E-09
17	KPNA2 *	rs189628481	68024502	C	T	0.3444720	-0.0157711	0.0027031	3.4E-09
17	KPNA2 *	rs192988621	68024504	C	T	0.3425550	-0.0157925	0.0026948	3.5E-09
17	KPNA2 *	rs183763906	68024506	C	T	0.3425550	-0.0157925	0.0026948	3.5E-09
17	KPNA2 *	rs200026262	68024507	A	G	0.3444720	-0.0157711	0.0027031	3.4E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	KPNA2 *	rs62086907	68025051	A	G	0.3349470	-0.0155014	0.0027193	4.7E-09
17	KPNA2 *	rs62086908	68025098	G	C	0.3365180	-0.0155904	0.0026919	5.2E-09
17	KPNA2 *	rs7405987	68025278	A	G	0.3370840	-0.0162694	0.0026827	8.4E-10
17	KPNA2 *	rs7406031	68025637	T	C	0.2988570	-0.0157051	0.0027570	7.6E-09
17	KPNA2 *	rs7406141	68025870	C	T	0.2988570	-0.0157051	0.0027570	7.6E-09
17	KPNA2 *	rs8076753	68026725	G	A	0.3368740	-0.0161989	0.0026821	1.1E-09
17	KPNA2 *	rs6504574	68026895	A	G	0.2988570	-0.0157051	0.0027570	7.6E-09
17	KPNA2 *	rs79778350	68027670	C	T	0.3248080	-0.0164298	0.0027618	2.7E-09
17	KPNA2 *	rs62084669	68028054	A	G	0.3367400	-0.0161941	0.0026823	1.1E-09
17	KPNA2 *	rs7211282	68028479	A	G	0.2985260	-0.0156003	0.0027574	1.0E-08
17	KPNA2 *	rs62084675	68030909	G	A	0.2960810	-0.0155771	0.0027648	1.1E-08
17	KPNA2 *	rs77536355	68032115	T	A	0.3450870	-0.0145164	0.0026703	3.0E-08
17	KPNA2 *	chr17:68032921_CT_C	68032921	CT	C	0.3532240	-0.0156388	0.0026833	3.2E-09
17	KPNA2 *	rs35229997	68033474	T	G	0.3388120	-0.0150396	0.0026777	1.3E-08
17	KPNA2 *	rs62084679	68033977	A	G	0.2959070	-0.0155538	0.0027658	1.1E-08
17	KPNA2 *	rs202202345	68034430	G	GGCT	0.2992960	-0.0157953	0.0027609	7.5E-09
17	KPNA2 *	rs10636181	68034433	T	TGC	0.2955740	-0.0154788	0.0027667	1.4E-08
17	KPNA2 *	rs7226002	68034719	T	C	0.3384950	-0.0150195	0.0026784	1.3E-08
17	KPNA2 *	rs62084681	68034876	G	A	0.3384950	-0.0150195	0.0026784	1.3E-08
17	KPNA2 *	rs75236169	68035083	T	C	0.2961440	-0.0154821	0.0027651	1.3E-08
17	KPNA2 *	rs62084682	68035405	G	C	0.3405500	-0.0149835	0.0026737	1.4E-08
17	KPNA2 *	rs62084683	68035609	G	A	0.2981360	-0.0155210	0.0027584	1.2E-08
17	KPNA2	rs12752	68035784	T	C	0.2955590	-0.0155809	0.0027677	9.9E-09
17	KPNA2	rs7214869	68036141	T	G	0.2961340	-0.0155106	0.0027648	1.3E-08
17	KPNA2	rs7214119	68036182	G	A	0.3385480	-0.0150545	0.0026787	1.2E-08
17	KPNA2	rs8075764	68036993	C	A	0.3384950	-0.0150195	0.0026784	1.3E-08
17	KPNA2	rs7503834	68037868	A	G	0.2946950	-0.0153748	0.0027704	2.0E-08
17	KPNA2	rs6504576	68038360	T	C	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2	rs146286181	68039012	CTA	C	0.3381800	-0.0148200	0.0026813	2.0E-08
17	KPNA2	rs62084689	68039173	T	C	0.3383350	-0.0149065	0.0026831	1.6E-08
17	KPNA2	rs62084691	68039402	C	T	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2	rs62084692	68039728	C	T	0.3392090	-0.0148399	0.0026833	2.1E-08
17	KPNA2	rs62084693	68039994	T	C	0.2937880	-0.0152169	0.0027767	2.6E-08
17	KPNA2	chr17:68040078_C_CA	68040078	C	CA	0.3474640	-0.0152415	0.0026930	1.2E-08
17	KPNA2	chr17:68040818_A_AT	68040818	A	AT	0.2966700	-0.0154309	0.0027683	1.5E-08
17	KPNA2	rs8078543	68041135	T	G	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2	rs62084694	68041478	G	T	0.3378700	-0.0149447	0.0026795	1.5E-08
17	KPNA2	rs62084696	68042065	G	C	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2	rs62084697	68042440	G	A	0.3378700	-0.0149447	0.0026795	1.5E-08
17	KPNA2	rs4638	68043234	G	A	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2	rs35594666	68043502	A	G	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2	rs35453056	68043552	G	A	0.2949350	-0.0153090	0.0027686	2.0E-08
17	KPNA2	rs62084701	68046122	T	C	0.2952440	-0.0155999	0.0027669	1.1E-08
17	KPNA2 *	rs62084702	68047041	T	C	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2 *	rs62084703	68047268	C	T	0.3379470	-0.0149286	0.0026791	1.6E-08
17	KPNA2 *	rs7405743	68047422	T	C	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2 *	rs62084704	68048913	A	G	0.2954450	-0.0154882	0.0027663	1.3E-08
17	KPNA2 *	rs78496681	68049047	C	CA	0.3368700	-0.0149576	0.0026851	1.6E-08
17	KPNA2 *	rs74354868	68049715	G	A	0.3379010	-0.0149759	0.0026794	1.4E-08
17	KPNA2 *	rs75885145	68050690	G	C	0.2954930	-0.0155120	0.0027664	1.3E-08
17	KPNA2 *	rs7214557	68051614	T	C	0.2955010	-0.0154435	0.0027678	1.5E-08
17	KPNA2 *	rs145024643	68052216	G	GC	0.2952140	-0.0156368	0.0027681	1.1E-08
17	KPNA2 *	rs7503050	68052346	G	T	0.3377680	-0.0150284	0.0026798	1.3E-08
17	KPNA2 *	rs7503056	68052533	C	G	0.2952860	-0.0155868	0.0027670	1.1E-08
17	KPNA2 *	rs34503060	68052563	G	A	0.2952860	-0.0155868	0.0027670	1.1E-08
17	KPNA2 *	rs7503096	68052679	C	T	0.2953170	-0.0155664	0.0027669	1.2E-08
17	KPNA2 *	rs35670842	68052729	ACT	A	0.2943840	-0.0153954	0.0027697	1.7E-08
17	KPNA2 *	rs7503206	68053058	G	A	0.2953420	-0.0155730	0.0027669	1.1E-08
17	KPNA2 *	rs7503810	68053415	G	A	0.3333690	-0.0153498	0.0026873	7.9E-09
17	KPNA2 *	rs62084708	68053591	G	A	0.3332370	-0.0154838	0.0026883	5.5E-09
17	KPNA2 *	rs7209959	68054289	T	C	0.2953420	-0.0155730	0.0027669	1.1E-08
17	KPNA2 *	rs62084711	68054795	T	C	0.2953420	-0.0155730	0.0027669	1.1E-08
17	KPNA2 *	rs28592929	68056618	C	T	0.2953460	-0.0155673	0.0027669	1.1E-08
17	KPNA2 *	rs3890640	68056912	T	C	0.2953460	-0.0155673	0.0027669	1.1E-08
17	KPNA2 *	rs34843489	68057215	T	C	0.2946820	-0.0156060	0.0027695	1.1E-08
17	KPNA2 *	rs139345647	68057409	CA	C	0.2953150	-0.0155877	0.0027670	1.1E-08
17	KPNA2 *	rs72318931	68058249	CTCTT	C	0.3367920	-0.0150126	0.0027356	3.3E-08
17	KPNA2 *	rs78429175	68058655	G	A	0.2950680	-0.0156086	0.0027681	1.0E-08
17	KPNA2 *	rs76542911	68059778	G	A	0.2955670	-0.0155316	0.0027669	1.1E-08
17	KPNA2 *	rs62084734	68060081	C	T	0.2955440	-0.0157621	0.0027682	7.7E-09
17	KPNA2 *	rs35040337	68060566	A	G	0.3332050	-0.0155490	0.0026885	4.7E-09
17	KPNA2 *	rs8072723	68060854	A	T	0.2953150	-0.0155877	0.0027670	1.1E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
17	KPNA2 *	rs6504578	68061850	A	G	0.2953150	-0.0155877	0.0027670	1.1E-08
17	KPNA2 *	rs200647245	68062663	A	AT	0.3406290	-0.0148656	0.0026980	2.2E-08
17	KPNA2 *	rs62084738	68063664	T	C	0.2953150	-0.0155877	0.0027670	1.1E-08
17	KPNA2 *	rs74976757	68064790	G	T	0.3378170	-0.0150941	0.0026804	1.1E-08
17	KPNA2 *	rs62084740	68065068	C	T	0.3378170	-0.0150941	0.0026804	1.1E-08
17	KPNA2 *	rs77194282	68065510	C	T	0.2953150	-0.0155877	0.0027670	1.1E-08
17	KPNA2 *	rs7213585	68066200	T	A	0.2952400	-0.0155956	0.0027673	1.1E-08
17	KPNA2 *	rs62084741	68066544	T	C	0.2953150	-0.0155877	0.0027670	1.1E-08
17	KPNA2 *	rs74900486	68066757	C	T	0.3378170	-0.0150941	0.0026804	1.1E-08
17	KPNA2 *	rs8075604	68066985	C	T	0.2909160	-0.0150089	0.0027828	4.3E-08
17	KPNA2 *	rs28850355	68068281	T	C	0.2916690	-0.0155367	0.0027897	1.7E-08
17	KPNA2 *	chr17:68069522_AT_A	68069522	AT	A	0.2952630	-0.0153153	0.0027727	1.7E-08
17	KPNA2 *	rs75544834	68070322	T	C	0.3338480	-0.0154274	0.0026941	9.0E-09
17	KPNA2 *	rs79415988	68070853	C	T	0.2947270	-0.0154970	0.0027720	1.7E-08
17	KPNA2 *	rs9674669	68071338	G	A	0.2950710	-0.0153321	0.0027743	2.5E-08
17	KPNA2 *	rs184478609	68071576	T	C	0.3353640	-0.0152721	0.0026937	7.4E-09
17	KPNA2 *	rs190151381	68071898	G	A	0.2999540	-0.0155954	0.0027789	1.2E-08
17	KPNA2 *	rs9747971	68073082	C	G	0.2945570	-0.0154724	0.0027730	1.8E-08
17	KPNA2 *	rs9330556	68073785	T	G	0.2954960	-0.0155119	0.0027723	1.5E-08
17	KPNA2 *	rs62084742	68079426	A	G	0.2946530	-0.0155161	0.0027735	1.6E-08
17	KPNA2 *	rs34937122	68079772	A	G	0.2942050	-0.0153616	0.0027753	2.3E-08
17	KPNA2 *	rs147170518	68079918	T	AAATCCT	0.3396920	-0.0147104	0.0026824	2.3E-08
17	KPNA2 *	rs78352159	68082103	C	G	0.3395660	-0.0145693	0.0026816	4.0E-08
17	KPNA2 *	rs75428197	68082271	A	G	0.2967010	-0.0154875	0.0027651	1.6E-08
17	KPNA2 *	rs62084744	68082412	T	C	0.3406460	-0.0146282	0.0026866	4.1E-08
17	KPNA2 *	rs111730207	68087657	G	C	0.2962990	-0.0153843	0.0027677	2.2E-08
19	ANGPTL4 *	rs111500536	8360674	A	G	0.0317929	-0.0426563	0.0072403	3.0E-08
19	HAPLN4	rs150641967	19259531	T	TGACA	0.0612752	-0.0397278	0.0052769	2.8E-14
19	TM6SF2	rs58542926	19268740	T	C	0.0670901	-0.0426248	0.0050396	9.3E-18
19	SUGP1	rs8107974	19277691	T	A	0.0967751	-0.0272001	0.0042625	5.6E-11
19	SUGP1	rs200210321	19283081	AG	A	0.1032220	-0.0259990	0.0041624	1.3E-10
19	SUGP1	rs10401969	19296909	C	T	0.0971610	-0.0253966	0.0042587	7.6E-10
19	SUGP1	rs739846	19308262	A	G	0.0966807	-0.0260311	0.0042649	3.3E-10
19	MAU2	rs2285626	19356736	T	C	0.1740490	-0.0179780	0.0033334	3.7E-08
19	MAU2	rs117970794	19357846	T	C	0.0912633	-0.0239878	0.0043777	1.6E-08
19	MAU2 *	rs56255430	19367068	C	A	0.0669343	-0.0356318	0.0050517	4.4E-13
19	GATAD2A	rs188552254	19406360	G	A	0.1343940	-0.0199032	0.0037044	4.9E-08
19	GATAD2A	rs2965185	19414983	C	T	0.1605300	-0.0206834	0.0034355	8.8E-10
19	GATAD2A	rs8182472	19429082	C	T	0.1370190	-0.0198448	0.0036663	4.5E-08
19	GATAD2A	rs79954596	19437834	G	T	0.1369030	-0.0197519	0.0036672	4.8E-08
19	GATAD2A	rs28720066	19461411	T	G	0.1360820	-0.0200061	0.0036795	3.7E-08
19	GATAD2A	rs73002956	19467934	G	A	0.0707496	-0.0333312	0.0049223	6.3E-12
19	GATAD2A	rs145702982	19468917	T	A	0.0667723	-0.0330032	0.0050595	2.4E-11
19	GATAD2A	rs73002960	19472183	T	C	0.1401980	-0.0202714	0.0036346	1.9E-08
19	GATAD2A	rs3794991	19499787	T	C	0.0739107	-0.0346370	0.0048180	3.5E-13
19	GATAD2A	rs57009615	19502813	G	A	0.1480060	-0.0215682	0.0035504	8.4E-10
19	CILP2 *	rs16996148	19547663	T	G	0.0698451	-0.0363409	0.0049480	7.2E-14
19	CILP2 *	rs17216525	19551411	T	C	0.0760565	-0.0328975	0.0047578	2.2E-12
19	CILP2 *	rs17216588	19553268	T	C	0.0744751	-0.0283325	0.0048350	1.6E-09
19	PBX4 *	rs143988316	19556445	T	C	0.0770041	-0.0280396	0.0047563	8.6E-10
19	PBX4 *	rs78916915	19558399	A	G	0.0763997	-0.0252507	0.0047609	3.5E-08
19	PBX4 *	rs150824230	19559801	A	G	0.0755871	-0.0267164	0.0047893	5.6E-09
19	PBX4 *	rs73004926	19560457	T	C	0.0755871	-0.0267164	0.0047893	5.6E-09
19	PBX4	rs73004933	19564887	T	C	0.0751405	-0.0275875	0.0047993	2.5E-09
19	PBX4	rs141756246	19574661	GT	G	0.0716387	-0.0267403	0.0049380	4.4E-08
19	PBX4	rs73004951	19584419	T	C	0.0957166	-0.0231126	0.0043083	2.6E-08
19	PBX4	rs73004966	19605749	T	C	0.0815147	-0.0252328	0.0046142	1.8E-08
19	PBX4	rs57504626	19609590	T	C	0.0851029	-0.0241899	0.0045240	3.3E-08
19	PBX4	rs58847337	19615213	A	G	0.0795512	-0.0249193	0.0046655	3.9E-08
19	CEBPA *	rs10402014	33322870	A	G	0.1696770	0.0195418	0.0033895	3.8E-08
19	CEBPA *	rs10411163	33323488	G	A	0.1653240	0.0194942	0.0034217	4.0E-08
19	CEBPA *	rs28885440	33323563	A	G	0.1651980	0.0195811	0.0034218	3.6E-08
19	CEBPA *	rs113811498	33323649	A	ATAT	0.1588710	0.0194891	0.0034726	4.6E-08
19	CEBPA *	rs7254869	33323787	C	T	0.1589790	0.0195973	0.0034704	3.4E-08
19	CEBPA *	rs7253713	33324221	A	G	0.1656120	0.0194306	0.0034127	3.6E-08
19	CEBPA *	rs10415737	33324300	C	G	0.1656200	0.0194240	0.0034127	3.6E-08
19	CEBPA *	rs10415770	33324336	A	G	0.1656290	0.0194443	0.0034126	3.4E-08
19	CEBPA *	rs60656848	33325591	C	T	0.1593650	0.0198032	0.0034644	2.5E-08
19	CEBPA *	rs12608723	33326227	G	A	0.1709350	0.0201328	0.0033626	9.3E-09
19	CEBPA *	rs112167957	33326622	GA	G	0.1709400	0.0201216	0.0033625	9.4E-09
19	CEBPA *	rs7251395	33327226	C	G	0.1643410	0.0201642	0.0034161	1.2E-08
19	CEBPA *	rs7256107	33327250	C	T	0.1707600	0.0201926	0.0033648	9.0E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	CEBPA *	rs10413354	33327308	G	C	0.1709530	0.0200770	0.0033623	1.0E-08
19	CEBPA *	rs10414141	33327311	T	A	0.1643430	0.0201654	0.0034161	1.2E-08
19	CEBPA *	rs7251758	33327479	A	G	0.1710880	0.0201421	0.0033616	9.6E-09
19	CEBPA *	rs112432604	33328149	G	A	0.1689260	0.0201291	0.0033987	1.5E-08
19	CEBPA *	rs10421445	33328331	G	A	0.1710870	0.0199649	0.0033617	1.2E-08
19	CEBPA *	rs10426997	33328338	C	T	0.1638630	0.0201561	0.0034203	1.2E-08
19	CEBPA *	rs7253865	33330342	G	T	0.1664160	0.0196237	0.0034056	2.6E-08
19	CEBPA *	rs149222436	33336002	T	C	0.1581240	0.0203271	0.0034774	1.5E-08
19	CEBPA *	rs141706710	33336121	T	C	0.1581810	0.0203391	0.0034768	1.5E-08
19	CEBPG *	rs16967971	33339692	T	G	0.1588120	0.0204863	0.0034717	9.6E-09
19	CEBPG *	rs12610763	33350705	A	G	0.1586630	0.0198617	0.0034761	2.8E-08
19	CEBPG *	rs10417389	33350819	T	C	0.1586580	0.0198483	0.0034763	2.8E-08
19	CEBPG *	rs10409981	33358189	T	C	0.1586540	0.0198141	0.0034772	3.2E-08
19	CEBPG *	rs10416682	33358955	T	C	0.1799880	0.0200514	0.0033195	5.9E-09
19	CEBPG *	rs4805872	33358978	C	T	0.1807870	0.0198287	0.0033109	9.2E-09
19	CEBPG *	rs1423065	33359589	T	C	0.1717510	0.0210855	0.0033581	1.2E-09
19	CEBPG *	chr19:33360112_C_CT	33360112	CT	C	0.1624930	0.0225058	0.0034683	3.1E-10
19	CEBPG *	rs10425856	33361416	C	T	0.1745520	0.0211339	0.0033347	9.7E-10
19	CEBPG *	rs11878996	33366074	C	T	0.1716430	0.0218198	0.0033577	2.7E-10
19	CEBPG *	rs2112820	33371182	C	T	0.1716140	0.0217364	0.0033574	3.1E-10
19	CEBPG *	rs77592544	33372029	G	T	0.1710120	0.0218036	0.0033680	2.4E-10
19	CEBPG *	rs78230685	33372898	C	A	0.1708350	0.0213745	0.0033676	5.5E-10
19	CEBPG	rs116494882	33374217	T	C	0.1714490	0.0214460	0.0033659	4.3E-10
19	CEBPG	rs151086462	33376066	TG	T	0.1713550	0.0209827	0.0033701	1.0E-09
19	CEBPG	rs77152611	33378116	T	C	0.1710950	0.0211132	0.0033675	8.0E-10
19	HPN	rs12461158	35049978	A	G	0.1378000	-0.0254649	0.0037438	4.8E-12
19	HPN	rs10406943	35050344	T	G	0.1296450	-0.0276641	0.0038212	1.2E-13
19	HPN	rs57035236	35050426	TA	T	0.1278970	-0.0263741	0.0038405	1.9E-12
19	HPN	rs1688025	35054215	T	C	0.1481640	-0.0236914	0.0035653	1.7E-11
19	HPN	rs73597479	35054481	T	C	0.1079860	-0.0222695	0.0041222	1.6E-08
19	HPN	rs1672981	35056147	T	C	0.1375840	-0.0237809	0.0036741	4.5E-11
19	HPN	rs1672980	35056214	T	C	0.1433470	-0.0234243	0.0036160	5.7E-11
19	HPN, HPN-AS1	rs8103570	35059337	T	C	0.1496100	-0.0235780	0.0035517	1.9E-11
19	HPN, HPN-AS1	rs1688044	35061175	C	G	0.1712950	-0.0216409	0.0033665	8.7E-11
19	HPN, HPN-AS1	rs60291566	35062059	TA	T	0.1634570	-0.0222909	0.0034214	4.0E-11
19	HPN, HPN-AS1	rs55726903	35062418	T	TA	0.1627450	-0.0223115	0.0034261	4.1E-11
19	HPN, HPN-AS1	rs1688043	35062437	C	T	0.1390320	-0.0234199	0.0036561	5.8E-11
19	HPN, HPN-AS1	rs2445818	35062545	A	G	0.1629380	-0.0224811	0.0034292	3.0E-11
19	HPN, HPN-AS1	rs1688042	35062684	A	T	0.1629000	-0.0222038	0.0034272	5.1E-11
19	HPN, HPN-AS1	rs1672979	35062693	G	A	0.1629000	-0.0222038	0.0034272	5.1E-11
19	HPN, HPN-AS1	rs1350292	35062852	C	T	0.1627680	-0.0223019	0.0034259	4.1E-11
19	HPN, HPN-AS1	rs1350291	35062860	T	G	0.1627680	-0.0223019	0.0034259	4.1E-11
19	HPN, HPN-AS1	rs3074472	35062896	TAACGG	A	0.1629380	-0.0219583	0.0034308	8.5E-11
19	HPN, HPN-AS1	rs1688040	35062926	G	C	0.1626820	-0.0221982	0.0034292	5.4E-11
19	HPN, HPN-AS1	rs1350290	35063068	C	T	0.1625980	-0.0222491	0.0034276	4.7E-11
19	HPN, HPN-AS1	rs2452000	35063480	G	A	0.1626100	-0.0223395	0.0034270	3.8E-11
19	HPN, HPN-AS1	rs2445819	35063499	G	A	0.1625900	-0.0223481	0.0034270	3.8E-11
19	HPN, HPN-AS1	rs1615767	35063863	C	T	0.1626530	-0.0221867	0.0034261	5.1E-11
19	HPN, HPN-AS1	rs10567974	35064149	CAGCAG	T	0.1641160	-0.0226029	0.0034323	2.6E-11
19	HPN, HPN-AS1	rs4806073	35064286	T	C	0.1628310	-0.0224339	0.0034236	3.3E-11
19	HPN, HPN-AS1	rs2305746	35065396	A	G	0.1599910	-0.0229867	0.0034531	1.4E-11
19	HPN, HPN-AS1	rs1688031	35065736	T	C	0.1601130	-0.0231253	0.0034544	1.3E-11
19	HPN, HPN-AS1	rs1672991	35065755	A	G	0.1592440	-0.0232122	0.0034617	1.1E-11
19	HPN, HPN-AS1	rs3835126	35065811	GT	G	0.1601180	-0.0231460	0.0034546	1.2E-11
19	HPN, HPN-AS1	rs1672992	35065825	C	T	0.1601220	-0.0231614	0.0034546	1.2E-11
19	HPN, HPN-AS1	rs1688030	35065840	T	C	0.1599890	-0.0230724	0.0034557	1.4E-11
19	PVRL2	rs12610605	44867581	G	A	0.4855390	0.0225561	0.0025341	1.4E-19
19	PVRL2	rs4803766	44867911	A	G	0.3719310	0.0178055	0.0026134	3.4E-12
19	PVRL2	rs34165484	44868428	A	AT	0.4859000	0.0222637	0.0025627	8.5E-19
19	PVRL2	rs200149544	44868448	T	TTTTTC	0.4871270	0.0221548	0.0025636	1.2E-18
19	PVRL2	rs404935	44869537	A	G	0.1387930	0.0228541	0.0036602	3.3E-10
19	PVRL2	rs395908	44870308	A	G	0.1319620	0.0226300	0.0037511	1.4E-09
19	PVRL2	rs148251724	44872787	TATTTA	G	0.4683110	0.0232010	0.0025524	1.1E-20
19	PVRL2	rs519113	44873027	G	C	0.1578670	0.0241145	0.0034559	4.2E-12
19	PVRL2	rs393584	44874077	G	A	0.3166840	0.0163430	0.0027266	2.3E-10
19	PVRL2	rs34278513	44874887	T	C	0.1342780	0.0241319	0.0037008	3.6E-11
19	PVRL2	rs387976	44875803	A	C	0.3153740	0.0160594	0.0027234	5.4E-10
19	PVRL2	rs369599	44876079	C	T	0.3153540	0.0159692	0.0027238	6.5E-10
19	PVRL2	rs412776	44876259	A	G	0.1312540	0.0314938	0.0037416	2.1E-17
19	PVRL2	rs3837923	44876309	AC	A	0.3160340	0.0158963	0.0027235	7.2E-10
19	PVRL2	rs370705	44876381	C	T	0.3159270	0.0162372	0.0027235	3.5E-10
19	PVRL2	rs385982	44876425	A	C	0.3153000	0.0159594	0.0027243	6.2E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	PVRL2	rs419925	44876869	G	C	0.3162180	0.0160099	0.0027235	5.7E-10
19	PVRL2	rs421812	44877288	G	T	0.3163520	0.0159500	0.0027277	7.2E-10
19	PVRL2	rs3865427	44877704	A	C	0.1263430	0.0302148	0.0038072	8.8E-16
19	PVRL2	rs11668861	44877713	G	T	0.2099950	0.0328196	0.0031165	7.3E-27
19	PVRL2	rs6859	44878777	A	G	0.2970490	0.0252767	0.0027720	1.6E-20
19	PVRL2	rs406456	44879460	G	A	0.1045920	0.0275770	0.0041625	6.1E-12
19	PVRL2	rs3852860	44879709	C	T	0.2148330	0.0363000	0.0030888	3.4E-33
19	PVRL2	rs71352237	44879822	C	T	0.1192590	0.0320573	0.0039112	6.1E-17
19	PVRL2	rs71171301	44879834	AC	A	0.1192350	0.0320637	0.0039120	6.2E-17
19	PVRL2	rs34224078	44879858	G	A	0.1192090	0.0321557	0.0039125	5.6E-17
19	PVRL2	rs35879138	44879882	A	T	0.1191820	0.0322156	0.0039127	4.9E-17
19	PVRL2	rs11083749	44880848	C	T	0.0922227	0.0343166	0.0044261	1.6E-15
19	PVRL2	rs406315	44880859	G	A	0.0857311	0.0320544	0.0045760	2.6E-13
19	PVRL2	rs34994196	44881075	GC	G	0.0916846	0.0345000	0.0044351	1.2E-15
19	PVRL2	rs142042446	44883210	GTAA	G	0.0863527	0.0461574	0.0044852	2.4E-27
19	PVRL2	rs283808	44883777	C	A	0.0853709	0.0393458	0.0045564	6.4E-19
19	PVRL2	rs283809	44883800	G	A	0.0859420	0.0394256	0.0045383	3.0E-19
19	PVRL2	rs12972156	44884202	G	C	0.0813662	0.0487236	0.0046245	8.0E-29
19	PVRL2	rs12972970	44884339	A	G	0.0813778	0.0487632	0.0046240	7.2E-29
19	PVRL2	rs34342646	44884873	A	G	0.0814682	0.0486943	0.0046206	8.7E-29
19	PVRL2	rs283810	44884984	G	T	0.0873330	0.0392302	0.0045020	1.6E-19
19	PVRL2	rs283811	44885243	G	A	0.1690520	0.0483886	0.0033808	1.1E-50
19	PVRL2	rs283813	44885917	A	T	0.0878200	0.0392646	0.0044780	1.0E-19
19	PVRL2	rs7254892	44886339	A	G	0.0620938	0.0466832	0.0052543	4.9E-21
19	PVRL2	rs283815	44887076	G	A	0.1733840	0.0466400	0.0033402	3.7E-48
19	PVRL2	rs148665049	44887875	T	C	0.0228929	0.0448806	0.0084650	2.7E-08
19	PVRL2	rs6857	44888997	T	C	0.0828653	0.0475008	0.0045841	4.9E-28
19	TOMM40 *	rs71352238	44891079	C	T	0.0828005	0.0486620	0.0045858	4.5E-29
19	TOMM40	rs184017	44891712	G	T	0.1753230	0.0455862	0.0033282	6.8E-47
19	TOMM40	rs157580	44892009	A	G	0.4335490	0.0308102	0.0025411	1.0E-36
19	TOMM40	rs2075650	44892362	G	A	0.0830303	0.0483206	0.0045815	9.5E-29
19	TOMM40	rs34404554	44892652	G	C	0.0824571	0.0489084	0.0045936	3.2E-29
19	TOMM40	rs11556505	44892887	T	C	0.0825692	0.0487655	0.0045925	5.1E-29
19	TOMM40	rs157582	44892962	T	C	0.1735270	0.0474819	0.0033405	7.6E-50
19	TOMM40	rs157584	44893642	C	T	0.3155420	0.0226941	0.0027236	6.2E-18
19	TOMM40	rs1160983	44893972	A	G	0.0668708	0.0411691	0.0050950	6.4E-18
19	TOMM40	rs157585	44894255	C	A	0.3209720	0.0235724	0.0027157	2.2E-19
19	TOMM40	rs157588	44895007	T	C	0.3158040	0.0241397	0.0027214	5.3E-20
19	TOMM40	rs157590	44895459	C	A	0.3228660	0.0231869	0.0027034	3.7E-19
19	TOMM40	rs61679753	44897490	A	T	0.0742889	0.0486810	0.0048349	4.0E-26
19	TOMM40	rs111784051	44899005	G	T	0.0730979	0.0479908	0.0048714	3.8E-25
19	TOMM40	chr19:44899618_ATT_A	44899618	A	ATT	0.3141670	0.0220809	0.0027331	2.5E-17
19	TOMM40	rs1160985	44900155	T	C	0.3131210	0.0221995	0.0027311	2.0E-17
19	TOMM40	rs760136	44900601	G	A	0.3131340	0.0222435	0.0027312	1.7E-17
19	TOMM40	rs741780	44901174	C	T	0.3133950	0.0222897	0.0027305	1.4E-17
19	TOMM40	rs405697	44901434	G	A	0.4015710	0.0384827	0.0025794	1.9E-54
19	TOMM40	rs1038025	44901715	C	T	0.3126950	0.0224382	0.0027342	9.1E-18
19	TOMM40	rs1038026	44901805	G	A	0.3133420	0.0223713	0.0027308	1.1E-17
19	TOMM40	rs34215622	44903281	CG	C	0.2928660	0.0222813	0.0027845	5.8E-17
19	TOMM40	rs10119	44903416	A	G	0.0875785	0.0558328	0.0044801	5.3E-38
19	TOMM40 *	rs7259620	44904531	A	G	0.3118630	0.0219849	0.0027346	4.5E-17
19	APOE *	rs769446	44905371	C	T	0.0705372	0.0477213	0.0049909	8.2E-24
19	APOE *	rs405509	44905579	G	T	0.2950110	0.0252974	0.0027748	3.7E-21
19	APOE	rs440446	44905910	G	C	0.3889030	0.0411709	0.0025930	1.8E-60
19	APOE	rs769449	44906745	A	G	0.0769100	0.0572386	0.0047438	3.6E-36
19	APOE	rs429358	44908684	C	T	0.0871414	0.0567085	0.0044852	3.2E-39
19	APOE	rs7412	44908822	T	C	0.0726931	0.0494074	0.0048782	2.9E-26
19	APOE *	rs1065853	44909976	T	G	0.0726557	0.0499036	0.0048782	8.5E-27
19	APOE *	rs376097536	44909977	G	GGT	0.0875880	0.0538986	0.0045171	2.1E-35
19	APOE *	rs75627662	44910319	T	C	0.1688320	0.0507211	0.0033796	3.5E-54
19	APOE *	rs72654473	44911142	A	C	0.0759549	0.0482298	0.0047781	1.9E-26
19	APOE *	rs439401	44911194	C	T	0.4067830	0.0402541	0.0025726	5.1E-58
19	APOC1 *	rs445925	44912383	A	G	0.0832505	0.0496211	0.0045780	1.1E-29
19	APOC1 *	rs10414043	44912456	A	G	0.0911353	0.0478955	0.0043946	5.0E-29
19	APOC1 *	rs7256200	44912678	T	G	0.0912871	0.0477362	0.0043951	7.8E-29
19	APOC1 *	rs483082	44912921	T	G	0.1746340	0.0538541	0.0033325	1.1E-62
19	APOC1 *	rs584007	44913221	G	A	0.4060260	0.0405459	0.0025754	6.1E-59
19	APOC1 *	rs438811	44913484	T	C	0.1746730	0.0538506	0.0033329	1.1E-62
19	APOC1 *	rs390082	44913574	G	T	0.0830807	0.0495191	0.0045858	1.3E-29
19	APOC1 *	rs11568822	44914381	CTTCG	C	0.1689150	0.0525900	0.0033785	1.4E-58
19	APOC1	rs5117	44915533	C	T	0.1693710	0.0506237	0.0033872	9.2E-55
19	APOC1	rs3826688	44915704	C	T	0.4107640	0.0395825	0.0025831	4.7E-56

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	APOC1	rs73052335	44916825	C	A	0.0926231	0.0470462	0.0044049	2.0E-27
19	APOC1	rs12721046	44917997	A	G	0.1013130	0.0477790	0.0042029	5.5E-31
19	APOC1	rs484195	44918620	G	A	0.4061000	0.0393962	0.0025992	3.5E-55
19	APOC1	rs12721051	44918903	G	C	0.1018000	0.0468337	0.0041859	3.0E-30
19	APOC1 *	rs56131196	44919589	A	G	0.1021470	0.0466433	0.0041764	3.2E-30
19	APOC1 *	rs4420638	44919689	G	A	0.1021790	0.0465112	0.0041757	4.8E-30
19	APOC1 *	rs117569256	44920073	G	A	0.0355061	0.0512118	0.0068512	1.8E-14
19	APOC1 *	chr19:44920730_C_CA	44920730	CA	C	0.0885619	0.0475577	0.0045247	1.3E-26
19	APOC1 *	rs199769815	44921765	A	G	0.0234359	0.0507143	0.0084082	1.1E-09
19	APOC1 *	rs190712692	44921921	A	G	0.0734383	0.0452116	0.0048694	6.5E-23
19	APOC1 *	rs141622900	44923535	A	G	0.0738725	0.0448142	0.0048396	9.7E-23
19	APOC1P1	rs114448690	44928196	A	G	0.2199750	0.0326071	0.0031155	5.3E-27
19	APOC1P1	rs113345881	44928379	G	A	0.2301380	0.0321086	0.0030599	2.6E-27
19	APOC1P1	rs112871012	44928640	A	G	0.2282110	0.0317075	0.0030584	9.0E-27
19	APOC1P1	rs111271293	44928832	C	T	0.2315790	0.0316887	0.0030274	2.3E-27
19	APOC1P1	chr19:44928869_AAAAAC_	44928869	A	AAAAAC	0.2309040	0.0316095	0.0030321	2.8E-27
19	APOC1P1	rs7259350	44929021	C	T	0.2408950	0.0333071	0.0029596	2.9E-31
19	APOC1P1	rs7259004	44929300	C	G	0.2421680	0.0327752	0.0029485	8.7E-31
19	APOC1P1	chr19:44930070_T_TA	44930070	TA	T	0.2223040	0.0326182	0.0030893	1.2E-27
20	LINC00261	rs1203896	22570456	G	A	0.1684230	-0.0182268	0.0034031	3.7E-08
20	LINC00261	rs73300991	22570688	T	C	0.1307750	-0.0214285	0.0037636	1.0E-08
20	LINC00261	rs73300993	22570865	A	G	0.1307750	-0.0214261	0.0037636	1.0E-08
20	LINC00261	rs6048202	22571368	A	G	0.1308010	-0.0213356	0.0037638	1.2E-08
20	LINC00261	rs1203898	22572502	C	T	0.1693500	-0.0206164	0.0033970	5.5E-10
20	LINC00261	rs1203899	22572658	T	C	0.1691960	-0.0207048	0.0033964	4.5E-10
20	LINC00261	rs148030607	22572923	C	CTT	0.1330190	-0.0245328	0.0037349	3.3E-11
20	LINC00261	rs11477526	22574444	A	AT	0.1330730	-0.0246045	0.0037328	2.9E-11
20	LINC00261	rs6036152	22575955	C	A	0.1413380	-0.0241011	0.0036262	1.2E-11
20	LINC00261	rs6113722	22576461	A	G	0.1411320	-0.0240011	0.0036278	1.3E-11
20	LINC00261	rs1203902	22578486	C	T	0.1986810	-0.0183139	0.0032095	3.1E-09
20	FOXA2 *	chr20:22578744_C_CAAA	22578744	CAAA	C	0.1694420	-0.0207537	0.0033994	2.8E-10
20	FOXA2 *	rs6048205	22578963	G	A	0.1416160	-0.0237643	0.0036214	2.4E-11
20	FOXA2 *	rs1203905	22580051	G	A	0.1760890	-0.0207171	0.0033378	1.7E-10
20	FOXA2 *	rs72470563	22580294	A	T	0.1402570	-0.0238942	0.0036522	2.5E-11
20	FOXA2 *	rs1203907	22580333	C	T	0.1765300	-0.0205695	0.0033372	1.9E-10
20	FOXA2 *	rs6048206	22580744	C	T	0.1402140	-0.0239496	0.0036530	2.3E-11
20	FOXA2	rs112021763	22581333	CT	C	0.1762930	-0.0206789	0.0033451	1.1E-10
20	FOXA2	rs1974	22581673	A	G	0.1360850	-0.0245661	0.0037086	1.3E-11
20	FOXA2	rs3833331	22581688	AG	A	0.1360470	-0.0245597	0.0037092	1.3E-11
20	FOXA2	rs1055080	22581800	A	G	0.1766160	-0.0213763	0.0033422	3.7E-11
20	FOXA2	rs1203910	22582387	C	T	0.1805490	-0.0201372	0.0033131	7.1E-10
20	FOXA2	rs1800847	22582933	A	G	0.1350540	-0.0252806	0.0037229	5.4E-12
20	FOXA2 *	rs2277764	22585486	C	T	0.1354730	-0.0250377	0.0037159	9.1E-12
20	FOXA2 *	rs1337918	22586970	A	C	0.1377030	-0.0242707	0.0036753	2.7E-11
20	FOXA2 *	rs1209523	22587304	T	C	0.1806150	-0.0203418	0.0032875	2.3E-10
20	LOC101929685	rs1337919	22587957	T	G	0.1368790	-0.0241841	0.0036842	2.4E-11
20	LOC101929685	rs6048209	22590445	G	A	0.1383350	-0.0238354	0.0036688	3.9E-11
20	LOC101929685	rs1337920	22590566	T	A	0.1809660	-0.0198316	0.0032863	4.4E-10
20	LOC101929685	rs1337921	22590570	G	T	0.1809660	-0.0198316	0.0032863	4.4E-10
20	LOC101929685	rs1203915	22591866	C	T	0.1795950	-0.0202401	0.0032937	2.0E-10
20	LOC101929685	rs8123991	22592696	T	C	0.1369550	-0.0244016	0.0036816	1.6E-11
20	LOC101929685	rs6048211	22593298	A	C	0.1365270	-0.0244051	0.0036925	1.7E-11
20	LOC101929685	rs200638849	22595154	G	T	0.1335560	-0.0238689	0.0037415	6.8E-11
20	LOC101929685	rs1203916	22595643	C	G	0.1789080	-0.0201651	0.0033231	3.0E-10
20	LOC101929685	rs1203917	22595877	C	T	0.1768160	-0.0206406	0.0033346	2.0E-10
20	LOC101929685	rs7266093	22596998	G	A	0.1360620	-0.0246295	0.0036916	1.4E-11
20	LOC101929685	rs910958	22597366	A	G	0.1768350	-0.0208492	0.0033352	1.3E-10
20	LOC101929685	rs910959	22597373	C	T	0.1359860	-0.0246670	0.0036914	1.3E-11
20	LOC101929685	rs6036157	22597777	A	G	0.1359860	-0.0246670	0.0036914	1.3E-11
20	LOC101929685	rs1203918	22598869	G	A	0.1763800	-0.0207607	0.0033375	1.8E-10
20	LOC101929685	rs2003076	22598907	A	G	0.1355770	-0.0245936	0.0036953	1.7E-11
20	LOC101929685	rs16984154	22600263	A	G	0.1355210	-0.0246705	0.0036956	1.6E-11
20	LOC101929685	rs6036158	22600422	C	T	0.1356320	-0.0246737	0.0036946	1.5E-11
20	LOC101929685	rs6048216	22600630	C	T	0.1363050	-0.0242806	0.0036906	3.5E-11
20	LOC101929685	rs1203919	22602316	T	G	0.1733080	-0.0208584	0.0033723	1.6E-10
20	LOC101929685	rs1203920	22604789	G	A	0.1130880	-0.0236296	0.0039964	6.1E-09
20	LOC101929685	rs1203921	22604846	T	G	0.1536840	-0.0206719	0.0035083	2.1E-09
20	LOC101929685	rs1203922	22605062	G	T	0.1557820	-0.0208092	0.0034827	1.3E-09
20	LOC101929685	rs1203923	22605190	T	G	0.1557670	-0.0208132	0.0034829	1.3E-09
20	LOC101929685	rs11480708	22605448	C	CT	0.1557820	-0.0208092	0.0034827	1.3E-09
20	LOC101929685	rs1203924	22605670	G	A	0.1559920	-0.0210288	0.0034802	8.6E-10
20	LOC101929685	rs11474135	22605991	C	CAA	0.1559920	-0.0210288	0.0034802	8.6E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	LOC101929685	rs11087391	22606202	GC	G	0.1559920	-0.0210288	0.0034802	8.6E-10
20	LOC101929685	rs1007458	22607038	G	A	0.1565990	-0.0208438	0.0034730	1.1E-09
20	LOC101929685	rs995734	22607370	G	T	0.1560080	-0.0210195	0.0034803	8.8E-10
20	FOXA2 *	rs1203925	22608135	G	A	0.1560080	-0.0210195	0.0034803	8.8E-10
20	FOXA2 *	rs1203926	22608279	A	T	0.1573890	-0.0207700	0.0034768	1.1E-09
20	FOXA2 *	rs1007202	22608882	T	G	0.1557920	-0.0210571	0.0034831	8.5E-10
20	FOXA2 *	rs1203927	22608927	G	A	0.1133500	-0.0233995	0.0039954	9.0E-09
20	FOXA2 *	rs1203928	22609245	G	A	0.1559660	-0.0209887	0.0034810	9.4E-10
20	FOXA2 *	rs1203929	22609266	C	G	0.1559660	-0.0209887	0.0034810	9.4E-10
20	FOXA2 *	rs2424435	22609912	C	T	0.1560050	-0.0208530	0.0034816	1.2E-09
20	FOXA2 *	rs2424436	22609914	G	T	0.1560050	-0.0208530	0.0034816	1.2E-09
20	FOXA2 *	rs1203930	22610197	A	G	0.1576860	-0.0209220	0.0034715	1.0E-09
20	FOXA2 *	rs1203931	22610325	A	G	0.1558240	-0.0208191	0.0034833	1.2E-09
20	FOXA2 *	chr20:22610445_ATTT_A	22610445	ATTT	A	0.1603280	-0.0205664	0.0034703	1.7E-09
20	FOXA2 *	rs1203932	22610530	T	G	0.1558110	-0.0207404	0.0034836	1.3E-09
20	FOXA2 *	rs1203933	22610551	T	C	0.1558110	-0.0207404	0.0034836	1.3E-09
20	FOXA2 *	rs1203934	22611326	A	C	0.1557900	-0.0207638	0.0034847	1.3E-09
20	FOXA2 *	rs1203935	22611348	G	A	0.1129470	-0.0236126	0.0039996	6.5E-09
20	FOXA2 *	rs1203936	22611792	G	T	0.1558020	-0.0207245	0.0034846	1.4E-09
20	FOXA2 *	rs12479757	22612556	T	C	0.1126410	-0.0236100	0.0040104	8.2E-09
20	FOXA2 *	rs1203937	22612728	T	C	0.1556720	-0.0205781	0.0034865	1.9E-09
20	FOXA2 *	rs1203938	22614320	G	A	0.1559230	-0.0204909	0.0034861	2.5E-09
20	FOXA2 *	rs1203939	22614618	A	G	0.1558340	-0.0206995	0.0034875	1.8E-09
20	FOXA2 *	rs1203940	22615005	T	C	0.1557850	-0.0206970	0.0034880	1.8E-09
20	FOXA2 *	rs61186493	22615369	TG	T	0.1556780	-0.0207281	0.0034901	1.7E-09
20	FOXA2 *	rs1203941	22615951	T	C	0.1554600	-0.0208763	0.0034926	1.4E-09
20	FOXA2 *	rs1203942	22615997	C	G	0.1554520	-0.0208683	0.0034926	1.4E-09
20	FOXA2 *	rs1203943	22616187	T	C	0.1554240	-0.0208091	0.0034932	1.6E-09
20	FOXA2 *	rs1203944	22616241	T	C	0.1554200	-0.0208017	0.0034932	1.6E-09
20	FOXA2 *	rs1203945	22616255	G	T	0.1554160	-0.0208023	0.0034933	1.6E-09
20	FOXA2 *	rs5840968	22617806	G	GA	0.1553890	-0.0207891	0.0034935	1.7E-09
20	FOXA2 *	rs1203946	22620340	A	C	0.1553220	-0.0207868	0.0034944	1.7E-09
20	FOXA2 *	chr20:22621385_GA_G	22621385	GA	G	0.1553250	-0.0207349	0.0034950	1.9E-09
20	FOXA2 *	rs1203947	22621725	C	T	0.1552930	-0.0207433	0.0034947	1.9E-09
20	FOXA2 *	rs1203948	22624134	G	A	0.1568140	-0.0202254	0.0034811	3.5E-09
20	FOXA2 *	rs1203949	22625059	T	C	0.1568020	-0.0201910	0.0034812	3.7E-09
20	FOXA2 *	rs1146365	22628040	A	G	0.1127130	-0.0235976	0.0040084	8.4E-09
20	FOXA2 *	rs1203950	22628463	A	G	0.1126860	-0.0234617	0.0040090	1.1E-08
20	FOXA2 *	rs1203952	22633494	G	A	0.1897980	-0.0193605	0.0032746	9.5E-10
20	FOXA2 *	rs1203953	22635505	T	C	0.1540060	-0.0204990	0.0035022	2.3E-09
20	FOXA2 *	rs6137704	22639060	A	T	0.1539610	-0.0205911	0.0035031	2.0E-09
20	FOXA2 *	rs2424439	22639402	G	A	0.1539610	-0.0205911	0.0035031	2.0E-09
20	FOXA2 *	rs2208168	22642628	C	T	0.1562300	-0.0202993	0.0034851	1.9E-09
20	FOXA2 *	rs2424440	22643338	C	T	0.1562180	-0.0203062	0.0034851	1.9E-09
20	FOXA2 *	rs2208169	22643647	T	C	0.1120450	-0.0237378	0.0040166	6.5E-09
20	FOXA2 *	rs2424442	22644151	C	T	0.1561740	-0.0202794	0.0034857	2.1E-09
20	FOXA2 *	rs6082762	22644378	A	T	0.1561770	-0.0202927	0.0034861	2.1E-09
20	FOXA2 *	rs2424443	22644497	G	A	0.1562570	-0.0201582	0.0034851	2.7E-09
20	FOXA2 *	rs6075931	22644757	C	A	0.1614530	-0.0189690	0.0034501	1.5E-08
20	FOXA2 *	rs910960	22647249	G	C	0.1129500	-0.0230944	0.0040012	1.9E-08
20	FOXA2 *	rs6137712	22648298	C	T	0.1126530	-0.0230089	0.0040059	2.4E-08
20	FOXA2 *	rs2424444	22648681	C	T	0.1130030	-0.0232425	0.0039985	1.5E-08
20	FOXA2 *	chr20:22649863_C_CT	22649863	C	CT	0.1166100	-0.0226222	0.0039777	4.3E-08
20	FOXA2 *	rs8118625	22649878	C	A	0.1131840	-0.0230024	0.0039924	2.0E-08
20	FOXA2 *	rs2224316	22651202	T	C	0.1131920	-0.0229558	0.0039920	2.2E-08
20	FOXA2 *	rs6082765	22651338	T	C	0.1132050	-0.0230067	0.0039922	2.0E-08
20	FOXA2 *	rs747911	22652293	T	C	0.1133650	-0.0230681	0.0039890	1.9E-08
20	FOXA2 *	rs910956	22652517	A	G	0.1130480	-0.0231561	0.0039936	1.7E-08
20	FOXA2 *	rs754855	22653005	T	C	0.1123380	-0.0227757	0.0040131	3.5E-08
20	FOXA2 *	rs910957	22653216	C	G	0.1123210	-0.0234426	0.0040170	1.4E-08
20	FOXA2 *	chr20:22654266_T_TAC	22654266	T	TAC	0.1152330	-0.0222498	0.0039708	4.6E-08
20	FOXA2 *	rs4815129	22654716	G	C	0.1150430	-0.0222637	0.0039732	4.3E-08
20	FOXA2 *	rs2424446	22656118	A	G	0.1151280	-0.0223284	0.0039719	3.9E-08
20	FOXA2 *	rs2424450	22657348	C	A	0.1152090	-0.0221919	0.0039698	4.6E-08
20	FOXA2 *	rs4815131	22658994	T	C	0.1220970	-0.0223405	0.0038705	1.4E-08
20	FOXA2 *	rs975525	22659774	G	A	0.1221360	-0.0224342	0.0038699	1.3E-08
20	FOXA2 *	rs2145058	22660132	T	C	0.1221720	-0.0224154	0.0038697	1.3E-08
20	FOXA2 *	rs4815132	22661195	T	C	0.1252390	-0.0219058	0.0038360	2.8E-08
20	FOXA2 *	rs2424454	22662292	G	A	0.1259120	-0.0227464	0.0038708	6.7E-09
20	FOXA2 *	rs6036168	22662688	G	A	0.1224410	-0.0222136	0.0038614	1.5E-08
20	FOXA2 *	rs2424456	22663024	C	A	0.1224540	-0.0222391	0.0038609	1.5E-08
20	FOXA2 *	rs4815134	22663923	C	T	0.1224500	-0.0222488	0.0038608	1.4E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	FOXA2 *	rs4815135	22663951	C	G	0.1224500	-0.0222488	0.0038608	1.4E-08
20	FOXA2 *	rs55803110	22664344	C	T	0.1228180	-0.0217290	0.0038562	2.9E-08
20	FOXA2 *	rs2424457	22664411	C	T	0.1230090	-0.0219795	0.0038535	2.0E-08
20	FOXA2 *	rs2424458	22664505	C	T	0.1230130	-0.0219477	0.0038534	2.1E-08
20	FOXA2 *	rs2145059	22664889	C	T	0.1223670	-0.0220440	0.0038618	1.7E-08
20	FOXA2 *	rs2145060	22664994	T	A	0.1223670	-0.0220440	0.0038618	1.7E-08
20	FOXA2 *	rs2145061	22665097	A	G	0.1223670	-0.0220440	0.0038618	1.7E-08
20	FOXA2 *	rs6036169	22665239	G	A	0.1224260	-0.0220814	0.0038607	1.6E-08
20	FOXA2 *	rs35336166	22666799	TC	T	0.1222040	-0.0221163	0.0038644	1.7E-08
20	FOXA2 *	rs6036170	22666949	T	C	0.1222040	-0.0221163	0.0038644	1.7E-08
20	FOXA2 *	rs6113758	22667010	C	T	0.1222040	-0.0221163	0.0038644	1.7E-08
20	FOXA2 *	rs2424459	22667434	C	A	0.1222050	-0.0221283	0.0038644	1.6E-08
20	FOXA2 *	rs11087394	22669346	TC	T	0.1221980	-0.0221558	0.0038645	1.6E-08
20	FOXA2 *	rs6082774	22669410	G	A	0.1221980	-0.0221558	0.0038645	1.6E-08
20	FOXA2 *	rs6137721	22670000	G	A	0.1221980	-0.0221558	0.0038645	1.6E-08
20	FOXA2 *	rs7273357	22671324	T	C	0.1221980	-0.0221558	0.0038645	1.6E-08
20	FOXA2 *	rs10708423	22672870	T	TG	0.1212540	-0.0216521	0.0038798	3.7E-08
20	FOXA2 *	rs6132536	22673262	T	C	0.1219920	-0.0219666	0.0038674	2.2E-08
20	FOXA2 *	rs6082778	22673436	T	C	0.1224150	-0.0219872	0.0038625	2.1E-08
20	FOXA2 *	rs73304707	22673921	A	C	0.1221780	-0.0223096	0.0038650	1.3E-08
20	FOXA2 *	rs6048245	22674559	A	C	0.1221380	-0.0223798	0.0038662	1.2E-08
20	FOXA2 *	rs6082779	22675057	T	C	0.1220460	-0.0223540	0.0038684	1.3E-08
20	FOXA2 *	rs6132537	22675285	C	T	0.1219380	-0.0224443	0.0038717	1.2E-08
20	PLTP	rs6065904	45906012	A	G	0.2974730	0.0194744	0.0027610	1.3E-13
20	PLTP	rs148753678	45907567	C	CACA	0.0669850	0.0469287	0.0050899	5.9E-21
20	PLTP	rs378114	45909788	T	C	0.4066520	-0.0152190	0.0025763	6.3E-10
20	PLTP	rs435306	45909845	G	T	0.4091790	-0.0153984	0.0025705	3.4E-10
20	PLTP	rs200238866	45912201	C	CCCT	0.0670323	0.0473175	0.0050622	1.6E-21
20	PLTP *	rs76083992	45916159	T	C	0.0674683	0.0466881	0.0050448	3.9E-21
20	PLTP *	rs4810479	45916409	T	C	0.3988680	-0.0155571	0.0025816	1.5E-10
20	PLTP *	rs4812975	45916821	A	G	0.3991110	-0.0154535	0.0025818	2.0E-10
20	PLTP *	rs6130967	45919050	A	G	0.0674746	0.0467254	0.0050443	3.6E-21
20	PLTP *	rs2868346	45919331	T	C	0.3982830	-0.0154757	0.0025886	2.1E-10
20	PLTP *	rs3843763	45919554	T	C	0.3978410	-0.0152016	0.0025905	4.4E-10
20	PLTP *	rs6130969	45920383	T	G	0.0673460	0.0463038	0.0050481	7.9E-21
20	PLTP *	rs6073958	45923216	C	T	0.1266920	0.0365337	0.0038128	3.9E-23
20	PCIF1 *	rs2903809	45924256	A	C	0.3962790	-0.0156671	0.0026098	1.6E-10
20	PCIF1 *	rs1810322	45925065	A	G	0.0652485	0.0475133	0.0051325	4.3E-21
20	PCIF1 *	rs6065906	45925376	C	T	0.0240443	0.0432055	0.0082530	3.1E-08
20	PCIF1 *	rs111859808	45930210	A	G	0.0668444	0.0466230	0.0050704	7.3E-21
20	PCIF1 *	rs6032589	45930959	C	T	0.3617280	-0.0156989	0.0026394	3.6E-10
20	PCIF1 *	rs113232549	45931069	T	C	0.0668444	0.0466230	0.0050704	7.3E-21
20	PCIF1	rs74436333	45937405	G	A	0.0668448	0.0466434	0.0050702	7.0E-21
20	PCIF1	rs6032597	45938696	T	G	0.3606330	-0.0156911	0.0026393	3.3E-10
20	PCIF1	rs6094229	45941824	G	C	0.3611200	-0.0156430	0.0026395	3.8E-10
20	PCIF1	rs2297194	45945077	G	A	0.0668444	0.0467764	0.0050700	5.5E-21
20	PCIF1	rs11111750	45945599	C	T	0.0668598	0.0467164	0.0050695	5.8E-21
20	PCIF1	rs7679	45947863	C	T	0.0241569	0.0439196	0.0082164	1.6E-08
20	ZNF335 *	rs6130975	45948343	A	G	0.0668421	0.0467780	0.0050700	5.4E-21
20	ZNF335 *	rs6124759	45948363	G	C	0.3842260	-0.0144294	0.0026002	3.0E-09
20	ZNF335	rs3363	45948675	T	C	0.3606780	-0.0156842	0.0026341	3.0E-10
20	ZNF335	rs16990951	45950035	A	T	0.3847830	-0.0143130	0.0025993	3.4E-09
20	ZNF335	rs3746503	45950322	G	A	0.3838480	-0.0144248	0.0025974	3.3E-09
20	ZNF335	rs6130976	45950933	T	C	0.0666976	0.0470637	0.0050747	3.3E-21
20	ZNF335	rs34240177	45951651	C	G	0.0669751	0.0467093	0.0050641	5.9E-21
20	ZNF335	rs6124760	45952814	G	C	0.0672721	0.0471822	0.0050514	1.9E-21
20	ZNF335	rs6032601	45956315	A	G	0.3819890	-0.0146438	0.0026051	2.0E-09
20	ZNF335	rs4465830	45956781	G	A	0.0241693	0.0425046	0.0082284	4.2E-08
20	ZNF335	rs3848718	45957124	A	G	0.0656493	0.0473266	0.0051087	5.9E-21
20	ZNF335	rs111434827	45958597	T	C	0.0670500	0.0472861	0.0050594	1.6E-21
20	ZNF335	rs6032602	45958731	C	T	0.3827830	-0.0146718	0.0026013	1.9E-09
20	ZNF335	rs6130977	45959191	A	C	0.0670500	0.0472861	0.0050594	1.6E-21
20	ZNF335	rs3746508	45959540	A	G	0.3860350	-0.0145740	0.0026002	2.3E-09
20	ZNF335	rs3746509	45959602	C	T	0.3827450	-0.0147612	0.0026016	1.5E-09
20	ZNF335	rs6130978	45959766	G	A	0.0670451	0.0472768	0.0050596	1.6E-21
20	ZNF335	rs79645412	45960177	C	G	0.0669548	0.0472605	0.0050640	1.7E-21
20	ZNF335	rs6104404	45961203	A	C	0.3831070	-0.0148471	0.0026026	1.3E-09
20	ZNF335	rs6073971	45961331	T	C	0.0240120	0.0427301	0.0082534	4.5E-08
20	ZNF335	rs6073972	45961659	G	C	0.0240117	0.0427286	0.0082534	4.5E-08
20	ZNF335	rs16990964	45962093	A	G	0.0670835	0.0472490	0.0050582	1.6E-21
20	ZNF335	rs147204976	45963071	A	G	0.0960647	0.0350665	0.0043090	8.6E-17
20	ZNF335	rs3746511	45963725	T	C	0.3814280	-0.0147988	0.0026112	1.8E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
20	ZNF335	rs3746512	45963997	T	C	0.3812100	-0.0147698	0.0026130	2.1E-09
20	ZNF335	rs74880664	45965956	A	G	0.0670726	0.0472586	0.0050587	1.6E-21
20	ZNF335	rs143167649	45966533	C	CTCTGTT	0.0652561	0.0475208	0.0051272	5.1E-21
20	ZNF335	rs76907877	45967688	T	C	0.0668257	0.0471848	0.0050701	2.2E-21
20	ZNF335	rs78558150	45970350	T	C	0.0528406	0.0440002	0.0056878	1.7E-15
20	ZNF335 *	rs16990971	45972654	G	A	0.0674105	0.0455654	0.0050597	3.0E-20
20	ZNF335 *	rs11469011	45973042	G	GCCTAT/	0.3793720	-0.0153553	0.0026397	8.8E-10
20	ZNF335 *	rs6017717	45975324	C	G	0.3792690	-0.0151164	0.0026423	1.5E-09
20	MMP9 *	rs78295912	45993859	T	C	0.0657480	0.0421520	0.0051468	1.5E-16
20	MMP9 *	rs1888235	45995328	T	C	0.1170140	0.0301473	0.0039851	4.6E-14
20	MMP9 *	rs145026700	45996044	T	C	0.0652516	0.0420644	0.0051646	1.8E-16
20	MMP9 *	rs6073984	46002014	G	A	0.1151360	0.0306954	0.0040068	3.3E-14
20	MMP9 *	rs3918241	46007096	A	T	0.1206340	0.0282605	0.0039160	7.1E-13
20	MMP9 *	rs3918242	46007337	T	C	0.1206510	0.0282171	0.0039155	7.8E-13
20	MMP9	rs2274755	46011053	T	G	0.1227860	0.0280528	0.0038675	6.4E-13
20	MMP9	rs2236416	46011936	G	A	0.1234880	0.0276147	0.0038523	1.1E-12
20	MMP9	rs17577	46014472	A	G	0.1257540	0.0267919	0.0038128	2.3E-12
20	MMP9	rs3918261	46014953	G	A	0.1257640	0.0267478	0.0038126	2.5E-12
20	MMP9	rs13925	46016326	A	G	0.1257680	0.0267505	0.0038122	2.5E-12
20	MMP9 *	rs3918270	46016700	A	G	0.1219710	0.0261883	0.0038844	1.3E-11
20	MMP9 *	rs8184490	46016794	G	C	0.0711836	0.0366012	0.0049355	5.6E-14
20	MMP9 *	rs3918271	46016954	A	G	0.1193240	0.0273800	0.0039213	3.7E-12
20	SLC12A5 *	rs10432735	46021679	T	A	0.1253110	0.0266580	0.0038143	3.0E-12
20	SLC12A5	rs62215576	46023758	T	C	0.1257890	0.0266737	0.0038113	2.7E-12
20	SLC12A5	rs6124764	46027498	A	T	0.1227710	0.0266307	0.0038734	3.8E-12
20	SLC12A5	rs11908352	46027501	A	C	0.1227690	0.0266562	0.0038735	3.6E-12
20	SLC12A5	rs6124765	46039572	T	C	0.1234690	0.0279059	0.0039201	1.6E-12
20	SLC12A5	rs116878061	46057452	T	G	0.0688700	0.0327402	0.0050064	7.1E-12
22	PPARA	rs1800234	46219983	C	T	0.0438586	-0.0360622	0.0061935	2.7E-09

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error

Supplementary Table 19. Summary of variants exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the male cohort using the Taiwan Biobank.

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAf	BETA	SE	P
1	USP1 *	rs60500353	62433313	T	C	0.2100350	-0.0262338	0.0042744	1.2E-10
1	USP1 *	rs624698	62435140	G	A	0.2594020	-0.0309272	0.0039195	3.2E-16
1	USP1 *	rs624700	62435141	C	G	0.2594020	-0.0309272	0.0039195	3.2E-16
1	USP1 *	rs626787	62435572	G	C	0.2586970	-0.0314794	0.0039078	8.5E-17
1	USP1 *	rs631106	62436136	A	C	0.2586260	-0.0314070	0.0039076	9.6E-17
1	USP1	rs646179	62437203	G	A	0.3816970	-0.0227083	0.0035375	5.4E-11
1	USP1	rs9436221	62437688	C	T	0.2529400	-0.0314462	0.0039327	8.6E-17
1	USP1	rs9436222	62437692	G	C	0.2529400	-0.0314462	0.0039327	8.6E-17
1	USP1	rs9436223	62437876	T	C	0.2530000	-0.0314480	0.0039319	9.5E-17
1	USP1	rs12029068	62438624	T	C	0.2530000	-0.0314480	0.0039319	9.5E-17
1	USP1	rs9436661	62438904	G	T	0.2530060	-0.0314391	0.0039319	9.7E-17
1	USP1	rs11588261	62439265	A	G	0.2530060	-0.0314391	0.0039319	9.7E-17
1	USP1	rs10493322	62440222	T	C	0.2107640	-0.0345458	0.0041878	1.9E-17
1	USP1	rs60688353	62440418	CAA	C	0.2107470	-0.0346756	0.0041878	1.6E-17
1	USP1	rs638714	62440818	T	G	0.2525850	-0.0316523	0.0039343	8.0E-17
1	USP1	rs638305	62440866	T	G	0.2531020	-0.0316029	0.0039303	7.3E-17
1	USP1	chr1:62441011_A_AT	62441011	AT	A	0.2384690	-0.0323043	0.0040572	2.4E-16
1	USP1	rs637723	62441057	T	C	0.2503340	-0.0322891	0.0039577	2.6E-17
1	USP1	rs656297	62441924	G	A	0.2531020	-0.0316029	0.0039303	7.3E-17
1	USP1	rs642845	62442564	C	T	0.2604640	-0.0298273	0.0039042	2.6E-15
1	USP1	rs641540	62442867	G	A	0.2531020	-0.0316029	0.0039303	7.3E-17
1	USP1	rs527281380	62444278	A	AAAG	0.2240780	-0.0330692	0.0041448	1.8E-16
1	USP1	rs1553145497	62445632	GTGTA	G	0.2531260	-0.0314743	0.0039323	9.5E-17
1	USP1	rs10647753	62445634	GTA	G	0.2534010	-0.0317643	0.0039335	5.5E-17
1	USP1	rs598253	62445670	C	T	0.2530770	-0.0315851	0.0039306	7.6E-17
1	USP1	rs11207969	62446080	G	A	0.2530770	-0.0315851	0.0039306	7.6E-17
1	USP1	rs659656	62446449	G	C	0.2530770	-0.0315851	0.0039306	7.6E-17
1	USP1	rs10158897	62447248	T	C	0.2107850	-0.0347414	0.0041883	1.4E-17
1	USP1	rs783291	62449307	A	G	0.2530820	-0.0316053	0.0039305	7.0E-17
1	USP1	rs11207970	62449802	T	C	0.2097590	-0.0348955	0.0042005	1.3E-17
1	USP1	rs583609	62451125	C	T	0.2531030	-0.0315969	0.0039305	7.2E-17
1	USP1 *	rs597470	62452125	G	T	0.2530820	-0.0316053	0.0039305	7.0E-17
1	USP1 *	rs597078	62452186	A	G	0.2526430	-0.0316765	0.0039357	6.0E-17
1	USP1 *	rs597076	62452194	A	T	0.2526430	-0.0316765	0.0039357	6.0E-17
1	USP1 *	rs630144	62453193	G	A	0.2530870	-0.0315915	0.0039305	7.2E-17
1	DOCK7 *	chr1:62453356_GT_G	62453356	G	GT	0.2503810	-0.0326251	0.0039781	2.3E-17
1	DOCK7 *	rs79346928	62454307	CAT	C	0.2107470	-0.0347315	0.0041881	1.4E-17
1	DOCK7 *	rs636523	62454337	G	A	0.2104140	-0.0345662	0.0041912	1.7E-17
1	DOCK7 *	rs636497	62454358	G	A	0.2531080	-0.0316250	0.0039303	6.8E-17
1	DOCK7 *	rs624660	62454717	A	C	0.2537300	-0.0315309	0.0039320	8.5E-17
1	DOCK7	rs634341	62455751	C	T	0.2501670	-0.0326352	0.0039576	1.4E-17
1	DOCK7	rs3913007	62455915	C	T	0.2107500	-0.0347800	0.0041882	1.2E-17
1	DOCK7	rs4350231	62456989	A	G	0.2085770	-0.0351426	0.0042071	1.2E-17
1	DOCK7	rs12023489	62458187	A	G	0.2525510	-0.0317343	0.0039358	6.0E-17
1	DOCK7	rs12037659	62458192	T	C	0.2101460	-0.0349317	0.0041957	1.1E-17
1	DOCK7	rs62932760	62458534	TG	T	0.2360260	-0.0300585	0.0040749	3.4E-14
1	DOCK7	rs9988450	62458777	T	C	0.2531130	-0.0316691	0.0039304	6.2E-17
1	DOCK7	rs77064258	62460056	T	C	0.1755560	-0.0362763	0.0045175	9.9E-17
1	DOCK7	rs1305520	62460386	A	T	0.2532240	-0.0316459	0.0039331	6.7E-17
1	DOCK7	rs7547965	62460700	G	A	0.2533070	-0.0317947	0.0039335	5.0E-17
1	DOCK7	chr1:62462070_CA_C	62462070	C	CA	0.2300450	-0.0332183	0.0041517	2.3E-16
1	DOCK7	rs1167996	62462126	T	G	0.2508100	-0.0315941	0.0039440	1.1E-16
1	DOCK7	rs998403	62462878	A	G	0.2088890	-0.0352747	0.0042026	6.5E-18
1	DOCK7	rs11356503	62463707	T	TA	0.2088890	-0.0352747	0.0042026	6.5E-18
1	DOCK7	rs1177541	62464221	G	A	0.2517200	-0.0321202	0.0039399	2.9E-17
1	DOCK7	rs77083979	62464435	A	G	0.2005810	-0.0362275	0.0042663	1.9E-18
1	DOCK7	rs11207972	62464553	G	A	0.2517250	-0.0321057	0.0039398	3.0E-17
1	DOCK7	rs1167998	62465961	C	A	0.2606720	-0.0308583	0.0038905	1.5E-16
1	DOCK7	rs77907749	62466449	T	C	0.2005750	-0.0361855	0.0042662	2.1E-18
1	DOCK7	rs1168001	62468087	G	A	0.2517300	-0.0321472	0.0039398	2.8E-17
1	DOCK7	rs12124284	62468356	A	G	0.2091280	-0.0355644	0.0042012	3.4E-18
1	DOCK7	rs1168002	62468637	A	G	0.2524770	-0.0322002	0.0039424	2.7E-17
1	DOCK7	rs1168003	62469175	G	A	0.2517300	-0.0321472	0.0039398	2.8E-17
1	DOCK7	rs12043877	62469328	T	C	0.2005890	-0.0362774	0.0042662	1.7E-18
1	DOCK7	rs1007205	62471241	T	C	0.2516580	-0.0321242	0.0039414	3.3E-17
1	DOCK7	rs10889330	62473795	C	G	0.2517300	-0.0321389	0.0039398	2.8E-17
1	DOCK7	rs1979722	62474426	A	G	0.2089030	-0.0353036	0.0042024	6.1E-18
1	DOCK7	rs11442941	62474595	T	TG	0.2517000	-0.0320647	0.0039415	3.5E-17
1	DOCK7	chr1:62475497_GA_G	62475497	GA	G	0.2547440	-0.0325384	0.0039560	2.3E-17
1	DOCK7	rs10889331	62477336	G	T	0.2517350	-0.0321247	0.0039398	2.9E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs1168009	62478283	G	A	0.2519510	-0.0320959	0.0039414	3.0E-17
1	DOCK7	rs1168010	62478308	G	A	0.2520200	-0.0320590	0.0039417	3.2E-17
1	DOCK7	rs35913674	62479276	CA	C	0.2522840	-0.0319621	0.0039411	4.7E-17
1	DOCK7	rs1183260	62479747	A	G	0.2514910	-0.0320457	0.0039408	3.8E-17
1	DOCK7	rs6587976	62479960	T	C	0.2514910	-0.0320457	0.0039408	3.8E-17
1	DOCK7	rs1305521	62483363	A	G	0.2526260	-0.0316705	0.0039395	9.6E-17
1	DOCK7	rs11207974	62484289	C	T	0.2514280	-0.0320363	0.0039411	3.9E-17
1	DOCK7	rs10889332	62485187	T	C	0.2514330	-0.0320848	0.0039426	3.7E-17
1	DOCK7	rs2489835	62489300	T	C	0.2514030	-0.0320497	0.0039414	3.8E-17
1	DOCK7	rs1690761	62490191	C	T	0.2514230	-0.0320338	0.0039413	3.8E-17
1	DOCK7	rs10889333	62491359	A	G	0.2088670	-0.0355070	0.0042032	4.2E-18
1	DOCK7	rs10889334	62491528	G	C	0.2088300	-0.0354735	0.0042033	4.4E-18
1	DOCK7	rs10789112	62492087	C	T	0.2088360	-0.0354987	0.0042036	4.1E-18
1	DOCK7	rs1183851	62492987	T	C	0.3768910	-0.0233405	0.0035455	1.4E-11
1	DOCK7	rs10889335	62494430	G	A	0.2012460	-0.0336036	0.0042868	7.6E-16
1	DOCK7	rs1168041	62494579	T	C	0.2158070	-0.0302172	0.0041608	3.9E-14
1	DOCK7	chr1:62494664_T_TG	62494664	TG	T	0.1550330	-0.0389008	0.0048275	7.1E-17
1	DOCK7	rs1168040	62494904	T	C	0.2513050	-0.0326125	0.0039422	1.0E-17
1	DOCK7	rs1168036	62497063	A	G	0.2500210	-0.0325187	0.0039450	1.2E-17
1	DOCK7	rs1002687	62498066	G	A	0.2516500	-0.0321902	0.0039424	2.1E-17
1	DOCK7	chr1:62498080_A_AT	62498080	A	AT	0.2595150	-0.0317101	0.0039750	9.8E-17
1	DOCK7	rs1168034	62498243	G	C	0.2501760	-0.0326767	0.0039433	8.2E-18
1	DOCK7	chr1:62499937_GA_G	62499937	GA	G	0.2508130	-0.0324209	0.0039477	1.3E-17
1	DOCK7	rs35529421	62499950	A	T	0.2032190	-0.0357502	0.0042711	1.2E-17
1	DOCK7	rs1168032	62502076	A	G	0.2498500	-0.0330877	0.0039459	3.8E-18
1	DOCK7	rs1168031	62502316	C	T	0.2501760	-0.0326767	0.0039433	8.2E-18
1	DOCK7	chr1:62502762_A_AT	62502762	AT	A	0.2074510	-0.0360736	0.0042131	1.3E-18
1	DOCK7	rs1168030	62502820	C	T	0.2503640	-0.0327983	0.0039441	5.9E-18
1	DOCK7	rs56342264	62503238	T	TA	0.2076130	-0.0361849	0.0042110	1.0E-18
1	DOCK7	rs1168029	62503731	G	A	0.2510320	-0.0326610	0.0039429	7.3E-18
1	DOCK7	rs1168028	62503760	G	A	0.2501760	-0.0326767	0.0039433	8.2E-18
1	DOCK7	rs1168027	62504513	T	C	0.2500210	-0.0325187	0.0039450	1.2E-17
1	DOCK7	rs1168026	62505325	T	C	0.2501760	-0.0326767	0.0039433	8.2E-18
1	DOCK7	chr1:62506471_CT_C	62506471	CT	C	0.2524080	-0.0324515	0.0039491	1.5E-17
1	DOCK7	rs7527004	62506557	G	A	0.2501970	-0.0326758	0.0039451	8.6E-18
1	DOCK7	rs12027778	62507642	G	C	0.1907960	-0.0377436	0.0043417	3.4E-19
1	DOCK7	rs1184865	62508124	A	G	0.2501820	-0.0326943	0.0039433	7.8E-18
1	DOCK7	rs1168042	62508479	A	T	0.2500210	-0.0325618	0.0039450	1.1E-17
1	DOCK7	rs35836805	62508787	T	TTTAC	0.2072380	-0.0358816	0.0042164	2.0E-18
1	DOCK7	rs11207976	62511080	A	G	0.2500210	-0.0325618	0.0039450	1.1E-17
1	DOCK7	rs11207977	62511636	T	C	0.2078910	-0.0358003	0.0042137	2.3E-18
1	DOCK7	rs1781212	62511748	G	A	0.2520900	-0.0323440	0.0039612	2.2E-17
1	DOCK7	rs1168044	62511887	A	C	0.2532140	-0.0328044	0.0039487	5.8E-18
1	DOCK7	rs1690755	62514490	A	G	0.2502230	-0.0327378	0.0039435	7.1E-18
1	DOCK7	rs10557760	62514728	CACA	C	0.2504050	-0.0326283	0.0039446	1.1E-17
1	DOCK7	rs10889336	62514739	C	T	0.2078140	-0.0360934	0.0042122	1.4E-18
1	DOCK7	rs10889337	62514936	A	G	0.2501820	-0.0326943	0.0039433	7.8E-18
1	DOCK7	rs12090886	62515769	G	A	0.2501820	-0.0326943	0.0039433	7.8E-18
1	DOCK7	rs11207979	62517323	A	G	0.2500210	-0.0325618	0.0039450	1.1E-17
1	DOCK7	rs1168046	62518022	A	C	0.2499070	-0.0325992	0.0039454	1.1E-17
1	DOCK7	rs1168047	62518080	C	T	0.2500210	-0.0325618	0.0039450	1.1E-17
1	DOCK7	rs10889338	62519226	T	C	0.2074590	-0.0359999	0.0042132	1.6E-18
1	DOCK7	rs1168050	62521284	C	T	0.2500420	-0.0325161	0.0039453	1.2E-17
1	DOCK7	rs1690766	62521618	T	C	0.2500210	-0.0325618	0.0039450	1.1E-17
1	DOCK7	rs1781195	62523301	T	C	0.2506850	-0.0326090	0.0039409	8.5E-18
1	DOCK7	rs1627591	62524136	C	T	0.2500160	-0.0325722	0.0039450	1.1E-17
1	DOCK7	rs11577840	62525698	T	C	0.2500160	-0.0325722	0.0039450	1.1E-17
1	DOCK7	rs12062275	62526234	T	C	0.2500160	-0.0325722	0.0039450	1.1E-17
1	DOCK7	rs11207980	62527078	C	T	0.2077500	-0.0357678	0.0042155	2.3E-18
1	DOCK7	rs4915838	62527397	G	A	0.2500160	-0.0325722	0.0039450	1.1E-17
1	DOCK7	rs12403207	62527949	T	C	0.2507770	-0.0324694	0.0039512	1.8E-17
1	DOCK7	rs12039115	62529592	T	C	0.1991340	-0.0368007	0.0042772	6.6E-19
1	DOCK7	rs1168015	62530375	C	G	0.2500160	-0.0325982	0.0039450	1.1E-17
1	DOCK7	rs1168013	62531167	C	G	0.2500160	-0.0325143	0.0039446	1.2E-17
1	DOCK7	rs10458569	62531930	A	C	0.1800470	-0.0367218	0.0044465	1.3E-17
1	DOCK7	rs35664253	62532065	C	CAG	0.2500310	-0.0325642	0.0039447	1.1E-17
1	DOCK7	chr1:62533439_A_AT	62533439	A	AT	0.2501250	-0.0325825	0.0039454	1.1E-17
1	DOCK7	rs4915840	62533924	C	G	0.2502290	-0.0327947	0.0039464	7.1E-18
1	DOCK7	rs61393465	62535060	G	GC	0.2074690	-0.0359722	0.0042129	1.7E-18
1	DOCK7	rs1168018	62535449	A	C	0.2499900	-0.0325612	0.0039449	1.1E-17
1	DOCK7	rs1168017	62536880	A	G	0.2500310	-0.0325642	0.0039447	1.1E-17
1	DOCK7	rs76176236	62538722	C	T	0.1201270	-0.0385568	0.0052670	3.1E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs56115463	62540080	A	C	0.1981240	-0.0368664	0.0042920	7.2E-19
1	DOCK7	rs7548877	62540279	T	C	0.2500260	-0.0325625	0.0039450	1.1E-17
1	DOCK7	rs11207981	62540416	C	A	0.2502130	-0.0326839	0.0039469	8.9E-18
1	DOCK7	rs1168023	62540924	A	T	0.2500260	-0.0325625	0.0039450	1.1E-17
1	DOCK7	rs66827188	62541132	TTTATAGAC	T	0.2505360	-0.0325632	0.0039474	1.2E-17
1	DOCK7	rs1781221	62541171	A	C	0.2500990	-0.0325612	0.0039453	1.1E-17
1	DOCK7	rs11207982	62541511	T	C	0.2074650	-0.0359759	0.0042132	1.7E-18
1	DOCK7	rs1184547	62541557	G	A	0.2500260	-0.0325625	0.0039450	1.1E-17
1	DOCK7	rs1168022	62542050	A	T	0.2500100	-0.0325830	0.0039453	1.1E-17
1	DOCK7	rs1168021	62544229	A	G	0.2508370	-0.0321858	0.0039437	2.6E-17
1	DOCK7	rs1168020	62544285	C	T	0.2509740	-0.0324009	0.0039473	2.0E-17
1	DOCK7	rs1179765	62544439	G	C	0.2500310	-0.0326284	0.0039451	9.5E-18
1	DOCK7	rs12074528	62545200	T	C	0.2500310	-0.0326284	0.0039451	9.5E-18
1	DOCK7	rs10889339	62546385	A	G	0.2502030	-0.0326644	0.0039462	8.8E-18
1	DOCK7	rs10889340	62546400	A	C	0.2500620	-0.0326389	0.0039455	9.2E-18
1	DOCK7	rs11207983	62546436	C	T	0.2500310	-0.0326284	0.0039451	9.5E-18
1	DOCK7	rs2029763	62547463	G	A	0.2074690	-0.0360537	0.0042133	1.4E-18
1	DOCK7	rs11207984	62547725	C	T	0.2500310	-0.0326284	0.0039451	9.5E-18
1	DOCK7	rs11207985	62548115	A	G	0.2500990	-0.0324983	0.0039450	1.2E-17
1	DOCK7	rs10789113	62549528	T	A	0.2075040	-0.0360658	0.0042134	1.4E-18
1	DOCK7	chr1:62550719_AT_A	62550719	AT	A	0.2621720	-0.0306712	0.0039741	1.4E-15
1	DOCK7	rs11207986	62552499	T	C	0.2500570	-0.0326620	0.0039453	9.0E-18
1	DOCK7	rs10889342	62553181	T	C	0.2053260	-0.0363146	0.0042366	1.5E-18
1	DOCK7	rs11207988	62553316	T	A	0.1869840	-0.0298089	0.0044533	9.5E-12
1	DOCK7	rs7519785	62554248	G	A	0.2500670	-0.0325657	0.0039451	1.1E-17
1	DOCK7	rs10159255	62555145	A	C	0.2075260	-0.0359935	0.0042131	1.6E-18
1	DOCK7	rs2131925	62560271	G	T	0.2513440	-0.0327973	0.0039419	6.1E-18
1	DOCK7	rs2131926	62560340	C	T	0.2502330	-0.0327449	0.0039432	6.9E-18
1	DOCK7	rs10889343	62560758	T	G	0.2502330	-0.0327449	0.0039432	6.9E-18
1	DOCK7	rs4329540	62561353	C	T	0.2508460	-0.0323102	0.0039408	1.8E-17
1	DOCK7	chr1:62562233_CTTT_C	62562233	C	CTTT	0.2076610	-0.0362232	0.0042114	9.2E-19
1	DOCK7	rs4915621	62563762	A	G	0.2501140	-0.0328614	0.0039450	5.5E-18
1	DOCK7	rs12025714	62565940	A	C	0.1952160	-0.0363555	0.0043208	2.6E-18
1	DOCK7	rs6693353	62565945	A	C	0.2501090	-0.0328409	0.0039450	5.8E-18
1	DOCK7	rs10889344	62568270	T	C	0.2501090	-0.0328409	0.0039450	5.8E-18
1	DOCK7	rs10789114	62568551	C	T	0.2063220	-0.0364015	0.0042283	8.9E-19
1	DOCK7	rs7555577	62568692	A	C	0.2499790	-0.0322231	0.0039528	2.1E-17
1	DOCK7	rs10789115	62570458	A	G	0.2500990	-0.0328638	0.0039452	5.3E-18
1	DOCK7	rs12735272	62571136	G	A	0.2500990	-0.0328638	0.0039452	5.3E-18
1	DOCK7	rs12116574	62572166	T	C	0.2038340	-0.0358660	0.0042507	3.2E-18
1	DOCK7	rs142666378	62572632	T	TGG	0.2500990	-0.0328638	0.0039452	5.3E-18
1	DOCK7	rs6696502	62573862	C	T	0.2500830	-0.0329214	0.0039455	4.8E-18
1	DOCK7	rs12038768	62575057	T	G	0.2076500	-0.0362512	0.0042117	8.8E-19
1	DOCK7	rs11207990	62575415	T	C	0.2500830	-0.0329214	0.0039455	4.8E-18
1	DOCK7	rs11207992	62576129	G	T	0.2076500	-0.0362512	0.0042117	8.8E-19
1	DOCK7	rs1472257	62576455	A	G	0.2500830	-0.0329214	0.0039455	4.8E-18
1	DOCK7	rs10789116	62577067	G	A	0.2076500	-0.0362512	0.0042117	8.8E-19
1	DOCK7	rs1748201	62579835	A	C	0.2489400	-0.0331789	0.0039545	3.5E-18
1	DOCK7	rs1748200	62580368	T	C	0.2502280	-0.0328039	0.0039452	6.5E-18
1	DOCK7	rs1629122	62580907	C	A	0.2503900	-0.0328020	0.0039454	6.0E-18
1	DOCK7	chr1:62582603_C_CCCCA	62582603	CCCCA	C	0.2048710	-0.0343553	0.0043155	2.7E-16
1	DOCK7	rs9436224	62582604	C	A	0.2280500	-0.0325050	0.0041645	7.5E-16
1	DOCK7	rs34465969	62582605	C	A	0.2257070	-0.0326756	0.0041679	6.4E-16
1	DOCK7	rs35194512	62582606	C	A	0.1839030	-0.0363434	0.0044981	1.9E-16
1	DOCK7	rs11207995	62583880	C	A	0.2095850	-0.0361870	0.0042080	7.0E-19
1	DOCK7	rs1748195	62583922	G	C	0.2399730	-0.0322293	0.0040045	8.2E-17
1	DOCK7	rs12042319	62584148	A	G	0.2076730	-0.0361143	0.0042120	1.2E-18
1	DOCK7	rs3850634	62584927	G	T	0.2077180	-0.0361016	0.0042106	1.2E-18
1	DOCK7	rs12030293	62586017	T	C	0.1992880	-0.0369760	0.0042763	4.1E-19
1	DOCK7	rs12048208	62589609	A	G	0.1980010	-0.0369895	0.0042896	4.9E-19
1	DOCK7	rs11207996	62589799	A	G	0.2079280	-0.0360851	0.0042147	1.3E-18
1	DOCK7	rs1748197	62590441	A	G	0.2195070	-0.0347639	0.0041252	4.2E-18
1	DOCK7	rs2366636	62590999	A	G	0.2195070	-0.0347639	0.0041252	4.2E-18
1	DOCK7	rs1748199	62591465	C	T	0.2195070	-0.0347639	0.0041252	4.2E-18
1	DOCK7	rs79439217	62594366	TAAGAA	T	0.2500880	-0.0331069	0.0039481	3.7E-18
1	DOCK7	rs6690733	62594640	C	A	0.2500520	-0.0328837	0.0039455	5.4E-18
1	DOCK7	rs11207997	62596235	T	C	0.2500780	-0.0328947	0.0039455	5.3E-18
1	ANGPTL3, DOCK7	rs34483103	62604866	A	GTTAATGT	0.2074460	-0.0358742	0.0042155	2.2E-18
1	DOCK7	rs10789117	62606594	C	A	0.2520220	-0.0324189	0.0039364	1.1E-17
1	DOCK7	rs59952505	62607196	C	CA	0.2520370	-0.0321729	0.0039350	1.8E-17
1	DOCK7	rs6675401	62608304	T	C	0.2517860	-0.0323565	0.0039349	1.3E-17
1	DOCK7	rs6678483	62608771	A	C	0.2517910	-0.0323659	0.0039350	1.3E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7	rs71776858	62608856	C	CTCAT	0.2075970	-0.0360393	0.0042149	1.4E-18
1	DOCK7	rs10889347	62610155	A	G	0.2517910	-0.0323659	0.0039350	1.3E-17
1	DOCK7	rs10889348	62612551	T	A	0.2076590	-0.0362202	0.0042149	9.7E-19
1	DOCK7	rs10889349	62616248	G	A	0.2449140	-0.0333151	0.0039871	9.9E-18
1	DOCK7	rs2031373	62617618	A	C	0.3847370	-0.0238265	0.0035226	3.5E-12
1	DOCK7	rs61471917	62618359	A	G	0.2518010	-0.0323568	0.0039347	1.3E-17
1	DOCK7	rs10889350	62619595	T	C	0.2520430	-0.0324565	0.0039361	1.1E-17
1	DOCK7	chr1:62619812_T_TA	62619812	TA	T	0.3752720	-0.0222162	0.0035835	1.9E-10
1	DOCK7	rs12239736	62620326	A	T	0.2065870	-0.0363241	0.0042282	9.7E-19
1	DOCK7	rs12239737	62620330	A	T	0.1519250	-0.0345854	0.0048492	5.8E-13
1	DOCK7	rs6587980	62625187	T	C	0.2500100	-0.0325693	0.0039461	9.2E-18
1	DOCK7	rs11207998	62625800	C	G	0.1991260	-0.0368613	0.0042784	5.8E-19
1	DOCK7	rs10157265	62627946	T	C	0.2517810	-0.0324002	0.0039352	1.2E-17
1	DOCK7	rs34211669	62627990	G	GT	0.2074940	-0.0361116	0.0042140	1.3E-18
1	DOCK7	rs11485618	62628536	G	A	0.2074800	-0.0360559	0.0042135	1.4E-18
1	DOCK7	rs10789118	62629021	G	A	0.2074670	-0.0360509	0.0042137	1.4E-18
1	DOCK7	rs7520810	62630040	T	C	0.2516930	-0.0324488	0.0039363	1.1E-17
1	DOCK7	rs12025800	62631110	G	C	0.2517810	-0.0324002	0.0039352	1.2E-17
1	DOCK7	rs141409973	62631753	AG	A	0.2517810	-0.0324002	0.0039352	1.2E-17
1	DOCK7	rs10789119	62632564	A	G	0.2074880	-0.0360596	0.0042136	1.3E-18
1	DOCK7	rs11207999	62632970	C	A	0.2517810	-0.0324002	0.0039352	1.2E-17
1	DOCK7	rs10889352	62633352	C	T	0.2074670	-0.0360509	0.0042137	1.4E-18
1	DOCK7	rs2366638	62633906	A	G	0.2517810	-0.0323995	0.0039353	1.2E-17
1	DOCK7	rs377031118	62634374	GA	G	0.2513560	-0.0326655	0.0039403	6.7E-18
1	DOCK7	rs10789120	62635452	A	G	0.2069040	-0.0360878	0.0042195	1.5E-18
1	DOCK7	rs1570694	62637546	G	A	0.2074590	-0.0360691	0.0042136	1.3E-18
1	DOCK7	rs6657050	62639582	G	A	0.2508840	-0.0325390	0.0039427	1.2E-17
1	DOCK7	rs12047226	62639867	C	T	0.2074540	-0.0360768	0.0042136	1.3E-18
1	DOCK7	rs113795489	62640503	A	AAAGC	0.2074540	-0.0360768	0.0042136	1.3E-18
1	DOCK7	rs7538689	62640577	A	G	0.3850660	-0.0236311	0.0035162	5.0E-12
1	DOCK7	rs7539035	62641096	A	C	0.2517600	-0.0324478	0.0039352	1.1E-17
1	DOCK7	rs995000	62641855	T	C	0.2064670	-0.0362567	0.0042233	9.7E-19
1	DOCK7	rs10789121	62642348	C	T	0.3848990	-0.0238409	0.0035172	3.2E-12
1	DOCK7	rs11208000	62642703	G	A	0.2482990	-0.0329562	0.0039663	7.1E-18
1	DOCK7	rs66531495	62643009	A	AGGCCACA	0.2488180	-0.0325741	0.0039656	1.5E-17
1	DOCK7	rs993013	62645398	G	T	0.2531020	-0.0323006	0.0039309	1.4E-17
1	DOCK7	rs1168085	62646649	C	G	0.2517700	-0.0324685	0.0039352	1.0E-17
1	DOCK7	rs1168086	62646718	A	G	0.2517700	-0.0324685	0.0039352	1.0E-17
1	DOCK7	rs746735	62647840	C	A	0.2520080	-0.0325668	0.0039371	7.6E-18
1	DOCK7	rs1168089	62648048	T	C	0.2506380	-0.0325932	0.0039433	8.2E-18
1	DOCK7	rs33999917	62650370	GA	G	0.2506440	-0.0325098	0.0039411	9.4E-18
1	DOCK7	rs1168093	62650556	G	A	0.2506590	-0.0324960	0.0039408	9.6E-18
1	DOCK7	rs112957492	62651339	C	T	0.2063390	-0.0362372	0.0042227	9.5E-19
1	DOCK7	rs35107877	62651507	A	AG	0.2506690	-0.0325324	0.0039408	8.8E-18
1	DOCK7	rs10889353	62652525	C	A	0.2071120	-0.0360272	0.0042190	1.4E-18
1	DOCK7	rs1168097	62654700	C	T	0.2551890	-0.0313472	0.0039308	9.0E-17
1	DOCK7	rs60286666	62655430	T	TC	0.2519540	-0.0326375	0.0039360	6.6E-18
1	DOCK7	rs1168098	62655623	G	A	0.2516950	-0.0324866	0.0039385	9.3E-18
1	DOCK7	rs1168099	62657188	C	A	0.2519950	-0.0325420	0.0039351	8.1E-18
1	DOCK7	rs4495740	62658794	G	T	0.2063600	-0.0363601	0.0042226	7.3E-19
1	DOCK7	rs1168100	62658871	T	C	0.4507750	-0.0193387	0.0034678	1.3E-08
1	DOCK7	rs1168102	62662034	C	T	0.2506230	-0.0325326	0.0039415	9.4E-18
1	DOCK7	rs1168103	62662410	C	T	0.2506800	-0.0324348	0.0039414	1.2E-17
1	DOCK7	rs1168104	62662654	A	G	0.2506230	-0.0325326	0.0039415	9.4E-18
1	DOCK7	rs10889354	62663411	C	T	0.2064550	-0.0362758	0.0042238	8.7E-19
1	DOCK7	rs11208001	62664760	T	C	0.2501260	-0.0317645	0.0039701	1.1E-16
1	DOCK7	rs12024419	62664854	A	G	0.1793230	-0.0368651	0.0044603	1.5E-17
1	DOCK7	rs2479464	62665320	G	A	0.2505820	-0.0325028	0.0039441	1.1E-17
1	DOCK7	rs1168132	62667797	T	A	0.2505820	-0.0323060	0.0039440	1.8E-17
1	DOCK7	rs4587594	62668259	A	G	0.2063380	-0.0360978	0.0042244	1.4E-18
1	DOCK7	rs28399032	62669953	C	G	0.2062810	-0.0360670	0.0042254	1.5E-18
1	DOCK7	rs1168128	62670175	C	G	0.2506560	-0.0325036	0.0039477	1.2E-17
1	DOCK7	rs181835401	62670284	A	G	0.2493750	-0.0323065	0.0039567	2.1E-17
1	DOCK7	rs1168124	62674059	C	T	0.2504890	-0.0323798	0.0039452	1.5E-17
1	DOCK7	rs11208004	62679768	A	G	0.2067290	-0.0357563	0.0042247	2.4E-18
1	DOCK7	rs4459145	62680578	A	C	0.2456340	-0.0313715	0.0039883	3.2E-16
1	DOCK7	rs7531579	62681369	C	A	0.2061110	-0.0360044	0.0042286	1.7E-18
1	DOCK7	chr1:62686882_G_GA	62686882	GA	G	0.1944240	-0.0357566	0.0043627	3.1E-17
1	DOCK7	rs56280080	62687528	T	TCAGAA	0.2056890	-0.0361741	0.0042465	1.6E-18
1	DOCK7	rs4344355	62688282	T	C	0.2062230	-0.0359609	0.0042458	2.5E-18
1	DOCK7 *	rs10889356	62689678	A	G	0.2057630	-0.0356658	0.0042426	4.8E-18
1	DOCK7 *	rs1168114	62690372	A	G	0.2139050	-0.0347043	0.0041887	1.6E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
1	DOCK7 *	rs1168113	62690427	T	C	0.2343610	-0.0302001	0.0040465	1.1E-14
1	DOCK7 *	rs35834397	62693541	TA	T	0.2244980	-0.0314417	0.0041051	2.8E-15
1	DOCK7 *	rs10889357	62694611	T	C	0.1918030	-0.0369975	0.0043592	3.7E-18
1	DOCK7 *	rs1168107	62695502	A	T	0.2245020	-0.0313511	0.0041055	3.5E-15
1	DOCK7 *	rs12136083	62697402	C	T	0.1918800	-0.0368864	0.0043579	4.4E-18
1	DOCK7 *	rs9659790	62700090	G	A	0.2244960	-0.0313752	0.0041044	3.3E-15
1	DOCK7 *	rs11208006	62704195	T	C	0.2245070	-0.0313364	0.0041049	3.6E-15
1	DOCK7 *	rs12041843	62704478	G	T	0.1765820	-0.0374683	0.0045218	7.4E-18
1	DOCK7 *	rs6682423	62705392	C	T	0.2244600	-0.0313939	0.0041047	3.2E-15
1	DOCK7 *	rs6666816	62705528	C	T	0.2244660	-0.0313843	0.0041046	3.2E-15
1	DOCK7 *	rs880694	62707613	C	T	0.2245590	-0.0313401	0.0041038	3.4E-15
1	DOCK7 *	rs10889360	62708247	T	C	0.1918660	-0.0370040	0.0043575	3.5E-18
1	DOCK7 *	rs11208007	62710412	T	A	0.1919360	-0.0369559	0.0043565	3.9E-18
1	DOCK7 *	rs4409689	62711694	C	T	0.2245270	-0.0315457	0.0041046	2.3E-15
1	DOCK7 *	rs60152331	62711868	G	T	0.3694400	-0.0216783	0.0035872	4.7E-10
1	DOCK7 *	rs7518497	62712025	C	A	0.1918550	-0.0370907	0.0043578	2.9E-18
1	DOCK7 *	rs9787151	62713467	C	T	0.2246040	-0.0315022	0.0041033	2.4E-15
1	DOCK7 *	rs9787156	62713541	G	A	0.2246040	-0.0315022	0.0041033	2.4E-15
1	DOCK7 *	rs12043910	62715877	A	G	0.1835200	-0.0383482	0.0044339	6.5E-19
1	DOCK7 *	rs6686331	62716464	C	T	0.2245100	-0.0314866	0.0041061	2.8E-15
1	DOCK7 *	rs75650238	62717743	C	CCA	0.1829110	-0.0387518	0.0044444	3.7E-19
1	DOCK7 *	rs6661669	62720298	T	C	0.2248070	-0.0317457	0.0041062	1.7E-15
1	DOCK7 *	rs76609868	62720544	C	A	0.1814520	-0.0385665	0.0044623	8.8E-19
1	DOCK7 *	rs12031537	62722415	A	C	0.1817750	-0.0387406	0.0044476	3.4E-19
1	DOCK7 *	rs7517372	62723893	G	A	0.2107560	-0.0321309	0.0042067	1.7E-15
1	DOCK7 *	rs4915624	62725847	G	A	0.2140240	-0.0322538	0.0041757	1.2E-15
1	DOCK7 *	rs76794398	62725894	A	G	0.1820190	-0.0380336	0.0044426	1.3E-18
1	DOCK7 *	rs4915853	62725906	C	A	0.2229150	-0.0312516	0.0041123	4.4E-15
1	DOCK7 *	rs199747920	62727151	ATTTTC	A	0.2144940	-0.0319704	0.0041715	2.0E-15
1	DOCK7 *	rs149188767	62727166	CTTTTCT	C	0.2231410	-0.0326033	0.0041683	5.8E-16
1	DOCK7 *	chr1:62727171_CT_C	62727171	C	CT	0.2125110	-0.0321135	0.0041917	2.3E-15
1	DOCK7 *	rs12029452	62727599	C	A	0.1820040	-0.0380391	0.0044425	1.3E-18
1	DOCK7 *	rs12026283	62728242	A	T	0.1820040	-0.0380391	0.0044425	1.3E-18
1	DOCK7 *	rs2149116	62728301	G	A	0.3733110	-0.0201741	0.0035924	7.6E-09
1	DOCK7 *	rs12023282	62728306	A	G	0.1820550	-0.0379211	0.0044430	1.6E-18
1	DOCK7 *	rs6664692	62729989	C	T	0.2108620	-0.0322165	0.0042011	2.4E-15
1	DOCK7 *	rs11208009	62730021	C	T	0.2192790	-0.0314592	0.0041401	5.6E-15
1	DOCK7 *	rs10889364	62731143	T	C	0.1820940	-0.0380308	0.0044405	1.2E-18
1	DOCK7 *	rs12049254	62731481	C	G	0.1821280	-0.0380535	0.0044403	1.2E-18
1	DOCK7 *	rs76753312	62733237	C	G	0.1821100	-0.0375010	0.0044365	4.2E-18
1	DOCK7 *	chr1:62733488_GA_G	62733488	GA	G	0.1832230	-0.0379939	0.0044373	2.2E-18
1	DOCK7 *	rs4630152	62733601	C	T	0.2113420	-0.0319489	0.0041924	4.6E-15
1	DOCK7 *	rs150990100	62733676	TG	T	0.2206550	-0.0308614	0.0041488	2.1E-14
1	DOCK7 *	rs61775961	62733677	G	T	0.2202580	-0.0307480	0.0041541	2.7E-14
1	DOCK7 *	rs61775962	62733679	A	G	0.2202580	-0.0307480	0.0041541	2.7E-14
1	DOCK7 *	rs6679002	62734265	G	T	0.2198930	-0.0311519	0.0041301	1.1E-14
1	DOCK7 *	rs12024044	62734645	A	G	0.1826550	-0.0378663	0.0044305	2.1E-18
1	DOCK7 *	rs12025111	62735769	A	G	0.1824990	-0.0377368	0.0044324	2.8E-18
1	DOCK7 *	rs12028944	62735867	A	T	0.1826140	-0.0377120	0.0044310	2.9E-18
1	ATG4C *	chr1:62736501_AT_A	62736501	AT	A	0.1933680	-0.0363505	0.0044373	9.1E-17
1	ATG4C *	rs12121288	62736790	G	A	0.2109940	-0.0321008	0.0042010	4.2E-15
1	ATG4C *	rs72915166	62736922	A	G	0.2106530	-0.0323481	0.0042071	2.6E-15
1	ATG4C *	rs78731792	62736973	A	G	0.1819140	-0.0383391	0.0044509	1.4E-18
1	ATG4C *	rs66676942	62737728	A	AT	0.1790650	-0.0379913	0.0045128	9.2E-18
1	ATG4C *	rs10789123	62737950	T	A	0.2070130	-0.0321658	0.0042853	1.3E-14
1	ATG4C *	rs12027341	62738235	A	G	0.1775030	-0.0374823	0.0045379	4.4E-17
1	ATG4C *	rs77870744	62738693	C	T	0.1793120	-0.0367212	0.0045294	1.6E-16
2	APOB *	rs10201379	20943917	C	A	0.1319710	0.0283637	0.0050994	6.0E-09
2	APOB *	rs4426495	20944222	C	T	0.1319440	0.0284204	0.0050987	5.4E-09
2	APOB *	rs10180633	20945069	G	T	0.1284490	0.0281546	0.0051603	1.2E-08
2	APOB *	rs10183548	20945739	G	A	0.1269580	0.0278127	0.0051715	1.7E-08
2	APOB *	rs5829761	20946172	AC	A	0.1269710	0.0278195	0.0051714	1.8E-08
2	APOB *	rs6732011	20946761	G	T	0.1271220	0.0280930	0.0051691	1.2E-08
2	APOB *	rs3923037	20948514	A	C	0.1248650	0.0276571	0.0052079	2.5E-08
2	APOB *	rs148458076	20955854	C	T	0.1236930	0.0316114	0.0052246	2.8E-10
2	APOB *	rs36145916	20956506	T	C	0.1229630	0.0319327	0.0052372	2.2E-10
2	APOB *	rs36187918	20958070	G	A	0.1231660	0.0314804	0.0052328	3.5E-10
2	APOB *	rs1344063	20961673	T	C	0.1263250	0.0317569	0.0051641	1.7E-10
2	APOB *	rs2337382	20961892	A	G	0.0894322	0.0329797	0.0060148	9.5E-09
2	APOB *	rs4665639	20964019	A	G	0.1227090	0.0320565	0.0052194	1.9E-10
2	APOB *	rs6707950	20964769	T	C	0.0872770	0.0342033	0.0060774	4.4E-09
2	APOB *	rs4665790	20965698	T	A	0.1231620	0.0322679	0.0052102	1.3E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs17041662	20966196	C	T	0.1231100	0.0322638	0.0052111	1.4E-10
2	APOB *	rs17041663	20967366	G	T	0.1226140	0.0320293	0.0052198	1.9E-10
2	APOB *	rs35695820	20967415	G	GCGCC	0.1327600	0.0275929	0.0050721	1.3E-08
2	APOB *	rs6706783	20968537	A	T	0.0871931	0.0341170	0.0060787	4.8E-09
2	APOB *	rs1320144	20969240	A	C	0.1225380	0.0321419	0.0052214	1.8E-10
2	APOB *	rs1320145	20969490	G	A	0.1229870	0.0323922	0.0052147	1.2E-10
2	APOB *	rs35893087	20969651	A	G	0.1225590	0.0321874	0.0052217	1.6E-10
2	APOB *	rs17041679	20972540	T	C	0.1229650	0.0316537	0.0052133	3.0E-10
2	APOB *	rs34335269	20973378	A	G	0.1221440	0.0318864	0.0052273	2.2E-10
2	APOB *	rs6733447	20975264	G	A	0.1233750	0.0321251	0.0052059	1.4E-10
2	APOB *	rs10495713	20977647	A	G	0.1216170	0.0331033	0.0052383	5.2E-11
2	APOB *	rs7608123	20980007	T	G	0.1215870	0.0331521	0.0052381	4.9E-11
2	APOB *	rs7571469	20981609	G	C	0.1216040	0.0331215	0.0052364	5.2E-11
2	APOB *	rs35131127	20983042	C	T	0.0876653	0.0343477	0.0060620	3.7E-09
2	APOB *	rs9789416	20983180	A	G	0.1214750	0.0331140	0.0052388	6.1E-11
2	APOB *	rs56327713	20983964	T	G	0.0876798	0.0347545	0.0060677	2.5E-09
2	APOB *	rs56403064	20984034	C	T	0.1219920	0.0336250	0.0052306	2.8E-11
2	APOB *	rs56213756	20984123	G	C	0.1217020	0.0337799	0.0052367	2.3E-11
2	APOB *	rs34059329	20986894	T	C	0.0877389	0.0352780	0.0060636	1.6E-09
2	APOB *	chr2:20986987_TG_T	20986987	TG	T	0.1726720	0.0260021	0.0046312	1.1E-08
2	APOB *	rs1320143	20989476	G	A	0.1206240	0.0345351	0.0052670	1.4E-11
2	APOB *	rs6721844	20989699	T	G	0.0872996	0.0344204	0.0060842	4.0E-09
2	APOB *	rs6722374	20990190	T	G	0.1201780	0.0342711	0.0052787	1.7E-11
2	APOB *	rs4665642	20990313	G	A	0.1201820	0.0342773	0.0052791	1.7E-11
2	APOB *	rs1318006	20991280	G	A	0.1207750	0.0340283	0.0052740	2.4E-11
2	APOB *	rs1318005	20991336	G	A	0.1205000	0.0337008	0.0052807	3.6E-11
2	APOB *	rs1318004	20991337	C	T	0.1205000	0.0337008	0.0052807	3.6E-11
2	APOB *	rs12992267	20992773	T	C	0.0718893	0.0379201	0.0066492	1.1E-08
2	APOB *	rs34776010	20993375	G	C	0.0719042	0.0379868	0.0066484	1.0E-08
2	APOB *	rs57947200	20994357	A	T	0.0699668	0.0372986	0.0067715	3.6E-08
2	APOB *	rs56984418	20994358	G	A	0.0721084	0.0375550	0.0066409	1.4E-08
2	APOB *	rs4665709	20998083	A	G	0.0722574	0.0371220	0.0066353	2.0E-08
2	APOB *	rs4371387	20998261	A	G	0.0721603	0.0371784	0.0066382	1.8E-08
2	APOB	rs2854725	21014914	G	T	0.1554430	-0.0254457	0.0047435	2.4E-08
2	APOB	rs57825321	21024193	A	T	0.1469170	-0.0309778	0.0048718	4.1E-11
2	APOB	rs13306194	21029662	A	G	0.1433950	-0.0341959	0.0049345	8.9E-13
2	APOB *	rs11893021	21050706	G	T	0.1786390	-0.0254215	0.0045583	3.8E-09
2	APOB *	rs58612563	21051291	G	A	0.1788920	-0.0250849	0.0045500	5.6E-09
2	APOB *	rs75022238	21052006	C	T	0.1789340	-0.0252955	0.0045477	3.9E-09
2	APOB *	rs111397565	21052832	CA	C	0.1790450	-0.0251700	0.0045445	4.1E-09
2	APOB *	chr2:21054688_TTTG_T	21054688	T	TTTG	0.1779800	-0.0252708	0.0045769	5.4E-09
2	APOB *	rs57922105	21055341	T	C	0.1734790	-0.0251921	0.0045906	6.4E-09
2	APOB *	rs75565290	21055810	G	A	0.1735170	-0.0252771	0.0045885	5.5E-09
2	APOB *	rs75208098	21060292	C	T	0.1742640	-0.0253942	0.0045756	3.9E-09
2	APOB *	rs60857806	21061227	G	T	0.1738500	-0.0252703	0.0045811	4.6E-09
2	APOB *	rs56885855	21061405	T	C	0.1738660	-0.0253272	0.0045815	4.3E-09
2	APOB *	rs75953246	21061841	A	G	0.1738600	-0.0252903	0.0045809	4.5E-09
2	APOB *	rs77257367	21062230	T	C	0.1730960	-0.0254907	0.0045890	4.2E-09
2	APOB *	rs11894096	21062695	G	A	0.1716170	-0.0252803	0.0046126	5.8E-09
2	APOB *	chr2:21062703_C_CA	21062703	CA	C	0.1742180	-0.0253754	0.0045757	4.0E-09
2	APOB *	rs11894310	21063145	G	A	0.1747120	-0.0256014	0.0045680	2.8E-09
2	APOB *	rs57024468	21064771	C	T	0.1747420	-0.0256459	0.0045668	2.6E-09
2	APOB *	rs67608778	21067028	A	AAG	0.1725530	-0.0245754	0.0046003	1.3E-08
2	APOB *	rs75207863	21068360	A	G	0.1750460	-0.0252303	0.0045653	4.3E-09
2	APOB *	rs79662771	21068361	G	A	0.1750460	-0.0252303	0.0045653	4.3E-09
2	APOB *	rs113414662	21068827	T	TAAAG	0.1750460	-0.0252303	0.0045653	4.3E-09
2	APOB *	rs17041755	21069695	A	G	0.1750600	-0.0252174	0.0045652	4.4E-09
2	APOB *	rs1897084	21074114	G	A	0.1744060	-0.0248335	0.0045556	7.4E-09
2	APOB *	rs7422168	21074322	C	G	0.1744090	-0.0249381	0.0045554	6.4E-09
2	APOB *	rs58420813	21077134	C	T	0.1748580	-0.0249279	0.0045463	6.5E-09
2	APOB *	rs80196520	21078435	A	C	0.1750430	-0.0248997	0.0045436	6.5E-09
2	APOB *	rs59263713	21079390	T	G	0.1750900	-0.0247061	0.0045427	8.4E-09
2	APOB *	rs11886946	21082715	C	A	0.1754520	-0.0251072	0.0045363	4.9E-09
2	APOB *	rs79721590	21083359	C	G	0.1754000	-0.0249906	0.0045365	5.8E-09
2	APOB *	rs112680646	21084238	A	G	0.1754550	-0.0246939	0.0045345	7.7E-09
2	APOB *	rs138654155	21091983	A	ATATCT	0.1767440	-0.0242376	0.0045046	1.2E-08
2	APOB *	rs57666320	21093675	T	C	0.1761740	-0.0245745	0.0045020	7.6E-09
2	APOB *	rs11899839	21095586	A	T	0.1770310	-0.0234940	0.0044858	2.7E-08
2	APOB *	rs1544977	21097940	G	C	0.1770310	-0.0235688	0.0044827	2.5E-08
2	APOB *	rs76234631	21101118	A	C	0.1772080	-0.0234501	0.0044804	2.8E-08
2	APOB *	rs77449706	21104188	T	C	0.1772170	-0.0232334	0.0044834	3.8E-08
2	APOB *	rs77809614	21105146	A	C	0.1769700	-0.0236308	0.0044837	2.2E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	APOB *	rs57334943	21105494	GCTTC	G	0.1768400	-0.0234314	0.0044870	2.9E-08
2	APOB *	rs6757883	21107738	G	A	0.1771140	-0.0233904	0.0044824	2.9E-08
2	APOB *	rs2337384	21110978	G	A	0.1771320	-0.0233223	0.0044821	3.2E-08
2	APOB *	rs78943787	21111867	A	T	0.1771320	-0.0233223	0.0044821	3.2E-08
2	APOB *	rs74367604	21112857	C	T	0.1771320	-0.0233223	0.0044821	3.2E-08
2	APOB *	rs112223447	21113105	CACTG	C	0.1771320	-0.0233223	0.0044821	3.2E-08
2	APOB *	rs61086479	21114871	T	C	0.1770920	-0.0233179	0.0044819	3.2E-08
2	APOB *	rs12172886	21116332	G	C	0.1770920	-0.0233179	0.0044819	3.2E-08
2	APOB *	rs11892905	21116651	G	A	0.1771040	-0.0232716	0.0044822	3.4E-08
2	APOB *	rs74957119	21118017	C	T	0.1771180	-0.0232566	0.0044821	3.5E-08
2	APOB *	rs72207140	21118375	T	TA	0.1771050	-0.0233030	0.0044818	3.3E-08
2	APOB *	rs312955	21119021	G	A	0.2704800	0.0198443	0.0038671	3.0E-08
2	APOB *	rs79542263	21121389	G	A	0.1771450	-0.0233074	0.0044819	3.2E-08
2	APOB *	rs76885666	21121682	C	A	0.1771450	-0.0233074	0.0044819	3.2E-08
2	APOB *	rs78051902	21122133	A	C	0.1719230	-0.0237772	0.0045470	3.0E-08
2	APOB *	rs61517696	21126306	C	T	0.1772020	-0.0232586	0.0044811	3.3E-08
2	APOB *	rs74582026	21127869	C	T	0.1772610	-0.0232305	0.0044820	3.3E-08
2	APOB *	rs61142046	21129214	C	T	0.1766140	-0.0231257	0.0044894	4.2E-08
2	APOB *	rs77258720	21129410	A	G	0.1771990	-0.0232539	0.0044811	3.3E-08
2	APOB *	rs79909173	21129857	C	T	0.1771990	-0.0232539	0.0044811	3.3E-08
2	APOB *	rs61437001	21131249	A	G	0.1772370	-0.0231535	0.0044802	3.8E-08
2	APOB *	rs11903814	21133608	C	T	0.1768170	-0.0231590	0.0044870	4.0E-08
2	APOB *	rs59537367	21134007	A	T	0.1765780	-0.0232731	0.0044877	3.5E-08
2	APOB *	rs79538365	21136575	G	C	0.1769750	-0.0233297	0.0044838	3.4E-08
2	APOB *	rs78059021	21148150	T	C	0.1769350	-0.0234543	0.0044845	2.9E-08
2	APOB *	rs140043113	21149823	T	G	0.1769560	-0.0234426	0.0044850	2.9E-08
2	APOB *	rs11900335	21150887	C	T	0.1769400	-0.0233862	0.0044849	3.2E-08
2	APOB *	rs113725991	21151946	T	C	0.1754520	-0.0232089	0.0045042	4.7E-08
2	APOB *	rs11893753	21152259	G	A	0.1769210	-0.0234082	0.0044846	3.0E-08
2	APOB *	rs60403956	21153184	G	A	0.1765770	-0.0233580	0.0044900	3.6E-08
2	APOB *	rs58658975	21153912	T	C	0.1762710	-0.0235430	0.0044926	3.0E-08
2	APOB *	rs60132502	21153937	A	G	0.1762710	-0.0235430	0.0044926	3.0E-08
2	APOB *	rs74369686	21154770	G	T	0.1772230	-0.0232730	0.0044823	3.5E-08
2	APOB *	rs34468875	21160481	T	C	0.2708780	0.0197930	0.0038686	4.1E-08
2	APOB *	rs114624425	21162078	G	A	0.1769360	-0.0233747	0.0044871	3.3E-08
2	ABHD1	rs4665946	27125063	A	C	0.3003460	0.0207655	0.0037599	1.5E-08
2	ABHD1	rs4665947	27125161	C	T	0.3013410	0.0206473	0.0037671	2.7E-08
2	ABHD1	rs6741646	27125330	T	C	0.3077240	0.0203766	0.0037228	2.5E-08
2	PRR30 *	chr2:27141287_CT_C	27141287	C	CT	0.2912460	0.0212467	0.0038346	3.6E-08
2	SLC5A6 *	rs74684611	27191771	C	T	0.1061800	-0.0392144	0.0056662	4.2E-12
2	PPM1G	rs79803862	27399271	A	T	0.0664130	-0.0424152	0.0069907	1.0E-09
2	PPM1G *	rs1728918	27412596	A	G	0.2082430	0.0254021	0.0042156	1.5E-09
2	NRBP1 *	rs147530299	27419228	A	AGTGGC	0.1576030	0.0261863	0.0047341	1.8E-08
2	GCKR	rs1260326	27508073	T	C	0.4923840	0.0649157	0.0034249	1.5E-85
2	GCKR	rs3817588	27508345	C	T	0.3586490	-0.0613679	0.0035533	8.3E-72
2	GCKR	rs148527487	27509703	AT	A	0.3538230	-0.0614450	0.0035883	1.7E-70
2	GCKR	rs6547692	27512105	G	A	0.4912770	0.0637266	0.0034329	4.4E-82
2	GCKR	rs780096	27518205	C	G	0.4906700	0.0634371	0.0034259	1.7E-81
2	GCKR	rs780095	27518238	A	G	0.4893160	0.0630616	0.0034290	2.9E-80
2	GCKR	rs780094	27518370	T	C	0.4800890	0.0629140	0.0034249	2.2E-80
2	GCKR	rs780093	27519736	T	C	0.4829110	0.0615249	0.0034267	6.6E-77
2	GCKR	rs780092	27520287	G	A	0.3609540	-0.0599885	0.0035489	1.1E-68
2	GCKR	rs814295	27520348	G	A	0.3625950	-0.0597342	0.0035453	3.5E-68
2	GCKR	rs74928908	27521222	G	A	0.3597940	-0.0600414	0.0035531	1.4E-68
2	GCKR *	rs1260334	27525730	C	A	0.4863690	0.0616551	0.0034416	1.0E-76
2	GCKR *	rs1260333	27525757	A	G	0.4855880	0.0608223	0.0034197	1.6E-75
2	GCKR *	rs1313566	27526037	G	A	0.4831060	0.0620103	0.0034450	2.2E-77
2	GCKR *	rs11336847	27526125	AT	A	0.4833780	0.0612796	0.0034566	4.4E-75
2	GCKR *	rs6744393	27527272	T	C	0.3600610	-0.0600084	0.0035901	2.0E-67
2	GCKR *	rs2950835	27527678	A	G	0.4848640	0.0617507	0.0034712	1.0E-75
2	GCKR *	rs2911711	27527679	T	A	0.4848640	0.0617517	0.0034712	1.0E-75
2	GCKR *	rs78680773	27528695	C	A	0.3585840	-0.0598243	0.0035915	5.7E-67
2	GCKR *	rs6753534	27530004	C	T	0.4861880	0.0554696	0.0034823	6.4E-61
2	GCKR *	rs74450311	27531758	C	CAT	0.3752080	-0.0472782	0.0035312	2.9E-43
2	GCKR *	rs62131879	27532245	G	T	0.3759780	-0.0474699	0.0035298	1.2E-43
2	GCKR *	rs7606605	27532849	T	A	0.2107780	0.0288565	0.0042774	1.6E-12
2	GCKR *	rs4665987	27532958	A	G	0.4737900	0.0510694	0.0034308	9.2E-53
2	GCKR *	rs10181342	27534476	G	A	0.3759180	-0.0474540	0.0035293	1.3E-43
2	GCKR *	rs4665988	27538569	A	C	0.4739030	0.0511350	0.0034306	6.7E-53
2	GCKR *	rs116443177	27541255	T	C	0.3775590	-0.0467432	0.0035263	2.0E-42
2	GCKR *	rs62131881	27541914	T	G	0.3758110	-0.0474857	0.0035288	1.2E-43
2	GCKR *	rs62131882	27542613	C	T	0.3773110	-0.0468768	0.0035239	1.1E-42

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	GCKR *	rs12473139	27542720	C	T	0.4746930	0.0515177	0.0034296	1.2E-53
2	GCKR *	rs4665991	27543417	A	G	0.4743060	0.0513882	0.0034324	2.7E-53
2	GCKR *	rs67080990	27544621	G	GC	0.4748140	0.0514337	0.0034303	1.9E-53
2	GCKR *	rs62141278	27545514	T	C	0.3780190	-0.0467610	0.0035248	1.6E-42
2	GCKR *	rs59210625	27546607	C	A	0.2109890	0.0289240	0.0042745	1.3E-12
2	GCKR *	rs62141279	27548548	T	C	0.3766890	-0.0468336	0.0035280	1.7E-42
2	C2orf16 *	chr2:27550224_C_CT	27550224	CT	C	0.3723320	-0.0463387	0.0035591	8.0E-41
2	C2orf16 *	rs2384627	27551582	A	G	0.3761050	-0.0466218	0.0035263	3.7E-42
2	C2orf16 *	rs202103665	27553764	A	AT	0.4728500	0.0513999	0.0034292	2.7E-53
2	C2orf16 *	rs62141281	27554784	T	G	0.3767080	-0.0467968	0.0035232	1.8E-42
2	C2orf16 *	rs6751087	27555149	C	T	0.3767080	-0.0467968	0.0035232	1.8E-42
2	C2orf16 *	rs12995461	27555300	C	A	0.4732400	0.0514022	0.0034269	2.5E-53
2	C2orf16 *	rs10169065	27555693	G	A	0.4732400	0.0514033	0.0034269	2.5E-53
2	C2orf16 *	rs10179872	27555705	A	G	0.4719480	0.0509214	0.0034294	2.2E-52
2	C2orf16 *	rs79414972	27558930	G	A	0.3640810	-0.0460415	0.0035901	1.4E-39
2	C2orf16 *	rs62141288	27560331	A	G	0.3544280	-0.0445219	0.0036168	5.9E-37
2	C2orf16 *	rs200969564	27560335	GAC	G	0.3544280	-0.0445219	0.0036168	5.9E-37
2	C2orf16 *	rs62141290	27560525	C	T	0.3748310	-0.0468481	0.0035335	2.6E-42
2	C2orf16 *	rs4665382	27560934	C	T	0.4732670	0.0513603	0.0034272	3.1E-53
2	C2orf16 *	rs62141291	27561167	T	C	0.3767260	-0.0467559	0.0035228	2.2E-42
2	C2orf16 *	rs62141292	27561433	C	A	0.3767180	-0.0467722	0.0035227	2.0E-42
2	C2orf16 *	rs7570476	27561791	T	C	0.4731870	0.0514327	0.0034273	2.3E-53
2	C2orf16 *	rs10208529	27563321	T	A	0.4731870	0.0514324	0.0034273	2.3E-53
2	C2orf16 *	rs60854669	27564062	C	T	0.3766790	-0.0467357	0.0035231	2.3E-42
2	C2orf16 *	rs965813	27566994	A	T	0.3766790	-0.0467189	0.0035231	2.5E-42
2	C2orf16 *	rs4665383	27568688	G	C	0.4731870	0.0514324	0.0034273	2.3E-53
2	C2orf16 *	rs59876138	27569456	C	A	0.3766870	-0.0467126	0.0035232	2.5E-42
2	C2orf16 *	rs7577311	27571054	T	G	0.4733640	0.0514031	0.0034288	3.0E-53
2	C2orf16 *	rs6704596	27574060	G	A	0.3766870	-0.0467126	0.0035232	2.5E-42
2	C2orf16	rs1919127	27578626	C	T	0.4731880	0.0512774	0.0034259	4.0E-53
2	C2orf16	rs1919128	27578892	G	A	0.4732100	0.0512693	0.0034257	4.1E-53
2	C2orf16	rs3811644	27579938	G	A	0.3766810	-0.0466381	0.0035226	3.3E-42
2	ZNF512	rs6734059	27585287	C	T	0.3767870	-0.0466031	0.0035228	3.5E-42
2	ZNF512	rs12478841	27588855	G	A	0.4740370	0.0515352	0.0034256	1.2E-53
2	ZNF512	rs6760250	27589385	A	G	0.4740370	0.0515352	0.0034256	1.2E-53
2	ZNF512	rs62138963	27591507	T	C	0.3766420	-0.0466390	0.0035227	3.2E-42
2	ZNF512	rs62138964	27591571	T	C	0.3766420	-0.0466390	0.0035227	3.2E-42
2	ZNF512	rs145275920	27591660	T	C	0.0576741	-0.0401941	0.0074090	1.1E-08
2	ZNF512	rs13022873	27592643	C	A	0.4741330	0.0515268	0.0034266	1.4E-53
2	ZNF512	rs76013440	27593448	A	G	0.3754730	-0.0468848	0.0035303	2.7E-42
2	ZNF512	rs62138965	27593726	C	T	0.3758030	-0.0464595	0.0035281	1.1E-41
2	ZNF512	rs13010586	27594950	A	G	0.4740590	0.0515202	0.0034254	1.3E-53
2	ZNF512	rs1919129	27595854	G	C	0.3766470	-0.0466373	0.0035227	3.2E-42
2	ZNF512	rs62138966	27596305	A	G	0.3764140	-0.0468299	0.0035237	1.7E-42
2	ZNF512	rs12989678	27598615	T	C	0.4735070	0.0520438	0.0034379	4.2E-54
2	ZNF512	rs78378018	27599416	GAC	G	0.3767200	-0.0467388	0.0035230	2.3E-42
2	ZNF512	rs117655217	27600099	C	T	0.0574302	-0.0404691	0.0074146	9.6E-09
2	ZNF512	rs56725354	27601301	C	G	0.3766470	-0.0466373	0.0035227	3.2E-42
2	ZNF512	rs62138968	27601618	G	C	0.3766450	-0.0466461	0.0035227	3.1E-42
2	ZNF512	rs112927528	27601644	TTTTTG	T	0.3755740	-0.0469588	0.0035276	1.5E-42
2	ZNF512	rs12467476	27602848	C	T	0.4726600	0.0509932	0.0034289	1.5E-52
2	ZNF512	rs12464616	27604225	T	C	0.4740100	0.0514827	0.0034257	1.5E-53
2	ZNF512	rs2141372	27604329	T	G	0.3766530	-0.0465763	0.0035231	4.2E-42
2	ZNF512	rs66497975	27604459	T	AGTCATGT/	0.4726860	0.0513004	0.0034324	4.0E-53
2	ZNF512	rs6719960	27607200	G	A	0.3765980	-0.0466931	0.0035230	2.6E-42
2	ZNF512	rs6547735	27608740	C	T	0.3765910	-0.0467073	0.0035231	2.6E-42
2	ZNF512	rs2384656	27609188	G	A	0.4740170	0.0515204	0.0034259	1.3E-53
2	ZNF512	rs1881397	27609418	G	A	0.3770890	-0.0463975	0.0035253	1.1E-41
2	ZNF512	chr2:27609869_CA_C	27609869	C	CA	0.3962840	-0.0431624	0.0035638	1.3E-35
2	ZNF512	rs112427483	27610460	T	TTATATATC	0.3313870	-0.0484596	0.0037004	2.9E-41
2	ZNF512	rs74175068	27610635	C	T	0.4609180	0.0505056	0.0034975	7.3E-50
2	ZNF512	rs34016998	27610820	T	C	0.4734260	0.0515284	0.0034266	1.5E-53
2	ZNF512	rs12987055	27611285	C	T	0.4739400	0.0510923	0.0034259	1.1E-52
2	ZNF512	rs13405762	27611748	C	A	0.3741010	-0.0467988	0.0035359	5.1E-42
2	ZNF512	rs78170284	27612215	A	G	0.3768270	-0.0463800	0.0035236	1.0E-41
2	ZNF512	rs13020949	27613738	T	C	0.4736070	0.0512122	0.0034279	6.8E-53
2	ZNF512	chr2:27614806_CT_C	27614806	C	CT	0.3765810	-0.0464307	0.0035262	1.0E-41
2	ZNF512	rs1881395	27615682	A	G	0.3764930	-0.0464260	0.0035268	1.1E-41
2	ZNF512	rs4666000	27616502	C	T	0.4734450	0.0509468	0.0034285	1.8E-52
2	ZNF512	rs2068834	27616672	C	T	0.4732710	0.0511324	0.0034287	1.0E-52
2	ZNF512	rs7571558	27616965	G	C	0.3765760	-0.0464287	0.0035269	1.1E-41
2	ZNF512	rs4666001	27617672	G	A	0.1570650	0.0284478	0.0047114	1.1E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	ZNF512	rs4666002	27617773	C	G	0.4730600	0.0513189	0.0034330	6.1E-53
2	ZNF512	rs62138971	27617887	A	G	0.3756190	-0.0475448	0.0035443	3.1E-43
2	ZNF512	rs1881396	27621734	G	T	0.3713280	-0.0474396	0.0035536	9.6E-43
2	GPN1	rs3749147	27629051	A	G	0.3148850	0.0408596	0.0036960	5.1E-30
2	GPN1	rs146892484	27629283	C	CG	0.4177300	0.0323177	0.0034916	1.3E-21
2	GPN1	rs34502053	27631657	A	G	0.3173420	0.0415581	0.0036921	5.5E-31
2	GPN1	rs10173720	27632530	A	T	0.4189400	0.0317289	0.0034853	6.4E-21
2	GPN1	rs6719175	27636484	A	T	0.3157800	0.0416345	0.0037112	7.9E-31
2	GPN1	rs77350364	27643272	A	G	0.4186050	0.0315351	0.0034953	1.3E-20
2	GPN1	rs12474585	27648726	C	T	0.4184860	0.0318283	0.0034936	5.0E-21
2	GPN1	rs35605899	27649445	A	AATAT	0.3364040	0.0369398	0.0036461	8.7E-26
2	GPN1	rs8731	27650459	C	G	0.4180620	0.0319521	0.0034942	3.7E-21
2	SUPT7L	chr2:27652149_AAAAT_A	27652149	AAAAT	A	0.4173730	0.0316469	0.0035003	8.9E-21
2	SUPT7L	rs67775899	27652169	TAAA	T	0.4179250	0.0310308	0.0035039	4.5E-20
2	SUPT7L	rs10202364	27652175	T	A	0.4184170	0.0312363	0.0034995	2.5E-20
2	SUPT7L	rs4666010	27655819	T	C	0.4179910	0.0320280	0.0034941	3.3E-21
2	SLC4A1AP	rs2272406	27669156	T	A	0.3364430	0.0368105	0.0036443	1.2E-25
2	SLC4A1AP	rs76586169	27674968	G	A	0.4178270	0.0319908	0.0034937	3.5E-21
2	SLC4A1AP	rs13021208	27678861	T	C	0.3364070	0.0373089	0.0036457	3.0E-26
2	SLC4A1AP	rs72613829	27680120	C	T	0.4168350	0.0322247	0.0034973	2.1E-21
2	SLC4A1AP	rs13023094	27687839	C	A	0.3365680	0.0368422	0.0036428	1.0E-25
2	SLC4A1AP	rs12998770	27690321	C	T	0.3367570	0.0369211	0.0036431	9.0E-26
2	SLC4A1AP *	rs80322731	27697569	G	A	0.2088700	0.0274140	0.0042891	2.1E-11
2	SLC4A1AP *	rs13030973	27705930	C	T	0.3337480	0.0363187	0.0036432	5.2E-25
2	SLC4A1AP *	rs4665385	27707970	C	T	0.4133860	0.0314891	0.0034963	1.7E-20
2	SLC4A1AP *	rs6727388	27709720	G	A	0.3329700	0.0363690	0.0036467	4.9E-25
2	SLC4A1AP *	rs4616435	27710775	T	C	0.3336860	0.0363326	0.0036440	5.1E-25
2	SLC4A1AP *	rs58199976	27711657	T	C	0.4126540	0.0317345	0.0034974	9.6E-21
2	SLC4A1AP *	rs6727215	27711864	A	G	0.3329390	0.0364360	0.0036470	4.0E-25
2	SLC4A1AP *	rs4665386	27712485	C	A	0.4140630	0.0321054	0.0034956	3.7E-21
2	SLC4A1AP *	rs6742571	27719021	G	A	0.4195850	0.0321158	0.0034933	2.8E-21
2	SLC4A1AP *	chr2:27724905_CT_C	27724905	C	CT	0.4120210	0.0303852	0.0035408	8.7E-19
2	SLC4A1AP *	rs1881394	27726185	G	A	0.4159800	0.0313225	0.0035202	4.3E-20
2	SLC4A1AP *	rs10432705	27727970	A	G	0.3325230	0.0366497	0.0036814	5.8E-25
2	SLC4A1AP *	rs867282	27728791	C	T	0.4159460	0.0312426	0.0035151	4.4E-20
2	SLC4A1AP *	rs2384655	27729368	T	A	0.4159860	0.0311427	0.0035151	5.6E-20
2	SLC4A1AP *	rs12994085	27729539	T	C	0.4159880	0.0311625	0.0035153	5.4E-20
2	SLC4A1AP *	rs12993377	27729900	C	G	0.4159790	0.0311698	0.0035153	5.2E-20
2	MRPL33 *	rs12624148	27733614	C	T	0.4161610	0.0313570	0.0035229	4.1E-20
2	MRPL33 *	rs6753736	27735988	G	C	0.4210200	0.0296609	0.0035145	2.8E-18
2	MRPL33 *	rs75429814	27738747	T	C	0.4113310	0.0278116	0.0035417	2.8E-16
2	MRPL33 *	rs111938697	27740266	C	T	0.4157380	0.0285310	0.0035292	5.9E-17
2	MRPL33 *	rs12714223	27740463	A	G	0.4147440	0.0280097	0.0035285	2.0E-16
2	MRPL33 *	rs36017854	27740804	AAT	A	0.4137510	0.0281003	0.0035354	1.8E-16
2	MRPL33 *	rs9678824	27741461	G	C	0.4148620	0.0278994	0.0035271	2.6E-16
2	MRPL33 *	rs13023194	27744393	C	G	0.3341970	0.0317956	0.0036721	3.5E-19
2	MRPL33 *	rs9967838	27745587	C	A	0.4148760	0.0279292	0.0035076	1.7E-16
2	MRPL33 *	chr2:27747209_A_AT	27747209	AT	A	0.4031410	0.0266052	0.0035292	5.5E-15
2	MRPL33 *	rs9677663	27749578	A	G	0.4100290	0.0279966	0.0034973	1.0E-16
2	MRPL33 *	rs57238885	27751393	C	G	0.4101130	0.0280924	0.0034934	7.0E-17
2	MRPL33 *	rs10201247	27752104	G	A	0.4101130	0.0280924	0.0034934	7.0E-17
2	MRPL33 *	rs6547796	27752527	C	T	0.4103730	0.0280448	0.0034939	8.3E-17
2	MRPL33 *	rs4666011	27758045	G	C	0.4101420	0.0281355	0.0034930	6.0E-17
2	MRPL33 *	rs10209020	27758077	T	C	0.4104290	0.0280756	0.0034942	7.1E-17
2	MRPL33 *	rs12471347	27758788	G	C	0.4102150	0.0281951	0.0034919	5.0E-17
2	MRPL33 *	rs77154381	27759252	A	G	0.4083720	0.0278759	0.0034968	1.0E-16
2	MRPL33 *	rs12477908	27764179	C	A	0.4112860	0.0278068	0.0034893	1.2E-16
2	MRPL33 *	rs13006480	27764354	G	C	0.3266360	0.0310207	0.0036871	2.9E-18
2	MRPL33 *	rs140124512	27764951	T	A	0.0434867	-0.0528272	0.0086032	1.7E-10
2	MRPL33 *	rs13013484	27765954	A	G	0.4102670	0.0281929	0.0034921	5.2E-17
2	MRPL33 *	rs4665390	27767042	C	T	0.4112880	0.0276082	0.0034912	2.0E-16
2	MRPL33 *	rs74429612	27770976	C	T	0.4114070	0.0277938	0.0034891	1.3E-16
2	MRPL33	rs3736594	27772914	C	A	0.4113590	0.0278748	0.0034890	9.9E-17
2	MRPL33	rs3792252	27773064	A	G	0.4102520	0.0281395	0.0034917	5.9E-17
2	MRPL33	rs35463245	27777857	C	G	0.4083180	0.0277559	0.0035026	2.0E-16
2	MRPL33	rs17006242	27778184	C	A	0.4112090	0.0278651	0.0034896	1.1E-16
2	MRPL33	rs3792253	27779135	T	C	0.4101200	0.0281915	0.0034927	5.4E-17
2	MRPL33 *	rs13030345	27780307	T	G	0.3070340	0.0297065	0.0037437	1.9E-16
2	RBKS	rs74327441	27784205	G	A	0.4039620	0.0274918	0.0035441	8.7E-16
2	RBKS	rs7596967	27789917	T	G	0.3899360	0.0251861	0.0035534	2.1E-13
2	RBKS	rs7593136	27794925	A	G	0.4115320	0.0274425	0.0034901	3.6E-16
2	RBKS	rs6744348	27795158	A	C	0.4115450	0.0274362	0.0034899	3.6E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
2	RBKS	rs36035825	27795264	T	G	0.4115450	0.0274362	0.0034899	3.6E-16
2	RBKS	rs4666012	27795426	A	G	0.4115450	0.0274362	0.0034899	3.6E-16
2	RBKS	rs11322614	27796225	AT	A	0.4102050	0.0280542	0.0034988	8.2E-17
2	RBKS	rs4666013	27796239	C	T	0.4115400	0.0274994	0.0034899	3.0E-16
2	RBKS	rs4666014	27796308	G	A	0.4116800	0.0273222	0.0034895	4.6E-16
2	RBKS	rs4666015	27796500	G	A	0.4115860	0.0274579	0.0034896	3.3E-16
2	RBKS	rs34181670	27796989	T	C	0.4115860	0.0274579	0.0034896	3.3E-16
2	RBKS	rs35679500	27797099	T	C	0.4115860	0.0274579	0.0034896	3.3E-16
2	RBKS	rs12623170	27797290	C	T	0.4118470	0.0272315	0.0034885	6.3E-16
2	RBKS	rs3935148	27798099	T	A	0.4088580	0.0278835	0.0034931	1.2E-16
2	RBKS	rs13027427	27798176	G	T	0.3807800	0.0259760	0.0035408	2.9E-14
2	RBKS	rs6745545	27798978	C	G	0.3806850	0.0259265	0.0035416	3.3E-14
2	RBKS	rs7570730	27799808	G	A	0.3805800	0.0254257	0.0035450	9.3E-14
2	RBKS	rs11127125	27800253	T	C	0.3798100	0.0255020	0.0035476	9.2E-14
2	RBKS	rs11127126	27800417	C	T	0.3806380	0.0252383	0.0035458	1.4E-13
2	RBKS	rs12473340	27800930	G	A	0.3805650	0.0254008	0.0035468	1.1E-13
2	RBKS	rs12473400	27801157	G	T	0.3814980	0.0252732	0.0035474	1.3E-13
2	RBKS	rs4630723	27801464	T	C	0.3901250	0.0242836	0.0035773	1.8E-12
2	RBKS	rs13019037	27801775	C	T	0.3805990	0.0253278	0.0035501	1.3E-13
2	RBKS	rs4632296	27802117	T	C	0.3816940	0.0248863	0.0035603	3.8E-13
2	RBKS	rs13001060	27802194	T	C	0.3832800	0.0252810	0.0035572	1.3E-13
2	RBKS	rs12995865	27802199	A	C	0.3832770	0.0252808	0.0035572	1.3E-13
2	RBKS	rs11891769	27802713	G	C	0.3807410	0.0247916	0.0035504	3.9E-13
2	RBKS	rs12465012	27805324	C	T	0.3597310	0.0226448	0.0035918	5.6E-11
2	RBKS	rs4665392	27806782	A	G	0.3594240	0.0225878	0.0035920	6.5E-11
2	RBKS	rs12986980	27807570	A	G	0.3587140	0.0226575	0.0035921	5.6E-11
2	RBKS	rs13023003	27809270	G	C	0.3590420	0.0224235	0.0035880	7.9E-11
2	RBKS	rs4233716	27811517	C	T	0.3796450	0.0202820	0.0035496	2.5E-09
2	RBKS	rs4233717	27811813	A	T	0.3796450	0.0202820	0.0035496	2.5E-09
2	RBKS	chr2:27813039_TAA_T	27813039	TAA	T	0.3792340	0.0202841	0.0035500	2.6E-09
2	RBKS	rs4666016	27814273	T	A	0.3778940	0.0204385	0.0035511	2.1E-09
2	RBKS	rs4464229	27815213	C	T	0.3796180	0.0205149	0.0035540	1.7E-09
2	RBKS	rs12617171	27815932	C	T	0.3786180	0.0202754	0.0035504	2.8E-09
2	RBKS	rs4420671	27816433	G	C	0.3786740	0.0203363	0.0035493	2.4E-09
2	RBKS	rs4493211	27816605	G	T	0.3791230	0.0203808	0.0035507	2.4E-09
2	RBKS	rs4665393	27817409	G	A	0.3786870	0.0203252	0.0035492	2.5E-09
2	RBKS	rs4666017	27817658	C	A	0.3786870	0.0203252	0.0035492	2.5E-09
2	RBKS	rs12478766	27818333	T	C	0.3786480	0.0203398	0.0035498	2.6E-09
2	RBKS	rs13026758	27818406	A	G	0.3787160	0.0203670	0.0035496	2.4E-09
2	RBKS	rs4666018	27819192	C	T	0.3835640	0.0202407	0.0035481	3.1E-09
2	RBKS	rs66523005	27822746	TAGAA	T	0.3872890	0.0201570	0.0035446	3.3E-09
2	RBKS	rs4666020	27823161	G	A	0.3872460	0.0201950	0.0035437	3.0E-09
2	RBKS	chr2:27825136_CA_C	27825136	CA	C	0.3883370	0.0195044	0.0035523	1.0E-08
2	RBKS	rs9679543	27828084	C	T	0.3821070	0.0199600	0.0035359	4.6E-09
2	RBKS	rs10531773	27831894	GAA	G	0.3823360	0.0199217	0.0035372	5.0E-09
2	RBKS	rs4666021	27833014	A	G	0.3816720	0.0196876	0.0035362	7.3E-09
2	RBKS	rs9678430	27834262	G	C	0.3815960	0.0196682	0.0035370	7.5E-09
2	RBKS	rs12463914	27834492	C	T	0.3817520	0.0196682	0.0035363	7.6E-09
2	RBKS	rs7560060	27834657	T	C	0.3816720	0.0196876	0.0035362	7.3E-09
2	RBKS	rs4666022	27834956	T	C	0.3815870	0.0197593	0.0035363	6.5E-09
2	RBKS	rs12464988	27835359	C	T	0.3801470	0.0196434	0.0035538	8.3E-09
2	RBKS	rs13027666	27835566	T	C	0.3804840	0.0195370	0.0035437	1.0E-08
2	RBKS	rs11885959	27836033	C	G	0.3815870	0.0197593	0.0035363	6.5E-09
2	RBKS	rs4665394	27836155	T	C	0.3815320	0.0196588	0.0035364	7.6E-09
2	RBKS	rs12617110	27837044	A	G	0.3816320	0.0197264	0.0035364	6.8E-09
2	RBKS	rs12617113	27837070	A	G	0.3816320	0.0197264	0.0035364	6.8E-09
2	RBKS	rs12992890	27837964	T	C	0.3815870	0.0197593	0.0035363	6.5E-09
2	RBKS	rs34096628	27838123	A	C	0.3815870	0.0197593	0.0035363	6.5E-09
2	RBKS	rs4275987	27840089	A	G	0.3863310	0.0200355	0.0035493	4.5E-09
2	RBKS	rs4462754	27841127	C	T	0.3821380	0.0200360	0.0035355	4.1E-09
2	RBKS	rs9678336	27842537	A	G	0.3816170	0.0197354	0.0035364	6.8E-09
2	RBKS	rs74446114	27843255	C	T	0.3008960	0.0235829	0.0037552	7.5E-11
2	RBKS	rs4233718	27843493	A	G	0.3816990	0.0197034	0.0035365	7.0E-09
2	RBKS	rs11127127	27844037	G	T	0.3822560	0.0199659	0.0035358	4.6E-09
2	RBKS	rs11127128	27844103	T	A	0.3816990	0.0197034	0.0035365	7.0E-09
2	RBKS	rs4564736	27846676	A	T	0.3815890	0.0197594	0.0035363	6.5E-09
2	RBKS	rs11901133	27846846	T	G	0.3816360	0.0198036	0.0035365	5.9E-09
2	RBKS	rs4555299	27848323	A	G	0.3815890	0.0197594	0.0035363	6.5E-09
2	RBKS	rs35841453	27849835	T	C	0.3816750	0.0197265	0.0035364	6.8E-09
2	RBKS	rs4666024	27850112	C	G	0.3793330	0.0193417	0.0035424	1.3E-08
2	RBKS	rs4666025	27851027	C	T	0.3816750	0.0197265	0.0035364	6.8E-09
2	RBKS	rs4313931	27851834	C	T	0.3816750	0.0197265	0.0035364	6.8E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAf	BETA	SE	P
2	RBKS	rs4583413	27851957	C	T	0.3815890	0.0197594	0.0035363	6.5E-09
2	RBKS	rs4419196	27852431	A	G	0.3815890	0.0197594	0.0035363	6.5E-09
2	RBKS	rs4447576	27853381	T	C	0.3853080	0.0194906	0.0035496	9.3E-09
2	RBKS	rs11127129	27853841	C	G	0.3819660	0.0200365	0.0035436	4.5E-09
2	RBKS	rs77353560	27862677	A	C	0.2859480	0.0207700	0.0038183	2.5E-08
2	RBKS	rs71441095	27866981	A	G	0.4708340	-0.0281251	0.0034630	1.4E-16
2	RBKS	rs10171517	27867192	T	C	0.4709770	-0.0281959	0.0034627	1.1E-16
2	RBKS	rs898034	27867953	T	C	0.4710600	-0.0283076	0.0034625	8.1E-17
2	BRE	rs11691385	28076117	G	A	0.4688660	0.0194969	0.0035085	3.3E-08
2	BRE	rs6737313	28076400	G	A	0.4695520	0.0196342	0.0035074	2.8E-08
2	BRE	rs13395259	28096429	T	C	0.4514640	0.0190259	0.0034510	3.9E-08
2	BRE	rs9309659	28103391	C	G	0.4513370	0.0193328	0.0034587	2.6E-08
2	BRE	rs55796876	28107028	G	A	0.4584460	0.0196426	0.0034952	3.2E-08
3	SYN2	rs34831171	12132155	C	T	0.1172780	-0.0269385	0.0033483	4.9E-08
3	SYN2	rs7621569	12143057	G	A	0.1166700	-0.0275881	0.0033640	2.8E-08
3	SYN2	chr3:12147956_C_CA	12147956	CA	C	0.1133770	-0.0292367	0.0054407	6.9E-09
3	SYN2	chr3:12168855_AT_A	12168855	AT	A	0.1179690	-0.0281848	0.0053383	1.4E-08
3	SYN2	rs310763	12189204	T	C	0.1180580	-0.0274312	0.0053328	3.1E-08
3	SYN2 *	rs7637403	12200988	A	G	0.1178270	-0.0281839	0.0053365	1.2E-08
3	SYN2 *	rs13079837	12209346	A	T	0.1187050	-0.0275022	0.0053200	1.9E-08
3	SYN2 *	rs13099882	12209388	G	A	0.1187760	-0.0276212	0.0053177	1.7E-08
3	SYN2 *	rs310749	12232268	G	T	0.1375600	-0.0271344	0.0049982	1.7E-08
4	RGS12	rs1894442	3384588	T	C	0.4602780	-0.0215952	0.0034659	3.4E-10
4	RGS12	rs12644442	3385844	A	G	0.4948970	0.0211264	0.0034836	5.7E-10
4	RGS12	rs4690090	3387800	T	C	0.4423000	-0.0205436	0.0034922	2.1E-09
4	RGS12	rs6828057	3388084	A	G	0.4449160	-0.0209303	0.0034945	1.3E-09
4	RGS12	rs13127597	3388545	C	A	0.4646900	-0.0218380	0.0034465	1.5E-10
4	RGS12	rs17797467	3390588	G	C	0.4672970	-0.0198960	0.0034662	5.2E-09
4	RGS12	rs13152128	3390623	A	C	0.4614350	-0.0210662	0.0034596	6.8E-10
4	RGS12	rs62274930	3413609	T	C	0.4745810	-0.0202759	0.0034804	5.3E-09
4	RGS12	rs3213506	3415757	A	G	0.4740190	-0.0201983	0.0034845	6.2E-09
4	RGS12	rs16844307	3416438	T	C	0.4747400	-0.0204914	0.0034861	4.2E-09
4	RGS12	rs16844309	3416539	A	G	0.4742990	-0.0206154	0.0034859	3.4E-09
4	RGS12	rs3748036	3418644	T	C	0.4746340	-0.0203388	0.0034901	6.2E-09
4	RGS12	rs4690095	3419582	C	T	0.4850520	0.0215709	0.0035053	8.1E-10
4	RGS12	rs3789739	3421715	T	C	0.4768200	-0.0208750	0.0035041	2.6E-09
4	RGS12	rs58143210	3423303	T	C	0.4732380	-0.0202871	0.0035094	7.5E-09
4	HGFAC *	rs28766336	3452024	T	G	0.4757160	-0.0199805	0.0035077	7.8E-09
4	HGFAC *	rs4690099	3452727	T	C	0.4661710	-0.0197449	0.0035099	1.0E-08
4	DOK7 *	rs2091626	3460173	T	G	0.4680600	-0.0200921	0.0035108	5.6E-09
4	DOK7 *	rs1076903	3460467	G	A	0.4680720	-0.0201754	0.0035113	4.8E-09
4	DOK7 *	rs28478452	3461750	A	G	0.4671370	-0.0202432	0.0035157	4.2E-09
4	AFF1	rs3755983	87116640	A	G	0.3996560	0.0190607	0.0035180	4.7E-08
4	AFF1	rs3775211	87117939	C	T	0.3996640	0.0190290	0.0035188	4.9E-08
4	AFF1	rs3755980	87121099	T	C	0.3988180	0.0191142	0.0035234	4.8E-08
4	AFF1	rs3775209	87125794	A	G	0.3994050	0.0192691	0.0035151	2.9E-08
4	AFF1	rs3841986	87137491	CT	C	0.4028530	0.0197339	0.0035141	1.7E-08
4	AFF1	rs10029915	87138465	C	G	0.4028070	0.0200610	0.0035160	9.9E-09
4	AFF1	rs1842685	87139680	C	T	0.4046380	0.0197874	0.0035241	1.7E-08
4	AFF1 *	rs66477840	87142207	A	G	0.4019330	0.0203053	0.0035241	7.1E-09
4	AFF1 *	rs10023056	87143314	G	A	0.4035870	0.0204138	0.0035215	5.4E-09
4	AFF1 *	rs10032710	87145107	A	G	0.3873640	0.0204132	0.0035614	6.9E-09
4	AFF1 *	rs17012512	87146352	C	T	0.3897420	0.0202791	0.0035613	1.1E-08
4	KLHL8 *	rs55747890	87155474	G	A	0.3625390	0.0200220	0.0036305	2.1E-08
5	ANKRD55 *	rs459193	56510924	A	G	0.4703360	-0.0214944	0.0034338	1.2E-10
5	LOC101928448	rs464605	56511543	C	T	0.4706020	-0.0217543	0.0034357	7.1E-11
5	LOC101928448	rs392794	56512515	C	T	0.4705330	-0.0217312	0.0034362	7.6E-11
5	LOC101928448	rs465002	56512648	C	T	0.4705310	-0.0217289	0.0034362	7.6E-11
5	LOC101928448	rs256903	56513311	C	A	0.4698900	-0.0216752	0.0034400	9.6E-11
5	LOC101928448	rs173964	56513638	A	G	0.4696480	-0.0217269	0.0034406	8.6E-11
5	LOC101928448	rs256904	56514478	A	T	0.4702010	-0.0216052	0.0034411	1.1E-10
6	MUC22	rs6457300	31030965	G	T	0.3266200	0.0205720	0.0037889	1.7E-08
6	MUC22	rs6457301	31031102	C	T	0.3264130	0.0206014	0.0037888	1.6E-08
6	MUC22	rs10807077	31033690	G	A	0.3266410	0.0207382	0.0037897	1.3E-08
6	MUC22	rs10947124	31033719	T	G	0.3265890	0.0206763	0.0037893	1.5E-08
6	MUC22	rs10947125	31033856	G	A	0.3266410	0.0207061	0.0037893	1.4E-08
6	MUC22	rs10947126	31033891	A	G	0.3282080	0.0204450	0.0037653	1.6E-08
6	HCG27 *	rs7757622	31232987	T	C	0.4345490	0.0203354	0.0038217	1.8E-08
6	VEGFA *	rs4711750	43789345	T	A	0.4362100	-0.0190694	0.0034460	4.7E-08
6	VEGFA *	rs998584	43790159	C	A	0.4424570	-0.0192849	0.0034471	2.4E-08
7	GCK *	rs2971669	44192179	T	C	0.3527470	0.0218370	0.0035913	1.9E-09
7	CAMK2B *	rs878521	44216044	A	G	0.3537630	0.0216961	0.0035866	2.1E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	FZD9 *	rs42123	73425622	G	T	0.1079390	-0.0430265	0.0055943	2.1E-16
7	FZD9 *	rs42122	73427493	A	G	0.0912032	-0.0509034	0.0059704	5.7E-20
7	FZD9 *	chr7:73428127_GAC_G	73428127	G	GAC	0.0857577	-0.0492179	0.0061667	5.8E-18
7	FZD9 *	rs140439318	73428135	C	CAT	0.0859763	-0.0524881	0.0061661	9.0E-20
7	FZD9 *	chr7:73428147_GAC_G	73428147	G	GAC	0.0884957	-0.0511511	0.0060871	3.0E-19
7	FZD9 *	chr7:73428394_GAC_G	73428394	G	GAC	0.0915995	-0.0458360	0.0060830	6.3E-16
7	FZD9 *	rs200392099	73432411	CTTT	C	0.0855588	-0.0497207	0.0061478	3.5E-18
7	FZD9 *	rs868953856	73432413	T	A	0.0741852	-0.0520651	0.0066130	3.9E-17
7	FZD9 *	rs782289776	73432414	T	C	0.0741852	-0.0520651	0.0066130	3.9E-17
7	FZD9	rs1178947	73435848	C	T	0.0896945	-0.0509149	0.0060037	5.0E-20
7	BAZ1B	rs2240466	73441939	A	G	0.0909544	-0.0499959	0.0059546	1.2E-19
7	BAZ1B	rs1178979	73442100	C	T	0.0903318	-0.0501905	0.0059768	1.1E-19
7	BAZ1B	rs1178977	73442719	G	A	0.0902478	-0.0499755	0.0059790	1.6E-19
7	BAZ1B	rs34604283	73443383	C	CA	0.0902978	-0.0502716	0.0059778	9.5E-20
7	BAZ1B	rs13231516	73448919	G	T	0.0950983	-0.0491611	0.0058367	1.0E-19
7	BAZ1B	rs714052	73450539	G	A	0.0955820	-0.0487060	0.0058258	1.5E-19
7	BAZ1B	rs34763247	73452286	T	A	0.0950859	-0.0491303	0.0058369	1.1E-19
7	BAZ1B	rs1306476	73454192	G	A	0.0950854	-0.0490039	0.0058371	1.4E-19
7	BAZ1B	rs71071936	73455536	CT	C	0.0909752	-0.0489917	0.0059640	6.2E-19
7	BAZ1B	rs35330527	73455877	G	A	0.0964574	-0.0473710	0.0058088	1.3E-18
7	BAZ1B	rs60982449	73459090	G	A	0.0891726	-0.0501369	0.0060139	2.0E-19
7	BAZ1B	rs2074755	73462836	C	T	0.0944406	-0.0490841	0.0058520	1.2E-19
7	BAZ1B	rs35797675	73463714	G	T	0.0964056	-0.0482126	0.0058051	4.2E-19
7	BAZ1B	rs12056034	73464315	G	A	0.0955716	-0.0489408	0.0058273	1.3E-19
7	BAZ1B	rs71556715	73467477	T	C	0.0944218	-0.0493295	0.0058524	8.3E-20
7	BAZ1B	rs62465144	73468776	C	T	0.0949974	-0.0491142	0.0058394	1.1E-19
7	BAZ1B	rs6976930	73471480	A	G	0.0897300	-0.0502669	0.0059925	9.6E-20
7	BAZ1B	rs35695283	73479073	G	A	0.0902148	-0.0502314	0.0059797	9.1E-20
7	BAZ1B	rs75229905	73481616	C	T	0.0949777	-0.0491853	0.0058393	9.5E-20
7	BAZ1B	rs7797566	73482065	C	A	0.0949777	-0.0491853	0.0058393	9.5E-20
7	BAZ1B	rs17145713	73490480	T	C	0.0944406	-0.0492353	0.0058520	9.7E-20
7	BAZ1B	rs111837003	73493129	T	C	0.0896401	-0.0508025	0.0059961	4.2E-20
7	BAZ1B	rs13244268	73497513	C	T	0.0950380	-0.0496259	0.0058465	6.2E-20
7	BAZ1B	rs67243124	73497702	A	AAAAAAG	0.0940265	-0.0496833	0.0058653	4.9E-20
7	BAZ1B	rs201533187	73497710	A	AAAAAG	0.0858338	-0.0459712	0.0061488	5.3E-16
7	BAZ1B	rs34482346	73501191	C	G	0.0944095	-0.0495120	0.0058533	6.1E-20
7	BAZ1B	chr7:73505631_GA_G	73505631	G	GA	0.0887953	-0.0480099	0.0060789	8.9E-18
7	BAZ1B	rs79862839	73507279	C	T	0.0944134	-0.0495378	0.0058533	5.9E-20
7	BAZ1B	rs13221253	73507903	G	A	0.0943032	-0.0493627	0.0058558	8.0E-20
7	BAZ1B	rs34437827	73509008	G	A	0.0944095	-0.0495120	0.0058533	6.1E-20
7	BAZ1B	rs7811265	73520180	G	A	0.0857244	-0.0477799	0.0061431	4.2E-17
7	BAZ1B *	rs62466264	73524388	C	T	0.0947103	-0.0492620	0.0058487	9.4E-20
7	BAZ1B *	rs11983997	73524914	C	G	0.0943273	-0.0493289	0.0058556	8.9E-20
7	BAZ1B *	rs80189144	73525609	C	T	0.0943273	-0.0493289	0.0058556	8.9E-20
7	BCL7B	rs17145732	73555938	G	T	0.0986495	-0.0546187	0.0057410	2.5E-24
7	BCL7B	rs13233571	73556901	T	C	0.0948453	-0.0583453	0.0058329	1.2E-26
7	BCL7B	rs7793710	73557201	G	C	0.0947870	-0.0581328	0.0058364	1.8E-26
7	BCL7B	rs13234157	73557398	A	C	0.0937617	-0.0579198	0.0058812	6.5E-26
7	BCL7B *	rs13244614	73559524	A	C	0.0947968	-0.0581111	0.0058364	1.9E-26
7	BCL7B *	rs111269058	73561372	T	C	0.0948047	-0.0581161	0.0058365	1.9E-26
7	BCL7B *	rs13225333	73561688	T	C	0.0947800	-0.0581874	0.0058369	1.7E-26
7	BCL7B *	rs13225347	73561718	T	C	0.0948047	-0.0581161	0.0058365	1.9E-26
7	BCL7B *	rs13225450	73561793	T	C	0.0946810	-0.0580886	0.0058411	2.0E-26
7	BCL7B *	rs34594435	73562919	T	C	0.0948047	-0.0581161	0.0058365	1.9E-26
7	BCL7B *	rs6946689	73563307	A	T	0.0948439	-0.0580898	0.0058379	2.1E-26
7	TBL2 *	rs12539316	73563568	G	A	0.0956729	-0.0578356	0.0058225	3.1E-26
7	TBL2 *	rs12539351	73563782	G	A	0.0899919	-0.0597345	0.0059806	1.0E-26
7	TBL2 *	rs17145738	73568544	T	C	0.0949387	-0.0583169	0.0058316	1.2E-26
7	TBL2	rs13232120	73568980	T	A	0.0949688	-0.0582371	0.0058316	1.4E-26
7	TBL2	rs14415	73570450	C	T	0.0949688	-0.0582371	0.0058316	1.4E-26
7	TBL2	rs2286276	73573024	T	C	0.0950632	-0.0580156	0.0058292	1.8E-26
7	TBL2	rs35659126	73573739	T	C	0.0947175	-0.0586469	0.0058393	7.3E-27
7	TBL2	chr7:73574811_C_CA	73574811	CA	C	0.0953943	-0.0592570	0.0058268	2.3E-27
7	TBL2	rs11974409	73575060	G	A	0.0947588	-0.0587304	0.0058396	6.2E-27
7	TBL2	rs12540011	73577374	A	G	0.0948698	-0.0585038	0.0058350	9.6E-27
7	TBL2	rs13246490	73578020	T	C	0.0948466	-0.0584707	0.0058357	1.0E-26
7	TBL2 *	rs66553475	73579219	ACTGCTGGT	T	0.0941630	-0.0592911	0.0058595	2.7E-27
7	TBL2 *	chr7:73581580_C_CA	73581580	CA	C	0.0835004	-0.0570363	0.0062642	5.5E-23
7	TBL2 *	rs66506038	73581613	C	T	0.0948870	-0.0582845	0.0058347	1.3E-26
7	TBL2 *	rs67644909	73581624	T	C	0.0935808	-0.0575153	0.0058774	1.4E-25
7	TBL2 *	rs9638180	73584622	G	A	0.0948978	-0.0586089	0.0058360	7.8E-27
7	TBL2 *	rs9638181	73584713	G	A	0.0948978	-0.0586089	0.0058360	7.8E-27

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
7	TBL2 *	rs9638182	73584775	G	T	0.0948978	-0.0586089	0.0058360	7.8E-27
7	MLXIPL *	rs35173225	73586691	T	C	0.0949788	-0.0585926	0.0058347	7.9E-27
7	MLXIPL *	rs187404224	73588697	G	A	0.0948505	-0.0585134	0.0058357	9.3E-27
7	MLXIPL *	rs185081604	73588973	C	A	0.0948505	-0.0585134	0.0058357	9.3E-27
7	MLXIPL *	rs145099458	73589985	T	C	0.0905950	-0.0582889	0.0059823	2.7E-25
7	MLXIPL *	rs35866503	73591446	T	C	0.0948485	-0.0585223	0.0058357	9.1E-27
7	MLXIPL *	rs13225660	73592058	T	C	0.0948485	-0.0585223	0.0058357	9.1E-27
7	MLXIPL *	chr7:73592757_C_CA	73592757	CA	C	0.0879106	-0.0584254	0.0060879	1.5E-24
7	MLXIPL	rs1051921	73593613	A	G	0.0948485	-0.0585223	0.0058357	9.1E-27
7	MLXIPL	rs13247874	73596112	T	C	0.0969619	-0.0608356	0.0057833	5.5E-29
7	MLXIPL	rs35332062	73597712	A	G	0.0977401	-0.0603730	0.0057588	5.4E-29
7	MLXIPL	rs79624003	73598455	G	A	0.0976304	-0.0606415	0.0057643	3.9E-29
7	MLXIPL	rs35732917	73598939	C	T	0.0975615	-0.0607287	0.0057668	3.6E-29
7	MLXIPL	rs13235543	73599571	T	C	0.0975207	-0.0607402	0.0057667	3.5E-29
7	MLXIPL	rs13240065	73601039	A	G	0.0964669	-0.0615997	0.0058032	2.7E-29
7	MLXIPL	rs34346326	73601851	C	T	0.0972831	-0.0606942	0.0057750	4.7E-29
7	MLXIPL	rs13240994	73602532	C	T	0.0882069	-0.0657210	0.0060607	2.5E-30
7	MLXIPL	rs13226650	73602675	G	A	0.0974300	-0.0606914	0.0057748	4.7E-29
7	MLXIPL	rs35368205	73603327	T	C	0.0885733	-0.0651031	0.0060241	4.0E-30
7	MLXIPL	rs34166762	73604194	C	T	0.0888448	-0.0666495	0.0060280	1.8E-31
7	MLXIPL	rs61010704	73605645	G	A	0.0862799	-0.0685134	0.0060931	1.6E-32
7	MLXIPL	rs3812316	73606007	G	C	0.0863060	-0.0689007	0.0060910	7.1E-33
7	MLXIPL	rs6968170	73606346	A	G	0.0863303	-0.0685094	0.0060897	1.4E-32
7	MLXIPL	rs77048596	73607881	A	G	0.0863347	-0.0686943	0.0060903	1.1E-32
7	MLXIPL	rs13246993	73608416	A	G	0.0863418	-0.0687214	0.0060904	1.0E-32
7	MLXIPL	rs141854486	73608603	A	AAG	0.0783569	-0.0686394	0.0064066	7.8E-30
7	MLXIPL	rs12531645	73609551	A	G	0.0862767	-0.0688710	0.0060925	7.2E-33
7	MLXIPL	rs35512732	73610432	T	TC	0.0863386	-0.0687492	0.0060907	9.4E-33
7	MLXIPL	rs13234131	73611645	G	A	0.0993981	-0.0592165	0.0057004	5.1E-28
7	MLXIPL	rs13234378	73611821	T	A	0.0998794	-0.0590638	0.0056945	6.3E-28
7	MLXIPL	rs17145750	73612048	T	C	0.0997946	-0.0595209	0.0056904	2.7E-28
7	MLXIPL	rs7808877	73613120	G	C	0.0996263	-0.0590302	0.0056952	7.3E-28
7	MLXIPL	rs33951980	73615107	T	C	0.0996284	-0.0590321	0.0056952	7.3E-28
7	MLXIPL	rs2074768	73615773	C	A	0.0996284	-0.0590321	0.0056952	7.3E-28
7	MLXIPL	rs13229619	73615845	A	G	0.0996284	-0.0590321	0.0056952	7.3E-28
7	MLXIPL	rs7798357	73617935	C	G	0.0995576	-0.0592098	0.0056977	5.2E-28
7	MLXIPL	rs7785479	73618505	C	T	0.0995638	-0.0592183	0.0056977	5.0E-28
7	MLXIPL	rs34062580	73619229	A	G	0.0995617	-0.0591935	0.0056980	5.2E-28
7	MLXIPL	rs6975495	73619700	G	A	0.0995575	-0.0592832	0.0056982	4.4E-28
7	MLXIPL	rs71556736	73620599	T	C	0.0996033	-0.0595847	0.0056964	2.4E-28
7	MLXIPL	rs7800944	73621527	C	T	0.0999501	-0.0581869	0.0056922	3.2E-27
7	MLXIPL	rs55747707	73623036	A	G	0.0994886	-0.0595738	0.0057008	2.7E-28
7	MLXIPL	rs34060476	73623626	G	A	0.0994698	-0.0596462	0.0057014	2.3E-28
7	MLXIPL *	rs35493868	73625076	G	C	0.0994822	-0.0597030	0.0057015	1.9E-28
7	MLXIPL *	rs34121855	73626484	G	T	0.0972709	-0.0599348	0.0057690	3.4E-28
7	MLXIPL *	rs62466318	73627755	T	C	0.1078270	-0.0547517	0.0055034	1.3E-25
7	MLXIPL *	chr7:73627972_GCTTT_G	73627972	G	GCTTT	0.1080830	-0.0538979	0.0054993	6.8E-25
7	MLXIPL *	rs6460047	73628113	C	T	0.1093250	-0.0540035	0.0054766	5.8E-25
7	MLXIPL *	rs7805504	73628255	C	T	0.1092090	-0.0536989	0.0054774	9.7E-25
7	MLXIPL *	rs7786376	73628284	G	A	0.1104890	-0.0523568	0.0054515	7.3E-24
7	MLXIPL *	rs35340690	73628738	C	G	0.1525910	-0.0394374	0.0048203	3.6E-17
7	MLXIPL *	rs34958196	73628771	A	G	0.1402430	-0.0456506	0.0049776	8.7E-22
7	MLXIPL *	rs34430945	73629335	C	T	0.1398120	-0.0448718	0.0049803	3.9E-21
7	MLXIPL *	rs34321592	73630874	A	G	0.1675140	-0.0404093	0.0046290	2.7E-19
7	MLXIPL *	rs7784668	73631153	C	T	0.1393940	-0.0452473	0.0049913	2.3E-21
7	MLXIPL *	rs78815801	73631608	C	T	0.1304240	-0.0467088	0.0051867	2.0E-21
7	MLXIPL *	rs1412452301	73631935	CTTCCTTT	C	0.1662480	-0.0405212	0.0046553	3.7E-19
7	MLXIPL *	rs17145813	73632428	A	C	0.1660870	-0.0405645	0.0046598	4.7E-19
7	MLXIPL *	rs17145817	73632449	G	A	0.1660910	-0.0405588	0.0046598	4.8E-19
7	MLXIPL *	rs36091304	73633181	C	T	0.1643850	-0.0397952	0.0046890	2.5E-18
7	MLXIPL *	rs34899589	73633190	C	T	0.1629800	-0.0392769	0.0047146	1.1E-17
7	MLXIPL *	rs35855035	73633221	T	C	0.1627250	-0.0392144	0.0047170	1.6E-17
7	MLXIPL *	rs35703204	73633518	T	C	0.1657570	-0.0406948	0.0046715	3.8E-19
7	MLXIPL *	rs13230514	73633765	G	A	0.1655870	-0.0407813	0.0046718	3.1E-19
7	MLXIPL *	rs62466323	73634348	A	G	0.1655430	-0.0407524	0.0046750	3.4E-19
7	MLXIPL *	rs13234805	73634852	A	G	0.1359550	-0.0448271	0.0050761	1.6E-20
7	MLXIPL *	rs13222090	73635057	C	T	0.1657720	-0.0409499	0.0046711	2.0E-19
8	NAT2 *	rs7006687	18376073	C	T	0.4626500	-0.0182197	0.0034359	2.6E-08
8	NAT2 *	rs4481648	18378050	G	T	0.4613700	-0.0181520	0.0034564	3.4E-08
8	NAT2 *	rs4646243	18390099	C	T	0.4751760	0.0186743	0.0034240	2.8E-08
8	NAT2 *	rs4646267	18390403	G	A	0.4751070	0.0186655	0.0034237	2.8E-08
8	NAT2 *	rs4646246	18391151	G	A	0.4730810	0.0185080	0.0034262	3.4E-08

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	NAT2	rs55686478	18392865	A	G	0.4717820	0.0184268	0.0034305	3.5E-08
8	NAT2	rs1041983	18400285	T	C	0.4330520	-0.0183130	0.0034445	3.8E-08
8	INTS10 *	rs10503666	19887085	C	G	0.0865581	-0.0344206	0.0061085	5.1E-09
8	INTS10 *	rs17482310	19889365	T	G	0.0961409	-0.0320381	0.0058321	6.4E-09
8	INTS10 *	rs79396901	19890937	C	T	0.0868502	-0.0339048	0.0060942	6.8E-09
8	INTS10 *	rs138094414	19892729	C	G	0.0837722	-0.0359504	0.0061889	8.2E-10
8	INTS10 *	rs112861901	19893440	C	T	0.0867883	-0.0344469	0.0060932	4.1E-09
8	INTS10 *	rs12550077	19893888	A	G	0.0823072	-0.0363462	0.0062403	8.5E-10
8	LPL *	rs17482386	19896010	G	A	0.0979673	-0.0321729	0.0057857	6.0E-09
8	LPL *	chr8:19896793_C_CT	19896793	CT	C	0.1036430	-0.0315040	0.0056673	3.0E-09
8	LPL *	rs1919482	19897207	T	A	0.0997062	-0.0317901	0.0057457	3.3E-09
8	LPL *	rs76085257	19897616	A	C	0.0821723	-0.0367104	0.0062389	6.3E-10
8	LPL *	rs73597688	19897664	A	C	0.0968236	-0.0347862	0.0058201	1.9E-10
8	LPL *	rs73597690	19898115	A	C	0.0883542	-0.0363175	0.0060632	2.0E-10
8	LPL *	rs12543154	19898466	T	G	0.0875037	-0.0365306	0.0060841	2.0E-10
8	LPL *	rs10091649	19898910	G	T	0.0921539	-0.0365003	0.0059588	6.5E-11
8	LPL *	rs73597699	19899081	T	C	0.0783291	-0.0358187	0.0064247	6.7E-09
8	LPL *	rs10102717	19899302	T	C	0.0897541	-0.0378079	0.0060314	3.7E-11
8	LPL *	rs1441771	19899789	T	C	0.0897430	-0.0383323	0.0060379	2.3E-11
8	LPL *	rs1441770	19899808	A	G	0.0897022	-0.0384231	0.0060370	2.0E-11
8	LPL *	rs183801835	19904479	C	T	0.0198119	-0.0825912	0.0123238	9.4E-12
8	LPL *	rs77032723	19906481	T	C	0.1282360	-0.0406807	0.0051785	5.0E-16
8	LPL *	rs192423215	19907403	C	G	0.0189012	-0.0833349	0.0125992	1.4E-11
8	LPL *	rs60526148	19909692	T	C	0.1525350	-0.0463403	0.0047975	4.4E-23
8	LPL *	rs3988301	19912868	G	T	0.1569390	-0.0474508	0.0047497	4.1E-24
8	LPL *	rs28834434	19917379	A	C	0.1501690	-0.0485571	0.0047868	2.9E-25
8	LPL *	rs4466415	19919470	C	A	0.1613740	-0.0478062	0.0046802	3.6E-25
8	LPL *	rs77899453	19922799	A	G	0.1497280	-0.0490813	0.0048042	1.6E-25
8	LPL *	rs2119692	19922946	C	G	0.1507210	-0.0489067	0.0047949	1.8E-25
8	LPL *	rs3866470	19927611	A	G	0.0160542	-0.0889664	0.0136505	2.5E-11
8	LPL *	rs7816032	19929380	T	C	0.1558340	-0.0477317	0.0047185	4.0E-25
8	LPL *	rs139001474	19931094	A	T	0.1595140	-0.0474079	0.0046915	9.6E-25
8	LPL *	rs149764042	19931164	C	G	0.0666111	-0.0785609	0.0069065	3.4E-31
8	LPL *	rs4592053	19931255	G	A	0.1599350	-0.0475528	0.0046882	5.7E-25
8	LPL *	rs150331294	19932487	A	T	0.1552560	-0.0479511	0.0047343	3.7E-25
8	LPL *	rs9694336	19933560	T	C	0.1487350	-0.0480281	0.0048232	1.2E-24
8	LPL *	rs145353248	19933835	T	C	0.1486880	-0.0482478	0.0048234	7.8E-25
8	LPL	rs3779787	19940405	T	G	0.1560050	-0.0460347	0.0047388	1.9E-23
8	LPL	rs1534649	19942130	T	G	0.1562170	-0.0464952	0.0047298	4.1E-24
8	LPL	rs112127208	19944019	G	T	0.1548370	-0.0472423	0.0047418	1.4E-24
8	LPL	rs10104051	19944891	T	C	0.1549840	-0.0471868	0.0047425	1.6E-24
8	LPL	rs3779788	19945582	T	C	0.1541270	-0.0478736	0.0047512	4.4E-25
8	LPL	rs56321069	19946485	A	T	0.1535190	-0.0474852	0.0047722	1.8E-24
8	LPL	rs8176337	19949160	G	C	0.1529730	-0.0483095	0.0048026	6.8E-25
8	LPL	rs74304285	19950519	A	G	0.1516780	-0.0487839	0.0048503	5.7E-25
8	LPL	rs113023641	19950620	A	G	0.1516140	-0.0488845	0.0048530	4.9E-25
8	LPL	rs73667472	19952184	C	T	0.0586386	-0.0834552	0.0073502	4.8E-31
8	LPL	rs249	19953495	C	T	0.0590651	-0.0897300	0.0073256	1.8E-35
8	LPL	rs254	19954386	G	C	0.2175090	-0.0436594	0.0041980	7.9E-26
8	LPL	rs255	19954390	C	T	0.2174930	-0.0436330	0.0041982	8.4E-26
8	LPL	rs256	19954456	T	C	0.2178700	-0.0442168	0.0041922	1.7E-26
8	LPL	rs263	19955301	T	C	0.2192470	-0.0438264	0.0041542	1.4E-26
8	LPL	rs264	19955669	A	G	0.2096560	-0.0392672	0.0042120	5.3E-21
8	LPL	rs269	19956156	G	T	0.2188110	-0.0435185	0.0041771	6.8E-26
8	LPL	rs271	19956191	A	G	0.2182360	-0.0431156	0.0041801	2.2E-25
8	LPL	chr8:19956458_G_GT	19956458	GT	G	0.2146690	-0.0446732	0.0042321	2.1E-26
8	LPL	rs285	19957678	T	C	0.3524350	-0.0420751	0.0036523	8.7E-33
8	LPL	rs287	19958045	G	A	0.2039620	-0.0596183	0.0042590	2.9E-46
8	LPL	rs289	19958108	C	T	0.2036590	-0.0600874	0.0042578	5.3E-47
8	LPL	rs291	19958341	C	T	0.2043670	-0.0598995	0.0042518	6.7E-47
8	LPL	chr8:19958567_T_TA	19958567	TA	T	0.2036190	-0.0599409	0.0042627	1.4E-46
8	LPL	rs295	19958727	C	A	0.2046730	-0.0599204	0.0042471	4.6E-47
8	LPL	rs297	19958860	C	T	0.2036640	-0.0601486	0.0042569	4.5E-47
8	LPL	rs301	19959423	C	T	0.2034900	-0.0603979	0.0042615	2.7E-47
8	LPL	rs304	19959850	G	T	0.1980560	-0.0589346	0.0043313	1.6E-43
8	LPL	rs305	19959890	G	A	0.2026140	-0.0601244	0.0042714	1.2E-46
8	LPL	rs308	19959965	G	T	0.0786850	-0.0894621	0.0063850	2.2E-47
8	LPL	rs314	19960531	A	G	0.2035830	-0.0600745	0.0042606	7.7E-47
8	LPL	rs117026536	19961262	T	G	0.1023800	-0.0877474	0.0056700	1.1E-57
8	LPL	rs320	19961566	G	T	0.2040680	-0.0605430	0.0042519	1.1E-47
8	LPL	rs322	19961706	C	A	0.2042950	-0.0605492	0.0042574	1.5E-47
8	LPL	rs325	19961817	C	T	0.1016930	-0.0888194	0.0056747	1.1E-58

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL	rs326	19961928	G	A	0.2039990	-0.0609865	0.0042495	1.8E-48
8	LPL	rs327	19962025	G	T	0.2043180	-0.0607130	0.0042504	6.8E-48
8	LPL	rs328	19962213	G	C	0.1017040	-0.0885515	0.0056745	2.1E-58
8	LPL	rs331	19962894	A	G	0.2025060	-0.0603833	0.0042600	2.7E-47
8	LPL	rs12679834	19962922	C	T	0.1016560	-0.0887394	0.0056757	1.4E-58
8	LPL	rs117199990	19963405	T	C	0.0995835	-0.0894615	0.0057381	3.1E-58
8	LPL	rs145391587	19963422	C	A	0.0986425	-0.0897577	0.0057630	2.9E-58
8	LPL	rs75278536	19963914	G	T	0.1014490	-0.0892093	0.0056805	4.0E-59
8	LPL	rs146265243	19963956	G	GT	0.1014810	-0.0891868	0.0056814	4.4E-59
8	LPL	rs77069344	19964271	G	T	0.1014470	-0.0892050	0.0056804	4.0E-59
8	LPL	rs11570891	19965299	T	C	0.1015610	-0.0887707	0.0056777	1.4E-58
8	LPL	rs3208305	19966137	T	A	0.1964340	-0.0602347	0.0043210	7.6E-46
8	LPL	rs1803924	19966163	T	C	0.1015590	-0.0887766	0.0056777	1.4E-58
8	LPL	rs3735964	19966534	A	C	0.1016020	-0.0890084	0.0056764	6.6E-59
8	LPL	rs13702	19966981	C	T	0.2002430	-0.0609092	0.0042780	1.1E-47
8	LPL	rs1059611	19967052	C	T	0.1016460	-0.0890452	0.0056756	5.8E-59
8	LPL	rs10645926	19967115	CTT	C	0.1015960	-0.0890834	0.0056766	5.4E-59
8	LPL	rs15285	19967156	T	C	0.1998170	-0.0606013	0.0042808	4.3E-47
8	LPL *	rs3916027	19967357	A	G	0.1997880	-0.0606334	0.0042817	4.0E-47
8	LPL *	rs77150190	19968791	C	G	0.0933004	-0.0864612	0.0059103	1.0E-51
8	LPL *	rs77729186	19968807	G	A	0.0933004	-0.0864612	0.0059103	1.0E-51
8	LPL *	rs2197089	19968862	A	G	0.3461790	-0.0413384	0.0035960	9.9E-33
8	LPL *	rs79108221	19969190	T	C	0.0932842	-0.0865408	0.0059105	8.0E-52
8	LPL *	rs1563590475	19969589	A	ACTT	0.0793975	-0.0827756	0.0064056	1.2E-40
8	LPL *	rs10105606	19970337	A	C	0.1994750	-0.0611381	0.0042849	5.8E-48
8	LPL *	rs1569209	19972659	G	T	0.0213612	-0.0786527	0.0118662	7.6E-12
8	LPL *	rs1011685	19973258	T	C	0.1008720	-0.0888711	0.0056935	2.5E-58
8	LPL *	rs10096633	19973410	T	C	0.1009770	-0.0884634	0.0056917	7.2E-58
8	LPL *	rs17482753	19975135	T	G	0.1003960	-0.0888230	0.0057045	4.0E-58
8	LPL *	rs78963197	19979135	C	T	0.0974880	-0.0888072	0.0057991	2.6E-56
8	LPL *	rs74855321	19979473	T	C	0.0994454	-0.0882445	0.0057333	6.2E-57
8	LPL *	rs4464984	19980958	T	C	0.1956730	-0.0605475	0.0043271	2.6E-46
8	LPL *	rs58946909	19982830	A	G	0.1002620	-0.0885423	0.0057118	1.8E-57
8	LPL *	rs75551077	19982897	C	G	0.1002780	-0.0886205	0.0057114	1.4E-57
8	LPL *	rs1554519534	19985625	CA	C	0.0553561	-0.0855098	0.0076351	5.7E-31
8	LPL *	rs17091891	19985660	C	T	0.0909253	-0.0890305	0.0060095	2.0E-52
8	LPL *	rs17410914	19985951	A	C	0.0974985	-0.0892090	0.0057841	6.9E-57
8	LPL *	rs117227752	19986350	A	G	0.1003800	-0.0886735	0.0057057	7.1E-58
8	LPL *	rs59147390	19986368	C	T	0.1003760	-0.0886781	0.0057057	7.0E-58
8	LPL *	rs184371102	19986419	T	G	0.0772900	-0.0890388	0.0064306	2.9E-46
8	LPL *	rs12678919	19986711	G	A	0.1006250	-0.0882096	0.0056989	2.2E-57
8	LPL *	rs7819706	19986904	G	A	0.1002200	-0.0882890	0.0057106	2.6E-57
8	LPL *	rs115129770	19986928	G	C	0.1002200	-0.0882890	0.0057106	2.6E-57
8	LPL *	rs149670831	19986936	C	CT	0.1002200	-0.0882890	0.0057106	2.6E-57
8	LPL *	rs7841189	19987865	T	C	0.1007390	-0.0881525	0.0056993	2.5E-57
8	LPL *	rs78458743	19988803	G	T	0.1003320	-0.0887715	0.0057081	5.7E-58
8	LPL *	rs114566157	19988978	G	C	0.1003320	-0.0887715	0.0057081	5.7E-58
8	LPL *	rs139894713	19989069	A	C	0.0213559	-0.0787263	0.0118662	7.4E-12
8	LPL *	rs12682115	19989549	A	G	0.1003320	-0.0887715	0.0057081	5.7E-58
8	LPL *	rs78013771	19989712	C	T	0.1003300	-0.0887640	0.0057081	5.8E-58
8	LPL *	rs76496571	19989930	A	C	0.1003510	-0.0884900	0.0057067	1.2E-57
8	LPL *	rs10503669	19990179	A	C	0.1004900	-0.0881795	0.0056955	1.9E-57
8	LPL *	rs17410962	19990569	A	G	0.1004110	-0.0885571	0.0057046	8.7E-58
8	LPL *	rs117604010	19990885	A	G	0.0776485	-0.0887276	0.0064142	3.1E-46
8	LPL *	rs17489185	19990988	C	G	0.1004110	-0.0885571	0.0057046	8.7E-58
8	LPL *	rs17410983	19991182	T	C	0.1004110	-0.0885571	0.0057046	8.7E-58
8	LPL *	rs17489226	19991367	T	A	0.1004110	-0.0885571	0.0057046	8.7E-58
8	LPL *	rs17410996	19991761	G	T	0.1003630	-0.0886295	0.0057059	8.0E-58
8	LPL *	rs75801420	19992159	G	T	0.1004340	-0.0884725	0.0057070	1.3E-57
8	LPL *	rs17091905	19992246	A	G	0.1004900	-0.0886154	0.0057021	7.7E-58
8	LPL *	rs114964604	19992478	G	A	0.0996733	-0.0888945	0.0057302	1.0E-57
8	LPL *	rs73600084	19992481	C	T	0.0996733	-0.0888945	0.0057302	1.0E-57
8	LPL *	rs76975037	19993997	A	C	0.1004010	-0.0892549	0.0057059	1.1E-58
8	LPL *	rs17489268	19994534	A	T	0.1993070	-0.0603052	0.0042911	1.2E-46
8	LPL *	rs17411024	19994623	A	G	0.1001620	-0.0890359	0.0057113	2.5E-58
8	LPL *	rs17091909	19994645	T	G	0.1003840	-0.0892987	0.0057063	1.0E-58
8	LPL *	rs147729680	19994665	T	TTC	0.1993960	-0.0605368	0.0042903	5.3E-47
8	LPL *	rs17411031	19994799	G	C	0.1993430	-0.0604738	0.0042900	6.4E-47
8	LPL *	rs17411045	19994851	C	T	0.1992420	-0.0606327	0.0042932	4.2E-47
8	LPL *	rs17489282	19995007	T	C	0.1993960	-0.0605364	0.0042908	5.5E-47
8	LPL *	rs4922117	19995075	C	T	0.1993430	-0.0604738	0.0042900	6.4E-47
8	LPL *	rs1822200	19995318	T	G	0.1993430	-0.0604738	0.0042900	6.4E-47

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs1372344	19995428	T	A	0.1993430	-0.0604738	0.0042900	6.4E-47
8	LPL *	rs1992442	19995878	C	A	0.1995380	-0.0602249	0.0042912	1.4E-46
8	LPL *	rs2410618	19995989	A	G	0.1993840	-0.0604563	0.0042899	6.7E-47
8	LPL *	rs1992443	19996076	A	G	0.1993840	-0.0604563	0.0042899	6.7E-47
8	LPL *	rs920588	19996756	T	C	0.1994260	-0.0603226	0.0042898	1.0E-46
8	LPL *	rs920589	19996850	T	G	0.1993840	-0.0604563	0.0042899	6.7E-47
8	LPL *	rs4425772	19996989	T	C	0.1990220	-0.0604357	0.0042930	9.2E-47
8	LPL *	rs4628269	19996998	T	C	0.1990220	-0.0604357	0.0042930	9.2E-47
8	LPL *	rs2410619	19997042	A	C	0.1993840	-0.0604563	0.0042899	6.7E-47
8	LPL *	rs4320561	19997126	A	C	0.1991880	-0.0602944	0.0042923	1.2E-46
8	LPL *	rs2410620	19997149	T	C	0.1991880	-0.0602944	0.0042923	1.2E-46
8	LPL *	rs2410621	19997171	C	T	0.1991880	-0.0602944	0.0042923	1.2E-46
8	LPL *	rs2410623	19997378	G	A	0.1993840	-0.0604563	0.0042899	6.7E-47
8	LPL *	rs17411113	19997495	G	C	0.1005240	-0.0892721	0.0057054	1.0E-58
8	LPL *	rs79734126	19997519	T	C	0.0769920	-0.0885213	0.0064430	8.6E-46
8	LPL *	rs34564316	19997710	T	C	0.1994870	-0.0603023	0.0042935	1.3E-46
8	LPL *	rs17411126	19997761	C	T	0.1993740	-0.0604288	0.0042897	7.3E-47
8	LPL *	rs17411133	19997820	A	T	0.1994030	-0.0604924	0.0042893	6.0E-47
8	LPL *	rs17489373	19997833	A	G	0.1994030	-0.0604924	0.0042893	6.0E-47
8	LPL *	rs17411168	19998089	C	T	0.1997010	-0.0603358	0.0042849	8.4E-47
8	LPL *	rs34932218	19998150	G	A	0.1997800	-0.0603045	0.0042833	8.2E-47
8	LPL *	rs140426714	19998333	G	GTATTTT	0.1976970	-0.0596749	0.0043126	1.8E-45
8	LPL *	rs2165558	19998749	G	T	0.2194280	-0.0543936	0.0041994	1.4E-39
8	LPL *	rs4523270	19999028	C	T	0.1998150	-0.0602534	0.0042824	9.4E-47
8	LPL *	rs2103325	20000832	T	C	0.1995200	-0.0606060	0.0042846	3.1E-47
8	LPL *	rs1581675	20000988	A	T	0.1995270	-0.0605906	0.0042846	3.3E-47
8	LPL *	rs4490856	20001609	C	T	0.3540840	-0.0447829	0.0035979	6.3E-38
8	LPL *	rs2119690	20002028	A	G	0.1996180	-0.0604873	0.0042836	4.5E-47
8	LPL *	rs2165556	20002116	T	C	0.1996080	-0.0604430	0.0042839	5.3E-47
8	LPL *	rs12541912	20002280	C	G	0.1999520	-0.0600817	0.0042804	1.5E-46
8	LPL *	rs74869266	20002686	C	A	0.0214958	-0.0802840	0.0118285	2.7E-12
8	LPL *	rs79236614	20002949	G	C	0.1003180	-0.0893911	0.0057092	1.2E-58
8	LPL *	rs34818360	20003236	A	G	0.1993770	-0.0602220	0.0042852	1.3E-46
8	LPL *	rs4083261	20003715	C	T	0.1999730	-0.0602111	0.0042800	9.2E-47
8	LPL *	rs3844510	20003850	C	A	0.1996970	-0.0606715	0.0042827	2.2E-47
8	LPL *	rs2410625	20004709	T	C	0.1996820	-0.0606547	0.0042827	2.3E-47
8	LPL *	rs4644277	20005059	C	T	0.1996820	-0.0606547	0.0042827	2.3E-47
8	LPL *	rs4389957	20005235	A	G	0.3548650	-0.0438912	0.0035925	1.1E-36
8	LPL *	rs1441766	20005277	T	A	0.2016370	-0.0599920	0.0042773	1.9E-46
8	LPL *	rs1441764	20005513	T	C	0.1999900	-0.0602378	0.0042796	8.3E-47
8	LPL *	rs6586884	20005847	C	T	0.1004110	-0.0894096	0.0057059	7.8E-59
8	LPL *	rs6999813	20005960	A	T	0.1004110	-0.0894096	0.0057059	7.8E-59
8	LPL *	rs2119689	20005996	T	C	0.1996820	-0.0606547	0.0042827	2.3E-47
8	LPL *	chr8:20006328_G_GA	20006328	GA	G	0.1971430	-0.0614337	0.0043143	7.3E-48
8	LPL *	rs1441763	20007045	C	T	0.1996990	-0.0606529	0.0042823	2.2E-47
8	LPL *	rs1441762	20007176	A	G	0.1998420	-0.0607891	0.0042840	1.5E-47
8	LPL *	rs1441761	20007237	C	G	0.1990710	-0.0602686	0.0042879	1.1E-46
8	LPL *	rs1441760	20007238	T	C	0.1990710	-0.0602686	0.0042879	1.1E-46
8	LPL *	chr8:20007371_T_TAAA	20007371	TAAA	T	0.1927510	-0.0605439	0.0043703	9.5E-46
8	LPL *	rs2083637	20007664	G	A	0.1997030	-0.0605506	0.0042809	2.8E-47
8	LPL *	rs2083636	20007752	G	T	0.2001220	-0.0602769	0.0042773	5.9E-47
8	LPL *	rs77237194	20007944	T	A	0.1004590	-0.0893734	0.0057042	7.1E-59
8	LPL *	rs35495249	20007998	A	C	0.1986380	-0.0613159	0.0042948	4.2E-48
8	LPL *	rs894211	20008236	T	C	0.1986880	-0.0613428	0.0042943	3.5E-48
8	LPL *	rs894210	20008332	A	G	0.3559230	-0.0445393	0.0035860	8.9E-38
8	LPL *	rs765547	20008763	A	G	0.1998050	-0.0607157	0.0042803	1.5E-47
8	LPL *	rs765548	20009083	T	C	0.1997800	-0.0607135	0.0042805	1.5E-47
8	LPL *	rs765549	20009120	G	A	0.2000930	-0.0603038	0.0042775	5.5E-47
8	LPL *	rs1441758	20009367	T	A	0.1997800	-0.0607135	0.0042805	1.5E-47
8	LPL *	rs139547332	20009665	CT	C	0.0776404	-0.0888489	0.0064133	2.1E-46
8	LPL *	rs9644637	20009709	C	T	0.1997800	-0.0607135	0.0042805	1.5E-47
8	LPL *	rs9644638	20009889	T	C	0.1993790	-0.0603840	0.0042847	5.2E-47
8	LPL *	rs11986942	20009934	G	C	0.2000930	-0.0603038	0.0042775	5.5E-47
8	LPL *	rs34327087	20009983	T	G	0.1997010	-0.0605993	0.0042812	2.5E-47
8	LPL *	rs34345068	20010025	T	G	0.1996720	-0.0605185	0.0042820	3.3E-47
8	LPL *	rs2009493	20010342	A	G	0.1997740	-0.0607052	0.0042805	1.6E-47
8	LPL *	rs1837843	20010591	T	C	0.1959200	-0.0594680	0.0043146	5.1E-45
8	LPL *	rs1837842	20010779	C	T	0.1997740	-0.0607052	0.0042805	1.6E-47
8	LPL *	rs1441757	20010866	C	G	0.1997740	-0.0607052	0.0042805	1.6E-47
8	LPL *	rs1441755	20011377	C	T	0.1997740	-0.0607052	0.0042805	1.6E-47
8	LPL *	rs1441754	20011428	A	G	0.1990250	-0.0606731	0.0042887	3.0E-47
8	LPL *	rs4406409	20011460	C	T	0.1988050	-0.0610241	0.0042956	1.7E-47

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs1441753	20011553	A	G	0.1997740	-0.0607052	0.0042805	1.6E-47
8	LPL *	rs4126104	20011855	T	G	0.1997740	-0.0607052	0.0042805	1.6E-47
8	LPL *	rs1919484	20012165	A	G	0.1998010	-0.0606736	0.0042797	1.9E-47
8	LPL *	rs35687633	20012476	G	A	0.1992770	-0.0603895	0.0042916	7.9E-47
8	LPL *	rs34942551	20012504	G	T	0.1992810	-0.0603868	0.0042916	7.9E-47
8	LPL *	rs34499461	20012516	C	G	0.1991810	-0.0604575	0.0042931	6.4E-47
8	LPL *	rs35369244	20012533	C	G	0.1991850	-0.0604450	0.0042931	6.6E-47
8	LPL *	rs35739466	20012576	A	G	0.1961390	-0.0579419	0.0043225	7.0E-43
8	LPL *	rs35617716	20012752	A	T	0.1968690	-0.0587269	0.0043092	4.5E-44
8	LPL *	rs35237252	20012760	A	C	0.1968780	-0.0586074	0.0043089	6.7E-44
8	LPL *	rs1569213	20013224	A	G	0.1781960	-0.0525216	0.0045532	7.4E-32
8	LPL *	rs78810414	20013602	T	C	0.0836926	-0.0808898	0.0061934	1.5E-41
8	LPL *	rs1372343	20013809	T	C	0.1853640	-0.0549998	0.0044161	1.0E-36
8	LPL *	rs1372342	20013820	A	T	0.1853640	-0.0549998	0.0044161	1.0E-36
8	LPL *	rs1372341	20013821	A	T	0.1853640	-0.0549998	0.0044161	1.0E-36
8	LPL *	rs1372340	20013861	A	G	0.1822370	-0.0527831	0.0044481	1.2E-33
8	LPL *	rs2410627	20014002	C	T	0.1857880	-0.0541023	0.0044101	9.7E-36
8	LPL *	rs7461115	20014029	G	C	0.1857900	-0.0540900	0.0044099	1.0E-35
8	LPL *	rs2410628	20014118	T	C	0.1858010	-0.0543256	0.0044097	5.5E-36
8	LPL *	rs2410629	20014126	C	T	0.1858280	-0.0543218	0.0044092	5.3E-36
8	LPL *	rs2898495	20014381	G	A	0.1858470	-0.0542770	0.0044087	5.9E-36
8	LPL *	rs4593558	20014497	G	A	0.1858580	-0.0542959	0.0044087	5.6E-36
8	LPL *	rs6986010	20015269	C	T	0.1858440	-0.0542600	0.0044087	6.3E-36
8	LPL *	rs35465966	20016045	A	C	0.1855000	-0.0540180	0.0044125	1.2E-35
8	LPL *	rs34693282	20016055	G	A	0.1857740	-0.0542055	0.0044095	7.2E-36
8	LPL *	rs17489539	20016071	A	T	0.1855680	-0.0540886	0.0044121	1.2E-35
8	LPL *	rs4922118	20016634	T	C	0.1855730	-0.0540432	0.0044173	1.4E-35
8	LPL *	rs4922119	20016642	T	C	0.1855730	-0.0540432	0.0044173	1.4E-35
8	LPL *	rs4375019	20016987	A	T	0.1819210	-0.0527794	0.0044496	1.3E-33
8	LPL *	rs141287949	20017421	A	AAGAC	0.0840748	-0.0806634	0.0061727	2.0E-41
8	LPL *	rs4333617	20017493	G	A	0.1824910	-0.0524637	0.0044438	2.5E-33
8	LPL *	rs2410630	20017589	T	C	0.1825450	-0.0522603	0.0044432	4.3E-33
8	LPL *	rs6586886	20017897	A	G	0.1826760	-0.0526656	0.0044395	1.4E-33
8	LPL *	rs73208815	20018604	C	G	0.1824710	-0.0531499	0.0044419	3.8E-34
8	LPL *	rs28675909	20018723	T	A	0.0840539	-0.0819382	0.0061716	1.1E-42
8	LPL *	rs79198716	20018753	T	C	0.0842648	-0.0823339	0.0061631	3.2E-43
8	LPL *	chr8:20018790_G_GA	20018790	GA	G	0.1836990	-0.0536806	0.0044422	1.1E-34
8	LPL *	rs78300069	20019013	T	C	0.0846670	-0.0819244	0.0061494	5.8E-43
8	LPL *	rs76737188	20019083	C	G	0.0883128	-0.0828254	0.0060310	2.0E-45
8	LPL *	rs7016880	20019235	C	G	0.0883293	-0.0826477	0.0060302	3.1E-45
8	LPL *	rs7007609	20019286	C	T	0.0883128	-0.0828254	0.0060310	2.0E-45
8	LPL *	rs7007797	20019459	G	T	0.0883147	-0.0828225	0.0060311	2.0E-45
8	LPL *	rs7004149	20019697	G	A	0.0883147	-0.0828225	0.0060311	2.0E-45
8	LPL *	rs7004158	20019722	G	A	0.0883147	-0.0828225	0.0060311	2.0E-45
8	LPL *	rs6983430	20019742	C	G	0.0883147	-0.0828225	0.0060311	2.0E-45
8	LPL *	rs77219697	20019950	C	T	0.0883226	-0.0828322	0.0060314	2.0E-45
8	LPL *	rs12678603	20020221	T	C	0.0846692	-0.0818740	0.0061504	6.5E-43
8	LPL *	rs12678604	20020262	G	C	0.0846655	-0.0819889	0.0061500	5.0E-43
8	LPL *	rs1534650	20020643	C	T	0.3520560	-0.0394199	0.0035975	2.4E-29
8	LPL *	rs7013777	20020845	C	T	0.1869380	-0.0541325	0.0043998	5.1E-36
8	LPL *	rs4922120	20021087	G	A	0.3513440	-0.0392327	0.0035971	4.4E-29
8	LPL *	rs112994260	20021193	A	T	0.0882872	-0.0828762	0.0060328	1.8E-45
8	LPL *	rs142117848	20021359	A	C	0.0882927	-0.0829008	0.0060328	1.7E-45
8	LPL *	rs4335137	20021363	T	A	0.1879830	-0.0536215	0.0043907	1.8E-35
8	LPL *	rs1819092	20021566	C	T	0.1869040	-0.0542290	0.0044002	4.3E-36
8	LPL *	rs1819094	20021804	G	C	0.1835970	-0.0522317	0.0044341	3.1E-33
8	LPL *	rs75082673	20022298	A	G	0.0845897	-0.0819703	0.0061526	5.8E-43
8	LPL *	rs11989309	20022819	T	C	0.0882390	-0.0828877	0.0060340	1.8E-45
8	LPL *	rs75675187	20023215	T	C	0.0882170	-0.0829105	0.0060349	1.6E-45
8	LPL *	rs74511360	20023529	A	G	0.0845707	-0.0820106	0.0061523	4.8E-43
8	LPL *	rs78404258	20023547	G	A	0.0882842	-0.0828327	0.0060323	1.8E-45
8	LPL *	rs74615535	20023725	A	G	0.0882115	-0.0830863	0.0060341	1.1E-45
8	LPL *	rs60223219	20024290	G	A	0.0882445	-0.0830413	0.0060333	1.1E-45
8	LPL *	rs35048052	20024541	AT	A	0.3525380	-0.0388537	0.0035909	1.1E-28
8	LPL *	rs7816447	20025439	C	T	0.0869384	-0.0839423	0.0060841	5.3E-46
8	LPL *	rs1919487	20026019	A	T	0.1828620	-0.0529158	0.0044378	5.4E-34
8	LPL *	rs114650503	20026746	A	G	0.0845622	-0.0821804	0.0061530	3.2E-43
8	LPL *	rs9644639	20027436	G	C	0.0845363	-0.0822626	0.0061554	2.9E-43
8	LPL *	rs2410631	20028057	T	A	0.1841310	-0.0536872	0.0044241	2.2E-35
8	LPL *	rs2410632	20028146	A	G	0.1839910	-0.0538298	0.0044262	1.7E-35
8	LPL *	rs11984636	20028215	C	T	0.0849764	-0.0832280	0.0061436	2.1E-44
8	LPL *	rs11984698	20028423	C	T	0.0849873	-0.0833003	0.0061440	1.7E-44

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	LPL *	rs35147888	20028593	T	TG	0.1841170	-0.0538188	0.0044243	1.5E-35
8	LPL *	rs11995475	20029177	T	C	0.0849314	-0.0833619	0.0061450	1.7E-44
8	LPL *	rs75469215	20029651	T	A	0.0844327	-0.0847033	0.0061767	2.0E-45
8	LPL *	rs4543558	20030818	G	C	0.1841660	-0.0533498	0.0044286	4.1E-35
8	LPL *	rs2178296	20031614	T	G	0.1666280	-0.0530543	0.0045937	2.8E-32
8	LPL *	rs78358410	20031888	G	T	0.0983445	-0.0826170	0.0057941	4.0E-49
8	LPL *	rs10103634	20033101	A	G	0.2505040	-0.0376897	0.0039702	3.3E-23
8	LPL *	rs139315015	20035786	G	A	0.1131230	-0.0668763	0.0054316	3.4E-37
8	LPL *	rs28841897	20036993	C	T	0.3396830	-0.0376614	0.0036347	6.8E-27
8	LPL *	rs4244457	20041535	T	C	0.3285280	-0.0382225	0.0036388	2.4E-27
8	LPL *	rs76259755	20041650	C	T	0.1128190	-0.0651771	0.0054286	1.4E-35
8	LPL *	rs7826306	20043160	C	G	0.3309690	-0.0370417	0.0036343	7.1E-26
8	LPL *	rs6993414	20045407	G	A	0.1137120	-0.0657258	0.0054112	3.1E-36
8	LPL *	rs74983646	20045739	A	G	0.0969805	-0.0633067	0.0058246	2.5E-29
8	LPL *	rs118099376	20048449	A	G	0.0166088	-0.0837293	0.0134540	1.6E-10
8	LPL *	rs11991231	20050401	C	T	0.1134700	-0.0657670	0.0054191	3.7E-36
8	LPL *	rs66462329	20054549	A	G	0.2426590	-0.0406302	0.0040141	4.5E-26
8	LPL *	rs115849089	20054859	A	G	0.1101550	-0.0631951	0.0054867	9.0E-33
8	LPL *	rs4585763	20055743	T	A	0.3284560	-0.0383413	0.0036548	2.6E-27
8	SLC18A1 *	rs6586891	20057087	A	C	0.3242700	-0.0372942	0.0036688	8.1E-26
8	SLC18A1 *	rs10104610	20058043	C	G	0.2429900	-0.0407947	0.0040137	2.8E-26
8	SLC18A1 *	rs66778572	20058609	A	G	0.2419670	-0.0406549	0.0040217	4.4E-26
8	SLC18A1 *	rs4128744	20062144	T	C	0.1112470	-0.0635389	0.0054679	3.0E-33
8	SLC18A1 *	rs4637851	20065099	A	G	0.3435140	-0.0376255	0.0036497	2.7E-26
8	SLC18A1 *	rs6999158	20070502	A	T	0.2656730	-0.0404576	0.0039322	6.4E-27
8	SLC18A1 *	rs10106652	20070649	A	G	0.2641880	-0.0409277	0.0039394	1.8E-27
8	SLC18A1 *	rs9644568	20071071	A	G	0.1125090	-0.0632883	0.0054325	1.7E-33
8	SLC18A1 *	rs34351848	20071686	T	TC	0.2630310	-0.0398510	0.0039666	6.5E-26
8	SLC18A1 *	rs13281248	20077573	A	G	0.0557995	-0.0798911	0.0075847	1.0E-27
8	SLC18A1 *	rs13257289	20077715	C	T	0.0573774	-0.0774113	0.0075091	8.4E-27
8	TRIB1 *	rs2954017	125464631	T	C	0.4365470	0.0401702	0.0034461	3.3E-34
8	TRIB1 *	rs2954018	125464911	C	T	0.2988090	0.0369787	0.0037253	2.4E-26
8	TRIB1 *	rs2001945	125465736	G	C	0.4366250	0.0402242	0.0034458	2.5E-34
8	TRIB1 *	rs2980853	125466108	A	C	0.4435550	0.0394593	0.0034407	4.6E-33
8	TRIB1 *	rs2001846	125466208	T	C	0.4366920	0.0402139	0.0034463	2.8E-34
8	TRIB1 *	rs2001845	125466402	A	G	0.2988570	0.0371081	0.0037256	1.6E-26
8	TRIB1 *	rs2001844	125466503	A	G	0.4436150	0.0396831	0.0034412	1.9E-33
8	TRIB1 *	rs6982636	125467073	G	A	0.4437520	0.0396870	0.0034403	1.8E-33
8	TRIB1 *	rs6982502	125467120	C	T	0.4366560	0.0401779	0.0034448	2.8E-34
8	TRIB1 *	rs2980886	125467846	G	A	0.4438370	0.0396293	0.0034395	2.0E-33
8	TRIB1 *	rs4871603	125468125	C	T	0.3060970	0.0360477	0.0036969	1.7E-25
8	TRIB1 *	rs2980882	125468458	A	G	0.4438380	0.0396169	0.0034401	2.2E-33
8	TRIB1 *	rs2980880	125468730	G	A	0.2990070	0.0371020	0.0037222	1.3E-26
8	TRIB1 *	rs2980879	125469233	A	T	0.2987720	0.0366859	0.0037198	4.0E-26
8	TRIB1 *	rs2980876	125469452	C	T	0.2990570	0.0371210	0.0037222	1.2E-26
8	TRIB1 *	rs2980875	125469505	A	G	0.4507510	0.0396653	0.0034389	1.8E-33
8	TRIB1 *	rs2954020	125469710	A	G	0.2991970	0.0369877	0.0037204	1.7E-26
8	TRIB1 *	rs2954021	125469835	A	G	0.4423720	0.0407526	0.0034414	2.8E-35
8	TRIB1 *	rs2954022	125470379	C	A	0.4493500	0.0400708	0.0034357	3.3E-34
8	TRIB1 *	rs79658059	125470680	T	TA	0.2991230	0.0370623	0.0037235	1.4E-26
8	TRIB1 *	rs28495284	125470681	G	A	0.3117850	0.0343218	0.0037524	6.4E-23
8	TRIB1 *	rs2954024	125470688	A	G	0.2991230	0.0370623	0.0037235	1.4E-26
8	TRIB1 *	rs2980870	125471598	A	G	0.3133870	0.0357878	0.0037214	5.5E-25
8	TRIB1 *	chr8:125471601_TAA_T	125471601	TAA	T	0.3046140	0.0365735	0.0037115	3.9E-26
8	TRIB1 *	rs4336630	125472034	T	G	0.3066430	0.0359946	0.0036948	1.6E-25
8	TRIB1 *	rs2954025	125472221	C	T	0.3066470	0.0359827	0.0036947	1.6E-25
8	TRIB1 *	rs2954026	125472284	T	G	0.2994980	0.0369640	0.0037205	1.6E-26
8	TRIB1 *	rs2980862	125472396	G	C	0.2994850	0.0370243	0.0037207	1.4E-26
8	TRIB1 *	rs35575186	125472985	A	AT	0.3066470	0.0359827	0.0036947	1.6E-25
8	TRIB1 *	rs2954027	125473052	T	A	0.4498450	0.0402262	0.0034362	1.7E-34
8	TRIB1 *	rs2954028	125473054	T	C	0.2994850	0.0370243	0.0037207	1.4E-26
8	TRIB1 *	rs2980860	125473095	A	G	0.4499550	0.0402420	0.0034370	1.6E-34
8	TRIB1 *	rs7828113	125473225	A	G	0.3067100	0.0359906	0.0036954	1.6E-25
8	TRIB1 *	rs7846466	125473289	T	C	0.2996050	0.0370263	0.0037223	1.5E-26
8	TRIB1 *	chr8:125473988_G_GT	125473988	G	GT	0.3050870	0.0360073	0.0037286	3.5E-25
8	TRIB1 *	rs17321515	125474167	A	G	0.4500510	0.0402828	0.0034357	1.3E-34
8	TRIB1 *	rs2980867	125475449	T	G	0.2995870	0.0371143	0.0037227	1.1E-26
8	TRIB1 *	rs2980868	125475993	C	T	0.4501880	0.0406530	0.0034374	3.9E-35
8	TRIB1 *	rs2980869	125476008	C	T	0.4504180	0.0407125	0.0034380	3.3E-35
8	TRIB1 *	rs59871348	125476465	ATTG	A	0.3073900	0.0360809	0.0036977	1.3E-25
8	TRIB1 *	rs2954029	125478730	A	T	0.4498950	0.0403179	0.0034345	1.1E-34
8	TRIB1 *	rs5894757	125478769	T	TG	0.3069620	0.0359852	0.0036962	1.4E-25

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
8	TRIB1 *	rs2954030	125479062	T	C	0.3198020	0.0335643	0.0036606	1.3E-22
8	TRIB1 *	rs2954031	125479491	G	T	0.4632070	0.0389892	0.0034279	2.1E-32
8	TRIB1 *	rs12164213	125480206	T	C	0.4385390	0.0198975	0.0034552	8.2E-10
8	TRIB1 *	rs56116731	125480684	C	CT	0.3034960	0.0367131	0.0037358	4.8E-26
8	TRIB1 *	rs10956250	125480889	A	G	0.4384900	0.0198705	0.0034548	8.8E-10
8	TRIB1 *	rs2954032	125481150	A	G	0.2993410	0.0374438	0.0037274	4.1E-27
8	TRIB1 *	rs2954033	125481504	A	G	0.3000580	0.0373594	0.0037210	4.7E-27
8	TRIB1 *	rs4457349	125482075	G	A	0.4181650	-0.0295516	0.0034718	1.6E-18
8	TRIB1 *	chr8:125482151_G_GT	125482151	G	GT	0.4450710	0.0201743	0.0034820	9.4E-10
8	TRIB1 *	rs4350001	125482320	C	T	0.4386210	0.0197314	0.0034536	1.1E-09
8	TRIB1 *	rs4552916	125482522	A	G	0.4387810	0.0198557	0.0034543	8.6E-10
8	TRIB1 *	rs35192929	125482927	T	C	0.4380270	0.0200579	0.0034555	5.4E-10
8	TRIB1 *	rs7005535	125483343	T	C	0.4382960	0.0201215	0.0034581	5.1E-10
8	TRIB1 *	rs6470358	125483683	G	A	0.4380200	0.0203077	0.0034563	3.4E-10
8	TRIB1 *	rs16900644	125484533	C	T	0.4376660	0.0200289	0.0034601	6.0E-10
8	TRIB1 *	rs12681878	125484683	C	T	0.4376410	0.0200129	0.0034602	6.1E-10
8	TRIB1 *	rs4870942	125486661	C	T	0.4413120	0.0199803	0.0034681	5.7E-10
8	TRIB1 *	rs72442317	125486996	CCAGT	C	0.4378680	0.0201221	0.0034595	5.4E-10
8	TRIB1 *	rs1055748815	125486998	AGTCG	A	0.4378680	0.0201221	0.0034595	5.4E-10
8	TRIB1 *	rs2980859	125487187	C	G	0.2848640	0.0398327	0.0037896	7.8E-29
8	TRIB1 *	rs4351435	125487636	G	A	0.2848680	0.0398508	0.0037896	7.4E-29
8	TRIB1 *	rs28601761	125487789	G	C	0.1503730	-0.0250461	0.0047998	3.3E-08
8	TRIB1 *	rs2980858	125488935	T	C	0.2853850	0.0398096	0.0037876	7.6E-29
8	TRIB1 *	rs11320307	125489095	CA	C	0.4371200	0.0201208	0.0034631	6.4E-10
8	TRIB1 *	rs7846135	125489286	G	A	0.4353960	0.0193249	0.0034656	3.0E-09
8	TRIB1 *	rs6987702	125492484	T	C	0.4352240	0.0196633	0.0034600	1.4E-09
8	TRIB1 *	rs75998532	125493463	C	T	0.4029910	-0.0313431	0.0034991	1.9E-20
8	TRIB1 *	rs2980888	125495066	T	C	0.2824480	0.0398396	0.0037971	4.8E-29
8	TRIB1 *	rs2954038	125495147	C	A	0.2826060	0.0397817	0.0037956	5.4E-29
8	TRIB1 *	rs6987904	125495783	T	C	0.4020860	-0.0313947	0.0035206	2.4E-20
8	TRIB1 *	rs6989280	125496504	G	A	0.4410620	0.0201054	0.0034984	7.4E-10
11	DAGLA *	rs7925523	61675020	A	G	0.2525890	-0.0236582	0.0039611	3.4E-09
11	DAGLA *	rs60399071	61675683	A	G	0.2526880	-0.0236108	0.0039621	3.7E-09
11	DAGLA *	rs151242175	61679851	T	C	0.2520760	-0.0230958	0.0039730	8.4E-09
11	DAGLA *	rs115702847	61679884	A	T	0.2520760	-0.0230958	0.0039730	8.4E-09
11	DAGLA	rs59200224	61682665	G	A	0.2527400	-0.0232974	0.0039666	6.1E-09
11	DAGLA	rs59371352	61682823	A	G	0.2529550	-0.0235154	0.0039721	4.9E-09
11	DAGLA	rs72918042	61684076	G	C	0.2527350	-0.0233111	0.0039666	5.9E-09
11	DAGLA	rs35404524	61687658	C	CTT	0.2527510	-0.0232074	0.0039672	7.2E-09
11	DAGLA	rs4963308	61688954	A	G	0.2527260	-0.0232388	0.0039682	6.8E-09
11	DAGLA	rs883724	61690385	T	C	0.2524290	-0.0230246	0.0039702	1.1E-08
11	DAGLA	rs11827215	61691123	A	G	0.2530500	-0.0228590	0.0039663	1.3E-08
11	DAGLA	rs72315101	61695289	C	CTCTG	0.2527330	-0.0233232	0.0039696	6.2E-09
11	DAGLA	rs60507107	61696297	T	C	0.2527130	-0.0231422	0.0039699	8.2E-09
11	DAGLA	rs2097853	61698795	T	G	0.2528920	-0.0231604	0.0039700	7.7E-09
11	DAGLA	rs58217294	61702031	A	T	0.2528990	-0.0230631	0.0039711	8.9E-09
11	DAGLA	rs12274157	61710175	C	A	0.2530770	-0.0229537	0.0039741	1.1E-08
11	DAGLA	rs731842	61712719	C	T	0.2531710	-0.0229864	0.0039734	1.0E-08
11	DAGLA	rs17156244	61714923	G	T	0.2532700	-0.0231502	0.0039724	8.0E-09
11	DAGLA	rs2903825	61721496	T	C	0.2605120	-0.0244482	0.0039398	9.3E-10
11	DAGLA	rs9735635	61723408	A	C	0.2599560	-0.0246288	0.0039426	6.7E-10
11	DAGLA	rs4963243	61726855	A	G	0.2608970	-0.0246252	0.0039351	6.3E-10
11	DAGLA	rs2240287	61738111	A	G	0.2632130	-0.0238795	0.0039294	1.7E-09
11	DAGLA	rs2240286	61738982	C	T	0.2631880	-0.0238703	0.0039306	1.9E-09
11	DAGLA	rs4963255	61740134	A	G	0.2632220	-0.0239905	0.0039316	1.6E-09
11	DAGLA	rs3741252	61744026	T	C	0.2608840	-0.0244686	0.0039540	9.8E-10
11	MYRF	rs174528	61776027	T	C	0.4007140	-0.0213665	0.0035166	1.1E-09
11	MYRF	rs174529	61776489	T	C	0.4005290	-0.0209378	0.0035188	2.2E-09
11	MYRF	rs174530	61779120	A	G	0.4104280	-0.0229708	0.0034969	4.2E-11
11	MYRF	rs108499	61779765	C	T	0.4139930	-0.0230357	0.0034962	4.1E-11
11	MYRF	rs509360	61781087	A	G	0.4009250	-0.0219041	0.0035206	3.5E-10
11	MYRF	rs174533	61781553	G	A	0.4136890	-0.0231268	0.0034985	3.3E-11
11	MYRF	rs174534	61781986	A	G	0.4103990	-0.0222933	0.0034990	1.7E-10
11	MYRF	rs174535	61783884	T	C	0.4094610	-0.0227526	0.0034966	6.5E-11
11	MYRF	rs174536	61784455	A	C	0.4120430	-0.0230174	0.0034991	4.2E-11
11	MYRF	rs174537	61785208	G	T	0.4130170	-0.0229945	0.0034956	4.1E-11
11	TMEM258	rs102275	61790331	T	C	0.4126880	-0.0232141	0.0034945	2.6E-11
11	TMEM258	rs102274	61790354	T	C	0.4128400	-0.0233895	0.0034953	1.9E-11
11	TMEM258	rs174538	61792609	G	A	0.4152710	-0.0229409	0.0034931	4.3E-11
11	FEN1	rs4246215	61796827	G	T	0.4132480	-0.0234202	0.0034956	1.9E-11
11	FADS1 *	rs174541	61798436	T	C	0.4130300	-0.0237110	0.0034974	1.1E-11
11	FADS1	rs174544	61800281	C	A	0.4224150	-0.0224349	0.0034939	9.8E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	FADS1	rs174545	61801834	C	G	0.4134550	-0.0232364	0.0034953	2.7E-11
11	FADS1	rs174546	61802358	C	T	0.4134970	-0.0234735	0.0034959	1.7E-11
11	FADS1	rs174547	61803311	T	C	0.4133520	-0.0231126	0.0034959	3.5E-11
11	FADS1	rs174548	61803876	C	G	0.4213510	-0.0226993	0.0034871	5.7E-11
11	FADS1	rs174549	61803910	G	A	0.4220130	-0.0226833	0.0034896	6.1E-11
11	FADS1	rs174550	61804006	T	C	0.4134140	-0.0234701	0.0034955	1.7E-11
11	FADS1	rs174553	61807686	A	G	0.4137210	-0.0234199	0.0034953	1.9E-11
11	FADS1	rs72643557	61811955	T	C	0.4099660	-0.0245028	0.0035134	3.1E-12
11	FADS1	rs174554	61811991	A	G	0.4137250	-0.0233906	0.0034949	2.0E-11
11	FADS1	rs174555	61812288	T	C	0.4211320	-0.0226940	0.0034875	5.5E-11
11	FADS1	rs174556	61813163	C	T	0.4211660	-0.0227405	0.0034875	5.0E-11
11	FADS1	rs174559	61814184	G	A	0.4228940	-0.0227012	0.0034876	5.5E-11
11	FADS1	rs174560	61814292	T	C	0.4211510	-0.0228576	0.0034878	4.1E-11
11	FADS1, MIR1908	rs174561	61815236	T	C	0.4211180	-0.0229048	0.0034883	3.7E-11
11	FADS2	rs174562	61817672	A	G	0.4130100	-0.0235695	0.0034978	1.5E-11
11	FADS2	rs35473591	61818856	C	CT	0.4132400	-0.0236683	0.0034983	1.2E-11
11	FADS2	rs174564	61820833	A	G	0.4120300	-0.0231052	0.0035026	4.1E-11
11	FADS2	rs28456	61822009	A	G	0.4198520	-0.0222014	0.0034983	1.6E-10
11	FADS2	rs174565	61824164	C	G	0.4140490	-0.0224780	0.0035016	1.3E-10
11	FADS2	chr11:61824525_A_AAG	61824525	A	AAG	0.4162020	-0.0227704	0.0035109	8.9E-11
11	FADS2	rs174566	61824890	A	G	0.4120400	-0.0230581	0.0035025	4.4E-11
11	FADS2	rs174567	61825533	A	G	0.4149440	-0.0237540	0.0034985	1.1E-11
11	FADS2	rs174568	61826344	C	T	0.4139480	-0.0235132	0.0034966	1.6E-11
11	FADS2	rs3834458	61827448	CT	C	0.4131710	-0.0235730	0.0034990	1.5E-11
11	FADS2	rs5792235	61828850	CA	C	0.4120440	-0.0232249	0.0034977	3.0E-11
11	FADS2	rs99780	61829161	C	T	0.4120440	-0.0232249	0.0034977	3.0E-11
11	FADS2	rs174570	61829740	C	T	0.4141920	-0.0227516	0.0034952	7.1E-11
11	FADS2	rs1535	61830500	A	G	0.4120750	-0.0231848	0.0034970	3.3E-11
11	FADS2	rs174574	61832870	C	A	0.4119490	-0.0231507	0.0034988	3.4E-11
11	FADS2	rs199649489	61834989	A	C	0.4310240	-0.0235923	0.0035592	3.5E-11
11	FADS2	rs174576	61836038	C	A	0.4115880	-0.0228217	0.0034993	6.0E-11
11	FADS2	rs174577	61837342	C	A	0.4116870	-0.0227514	0.0034988	7.0E-11
11	FADS2	rs174578	61838027	T	A	0.4119290	-0.0229379	0.0034991	4.9E-11
11	FADS2	rs174580	61839170	A	G	0.4113160	-0.0228407	0.0035016	5.8E-11
11	FADS2	rs174581	61839211	G	A	0.4114260	-0.0229248	0.0035021	5.0E-11
11	FADS2	rs174583	61842278	C	T	0.4110170	-0.0228697	0.0035000	5.4E-11
11	FADS2	rs174584	61843278	G	A	0.4106490	-0.0228844	0.0035025	5.5E-11
11	FADS2	rs174592	61851136	A	G	0.4081950	-0.0229887	0.0034991	4.1E-11
11	FADS2	rs174594	61852357	A	C	0.4080200	-0.0231079	0.0035061	3.0E-11
11	FADS2	rs72643559	61852802	C	T	0.4040470	-0.0226673	0.0035267	9.3E-11
11	FADS2	chr11:61853156_AAACAAC	61853156	AAACAAC	A	0.4081840	-0.0219595	0.0035190	2.8E-10
11	FADS2	rs174598	61853722	G	A	0.4095030	-0.0229709	0.0035037	4.0E-11
11	FADS2	rs174599	61854084	G	C	0.4075580	-0.0231181	0.0035061	3.0E-11
11	FADS2	rs174600	61854755	T	C	0.4091540	-0.0227345	0.0035076	6.5E-11
11	FADS2	rs174601	61855668	C	T	0.4038370	-0.0226296	0.0035113	6.9E-11
11	FADS3 *	rs35870730	61891648	A	AC	0.2954430	0.0212065	0.0038516	1.8E-08
11	BUD13 *	rs10891999	116618165	T	A	0.1472680	0.0296992	0.0048743	1.0E-09
11	BUD13 *	rs11216043	116619262	C	T	0.1459940	0.0302346	0.0048868	5.1E-10
11	BUD13 *	rs148093284	116620192	C	T	0.0309289	0.0549655	0.0100173	1.6E-08
11	BUD13 *	rs11216045	116621694	C	T	0.1473030	0.0296640	0.0048700	1.0E-09
11	BUD13 *	rs184616707	116639841	G	C	0.0286399	0.0549464	0.0103636	3.3E-08
11	BUD13 *	rs116892227	116642030	A	G	0.0890399	-0.0320319	0.0060174	4.1E-08
11	BUD13 *	rs1145184	116642465	A	G	0.1382820	0.0436569	0.0050135	6.3E-19
11	BUD13 *	rs116859831	116642711	C	T	0.0926138	-0.0312479	0.0058971	4.9E-08
11	BUD13 *	rs78642155	116643375	C	G	0.0922423	-0.0318035	0.0059095	2.9E-08
11	BUD13 *	rs116948654	116643602	C	T	0.0922849	-0.0315870	0.0059119	3.4E-08
11	BUD13 *	rs117689643	116643612	T	G	0.0922887	-0.0315947	0.0059119	3.4E-08
11	BUD13 *	rs1145185	116643982	A	G	0.1378310	0.0447668	0.0049858	8.9E-20
11	BUD13 *	rs71480306	116644840	C	T	0.1426310	0.0454944	0.0048967	3.7E-21
11	BUD13 *	rs139668970	116645673	T	TAAAAC	0.1419420	0.0447911	0.0049031	1.7E-20
11	BUD13 *	rs869271932	116645674	A	AAAAC	0.1427990	0.0456472	0.0048880	2.6E-21
11	BUD13 *	rs2212428	116645870	T	C	0.0921481	-0.0321394	0.0059353	2.1E-08
11	BUD13 *	rs1002037	116646019	C	G	0.0969441	-0.0315010	0.0058243	1.7E-08
11	BUD13 *	rs71480307	116646156	A	G	0.1423060	0.0461947	0.0048916	9.4E-22
11	BUD13 *	rs35165288	116646608	C	T	0.1429430	0.0458306	0.0048841	1.8E-21
11	BUD13 *	rs513533	116648641	G	A	0.1157360	0.0551461	0.0053527	4.5E-25
11	BUD13 *	rs516043	116648867	G	C	0.1158260	0.0551615	0.0053510	4.3E-25
11	BUD13 *	rs499790	116649022	T	C	0.1158230	0.0551389	0.0053506	4.5E-25
11	BUD13 *	rs504268	116649487	T	C	0.1158260	0.0552382	0.0053504	3.8E-25
11	BUD13 *	rs544479	116649681	C	T	0.1158210	0.0551628	0.0053506	4.4E-25
11	BUD13 *	rs506222	116649717	C	A	0.1158230	0.0551623	0.0053506	4.4E-25
11	BUD13 *	rs549125	116650209	G	C	0.1199980	0.0585054	0.0052715	8.5E-29

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs533668	116650418	G	T	0.1200060	0.0586308	0.0052713	6.4E-29
11	BUD13 *	rs573985	116650599	A	G	0.1198140	0.0585492	0.0052755	9.3E-29
11	BUD13 *	rs575906	116650841	G	A	0.1202450	0.0585211	0.0052672	8.1E-29
11	BUD13 *	rs143762798	116650954	A	G	0.0208574	-0.0696810	0.0119648	3.0E-09
11	BUD13 *	rs562756	116651258	C	G	0.1199470	0.0594814	0.0052729	1.6E-29
11	BUD13 *	rs491022	116651271	C	T	0.1390130	0.0500589	0.0049979	7.8E-24
11	BUD13 *	rs563796	116651394	G	A	0.1208310	0.0589671	0.0052521	2.8E-29
11	BUD13 *	rs563917	116651439	T	C	0.1208650	0.0589409	0.0052510	2.8E-29
11	BUD13 *	rs492182	116651447	A	G	0.1208810	0.0589473	0.0052507	2.8E-29
11	BUD13 *	rs5795043	116651516	T	TC	0.1120600	0.0552923	0.0054792	5.4E-24
11	BUD13 *	rs565607	116651613	T	C	0.1207310	0.0589026	0.0052535	3.7E-29
11	BUD13 *	rs567576	116651842	G	A	0.1206670	0.0586940	0.0052489	5.8E-29
11	BUD13 *	rs567599	116651848	T	G	0.1206830	0.0585717	0.0052486	7.4E-29
11	BUD13 *	rs3017237	116651908	C	G	0.1208700	0.0586867	0.0052436	5.4E-29
11	BUD13 *	rs480028	116652053	G	C	0.1209160	0.0586445	0.0052419	5.7E-29
11	BUD13 *	rs480878	116652137	A	G	0.1214500	0.0583525	0.0052360	7.1E-29
11	BUD13 *	rs499563	116652244	T	C	0.1209710	0.0590379	0.0052420	2.7E-29
11	BUD13 *	rs138535309	116652253	C	CTT	0.1208230	0.0587343	0.0052439	4.6E-29
11	BUD13 *	rs202191031	116652259	A	AAGTGG	0.1208230	0.0587343	0.0052439	4.6E-29
11	BUD13 *	rs79770434	116652448	T	C	0.0863474	-0.0335534	0.0061258	1.2E-08
11	BUD13 *	rs483747	116652450	C	T	0.1209580	0.0586930	0.0052405	4.9E-29
11	BUD13 *	rs141584077	116652587	T	A	0.1128250	0.0518285	0.0054491	2.4E-21
11	BUD13 *	rs523980	116652589	T	A	0.1078630	0.0502443	0.0055738	2.5E-19
11	BUD13 *	rs485638	116652656	C	G	0.1209550	0.0586877	0.0052404	5.0E-29
11	BUD13 *	rs117742492	116652940	A	G	0.0862700	-0.0335970	0.0061318	1.2E-08
11	BUD13 *	rs528647	116653104	T	C	0.1209210	0.0587090	0.0052406	4.8E-29
11	BUD13 *	rs528732	116653127	A	G	0.1209210	0.0587090	0.0052406	4.8E-29
11	BUD13 *	rs3017778	116653214	T	C	0.1208710	0.0585782	0.0052420	6.3E-29
11	BUD13 *	rs3017779	116653271	T	C	0.1208210	0.0584206	0.0052427	9.1E-29
11	BUD13 *	rs76860051	116654589	C	A	0.0859809	-0.0347742	0.0061446	3.9E-09
11	BUD13 *	rs79862998	116654602	A	G	0.0858544	-0.0345114	0.0061485	5.0E-09
11	BUD13 *	rs480823	116655013	C	T	0.1161220	0.0617553	0.0053901	3.9E-30
11	BUD13 *	rs481843	116655150	T	C	0.1153000	0.0605341	0.0054129	7.6E-29
11	BUD13 *	rs116857027	116655278	T	C	0.0856961	-0.0346194	0.0061571	4.5E-09
11	BUD13 *	rs34485603	116655315	C	CCT	0.1153230	0.0604711	0.0054166	9.1E-29
11	BUD13 *	rs486394	116655605	C	A	0.1183840	0.0624992	0.0053635	3.9E-31
11	BUD13 *	rs78347813	116658413	T	C	0.0851763	-0.0390673	0.0061570	7.9E-11
11	BUD13 *	rs1892947	116659344	A	G	0.0872022	-0.0401354	0.0060692	1.3E-11
11	BUD13 *	rs116905034	116659391	C	G	0.0654231	0.0477783	0.0070341	2.2E-12
11	BUD13 *	rs146893332	116660321	TGAGGGGGGC	T	0.0656994	0.0475901	0.0070165	2.2E-12
11	BUD13 *	rs117889066	116660333	C	G	0.0879205	-0.0406032	0.0060396	7.0E-12
11	BUD13 *	rs117293980	116660758	G	T	0.0879034	-0.0405612	0.0060401	7.3E-12
11	BUD13 *	rs7117145	116661252	T	A	0.0880501	-0.0400516	0.0060331	1.3E-11
11	BUD13 *	rs78198334	116661566	C	G	0.0880691	-0.0399028	0.0060318	1.5E-11
11	BUD13 *	rs118175510	116661831	C	T	0.0832611	0.0749189	0.0062393	6.5E-34
11	BUD13 *	rs79291519	116662593	T	C	0.0865113	-0.0394630	0.0060789	3.4E-11
11	BUD13 *	rs75942205	116662878	C	T	0.0869254	-0.0396121	0.0060622	2.3E-11
11	BUD13 *	rs61659529	116662911	G	A	0.0868721	-0.0394519	0.0060653	2.8E-11
11	BUD13 *	rs486915	116663571	T	A	0.3698980	-0.0421801	0.0036258	2.0E-33
11	BUD13 *	rs146134775	116663577	C	CT	0.0868571	-0.0397357	0.0060710	2.1E-11
11	BUD13 *	rs76547220	116663833	G	T	0.0869263	-0.0396877	0.0060644	2.2E-11
11	BUD13 *	rs567209	116664111	T	C	0.1675520	0.0358665	0.0046279	3.7E-15
11	BUD13 *	rs2105609	116664370	A	G	0.0869263	-0.0396877	0.0060644	2.2E-11
11	BUD13 *	rs2105610	116664409	C	T	0.0866283	-0.0391094	0.0060745	4.5E-11
11	BUD13 *	rs77226464	116664718	T	C	0.0869868	-0.0394061	0.0060618	3.1E-11
11	BUD13 *	rs190069353	116664907	A	C	0.0869132	-0.0396589	0.0060653	2.3E-11
11	BUD13 *	rs117014628	116664914	T	C	0.0869303	-0.0396928	0.0060647	2.2E-11
11	BUD13 *	rs1240776	116665564	T	C	0.3761920	-0.0436420	0.0035382	3.5E-37
11	BUD13 *	rs12803249	116665701	G	A	0.1674920	0.0358047	0.0046274	4.1E-15
11	BUD13 *	rs1240778	116665773	C	A	0.3693490	0.0274111	0.0035893	5.0E-15
11	BUD13 *	rs10892010	116665939	C	A	0.2483350	0.0212610	0.0040076	3.4E-08
11	BUD13 *	rs79063991	116666103	T	C	0.0869308	-0.0396968	0.0060650	2.2E-11
11	BUD13 *	rs61906081	116666342	A	G	0.1674920	0.0358047	0.0046274	4.1E-15
11	BUD13 *	rs118103820	116666399	G	A	0.0869308	-0.0396968	0.0060650	2.2E-11
11	BUD13 *	rs6589557	116667044	T	C	0.4237390	0.0363840	0.0034668	3.3E-27
11	BUD13 *	rs140973748	116667081	C	T	0.0869326	-0.0397099	0.0060651	2.2E-11
11	BUD13 *	rs35933073	116667129	A	C	0.1674920	0.0358047	0.0046274	4.1E-15
11	BUD13 *	rs6589558	116667225	A	G	0.4237390	0.0363840	0.0034668	3.3E-27
11	BUD13 *	rs12787592	116667257	C	G	0.1675130	0.0357117	0.0046271	4.8E-15
11	BUD13 *	rs143380339	116667386	A	C	0.0869326	-0.0397099	0.0060651	2.2E-11
11	BUD13 *	rs1784126	116667498	T	G	0.3742680	-0.0430240	0.0035403	4.1E-36
11	BUD13 *	rs1784127	116667859	A	G	0.3745680	-0.0430600	0.0035395	3.6E-36

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs1784128	116667972	A	G	0.3745680	-0.0430600	0.0035395	3.6E-36
11	BUD13 *	rs150937658	116668605	G	A	0.0995288	-0.0492591	0.0057635	2.1E-17
11	BUD13 *	rs7925553	116670267	G	A	0.1676540	0.0357925	0.0046242	3.9E-15
11	BUD13 *	rs144188664	116670317	T	A	0.0869561	-0.0397719	0.0060652	2.0E-11
11	BUD13 *	rs1787686	116670755	A	G	0.2873020	-0.0339779	0.0037944	1.6E-20
11	BUD13 *	rs148462279	116672020	G	A	0.0869443	-0.0396561	0.0060658	2.3E-11
11	BUD13 *	rs144256947	116672308	C	T	0.0868522	-0.0399932	0.0060700	1.6E-11
11	BUD13 *	chr11:116672851_TA_T	116672851	TA	T	0.2873030	-0.0339614	0.0037944	1.7E-20
11	BUD13 *	chr11:116674066_A_ATATT	116674066	ATATT	A	0.0864526	-0.0400517	0.0060851	1.4E-11
11	BUD13 *	rs117179746	116674534	A	G	0.0866599	-0.0397498	0.0060792	2.0E-11
11	BUD13 *	rs11530558	116674881	C	A	0.0253631	0.0591580	0.0109167	2.4E-08
11	BUD13 *	rs1787688	116675006	C	T	0.2869250	-0.0339371	0.0037968	1.9E-20
11	BUD13 *	rs78106248	116675263	CA	C	0.1722210	0.0370573	0.0045856	1.8E-16
11	BUD13 *	rs61906102	116675786	C	T	0.1724880	0.0367279	0.0045820	3.1E-16
11	BUD13 *	rs116944258	116675916	A	C	0.0871099	-0.0389416	0.0060671	5.1E-11
11	BUD13 *	rs58672319	116676219	T	TG	0.2863890	-0.0341695	0.0037988	1.0E-20
11	BUD13 *	rs1960036	116676692	A	C	0.1724770	0.0367506	0.0045817	3.0E-16
11	BUD13 *	rs372407480	116677221	A	C	0.0144222	0.0810184	0.0143652	1.9E-08
11	BUD13 *	rs12801136	116677632	A	G	0.1725180	0.0367596	0.0045808	2.9E-16
11	BUD13 *	rs79678269	116678255	C	G	0.0872254	-0.0389668	0.0060655	5.0E-11
11	BUD13 *	rs1005705	116678399	C	A	0.0870986	-0.0390634	0.0060681	4.5E-11
11	BUD13 *	chr11:116678728_T_TGA	116678728	TGA	T	0.0870986	-0.0390634	0.0060681	4.5E-11
11	BUD13 *	rs58060512	116678740	A	AAT	0.1708870	0.0345663	0.0046255	2.8E-14
11	BUD13 *	rs35963862	116679180	C	T	0.1682370	0.0356201	0.0046144	4.4E-15
11	BUD13 *	rs117830617	116679254	A	G	0.0871045	-0.0390667	0.0060684	4.5E-11
11	BUD13 *	rs61906104	116679398	G	A	0.1726480	0.0367110	0.0045779	3.1E-16
11	BUD13 *	chr11:116681564_G_GA	116681564	GA	G	0.1726280	0.0367840	0.0045788	2.5E-16
11	BUD13 *	rs1787717	116682049	T	C	0.3721600	-0.0423748	0.0035504	5.0E-35
11	BUD13 *	rs12806224	116682098	C	T	0.1722900	0.0366749	0.0045847	3.1E-16
11	BUD13 *	rs12805061	116682308	G	A	0.1726560	0.0365458	0.0045785	3.7E-16
11	BUD13 *	rs5795046	116682757	T	TG	0.3720630	-0.0423423	0.0035516	6.2E-35
11	BUD13 *	rs11826999	116683062	A	G	0.1727850	0.0363141	0.0045784	5.9E-16
11	BUD13 *	rs66560466	116683783	T	TG	0.2853610	-0.0337303	0.0037974	3.2E-20
11	BUD13 *	rs35310854	116684317	TA	T	0.1727520	0.0367017	0.0045790	3.0E-16
11	BUD13 *	rs117341026	116684410	A	G	0.0862260	-0.0394329	0.0061053	3.3E-11
11	BUD13 *	rs35681250	116684670	T	A	0.1729320	0.0366840	0.0045800	3.1E-16
11	BUD13 *	rs3016357	116684699	T	C	0.2928140	-0.0346091	0.0038164	6.9E-21
11	BUD13 *	rs1145213	116684706	G	A	0.2959850	-0.0327167	0.0038134	7.0E-19
11	BUD13 *	rs77835865	116684713	G	A	0.1727520	0.0366607	0.0045790	3.2E-16
11	BUD13 *	rs956832572	116684717	T	A	0.0148147	0.0821950	0.0141853	8.1E-09
11	BUD13 *	rs61906112	116685049	A	T	0.1727000	0.0366238	0.0045800	3.5E-16
11	BUD13 *	rs17092638	116685520	G	C	0.1727210	0.0367970	0.0045812	2.6E-16
11	BUD13 *	rs1145212	116686149	A	G	0.4511290	0.0218633	0.0034849	5.3E-11
11	BUD13 *	rs1145211	116686500	A	C	0.2849720	-0.0349581	0.0038168	1.9E-21
11	BUD13 *	rs17092642	116686532	C	T	0.1727280	0.0368901	0.0045854	2.2E-16
11	BUD13 *	rs947990	116686598	T	G	0.0612357	-0.0399474	0.0071665	4.2E-08
11	BUD13 *	rs11216093	116687166	C	A	0.2506220	0.0213278	0.0040085	2.9E-08
11	BUD13 *	rs61906115	116687529	A	T	0.1680880	0.0358864	0.0046277	3.0E-15
11	BUD13 *	rs12799766	116687711	A	G	0.1681660	0.0359162	0.0046265	2.9E-15
11	BUD13 *	rs12799441	116687799	T	A	0.1682730	0.0360058	0.0046254	2.4E-15
11	BUD13 *	rs12799449	116687809	G	A	0.1683050	0.0361464	0.0046262	1.9E-15
11	BUD13 *	rs1623797	116689731	T	C	0.4341480	-0.0394287	0.0034869	1.5E-31
11	BUD13 *	rs1787714	116689894	A	G	0.2477380	-0.0441579	0.0040454	3.0E-29
11	BUD13 *	rs1787713	116689895	G	C	0.2477380	-0.0441579	0.0040454	3.0E-29
11	BUD13 *	rs12291024	116689951	G	T	0.3656260	0.0346814	0.0035809	1.5E-23
11	BUD13 *	rs3017229	116690251	A	G	0.2494410	-0.0443422	0.0040301	1.0E-29
11	BUD13 *	rs118013839	116690798	A	G	0.0843370	-0.0430091	0.0061851	1.6E-12
11	BUD13 *	rs1784121	116691074	T	G	0.4335310	-0.0396576	0.0034876	7.4E-32
11	BUD13 *	rs1787704	116691280	T	C	0.4347230	-0.0398419	0.0034852	2.7E-32
11	BUD13 *	rs11216096	116691864	A	C	0.3661210	0.0349275	0.0035752	6.3E-24
11	BUD13 *	rs117393825	116691971	T	C	0.1000440	-0.0501902	0.0057455	5.6E-18
11	BUD13 *	rs1784119	116692089	T	C	0.2494570	-0.0445583	0.0040278	4.9E-30
11	BUD13 *	rs12785772	116692892	A	G	0.3661150	0.0347684	0.0035760	1.0E-23
11	BUD13 *	rs12785990	116692990	A	G	0.3638190	0.0349865	0.0035812	7.2E-24
11	BUD13 *	rs79962987	116693078	T	G	0.0391570	-0.0631785	0.0088320	3.1E-13
11	BUD13 *	rs12420888	116693106	G	C	0.3640950	0.0350337	0.0035790	6.3E-24
11	BUD13 *	rs1787701	116693276	C	G	0.3384470	-0.0523183	0.0036705	2.6E-48
11	BUD13 *	rs117889337	116693777	T	C	0.0836714	-0.0421889	0.0062082	4.6E-12
11	BUD13 *	rs1787699	116693837	G	A	0.2490290	-0.0447020	0.0040322	4.1E-30
11	BUD13 *	rs1787698	116693846	T	C	0.2490240	-0.0446994	0.0040322	4.2E-30
11	BUD13 *	rs1784118	116694339	T	C	0.2516290	-0.0455403	0.0040149	2.0E-31
11	BUD13 *	rs117607796	116694887	A	C	0.0840936	-0.0429076	0.0061928	1.8E-12

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs111218525	116695822	T	C	0.2060270	0.0340809	0.0042758	7.7E-16
11	BUD13 *	rs59854309	116696047	T	C	0.2571320	-0.0469136	0.0040288	4.6E-33
11	BUD13 *	rs60954647	116696217	T	C	0.4101850	-0.0261372	0.0035689	1.5E-13
11	BUD13 *	rs1784106	116696733	A	C	0.2536950	-0.0456511	0.0040075	1.1E-31
11	BUD13 *	rs4938300	116696903	T	C	0.2029420	0.0357005	0.0042845	2.4E-17
11	BUD13 *	rs10892017	116697165	C	G	0.3596830	0.0368765	0.0035705	1.2E-26
11	BUD13 *	rs66473272	116697382	G	GT	0.3528550	0.0374939	0.0036118	8.6E-27
11	BUD13 *	rs11605568	116697452	A	G	0.3596200	0.0367172	0.0035700	1.8E-26
11	BUD13 *	rs11606013	116697509	T	G	0.3596860	0.0367425	0.0035696	1.7E-26
11	BUD13 *	rs140078194	116697574	A	C	0.0872345	-0.0426224	0.0060879	1.2E-12
11	BUD13 *	rs11608173	116697648	A	T	0.3596820	0.0367436	0.0035695	1.7E-26
11	BUD13 *	rs1787689	116697666	G	A	0.4448150	-0.0419295	0.0034632	7.9E-36
11	BUD13 *	rs1787690	116697800	T	G	0.2532210	-0.0461458	0.0040035	2.0E-32
11	BUD13 *	rs1787691	116697997	A	G	0.4441680	-0.0417471	0.0034615	1.4E-35
11	BUD13 *	rs947986	116698488	A	G	0.2520870	-0.0462761	0.0040105	1.5E-32
11	BUD13 *	rs3017338	116698629	A	G	0.4440150	-0.0412882	0.0034656	6.4E-35
11	BUD13 *	rs71037412	116699941	CA	C	0.4464920	-0.0406924	0.0034533	3.3E-34
11	BUD13 *	rs1145191	116700002	G	C	0.4464920	-0.0406924	0.0034533	3.3E-34
11	BUD13 *	rs200445365	116700100	A	AAAAAAAT	0.0870466	-0.0434229	0.0060963	4.5E-13
11	BUD13 *	rs1145193	116700226	G	A	0.4474560	-0.0412285	0.0034518	5.0E-35
11	BUD13 *	rs1145194	116700252	A	C	0.2505170	-0.0457481	0.0040238	1.4E-31
11	BUD13 *	rs11601168	116700422	A	T	0.0774813	-0.0476134	0.0064120	1.0E-13
11	BUD13 *	rs1145195	116700534	A	G	0.4467670	-0.0404592	0.0034528	7.2E-34
11	BUD13 *	rs11601584	116700568	C	T	0.3481500	0.0377994	0.0035771	5.2E-28
11	BUD13 *	rs1145196	116701489	T	C	0.4468540	-0.0409788	0.0034536	1.3E-34
11	BUD13 *	rs1240783	116701809	C	T	0.4467960	-0.0408988	0.0034539	1.7E-34
11	BUD13 *	rs11216100	116701814	G	C	0.3438690	0.0391427	0.0035922	1.6E-29
11	BUD13 *	rs947989	116702805	A	C	0.4530810	-0.0417055	0.0035085	1.4E-34
11	BUD13 *	rs77206548	116703747	A	G	0.0873985	-0.0428111	0.0060856	8.6E-13
11	BUD13 *	rs1240782	116703868	A	G	0.3532820	-0.0277505	0.0036289	1.6E-15
11	BUD13 *	rs10617144	116703898	CTG	C	0.3530940	-0.0276681	0.0036297	1.8E-15
11	BUD13 *	rs1240781	116704101	T	C	0.2457870	-0.0448819	0.0040577	9.3E-30
11	BUD13 *	rs4938301	116704757	A	G	0.2057560	0.0335815	0.0042604	1.1E-15
11	BUD13 *	rs76124005	116704898	G	T	0.0878626	-0.0435670	0.0060710	3.3E-13
11	BUD13 *	rs74939223	116705164	G	A	0.0878933	-0.0441975	0.0060726	1.7E-13
11	BUD13 *	rs59873384	116705494	T	C	0.0877987	-0.0439376	0.0060748	2.2E-13
11	BUD13 *	rs12802944	116705684	C	T	0.2041340	0.0347130	0.0042786	9.8E-17
11	BUD13 *	rs1263056	116705699	A	G	0.3448710	-0.0541304	0.0036619	7.3E-52
11	BUD13 *	rs1263055	116706327	A	G	0.2533550	-0.0455406	0.0040172	2.0E-31
11	BUD13 *	rs11216105	116706725	A	G	0.2535730	-0.0457116	0.0040186	1.2E-31
11	BUD13 *	rs117684324	116707255	T	A	0.0878576	-0.0436998	0.0060729	2.9E-13
11	BUD13 *	rs12221682	116707501	G	C	0.3076200	-0.0271708	0.0037567	9.5E-13
11	BUD13 *	rs11216107	116708947	C	T	0.4949440	0.0264228	0.0034406	2.8E-15
11	BUD13 *	rs148075162	116709936	C	G	0.0157552	0.0833130	0.0137153	1.1E-09
11	BUD13 *	rs61346349	116710082	G	A	0.1783540	-0.0652817	0.0044863	1.3E-48
11	BUD13 *	rs11216109	116710099	G	C	0.3085930	0.0760244	0.0037042	1.9E-96
11	BUD13 *	rs75476300	116710153	C	G	0.0544698	0.0915737	0.0075486	4.8E-34
11	BUD13 *	rs59620302	116710443	G	C	0.0867082	-0.0429851	0.0060966	8.3E-13
11	BUD13 *	rs2367970	116710925	A	G	0.3087820	0.0760578	0.0037055	1.5E-96
11	BUD13 *	rs77574778	116711084	T	C	0.0868221	-0.0429999	0.0060919	7.9E-13
11	BUD13 *	rs77646493	116711464	A	C	0.0868258	-0.0430956	0.0060919	7.1E-13
11	BUD13 *	rs74360954	116711826	T	C	0.0868518	-0.0431070	0.0060911	7.0E-13
11	BUD13 *	rs7480302	116712301	G	A	0.4929330	0.0263056	0.0034209	3.4E-15
11	BUD13 *	rs6589562	116712723	A	G	0.3093730	0.0757052	0.0037031	7.6E-96
11	BUD13 *	rs886022	116712797	A	C	0.2361120	-0.0549660	0.0040893	2.9E-43
11	BUD13 *	rs117450838	116712972	A	G	0.0688530	-0.0596052	0.0067820	1.8E-19
11	BUD13 *	rs151007118	116713148	T	G	0.1006480	0.0853099	0.0057277	6.9E-52
11	BUD13 *	rs1144035	116713601	C	T	0.2369920	-0.0552037	0.0040846	1.2E-43
11	BUD13 *	rs117837319	116713731	C	A	0.0852360	-0.0422178	0.0061490	2.8E-12
11	BUD13 *	rs4938302	116713788	C	T	0.4929870	0.0262225	0.0034177	3.6E-15
11	BUD13 *	rs4938303	116714271	C	T	0.4928930	0.0261934	0.0034153	3.9E-15
11	BUD13 *	rs79886324	116714728	A	G	0.0871453	-0.0429786	0.0060792	6.5E-13
11	BUD13 *	rs2000571	116714817	A	G	0.3082840	0.0758489	0.0037091	5.1E-96
11	BUD13 *	rs17119918	116714897	A	G	0.1074210	-0.0585568	0.0055533	7.6E-26
11	BUD13 *	rs117785509	116715515	A	G	0.0872271	-0.0435078	0.0060788	3.6E-13
11	BUD13 *	rs7350481	116715567	T	C	0.2339950	0.1136090	0.0040319	1.5E-179
11	BUD13 *	rs7926828	116715707	C	T	0.3114960	0.0807635	0.0036990	1.7E-109
11	BUD13 *	rs151061355	116716138	A	G	0.0881118	-0.0430964	0.0060505	4.1E-13
11	BUD13 *	rs555105607	116716397	CT	C	0.0883197	-0.0440132	0.0060357	1.2E-13
11	BUD13 *	rs373804009	116716399	T	TG	0.0879068	-0.0441301	0.0060494	1.2E-13
11	BUD13 *	rs142290703	116716430	A	G	0.0883197	-0.0440132	0.0060357	1.2E-13
11	BUD13 *	rs4938304	116717709	T	C	0.0784819	-0.0509735	0.0063559	1.1E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13 *	rs79408961	116717877	T	C	0.0539718	0.0929393	0.0075657	6.0E-35
11	BUD13 *	rs4938305	116717913	T	C	0.3098060	0.0832216	0.0037200	6.5E-115
11	BUD13 *	rs180378	116718193	A	G	0.3108720	0.0829722	0.0037150	1.5E-114
11	BUD13 *	rs10711344	116718401	TA	T	0.3101040	0.0832255	0.0037180	5.6E-115
11	BUD13 *	rs180377	116718411	T	C	0.3108460	0.0830317	0.0037154	1.1E-114
11	BUD13 *	rs10892020	116718936	G	C	0.3096110	0.0833015	0.0037224	7.9E-115
11	BUD13 *	rs180376	116719323	C	G	0.3299530	-0.0332667	0.0036759	9.8E-21
11	BUD13 *	rs118046012	116719812	A	G	0.0868358	-0.0445755	0.0060776	6.7E-14
11	BUD13 *	rs180375	116720324	T	C	0.3301150	-0.0334167	0.0036739	6.3E-21
11	BUD13 *	rs180373	116720837	A	C	0.1665650	-0.0645930	0.0046172	9.0E-46
11	BUD13 *	rs147232672	116721147	A	C	0.0113919	0.0959871	0.0160809	7.4E-10
11	BUD13 *	rs180372	116721218	A	G	0.3291860	-0.0333141	0.0036749	8.4E-21
11	BUD13 *	rs180371	116721487	A	G	0.4192280	-0.0451197	0.0034735	1.3E-40
11	BUD13 *	rs143315658	116721532	C	T	0.0872265	-0.0450393	0.0060632	3.5E-14
11	BUD13 *	rs180370	116721649	T	C	0.3291860	-0.0333141	0.0036749	8.4E-21
11	BUD13 *	rs74680844	116721744	C	G	0.1650850	-0.0658627	0.0046294	3.2E-47
11	BUD13 *	rs79100692	116722391	A	G	0.1647390	-0.0664689	0.0046349	6.2E-48
11	BUD13 *	rs12420920	116723315	A	G	0.1647390	-0.0664689	0.0046349	6.2E-48
11	BUD13 *	rs12421191	116723578	T	C	0.1647390	-0.0664689	0.0046349	6.2E-48
11	BUD13 *	rs180365	116725458	T	C	0.2963090	-0.0621295	0.0038148	1.8E-62
11	BUD13 *	rs61905078	116725593	C	A	0.1636250	-0.0642333	0.0046550	1.1E-44
11	BUD13 *	rs11216118	116725679	T	C	0.0758134	0.1149190	0.0064862	3.8E-71
11	BUD13 *	rs180364	116726036	G	A	0.2568080	-0.0646602	0.0039541	5.2E-62
11	BUD13 *	rs146714678	116726114	G	T	0.0922951	-0.0613243	0.0059447	4.4E-25
11	BUD13 *	rs75662937	116726178	T	C	0.0342979	0.1657060	0.0093953	4.5E-71
11	BUD13 *	rs144027752	116726289	A	G	0.0099230	0.1075950	0.0172364	4.8E-10
11	BUD13 *	rs180363	116727173	C	T	0.2553440	-0.0666487	0.0039532	7.0E-66
11	BUD13 *	rs78484485	116727349	A	G	0.2537510	-0.0675704	0.0039588	2.1E-67
11	BUD13 *	rs10892023	116727532	T	C	0.3071330	0.0848413	0.0037277	1.2E-118
11	BUD13 *	rs180361	116727933	T	C	0.3297080	-0.0332199	0.0036749	1.1E-20
11	BUD13 *	rs139283556	116728079	T	C	0.0122330	0.1039040	0.0155369	2.2E-11
11	BUD13 *	rs180360	116728272	G	A	0.2548680	-0.0674166	0.0039545	3.0E-67
11	BUD13 *	rs76240380	116728819	A	G	0.0344195	0.1664380	0.0093800	6.0E-72
11	BUD13 *	rs7123583	116729305	C	T	0.4353120	-0.0206117	0.0034869	1.3E-09
11	BUD13 *	rs141882698	116730622	C	A	0.0917761	-0.0609944	0.0059617	1.1E-24
11	BUD13 *	rs108533	116730995	T	A	0.3320510	-0.0326667	0.0036701	3.8E-20
11	BUD13 *	rs3212282	116731229	A	G	0.3080420	0.0841427	0.0037218	3.6E-117
11	BUD13 *	rs75387300	116731683	A	G	0.1643230	-0.0667774	0.0046391	2.1E-48
11	BUD13 *	rs2008915	116732418	C	G	0.3069430	0.0846444	0.0037255	2.6E-118
11	BUD13 *	rs1893460	116732961	A	G	0.3343570	-0.0749736	0.0036514	6.9E-96
11	BUD13 *	rs4938307	116733798	A	G	0.2430810	-0.0693211	0.0039965	8.7E-69
11	BUD13 *	rs117170971	116734549	A	G	0.0887391	-0.0451288	0.0060194	2.3E-14
11	BUD13 *	rs1974718	116736050	G	A	0.2041000	0.1083480	0.0042224	3.0E-149
11	BUD13 *	rs68149171	116736335	T	TTCTG	0.2412200	-0.0695315	0.0040108	1.5E-68
11	BUD13 *	rs1558860	116736652	A	C	0.2038470	0.1087060	0.0042225	2.7E-150
11	BUD13 *	rs1558861	116736721	C	T	0.2039260	0.1088490	0.0042212	8.6E-151
11	BUD13 *	rs180350	116739332	T	C	0.2806300	-0.0667791	0.0038486	7.8E-70
11	BUD13 *	rs61905084	116739578	C	T	0.3407250	-0.0764834	0.0036284	4.5E-101
11	BUD13 *	rs9326246	116741017	C	G	0.2038660	0.1087100	0.0042273	3.5E-149
11	BUD13 *	rs180349	116741111	A	T	0.2044320	0.1084760	0.0042231	6.4E-149
11	BUD13 *	rs180348	116741279	A	G	0.0674311	-0.0433723	0.0068318	1.8E-10
11	BUD13 *	rs11216125	116741558	A	G	0.2582120	-0.0675356	0.0039007	9.2E-69
11	BUD13 *	chr11:116741689_AACACA	116741689	A	ACACACA	0.0700330	0.1485030	0.0067747	3.7E-109
11	BUD13 *	rs180346	116741943	C	A	0.2801860	-0.0665566	0.0038428	2.0E-69
11	BUD13 *	rs117788500	116742318	C	G	0.0844440	-0.0471672	0.0061562	7.2E-15
11	BUD13 *	rs17518841	116744528	A	G	0.0848514	-0.0469824	0.0061394	7.4E-15
11	BUD13 *	rs11216126	116746524	C	A	0.2555670	-0.0693025	0.0039067	3.8E-72
11	BUD13 *	rs180339	116747066	T	C	0.4406350	-0.0605345	0.0034598	7.3E-70
11	BUD13 *	rs45539536	116747179	T	C	0.0849299	-0.0466767	0.0061375	1.1E-14
11	BUD13	rs34637368	116748889	A	G	0.2495510	-0.0677816	0.0039735	5.7E-67
11	BUD13	rs141923916	116749021	GA	G	0.0850381	-0.0469990	0.0061333	7.7E-15
11	BUD13	rs11216129	116749540	A	C	0.2514630	-0.0688429	0.0039413	3.2E-70
11	BUD13	rs57950207	116749954	C	T	0.0850763	-0.0471014	0.0061340	7.0E-15
11	BUD13	rs17440396	116751054	A	G	0.0838852	-0.0469099	0.0061784	1.4E-14
11	BUD13	rs74368849	116751583	A	G	0.0661475	0.1481720	0.0069747	1.1E-102
11	BUD13	chr11:116752497_TA_T	116752497	TA	T	0.3033700	0.0954883	0.0037155	1.4E-150
11	BUD13	rs180327	116752943	C	T	0.3046950	0.0954711	0.0037103	6.2E-151
11	BUD13	rs6589564	116753437	C	G	0.2016630	0.1118950	0.0042413	2.5E-157
11	BUD13	rs180326	116753987	G	T	0.2034490	0.1119350	0.0042255	1.7E-158
11	BUD13	rs7930786	116754011	C	G	0.2018830	0.1121290	0.0042414	5.1E-158
11	BUD13	rs12421652	116755159	T	G	0.2526140	-0.0690683	0.0039365	6.9E-71
11	BUD13	rs77112220	116755510	T	C	0.0848301	-0.0468245	0.0061392	9.8E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	BUD13	rs182500870	116755846	A	T	0.0110417	0.1612280	0.0163978	2.2E-23
11	BUD13	rs180322	116756019	C	T	0.3573170	-0.0477308	0.0035592	1.5E-41
11	BUD13	rs4938309	116756339	T	C	0.2528750	-0.0690018	0.0039336	1.1E-70
11	BUD13	rs117685786	116756907	C	T	0.0441085	-0.0520750	0.0083432	4.7E-10
11	BUD13	rs2075295	116757685	C	T	0.4407340	-0.0606892	0.0034600	4.6E-70
11	BUD13	rs17519093	116759189	A	G	0.0850681	-0.0471964	0.0061315	5.5E-15
11	BUD13	rs75955612	116759802	T	A	0.0417533	0.0976942	0.0085771	2.5E-30
11	BUD13	rs3741301	116760675	C	T	0.2826730	-0.0661539	0.0038333	4.5E-69
11	BUD13	rs3825041	116760991	T	C	0.2001990	0.1122560	0.0042521	1.1E-157
11	BUD13	rs139872819	116761196	C	T	0.0849785	-0.0464813	0.0061301	1.4E-14
11	BUD13	rs11602240	116762082	C	T	0.2567340	-0.0698592	0.0039169	7.7E-73
11	BUD13	rs918144	116763109	T	C	0.4412220	-0.0601027	0.0034591	6.8E-69
11	BUD13	rs10488698	116763231	A	G	0.0844410	-0.0475503	0.0061490	5.2E-15
11	BUD13	rs17440824	116763457	T	C	0.0871047	-0.0449835	0.0060642	4.7E-14
11	BUD13	rs116877083	116763581	C	A	0.0870138	-0.0449122	0.0060663	5.7E-14
11	BUD13	rs17119975	116763841	C	T	0.2542040	-0.0696697	0.0039351	6.1E-72
11	BUD13	rs10790162	116768388	A	G	0.2001440	0.1126890	0.0042546	1.2E-158
11	BUD13	rs1268353	116768976	T	C	0.3007500	-0.0737597	0.0037457	2.7E-88
11	BUD13	rs1263149	116769225	G	A	0.4548620	-0.0592521	0.0034353	5.0E-68
11	BUD13	rs622604	116769346	C	T	0.3035140	-0.0732742	0.0037313	7.0E-88
11	BUD13	rs610675	116769378	A	T	0.3035140	-0.0732742	0.0037313	7.0E-88
11	BUD13	rs6589565	116769521	A	G	0.2011830	0.1129910	0.0042453	3.0E-160
11	BUD13	rs623908	116769652	G	A	0.3036060	-0.0734594	0.0037311	3.0E-88
11	BUD13	rs1263151	116770312	T	C	0.3845040	-0.0218722	0.0035209	1.6E-10
11	BUD13	rs181315084	116770469	C	T	0.0122182	0.1080170	0.0155634	3.7E-12
11	BUD13 *	rs12422076	116773572	G	A	0.0703885	-0.0599147	0.0067260	4.9E-20
11	BUD13 *	rs2041967	116774433	G	A	0.4103870	-0.0553673	0.0034791	1.1E-57
11	BUD13 *	rs7118999	116774559	T	C	0.3853960	-0.0217304	0.0035157	1.9E-10
11	BUD13 *	rs11216135	116775346	G	C	0.3012350	-0.0743549	0.0037367	6.1E-90
11	ZPR1 *	rs11602073	116776142	T	C	0.3009050	-0.0732280	0.0037367	1.9E-87
11	ZPR1 *	rs11216136	116776404	G	T	0.3031860	-0.0732627	0.0037298	8.6E-88
11	ZPR1 *	rs2160669	116776891	C	T	0.2027650	0.1130330	0.0042304	2.5E-161
11	ZPR1 *	rs964184	116778201	G	C	0.2032410	0.1132890	0.0042256	1.7E-162
11	ZPR1	rs75198898	116779090	A	G	0.0648087	0.1609240	0.0069791	2.9E-121
11	ZPR1	rs113932726	116779922	T	C	0.0642354	0.1627630	0.0070063	4.7E-123
11	ZPR1	rs34248274	116779950	C	CTAGT	0.3012540	-0.0735418	0.0037336	2.1E-88
11	ZPR1	rs11604424	116780399	C	T	0.3535250	0.0842286	0.0035733	3.9E-126
11	ZPR1	rs200405951	116780493	G	C	0.0109187	0.1325550	0.0164145	1.5E-16
11	ZPR1	rs1942478	116780747	G	T	0.3027630	-0.0748275	0.0037296	1.8E-91
11	ZPR1	rs4417316	116781585	T	C	0.3009310	-0.0737824	0.0037313	5.5E-89
11	ZPR1	rs6589566	116781707	G	A	0.2031260	0.1131550	0.0042271	6.7E-162
11	ZPR1	rs7483863	116781775	A	G	0.2031260	0.1131550	0.0042271	6.7E-162
11	ZPR1	rs2075290	116782580	C	T	0.2212640	0.1004400	0.0041025	2.1E-136
11	ZPR1	rs603446	116783719	T	C	0.2802610	-0.0678689	0.0038219	4.5E-73
11	ZPR1	rs139678706	116784368	A	G	0.0188594	-0.0706197	0.0126391	1.2E-08
11	ZPR1	rs10750096	116786072	C	A	0.2031720	0.1135520	0.0042277	6.5E-163
11	ZPR1	rs3741298	116786845	C	T	0.3627700	0.0840433	0.0035480	1.6E-127
11	ZPR1	rs3741297	116786951	T	C	0.0638835	0.1684080	0.0070222	8.3E-131
11	APOA5	rs2266788	116789970	G	A	0.2031380	0.1136420	0.0042294	5.8E-163
11	APOA5	rs2075291	116790676	A	C	0.0639716	0.1694710	0.0070163	7.3E-133
11	APOA5	rs2072560	116791110	T	C	0.2021320	0.1136910	0.0042453	8.0E-162
11	APOA5	rs651821	116791863	C	T	0.2692070	0.1446920	0.0038678	1.1E-314
11	APOA5 *	rs662799	116792991	G	A	0.2695950	0.1444730	0.0038629	1.6E-314
11	APOA5 *	rs17120035	116793135	T	C	0.0819103	-0.0471221	0.0062624	3.0E-14
11	APOA5 *	rs7103224	116793250	A	G	0.0818520	-0.0470233	0.0062645	3.4E-14
11	APOA5 *	rs10750097	116793324	G	A	0.4342260	0.0293280	0.0035074	1.1E-17
11	APOA5 *	rs1787680	116794060	A	T	0.2674180	-0.0707144	0.0039541	5.2E-74
11	APOA5 *	rs9804646	116794363	T	C	0.2198790	-0.0653599	0.0042109	3.5E-55
11	APOA5 *	rs35904674	116795383	T	C	0.0543526	-0.0485895	0.0075892	4.0E-11
11	APOA5 *	chr11:116795401_C_CA	116795401	CA	C	0.0532080	-0.0479075	0.0076842	1.3E-10
11	APOA5 *	rs7123666	116796367	A	G	0.1584550	0.1073950	0.0047260	1.9E-115
11	APOA5 *	rs35606865	116798127	C	T	0.0540161	-0.0485397	0.0076105	4.5E-11
11	APOA5 *	rs11216137	116799112	A	G	0.0513326	-0.0472388	0.0078061	4.2E-10
11	APOA5 *	rs11600380	116799466	C	T	0.0541005	-0.0485655	0.0076042	3.9E-11
11	APOA5 *	rs12294065	116800824	C	G	0.0506137	-0.0482611	0.0078687	2.9E-10
11	APOA5 *	rs188651594	116802375	A	G	0.0284841	0.1030040	0.0102975	1.3E-24
11	APOA5 *	rs12791103	116802599	T	G	0.0504337	-0.0485984	0.0078895	2.7E-10
11	APOA5 *	rs1263164	116804575	A	C	0.3032770	-0.0314300	0.0038087	5.8E-17
11	APOA4 *	rs1729407	116806654	G	C	0.3056860	-0.0321370	0.0037819	5.5E-18
11	APOA4 *	rs1263168	116807283	T	C	0.3063350	-0.0301890	0.0037422	2.1E-16
11	APOA4 *	rs1263169	116807423	T	A	0.3080970	-0.0310753	0.0037443	2.8E-17
11	APOA4 *	rs11398704	116807533	CA	C	0.3534300	-0.0325739	0.0036603	1.0E-19

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	APOA4 *	rs1263170	116807697	C	T	0.3091640	-0.0306223	0.0037292	5.7E-17
11	APOA4 *	rs1729405	116808044	T	C	0.3087530	-0.0308135	0.0037280	3.4E-17
11	APOA4 *	rs75542613	116808439	A	G	0.0409979	-0.0517259	0.0086703	9.2E-10
11	APOA4 *	rs1263171	116809614	A	G	0.3060200	-0.0288600	0.0037184	2.8E-15
11	APOA4 *	rs6589571	116809702	T	C	0.1953390	0.0653323	0.0043814	5.1E-51
11	APOA4 *	rs1263172	116810202	A	G	0.3597220	-0.0318849	0.0035883	1.0E-19
11	APOA4 *	rs1263173	116810292	A	G	0.3062110	-0.0288637	0.0037164	2.8E-15
11	APOA4 *	rs1263174	116810527	T	G	0.3102220	-0.0283105	0.0037130	7.7E-15
11	APOA4 *	rs6589572	116810847	G	A	0.3055780	0.0695125	0.0037117	1.2E-80
11	APOA4 *	rs79538491	116811203	G	A	0.0597284	0.0465170	0.0072607	3.4E-11
11	APOA4 *	rs7927820	116811440	G	A	0.3044620	0.0698328	0.0037103	2.0E-81
11	APOA4 *	rs35180165	116811633	C	CAG	0.3048570	-0.0292024	0.0037273	1.6E-15
11	APOA4 *	rs76636922	116812279	A	G	0.3341010	-0.0327251	0.0036379	1.1E-19
11	APOA4 *	rs2727793	116812658	T	C	0.3049550	-0.0289912	0.0037333	2.5E-15
11	APOA4 *	rs75318540	116813146	T	C	0.2171630	-0.0320976	0.0041922	7.9E-15
11	APOA4 *	rs7396835	116813312	T	C	0.3050490	0.0695113	0.0037009	4.3E-81
11	APOA4 *	rs7396851	116813448	T	C	0.3047150	0.0696082	0.0037046	3.9E-81
11	APOA4 *	rs79841374	116813844	T	C	0.3333720	-0.0333790	0.0036383	2.2E-20
11	APOA4 *	rs2727791	116813846	G	C	0.3076380	-0.0296634	0.0037229	3.9E-16
11	APOA4 *	rs2849167	116814028	A	G	0.3075450	-0.0298393	0.0037248	3.0E-16
11	APOA4 *	rs2542063	116814051	A	G	0.3079890	-0.0297061	0.0037233	4.2E-16
11	APOA4 *	rs77535577	116814675	A	G	0.3327100	-0.0338274	0.0036517	8.6E-21
11	APOA4 *	rs6589573	116815050	C	G	0.3069420	0.0711670	0.0037384	3.3E-83
11	APOA4 *	rs7107757	116815572	T	C	0.3572000	0.0606754	0.0035879	7.2E-66
11	APOA4 *	chr11:116816190_CT_C	116816190	C	CT	0.3135630	-0.0331257	0.0037500	3.5E-19
11	APOA4 *	rs9735326	116818049	C	A	0.3262180	0.0670087	0.0036856	1.6E-76
11	APOA4 *	rs1263176	116819407	T	C	0.3687260	0.0597355	0.0035640	5.6E-65
11	APOA4 *	rs1268354	116819862	C	T	0.3691430	0.0597420	0.0035633	4.5E-65
11	APOA4 *	rs1263177	116819996	C	T	0.3675160	0.0599623	0.0035720	4.5E-65
11	APOA4	rs2234669	116820795	G	GGACA	0.3041700	-0.0308870	0.0037699	5.9E-17
11	APOA4	rs5104	116821618	C	T	0.3196000	0.0684997	0.0036869	1.0E-79
11	APOA4	rs5100	116821978	G	A	0.3729130	0.0590329	0.0035589	1.2E-63
11	APOA4	rs5096	116822379	G	A	0.3728450	0.0590034	0.0035593	1.7E-63
11	APOA4	rs2239013	116822637	T	C	0.0411476	-0.0511993	0.0086515	1.4E-09
11	APOA4	rs5093	116822638	A	G	0.2157420	-0.0325936	0.0042249	4.6E-15
11	APOA4	rs5092	116822748	C	T	0.3725590	0.0587885	0.0035629	8.2E-63
11	APOA4 *	rs1268833	116824150	G	A	0.3725370	0.0586353	0.0035640	1.3E-62
11	APOA4 *	rs10892035	116824222	A	G	0.3718720	0.0585415	0.0035658	2.7E-62
11	APOA4 *	rs182352602	116824894	A	G	0.2095220	-0.0324453	0.0042808	1.2E-14
11	APOA4 *	rs7111242	116825064	A	G	0.3201710	0.0673902	0.0037049	2.4E-76
11	APOA4 *	rs2216311	116825327	G	A	0.3723060	0.0591655	0.0035682	1.6E-63
11	APOA4 *	rs2098453	116825964	C	T	0.3717650	0.0592686	0.0035702	1.2E-63
11	APOA4 *	rs2727789	116826171	G	T	0.3732970	0.0591698	0.0035687	1.7E-63
11	APOA4 *	rs2849176	116826205	T	C	0.3723220	0.0594003	0.0035700	5.8E-64
11	APOA4 *	rs2542050	116826401	C	A	0.3717300	0.0592751	0.0035701	1.1E-63
11	APOC3 *	rs2849173	116826605	G	C	0.3717800	0.0592732	0.0035706	1.2E-63
11	APOC3 *	rs2071523	116826628	C	T	0.3717860	0.0592531	0.0035706	1.3E-63
11	APOC3 *	rs2071522	116826822	T	C	0.3717860	0.0591962	0.0035708	1.8E-63
11	APOC3 *	rs2542051	116827022	C	A	0.3719920	0.0591779	0.0035712	2.0E-63
11	APOC3 *	rs2071521	116827132	G	A	0.3718970	0.0592494	0.0035702	1.3E-63
11	APOC3 *	rs595049	116828729	C	A	0.3738690	0.0592054	0.0035590	7.2E-64
11	APOC3	rs734104	116830144	C	T	0.2926860	0.0566142	0.0037942	2.0E-52
11	APOC3	rs5128	116832924	G	C	0.2900360	0.0570154	0.0037748	1.6E-53
11	APOA1 *	rs10750098	116834852	G	T	0.2895560	0.0574959	0.0037856	5.6E-54
11	APOA1 *	rs613808	116840252	G	A	0.2774730	-0.0341462	0.0039055	3.8E-19
11	APOA1 *	rs2727784	116840425	T	C	0.2584300	-0.0351416	0.0040025	2.4E-19
11	SIK3 *	rs591592	116842850	T	C	0.2220820	-0.0282139	0.0041926	6.2E-12
11	SIK3 *	rs200408997	116842862	A	ACCC	0.0488229	0.0604704	0.0079590	8.2E-15
11	SIK3 *	rs579163	116842914	G	C	0.2224310	-0.0280923	0.0041912	7.3E-12
11	SIK3	rs371090973	116844640	T	TTA	0.0489944	0.0559545	0.0079512	6.8E-13
11	SIK3	rs201579941	116844674	A	ATAT	0.0480857	0.0570901	0.0080128	2.7E-13
11	SIK3	rs142174850	116845068	A	G	0.0828510	-0.0480521	0.0062410	1.1E-15
11	SIK3	rs143120617	116846722	T	C	0.0372549	-0.0587274	0.0090614	1.5E-11
11	SIK3	rs61905145	116847699	A	G	0.0496446	0.0583678	0.0078782	3.1E-14
11	SIK3	rs532815	116848142	A	G	0.2348110	-0.0300656	0.0040670	4.1E-14
11	SIK3	rs61905155	116848213	T	G	0.0495176	0.0575212	0.0078934	7.0E-14
11	SIK3	rs2289893	116849373	C	T	0.3512090	-0.0292942	0.0035977	9.1E-17
11	SIK3	rs660083	116850113	G	C	0.2313970	-0.0276087	0.0040782	4.5E-12
11	SIK3	rs10047462	116851325	T	G	0.4853700	-0.0303717	0.0034280	8.3E-20
11	SIK3	rs689243	116851977	C	G	0.2311290	-0.0273314	0.0040780	7.7E-12
11	SIK3	rs139952838	116852044	T	C	0.0285974	0.0947560	0.0102128	9.8E-22
11	SIK3	rs888245	116853021	G	C	0.0498983	0.0586458	0.0078539	1.7E-14

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs888246	116853516	T	C	0.0498734	0.0586334	0.0078546	1.6E-14
11	SIK3	rs12099358	116855332	A	C	0.0500602	0.0581059	0.0078404	2.4E-14
11	SIK3	rs112618266	116855993	T	C	0.0801452	-0.0463982	0.0063069	1.9E-14
11	SIK3	rs640621	116856053	G	C	0.2352450	-0.0298088	0.0040458	5.7E-14
11	SIK3	rs78857232	116856749	T	C	0.0498713	0.0583428	0.0078529	2.3E-14
11	SIK3	rs1035237	116857134	C	G	0.4870000	-0.0307451	0.0034417	3.4E-20
11	SIK3	rs6589574	116859922	A	G	0.3111540	0.0482243	0.0037353	5.4E-40
11	SIK3	rs567312	116860022	A	G	0.2341530	-0.0303003	0.0040517	2.4E-14
11	SIK3	rs4938315	116860489	A	G	0.4855970	-0.0306116	0.0034415	4.7E-20
11	SIK3	rs2075292	116861796	T	G	0.4848680	-0.0305795	0.0034477	5.3E-20
11	SIK3	rs117010832	116861803	A	G	0.1377230	-0.0327751	0.0050255	1.9E-11
11	SIK3	rs484646	116862140	G	A	0.2353600	-0.0300686	0.0040453	3.5E-14
11	SIK3	rs6589575	116862594	T	C	0.4862120	-0.0306996	0.0034405	3.7E-20
11	SIK3	rs2080586	116862600	C	T	0.0496917	0.0587049	0.0078635	1.7E-14
11	SIK3	rs476399	116863012	C	T	0.2353360	-0.0299927	0.0040443	3.9E-14
11	SIK3	rs718847	116863430	T	C	0.4854980	-0.0304979	0.0034400	6.2E-20
11	SIK3	rs17120099	116864744	C	A	0.0801967	-0.0464330	0.0063042	1.7E-14
11	SIK3	rs6589576	116865072	G	C	0.4860580	-0.0308111	0.0034394	2.9E-20
11	SIK3	rs573549	116865963	G	A	0.2359390	-0.0303191	0.0040468	2.3E-14
11	SIK3	chr11:116866441_C_CTTA	116866441	CTTTA	C	0.0398725	0.0578399	0.0088025	1.5E-11
11	SIK3	rs17120101	116867872	T	C	0.0330397	-0.0537505	0.0095770	5.5E-09
11	SIK3	rs11216168	116870837	A	G	0.0498308	0.0586761	0.0078539	1.6E-14
11	SIK3	rs533556	116870856	C	A	0.2361720	-0.0302035	0.0040382	2.4E-14
11	SIK3	rs17120111	116873302	T	C	0.0494285	0.0582402	0.0078865	3.2E-14
11	SIK3	rs11216169	116873673	C	T	0.0494035	0.0575236	0.0078903	6.5E-14
11	SIK3	rs9919599	116874768	G	C	0.4855930	-0.0308815	0.0034453	3.1E-20
11	SIK3	rs17120119	116876566	G	C	0.0781839	-0.0459187	0.0063811	5.7E-14
11	SIK3	rs77682889	116876596	T	C	0.0307530	0.0857717	0.0098483	2.8E-19
11	SIK3	rs12278117	116877453	A	G	0.0781718	-0.0460502	0.0063814	4.9E-14
11	SIK3	rs12279433	116877505	T	G	0.0795032	-0.0469511	0.0063269	1.1E-14
11	SIK3	rs12279464	116877766	T	C	0.0781718	-0.0460502	0.0063814	4.9E-14
11	SIK3	rs112867178	116877768	CTCTATT	C	0.4843060	-0.0310976	0.0034504	1.8E-20
11	SIK3	rs12292614	116877799	G	A	0.0781718	-0.0460502	0.0063814	4.9E-14
11	SIK3	rs12286581	116878028	C	T	0.0781702	-0.0460482	0.0063814	4.9E-14
11	SIK3	rs61907566	116878189	G	C	0.2339040	-0.0310163	0.0040626	7.2E-15
11	SIK3	rs75294699	116878356	A	C	0.0781702	-0.0460482	0.0063814	4.9E-14
11	SIK3	rs76523703	116878793	G	T	0.0494939	0.0574432	0.0078841	7.0E-14
11	SIK3	rs6589577	116879261	T	C	0.4855870	-0.0310909	0.0034459	1.9E-20
11	SIK3	rs543819	116879357	G	A	0.0843666	-0.0474651	0.0061773	1.5E-15
11	SIK3	rs7396061	116880158	C	A	0.3178680	-0.0309429	0.0036912	1.2E-17
11	SIK3	rs74341458	116880833	A	G	0.0493454	0.0573968	0.0078938	7.6E-14
11	SIK3	rs482371	116881447	C	T	0.2294390	-0.0298355	0.0040886	1.1E-13
11	SIK3	rs7124741	116881503	T	A	0.4853140	-0.0310708	0.0034435	1.8E-20
11	SIK3	rs12275565	116882836	G	A	0.0833872	-0.0468358	0.0062121	3.8E-15
11	SIK3	rs12416987	116883549	C	T	0.0795648	-0.0468715	0.0063243	1.2E-14
11	SIK3	rs1269329	116884325	C	T	0.2355290	-0.0307143	0.0040563	1.2E-14
11	SIK3	rs139733873	116884844	G	A	0.0121354	0.0942893	0.0155688	2.3E-10
11	SIK3	rs11827828	116884868	A	G	0.0494929	0.0574554	0.0078841	6.9E-14
11	SIK3	rs2044426	116885467	A	G	0.0775133	-0.0468502	0.0064097	2.3E-14
11	SIK3	rs35378097	116886122	G	GT	0.0346788	-0.0548045	0.0093352	9.0E-10
11	SIK3	rs10892040	116886270	A	G	0.0778002	-0.0460739	0.0063968	5.3E-14
11	SIK3	rs11216174	116886532	G	A	0.0778122	-0.0459417	0.0063965	6.1E-14
11	SIK3	rs11216175	116886682	T	C	0.0778002	-0.0460739	0.0063968	5.3E-14
11	SIK3	chr11:116886752_T_TA	116886752	TA	T	0.2348440	-0.0313094	0.0040557	3.8E-15
11	SIK3	rs12284346	116887077	C	T	0.0786530	-0.0469204	0.0063631	1.8E-14
11	SIK3	rs12292278	116887977	C	A	0.0843743	-0.0477155	0.0061755	9.7E-16
11	SIK3	rs1473177	116888616	C	T	0.0494004	0.0576484	0.0078903	5.6E-14
11	SIK3	rs17174502	116888939	G	A	0.4857800	-0.0311906	0.0034466	1.3E-20
11	SIK3	rs12294191	116889108	G	A	0.0845201	-0.0475233	0.0061708	1.2E-15
11	SIK3	rs10892042	116889829	A	G	0.0494004	0.0576484	0.0078903	5.6E-14
11	SIK3	rs660443	116889977	C	T	0.2296310	-0.0297982	0.0040885	1.1E-13
11	SIK3	rs12285074	116891312	G	A	0.4855840	-0.0311604	0.0034547	1.6E-20
11	SIK3	rs72645459	116891441	C	A	0.4848880	-0.0314066	0.0034511	7.5E-21
11	SIK3	chr11:116891662_AAG_A	116891662	AAG	A	0.4839970	-0.0314668	0.0034471	5.2E-21
11	SIK3	rs144010715	116891837	AG	A	0.0844682	-0.0477792	0.0061734	8.8E-16
11	SIK3	rs75158858	116892113	A	G	0.0494004	0.0576484	0.0078903	5.6E-14
11	SIK3	rs672058	116893305	T	C	0.4021290	-0.0275405	0.0035219	9.9E-16
11	SIK3	rs74885676	116894221	T	G	0.1357870	-0.0321489	0.0050481	5.9E-11
11	SIK3	rs77349713	116894760	C	T	0.0850141	-0.0473446	0.0061491	1.2E-15
11	SIK3	rs11820814	116894984	C	T	0.0493189	0.0578675	0.0078982	4.2E-14
11	SIK3	rs74881320	116895209	C	A	0.0850104	-0.0474090	0.0061488	1.1E-15
11	SIK3	rs149874218	116895594	TTG	T	0.0852255	-0.0471670	0.0061461	1.5E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs11216178	116895674	T	G	0.0492606	0.0577338	0.0079025	5.1E-14
11	SIK3	rs10892044	116896183	C	T	0.0493126	0.0579677	0.0078990	3.9E-14
11	SIK3	rs2270392	116896972	C	T	0.1234200	-0.0374017	0.0052152	1.0E-13
11	SIK3	chr11:116897883_CA_C	116897883	C	CA	0.0749066	-0.0454188	0.0065311	3.6E-13
11	SIK3	rs111884008	116898027	C	G	0.1183350	-0.0361898	0.0053014	1.4E-12
11	SIK3	rs190051172	116898198	G	C	0.0850104	-0.0474090	0.0061488	1.1E-15
11	SIK3	rs609177	116899801	G	A	0.2358860	-0.0314466	0.0040576	2.6E-15
11	SIK3	rs72645460	116900659	A	G	0.4829060	-0.0315217	0.0034517	5.6E-21
11	SIK3	rs1076485	116901725	C	T	0.4449600	-0.0303778	0.0034644	1.7E-19
11	SIK3	rs17120131	116901770	C	T	0.0853184	-0.0474044	0.0061427	1.1E-15
11	SIK3	rs518181	116902071	A	C	0.2283000	-0.0306872	0.0041004	2.2E-14
11	SIK3	rs17120132	116902602	A	T	0.0853610	-0.0471570	0.0061405	1.4E-15
11	SIK3	rs11216180	116902662	T	A	0.0493084	0.0582826	0.0078997	2.9E-14
11	SIK3	rs17120136	116903045	G	T	0.0835383	-0.0467784	0.0062084	4.3E-15
11	SIK3	rs17120139	116903485	G	A	0.4827140	-0.0314526	0.0034521	6.3E-21
11	SIK3	rs78694306	116903528	T	G	0.0787685	-0.0454795	0.0063570	7.7E-14
11	SIK3	rs11216181	116903758	T	A	0.0461140	0.0608882	0.0081762	2.1E-14
11	SIK3	rs78832854	116903759	A	T	0.0819515	-0.0397702	0.0062575	2.2E-11
11	SIK3	rs115971514	116903783	C	G	0.0787685	-0.0454795	0.0063570	7.7E-14
11	SIK3	rs12280030	116904480	A	T	0.0851477	-0.0473677	0.0061432	1.1E-15
11	SIK3	rs7111854	116906110	T	A	0.1235830	-0.0373858	0.0052110	9.6E-14
11	SIK3	rs12273762	116906347	A	T	0.0851477	-0.0473677	0.0061432	1.1E-15
11	SIK3	rs9651681	116907349	C	T	0.0853593	-0.0471526	0.0061405	1.5E-15
11	SIK3	rs4938317	116907559	C	T	0.0493073	0.0582739	0.0078997	2.9E-14
11	SIK3	rs35184536	116908097	G	A	0.0852137	-0.0473424	0.0061452	1.2E-15
11	SIK3	rs200905431	116909318	G	GA	0.0945744	-0.0374078	0.0059847	8.2E-11
11	SIK3	rs75920871	116909379	T	A	0.0493302	0.0590246	0.0079205	2.2E-14
11	SIK3	rs11216183	116910829	A	C	0.0758463	-0.0487645	0.0064535	4.6E-15
11	SIK3	rs11216185	116912258	G	T	0.0802362	-0.0462898	0.0062978	2.0E-14
11	SIK3	rs142195028	116913525	A	AG	0.0757205	-0.0486616	0.0064606	5.2E-15
11	SIK3	rs11357208	116913587	C	CT	0.0492886	0.0580228	0.0079029	3.8E-14
11	SIK3	rs7115583	116913660	T	G	0.1184490	-0.0362393	0.0053009	1.2E-12
11	SIK3	rs149566815	116913905	T	TAAAC	0.0757425	-0.0487323	0.0064607	4.7E-15
11	SIK3	rs11216186	116913976	C	T	0.0997297	-0.0466890	0.0057167	3.3E-17
11	SIK3	rs10892045	116914108	A	C	0.0456189	0.0593363	0.0082179	1.3E-13
11	SIK3	rs79711490	116914625	T	C	0.0997297	-0.0466890	0.0057167	3.3E-17
11	SIK3	rs11216187	116916432	T	C	0.0492886	0.0576920	0.0079029	5.2E-14
11	SIK3	rs12277181	116916604	A	G	0.0999584	-0.0464352	0.0057144	4.9E-17
11	SIK3	rs12277092	116916611	T	C	0.0997464	-0.0466869	0.0057162	3.3E-17
11	SIK3	rs7928298	116916811	T	A	0.0744903	-0.0360453	0.0065752	1.7E-08
11	SIK3	rs12418208	116916917	T	C	0.0970704	-0.0464153	0.0058007	1.1E-16
11	SIK3	rs12418209	116916925	T	C	0.0970704	-0.0464153	0.0058007	1.1E-16
11	SIK3	rs1006176	116917417	C	T	0.0999855	-0.0463916	0.0057081	4.4E-17
11	SIK3	chr11:116917733_AAGAG_/_	116917733	A	AAGAG	0.0971840	-0.0461089	0.0057966	2.5E-16
11	SIK3	rs76136280	116917775	T	C	0.0493240	0.0579944	0.0079000	3.8E-14
11	SIK3	rs1135663	116918121	T	C	0.0871111	-0.0461097	0.0061306	4.6E-15
11	SIK3	rs79530380	116918472	A	T	0.0407037	0.0612847	0.0087591	3.6E-13
11	SIK3	rs78692246	116920591	A	G	0.1005090	-0.0463734	0.0056932	4.0E-17
11	SIK3	rs7934763	116921641	G	T	0.0497733	0.0578073	0.0078698	3.4E-14
11	SIK3	rs7948838	116922245	G	A	0.1386090	-0.0382899	0.0049534	1.6E-15
11	SIK3	rs12225187	116922515	A	G	0.2034970	-0.0275518	0.0042724	4.2E-11
11	SIK3	rs12288386	116922907	T	C	0.1003070	-0.0463477	0.0056973	4.4E-17
11	SIK3	rs10892047	116922977	T	C	0.1002660	-0.0461892	0.0057007	6.1E-17
11	SIK3	rs117287138	116924163	A	G	0.0496579	0.0577960	0.0078810	4.0E-14
11	SIK3	rs56314469	116924187	A	G	0.0496579	0.0577960	0.0078810	4.0E-14
11	SIK3	rs12292371	116925232	C	G	0.1003760	-0.0462997	0.0056959	4.7E-17
11	SIK3	rs12292434	116925349	A	G	0.1003300	-0.0463573	0.0056964	4.3E-17
11	SIK3	rs7121898	116926130	T	A	0.2038960	-0.0271902	0.0042697	7.6E-11
11	SIK3	rs61907591	116926139	A	T	0.0497733	0.0578073	0.0078698	3.4E-14
11	SIK3	rs12285956	116926759	A	G	0.1003300	-0.0463573	0.0056964	4.3E-17
11	SIK3	rs11216190	116926968	C	T	0.1378020	-0.0388257	0.0049669	9.1E-16
11	SIK3	chr11:116927081_AT_A	116927081	A	AT	0.0980128	-0.0450032	0.0057750	6.1E-16
11	SIK3	rs1446105	116927828	T	C	0.2039310	-0.0270862	0.0042680	8.4E-11
11	SIK3	rs579890	116928247	G	A	0.4743460	-0.0299399	0.0034501	4.6E-19
11	SIK3	rs79157715	116929554	A	G	0.1004360	-0.0463228	0.0056923	4.4E-17
11	SIK3	rs10790167	116930227	C	T	0.2037840	-0.0271580	0.0042692	7.6E-11
11	SIK3	rs75776964	116930345	G	C	0.1004360	-0.0464216	0.0056923	3.8E-17
11	SIK3	rs645258	116930485	A	C	0.3135650	0.0437530	0.0037011	1.3E-33
11	SIK3	rs76690043	116930813	G	C	0.0497733	0.0578073	0.0078698	3.4E-14
11	SIK3	rs61907594	116931095	T	C	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs79974099	116931865	A	T	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs74615346	116932256	C	A	0.1005590	-0.0465759	0.0056900	3.1E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs12270974	116933289	T	C	0.1004360	-0.0464216	0.0056923	3.8E-17
11	SIK3	rs12272491	116933654	T	C	0.1004360	-0.0464216	0.0056923	3.8E-17
11	SIK3	rs12418735	116934046	G	T	0.1004360	-0.0464216	0.0056923	3.8E-17
11	SIK3	rs77204473	116934348	G	T	0.0651122	-0.0378620	0.0069257	2.4E-08
11	SIK3	rs562179	116934488	C	T	0.4387690	-0.0227490	0.0034660	1.8E-11
11	SIK3	rs79207844	116934725	A	G	0.0646608	-0.0380199	0.0069496	2.1E-08
11	SIK3	rs12274590	116934980	A	G	0.0646608	-0.0380199	0.0069496	2.1E-08
11	SIK3	rs144015791	116935158	T	G	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs2513095	116935553	C	T	0.4747130	-0.0299189	0.0034503	4.9E-19
11	SIK3	rs2513093	116935971	G	A	0.4745420	-0.0300859	0.0034490	3.0E-19
11	SIK3	rs12273769	116936457	G	T	0.1004320	-0.0464449	0.0056923	3.7E-17
11	SIK3	rs12294657	116936652	C	G	0.1004400	-0.0463981	0.0056921	3.9E-17
11	SIK3	rs77920516	116936711	C	T	0.0887431	0.0395986	0.0060481	1.1E-11
11	SIK3	rs473172	116937254	G	A	0.4745650	-0.0300518	0.0034488	3.2E-19
11	SIK3	rs77136879	116937737	T	C	0.1004750	-0.0462835	0.0056906	4.6E-17
11	SIK3	chr11:116938204_AGAGGGG	116938204	A	GGGAGGGC	0.1157400	-0.0323876	0.0054006	4.6E-10
11	SIK3	rs61907600	116938632	G	A	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs7480278	116939073	G	T	0.1004840	-0.0462362	0.0056904	4.9E-17
11	SIK3	rs61624438	116939229	A	C	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs80015203	116940190	G	A	0.1004840	-0.0462362	0.0056904	4.9E-17
11	SIK3	rs117877581	116940238	G	T	0.1006290	-0.0465439	0.0056885	3.1E-17
11	SIK3	rs116597701	116940771	G	C	0.0990808	-0.0447886	0.0057298	5.7E-16
11	SIK3	rs145705809	116940967	A	C	0.0129205	0.1085370	0.0151327	2.3E-13
11	SIK3	rs139127609	116940986	T	TTTTG	0.1004840	-0.0462362	0.0056904	4.9E-17
11	SIK3	rs473188	116941313	G	C	0.4741950	-0.0300504	0.0034485	3.3E-19
11	SIK3	rs78066444	116941342	C	A	0.0992259	-0.0450217	0.0057274	3.8E-16
11	SIK3	chr11:116941408_TA_T	116941408	T	TA	0.4826550	-0.0310408	0.0034859	8.2E-20
11	SIK3	rs17120157	116941912	C	T	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs75410648	116942722	T	C	0.1005100	-0.0463723	0.0056898	4.1E-17
11	SIK3	rs510988	116943088	T	C	0.4741850	-0.0300392	0.0034484	3.4E-19
11	SIK3	rs12292858	116943263	C	A	0.1385390	-0.0385963	0.0049508	9.5E-16
11	SIK3	rs10892048	116943880	G	A	0.2020830	-0.0270626	0.0042878	1.1E-10
11	SIK3	rs12421902	116943930	G	A	0.0986526	-0.0459712	0.0057474	1.6E-16
11	SIK3	chr11:116944465_GCAAT_C	116944465	G	GCAAT	0.4741850	-0.0300392	0.0034484	3.4E-19
11	SIK3	rs11216193	116944883	T	C	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	chr11:116944965_C_CTT	116944965	CTT	C	0.0809399	-0.0434697	0.0063927	1.5E-12
11	SIK3	rs11216194	116945022	C	G	0.1002040	-0.0464674	0.0057104	4.9E-17
11	SIK3	rs11216195	116945175	A	G	0.0984168	-0.0457166	0.0057574	2.1E-16
11	SIK3	rs11216196	116945176	G	T	0.0984168	-0.0457166	0.0057574	2.1E-16
11	SIK3	rs35485516	116945411	C	CAG	0.1004690	-0.0461857	0.0056909	5.4E-17
11	SIK3	rs10892049	116945500	C	G	0.1385180	-0.0386175	0.0049514	9.1E-16
11	SIK3	rs10892050	116945678	A	C	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs75958227	116945875	A	G	0.1386460	-0.0308674	0.0050009	2.3E-10
11	SIK3	rs7924318	116945914	G	C	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs11216197	116946062	G	A	0.1006670	-0.0461386	0.0056906	6.0E-17
11	SIK3	rs191655881	116946939	C	A	0.1385180	-0.0386175	0.0049514	9.1E-16
11	SIK3	rs111327557	116947068	T	C	0.0495882	0.0572355	0.0078886	7.4E-14
11	SIK3	rs146056222	116947627	G	A	0.1385180	-0.0386175	0.0049514	9.1E-16
11	SIK3	rs146503809	116948352	G	A	0.0274940	0.0820641	0.0104186	4.0E-16
11	SIK3	rs4316540	116948525	T	C	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs12293755	116948548	T	A	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs1241658	116948901	A	G	0.4736390	-0.0293136	0.0034503	2.4E-18
11	SIK3	rs139552563	116949016	CAAAT	C	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs112297132	116949116	GA	G	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs12419047	116949190	A	G	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs12421834	116949307	C	A	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs61907605	116949355	A	T	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs12420518	116949372	C	T	0.1385180	-0.0386175	0.0049514	9.1E-16
11	SIK3	rs142344418	116949918	C	CAG	0.0861146	0.0436270	0.0061333	1.6E-13
11	SIK3	rs12419437	116949974	A	G	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs1473324	116951202	G	T	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs1473325	116951318	T	C	0.0497743	0.0578156	0.0078698	3.4E-14
11	SIK3	rs76538122	116951618	G	A	0.0320319	-0.0580262	0.0097153	3.6E-10
11	SIK3	rs12286405	116951812	T	C	0.1385180	-0.0386175	0.0049514	9.1E-16
11	SIK3	rs11605327	116952346	A	G	0.2031560	-0.0274514	0.0042760	5.0E-11
11	SIK3	rs77467134	116952391	C	T	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs76654964	116952805	A	G	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs76146269	116952901	G	A	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs1473326	116952956	C	T	0.0497754	0.0578155	0.0078698	3.4E-14
11	SIK3	rs1473327	116953280	T	A	0.0497785	0.0578440	0.0078699	3.2E-14
11	SIK3	rs12275355	116953446	G	A	0.1005330	-0.0462680	0.0056894	4.5E-17
11	SIK3	rs12289974	116953570	T	C	0.1004810	-0.0462593	0.0056904	4.8E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs2289890	116953904	A	G	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs511676	116954168	G	T	0.4746510	-0.0302624	0.0034491	1.8E-19
11	SIK3	rs2289892	116954524	A	G	0.1003720	-0.0461768	0.0056931	5.7E-17
11	SIK3	rs12291040	116955901	C	T	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs12270837	116955927	C	A	0.1004810	-0.0462593	0.0056904	4.8E-17
11	SIK3	rs10502221	116956154	T	C	0.2030000	-0.0272914	0.0042764	6.5E-11
11	SIK3	rs17120177	116956653	C	T	0.1004010	-0.0457768	0.0056961	1.1E-16
11	SIK3	rs878692	116958223	A	C	0.1004090	-0.0458489	0.0056969	9.7E-17
11	SIK3	rs6589582	116958484	C	A	0.2050020	-0.0272915	0.0042591	6.8E-11
11	SIK3	rs12420857	116958726	T	G	0.1003930	-0.0458535	0.0056973	9.8E-17
11	SIK3	rs7120706	116959371	C	T	0.2050020	-0.0272915	0.0042591	6.8E-11
11	SIK3	rs7120963	116959545	C	T	0.2050020	-0.0272915	0.0042591	6.8E-11
11	SIK3	rs11216199	116960300	T	C	0.1003370	-0.0457254	0.0056990	1.2E-16
11	SIK3	rs145400227	116960788	CAGTAAA	C	0.1003280	-0.0458040	0.0056992	1.1E-16
11	SIK3	rs11216200	116961127	T	C	0.1384670	-0.0384002	0.0049557	1.3E-15
11	SIK3	rs7112967	116961196	T	C	0.0497858	0.0578358	0.0078692	3.3E-14
11	SIK3	rs10892051	116962002	A	C	0.1003280	-0.0458040	0.0056992	1.1E-16
11	SIK3	rs56134734	116962339	A	G	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs61905677	116962939	G	T	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs493134	116962963	T	C	0.4739380	-0.0300408	0.0034496	3.4E-19
11	SIK3	rs10502222	116963014	T	C	0.1852040	-0.0279943	0.0044331	1.0E-10
11	SIK3	rs10892052	116963597	A	G	0.1851930	-0.0279781	0.0044331	1.0E-10
11	SIK3	rs61905678	116964069	T	C	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs61905679	116964071	T	C	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs201165469	116964853	G	GC	0.1004220	-0.0457077	0.0056974	1.2E-16
11	SIK3	rs61905680	116965315	A	G	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs61905681	116965493	C	A	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs77320801	116965633	T	C	0.0497847	0.0578167	0.0078692	3.3E-14
11	SIK3	rs761823852	116965753	A	AT	0.0428416	0.0549762	0.0085454	3.8E-11
11	SIK3	rs78044162	116966373	T	C	0.1383580	-0.0384655	0.0049581	1.2E-15
11	SIK3	rs9971422	116966657	C	T	0.1379110	-0.0386584	0.0049675	8.9E-16
11	SIK3	rs12281729	116967414	C	A	0.1003680	-0.0458192	0.0056997	1.1E-16
11	SIK3	rs149144614	116968288	A	G	0.0449372	0.0600116	0.0082938	8.3E-14
11	SIK3	rs12417152	116968577	C	G	0.1002120	-0.0460832	0.0057056	7.4E-17
11	SIK3	rs11823013	116968819	C	T	0.0497358	0.0582053	0.0078736	2.4E-14
11	SIK3	rs11216204	116968898	A	G	0.1001980	-0.0461659	0.0057060	6.6E-17
11	SIK3	rs1241657	116969045	T	C	0.3123280	0.0436255	0.0037083	2.7E-33
11	SIK3	rs12272305	116969222	A	G	0.0969587	-0.0454227	0.0058049	5.0E-16
11	SIK3	rs12279266	116969317	C	T	0.0996629	-0.0460498	0.0057196	9.4E-17
11	SIK3	rs201227770	116969542	T	GGCATTTT	0.0357204	0.0562889	0.0093306	3.8E-10
11	SIK3	rs59294170	116970730	T	A	0.0497296	0.0582505	0.0078735	2.3E-14
11	SIK3	rs12418324	116971960	T	C	0.1001600	-0.0462243	0.0057063	6.2E-17
11	SIK3	rs11216206	116972709	G	C	0.3121820	-0.0277043	0.0036948	1.7E-14
11	SIK3	rs17120197	116974388	C	T	0.0497921	0.0579959	0.0078678	2.8E-14
11	SIK3	chr11:116974556_C_CTGTT	116974556	CTGTT	C	0.1002910	-0.0462188	0.0057012	5.7E-17
11	SIK3	rs74927399	116975550	C	T	0.1002910	-0.0462188	0.0057012	5.7E-17
11	SIK3	rs76949321	116975627	A	G	0.1002910	-0.0462188	0.0057012	5.7E-17
11	SIK3	rs11216209	116977470	C	T	0.1003080	-0.0462472	0.0057008	5.5E-17
11	SIK3	rs11216210	116977613	T	G	0.1386180	-0.0381790	0.0049507	1.6E-15
11	SIK3	rs7109876	116977932	A	C	0.0498097	0.0578911	0.0078665	3.1E-14
11	SIK3	chr11:116978213_C_CA	116978213	CA	C	0.1718110	-0.0351120	0.0045939	2.2E-15
11	SIK3	rs11216212	116979635	A	T	0.1003080	-0.0462472	0.0057008	5.5E-17
11	SIK3	rs146178826	116980651	G	A	0.1003080	-0.0462472	0.0057008	5.5E-17
11	SIK3	rs7358350	116980892	C	T	0.1386180	-0.0381790	0.0049507	1.6E-15
11	SIK3	rs11216215	116981971	A	T	0.1003080	-0.0462472	0.0057008	5.5E-17
11	SIK3	rs3863304	116982407	A	G	0.2017840	-0.0277060	0.0042970	3.8E-11
11	SIK3	rs3863305	116982408	T	C	0.2017840	-0.0277060	0.0042970	3.8E-11
11	SIK3	rs3863306	116982497	T	C	0.2026240	-0.0261845	0.0042869	4.0E-10
11	SIK3	rs7131351	116982890	A	G	0.2023270	-0.0259074	0.0042876	6.2E-10
11	SIK3	rs7117123	116982970	A	T	0.1929190	-0.0266077	0.0043763	7.1E-10
11	SIK3	rs10128690	116983206	A	G	0.0950061	-0.0459401	0.0058730	4.8E-16
11	SIK3	rs10128570	116983305	G	A	0.1003080	-0.0462472	0.0057008	5.5E-17
11	SIK3	rs10128571	116983465	G	A	0.1003080	-0.0462472	0.0057008	5.5E-17
11	SIK3	rs113184611	116984048	A	C	0.0498066	0.0578977	0.0078664	3.0E-14
11	SIK3	rs374519262	116984705	A	AC	0.1194750	-0.0373685	0.0053542	5.1E-13
11	SIK3	rs146725667	116985530	A	G	0.0343795	-0.0543319	0.0093774	1.2E-09
11	SIK3	rs12287768	116985606	C	A	0.1003220	-0.0462461	0.0057006	5.5E-17
11	SIK3	rs588918	116985926	C	T	0.4742010	-0.0291615	0.0034453	3.1E-18
11	SIK3	rs12274771	116985982	G	C	0.1003200	-0.0462393	0.0057006	5.6E-17
11	SIK3	rs12274773	116985993	T	C	0.1003200	-0.0462393	0.0057006	5.6E-17
11	SIK3	rs75212922	116986276	A	T	0.1003200	-0.0462393	0.0057006	5.6E-17
11	SIK3	rs10892053	116986287	T	C	0.2036090	-0.0263140	0.0042690	2.9E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs11216217	116986936	A	G	0.1003200	-0.0462393	0.0057006	5.6E-17
11	SIK3	chr11:116987321_TAA_T	116987321	T	TAA	0.1018710	-0.0442551	0.0056753	1.0E-15
11	SIK3	rs201445271	116987332	AC	A	0.0495007	0.0544529	0.0079026	1.2E-12
11	SIK3	rs10160754	116988278	C	A	0.1386140	-0.0382172	0.0049510	1.5E-15
11	SIK3	rs10160755	116988287	G	A	0.1386140	-0.0382172	0.0049510	1.5E-15
11	SIK3	rs11406946	116988385	CA	C	0.2069940	-0.0286594	0.0042518	5.6E-12
11	SIK3	rs519794	116988737	C	T	0.4746130	-0.0300742	0.0034455	3.1E-19
11	SIK3	rs10706688	116989575	T	TA	0.2027430	-0.0256611	0.0042833	9.6E-10
11	SIK3	rs61905687	116991428	C	T	0.0498607	0.0576261	0.0078622	4.0E-14
11	SIK3	rs80242245	116991529	G	C	0.1003120	-0.0462771	0.0057008	5.3E-17
11	SIK3	rs11216218	116991945	T	C	0.1003120	-0.0462771	0.0057008	5.3E-17
11	SIK3	rs11216219	116992039	T	C	0.1003120	-0.0462771	0.0057008	5.3E-17
11	SIK3	rs607273	116992102	A	T	0.3112310	0.0438580	0.0037007	1.3E-33
11	SIK3	rs12272973	116992331	C	A	0.1009160	-0.0463697	0.0057040	4.8E-17
11	SIK3	rs10128682	116992742	T	C	0.1004390	-0.0462027	0.0056970	5.5E-17
11	SIK3	rs7130531	116993117	T	C	0.0498607	0.0576261	0.0078622	4.0E-14
11	SIK3	rs11216220	116993272	C	T	0.1386430	-0.0381766	0.0049499	1.6E-15
11	SIK3	rs11375002	116993436	CA	C	0.4748750	-0.0301352	0.0034433	2.6E-19
11	SIK3	rs75826529	116994384	A	T	0.1004390	-0.0462027	0.0056970	5.5E-17
11	SIK3	rs74460214	116994491	C	T	0.1004390	-0.0462027	0.0056970	5.5E-17
11	SIK3	rs79349393	116994651	G	A	0.1004390	-0.0462027	0.0056970	5.5E-17
11	SIK3	rs7931665	116995524	G	A	0.1387230	-0.0382063	0.0049490	1.5E-15
11	SIK3	rs7931770	116995574	T	C	0.4738460	-0.0292040	0.0034425	2.6E-18
11	SIK3	rs7121347	116996493	T	G	0.4738460	-0.0292040	0.0034425	2.6E-18
11	SIK3	rs11604866	116996798	T	C	0.1004390	-0.0462027	0.0056970	5.5E-17
11	SIK3	rs7950213	116997938	A	C	0.0498607	0.0576261	0.0078622	4.0E-14
11	SIK3	chr11:116999579_G_GTTT	116999579	GTTTTC	G	0.0498607	0.0576261	0.0078622	4.0E-14
11	SIK3	rs10892056	116999695	C	G	0.1004390	-0.0462027	0.0056970	5.5E-17
11	SIK3	rs10502224	116999764	G	A	0.1387510	-0.0382110	0.0049495	1.5E-15
11	SIK3	rs17120233	117000507	G	A	0.0498607	0.0576261	0.0078622	4.0E-14
11	SIK3	rs10892057	117001318	C	A	0.1392840	-0.0382671	0.0049469	1.4E-15
11	SIK3	chr11:117001505_C_CA	117001505	CA	C	0.2817090	-0.0269401	0.0038279	3.7E-13
11	SIK3	rs75858236	117001547	G	A	0.0498701	0.0574650	0.0078615	4.6E-14
11	SIK3	rs12278943	117003642	C	T	0.1003120	-0.0462771	0.0057008	5.3E-17
11	SIK3	rs7946390	117004436	G	A	0.1387240	-0.0381722	0.0049488	1.5E-15
11	SIK3	rs11216224	117005208	C	T	0.1373940	-0.0378043	0.0049757	4.3E-15
11	SIK3	rs7114963	117005267	C	T	0.4693320	-0.0297757	0.0034588	8.5E-19
11	SIK3	rs1940625	117005726	G	A	0.1387240	-0.0381722	0.0049488	1.5E-15
11	SIK3	rs10892058	117005905	T	C	0.2029580	-0.0266511	0.0042706	1.7E-10
11	SIK3	rs10790169	117006443	C	A	0.4742680	-0.0294524	0.0034396	1.3E-18
11	SIK3	rs77250716	117006637	C	T	0.0494174	0.0584480	0.0078987	2.5E-14
11	SIK3	rs11216225	117007298	G	A	0.1387240	-0.0381722	0.0049488	1.5E-15
11	SIK3	rs11216226	117007350	G	C	0.1004410	-0.0462043	0.0056970	5.5E-17
11	SIK3	rs11216227	117007881	G	C	0.2031730	-0.0268420	0.0042720	1.3E-10
11	SIK3	rs12276805	117008043	C	T	0.0985340	-0.0462486	0.0057582	1.2E-16
11	SIK3	rs12271319	117008508	T	C	0.1387240	-0.0381722	0.0049488	1.5E-15
11	SIK3	rs12284696	117008803	G	A	0.1378170	-0.0385259	0.0049658	1.1E-15
11	SIK3	rs117901629	117008963	A	G	0.1003330	-0.0462699	0.0057007	5.4E-17
11	SIK3	rs138181556	117009007	A	G	0.1003220	-0.0462484	0.0057006	5.5E-17
11	SIK3	rs7112937	117009740	C	T	0.1387500	-0.0380803	0.0049481	1.8E-15
11	SIK3	rs61905691	117009987	G	A	0.0498701	0.0574650	0.0078615	4.6E-14
11	SIK3	rs7127881	117010082	A	G	0.2069730	-0.0275993	0.0042668	3.9E-11
11	SIK3	rs58176010	117010731	A	G	0.0185577	0.0760308	0.0126931	6.4E-10
11	SIK3	rs10892059	117010929	A	G	0.2033580	-0.0263642	0.0042647	2.5E-10
11	SIK3	rs10892060	117010946	A	C	0.2029680	-0.0262682	0.0042692	3.1E-10
11	SIK3	rs4245168	117011922	A	C	0.4738220	-0.0294008	0.0034372	1.3E-18
11	SIK3	rs35123861	117012098	CA	C	0.2041700	-0.0264684	0.0042615	2.3E-10
11	SIK3	rs7125788	117012680	C	T	0.0498701	0.0574650	0.0078615	4.6E-14
11	SIK3	rs1442498591	117012824	AG	A	0.1659620	-0.0287749	0.0047018	2.9E-10
11	SIK3	chr11:117012827_G_GTT	117012827	GTT	G	0.1003660	-0.0460549	0.0056981	6.9E-17
11	SIK3	rs10790170	117012828	G	T	0.2043070	-0.0263873	0.0042746	3.1E-10
11	SIK3	rs61905705	117013060	T	A	0.0498805	0.0573718	0.0078608	5.0E-14
11	SIK3	rs61905706	117013061	T	G	0.0498805	0.0573718	0.0078608	5.0E-14
11	SIK3	rs140947361	117013808	A	AC	0.0498805	0.0573718	0.0078608	5.0E-14
11	SIK3	rs374772197	117013968	C	T	0.0497349	0.0574573	0.0078730	5.6E-14
11	SIK3	rs11216230	117014073	A	G	0.1737690	-0.0243638	0.0045837	4.0E-08
11	SIK3	rs35190172	117014597	T	TC	0.0498805	0.0573718	0.0078608	5.0E-14
11	SIK3	rs10892061	117015398	T	C	0.2037890	-0.0267850	0.0042673	1.5E-10
11	SIK3	rs79870586	117016005	A	G	0.1004090	-0.0459581	0.0056962	7.9E-17
11	SIK3	rs66751419	117017528	T	TG	0.2039890	-0.0267043	0.0042677	1.7E-10
11	SIK3	rs80054374	117019951	G	A	0.1004090	-0.0459581	0.0056962	7.9E-17
11	SIK3	rs12808524	117020277	C	T	0.2039130	-0.0266677	0.0042678	1.8E-10

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3	rs17120237	117020330	C	T	0.0498805	0.0573718	0.0078608	5.0E-14
11	SIK3	rs77955134	117021652	A	G	0.1002830	-0.0460322	0.0057000	7.6E-17
11	SIK3	rs77594377	117021730	A	G	0.1002640	-0.0460987	0.0057004	6.9E-17
11	SIK3	rs142310263	117022278	C	AAATCTCA	0.0993379	-0.0467573	0.0057269	3.6E-17
11	SIK3	rs4936359	117023008	A	T	0.0498763	0.0573491	0.0078608	5.1E-14
11	SIK3	rs4936360	117023053	C	G	0.0498763	0.0573491	0.0078608	5.1E-14
11	SIK3	rs143791312	117024639	T	C	0.0633078	-0.0373966	0.0070336	4.7E-08
11	SIK3	rs10892063	117025439	C	A	0.2045960	-0.0261871	0.0042580	3.5E-10
11	SIK3	rs111860754	117025569	C	CA	0.0498732	0.0574072	0.0078599	4.8E-14
11	SIK3	rs10892064	117025837	C	G	0.2041180	-0.0263612	0.0042576	2.5E-10
11	SIK3	rs2186844	117026197	T	C	0.1002830	-0.0460322	0.0057000	7.6E-17
11	SIK3	rs10892065	117026308	C	T	0.2041180	-0.0263612	0.0042576	2.5E-10
11	SIK3	rs61905709	117027118	T	C	0.0498722	0.0574066	0.0078599	4.8E-14
11	SIK3	rs4938325	117027763	A	G	0.0498722	0.0574066	0.0078599	4.8E-14
11	SIK3	rs7950364	117028170	G	C	0.4734000	-0.0294405	0.0034384	1.3E-18
11	SIK3	rs12289032	117028864	T	C	0.1002990	-0.0460302	0.0056995	7.4E-17
11	SIK3	rs7926104	117029066	A	G	0.2036770	-0.0267708	0.0042639	1.4E-10
11	SIK3	rs112120205	117029070	A	G	0.0498722	0.0574066	0.0078599	4.8E-14
11	SIK3	rs146943088	117029109	C	A	0.1002990	-0.0460302	0.0056995	7.4E-17
11	SIK3	rs11216242	117030833	A	G	0.2036960	-0.0267811	0.0042639	1.4E-10
11	SIK3	rs7112191	117031340	A	G	0.0498608	0.0572280	0.0078624	5.8E-14
11	SIK3	chr11:117031495_C_CATT	117031495	CATTTT	C	0.4734320	-0.0294567	0.0034385	1.3E-18
11	SIK3	rs199986368	117031627	C	T	0.0148760	0.1127670	0.0141808	5.0E-16
11	SIK3	rs7481286	117031656	T	G	0.1004470	-0.0455111	0.0056944	1.5E-16
11	SIK3	rs12804122	117031900	G	C	0.2038370	-0.0266148	0.0042613	1.7E-10
11	SIK3	chr11:117032674_CTT_C	117032674	CTT	C	0.1065500	-0.0452932	0.0055759	4.9E-17
11	SIK3	rs4575311	117033641	A	G	0.2037360	-0.0267835	0.0042635	1.4E-10
11	SIK3	rs4938326	117034748	C	G	0.0498608	0.0572280	0.0078624	5.8E-14
11	SIK3	rs187437651	117034813	A	G	0.0180266	0.0824641	0.0129666	1.7E-10
11	SIK3	rs147518949	117035258	A	G	0.0180270	0.0824471	0.0129666	1.7E-10
11	SIK3	rs10732856	117036397	C	T	0.4739220	-0.0293442	0.0034358	1.6E-18
11	SIK3	rs75216569	117036999	G	A	0.1004590	-0.0457412	0.0056946	1.1E-16
11	SIK3	rs7115242	117037567	A	G	0.3128000	0.0426620	0.0036811	2.2E-32
11	SIK3	rs80273401	117037990	C	T	0.1004590	-0.0457412	0.0056946	1.1E-16
11	SIK3	rs61905712	117038577	A	G	0.0498836	0.0570033	0.0078610	7.0E-14
11	SIK3	rs112870705	117038708	T	TCAC	0.0496892	0.0573446	0.0078767	5.5E-14
11	SIK3	rs61905713	117038713	T	C	0.0496892	0.0573446	0.0078767	5.5E-14
11	SIK3	rs12273536	117040255	T	C	0.0977626	-0.0475888	0.0057668	2.1E-17
11	SIK3	rs12273545	117040296	T	C	0.0977626	-0.0475888	0.0057668	2.1E-17
11	SIK3	rs77999164	117041401	T	C	0.0977834	-0.0476706	0.0057664	1.8E-17
11	SIK3	rs80143284	117042854	A	C	0.0978898	-0.0474374	0.0057631	2.4E-17
11	SIK3	rs17120241	117044304	C	T	0.0498784	0.0572997	0.0078609	5.4E-14
11	SIK3	rs2155583	117044501	G	A	0.4735960	-0.0294857	0.0034394	1.2E-18
11	SIK3	chr11:117044615_GA_G	117044615	G	GA	0.2200290	-0.0245220	0.0042194	4.9E-09
11	SIK3	rs2000614	117045026	T	C	0.4734800	-0.0294989	0.0034388	1.1E-18
11	SIK3	rs2000615	117045103	T	C	0.4734800	-0.0294989	0.0034388	1.1E-18
11	SIK3	rs2000616	117045813	T	C	0.4734800	-0.0294989	0.0034388	1.1E-18
11	SIK3	rs76972960	117045962	C	T	0.0498784	0.0572997	0.0078609	5.4E-14
11	SIK3	rs10750100	117046528	C	T	0.4734700	-0.0294860	0.0034387	1.1E-18
11	SIK3	rs61905716	117048351	T	C	0.0498795	0.0573198	0.0078609	5.3E-14
11	SIK3	rs12280172	117048557	A	G	0.0985181	-0.0456037	0.0057442	2.6E-16
11	SIK3	rs112151056	117048652	A	G	0.0498795	0.0573198	0.0078609	5.3E-14
11	SIK3	rs61905718	117048961	T	C	0.0498795	0.0573198	0.0078609	5.3E-14
11	SIK3	rs75890305	117049253	G	A	0.0978146	-0.0475258	0.0057651	2.2E-17
11	SIK3	rs142341972	117049453	T	C	0.1387050	-0.0315441	0.0049937	1.1E-10
11	SIK3	chr11:117049961_T_TA	117049961	TA	T	0.4769670	-0.0300907	0.0034603	3.9E-19
11	SIK3	rs11826651	117049977	A	T	0.0498784	0.0573376	0.0078609	5.2E-14
11	SIK3	rs4938328	117050503	T	G	0.2070040	-0.0259782	0.0042364	3.2E-10
11	SIK3	rs1815786	117050674	T	C	0.3124160	0.0420139	0.0036959	3.0E-31
11	SIK3	rs1815787	117050681	C	T	0.4739220	-0.0295219	0.0034372	9.5E-19
11	SIK3	rs111530588	117051870	A	G	0.0978125	-0.0475293	0.0057651	2.2E-17
11	SIK3	rs61905719	117051998	T	C	0.0498784	0.0573376	0.0078609	5.2E-14
11	SIK3	rs7130297	117053154	T	C	0.4722590	-0.0306206	0.0034403	6.6E-20
11	SIK3	rs11216250	117053284	T	C	0.0970236	-0.0477226	0.0057884	2.2E-17
11	SIK3	rs80259223	117053602	A	G	0.0507806	0.0554485	0.0077997	2.1E-13
11	SIK3	rs201829635	117056603	T	TC	0.0491224	0.0571448	0.0079223	1.0E-13
11	SIK3	rs117091722	117056884	A	G	0.0614293	-0.0624295	0.0071702	7.3E-19
11	SIK3	rs10790172	117057024	T	G	0.4766830	-0.0305251	0.0034589	1.5E-19
11	SIK3	rs10892067	117057046	C	G	0.0978877	-0.0474409	0.0057631	2.4E-17
11	SIK3	rs11216252	117057507	A	G	0.0978125	-0.0475293	0.0057651	2.2E-17
11	SIK3	rs11216253	117057509	C	A	0.0978125	-0.0475293	0.0057651	2.2E-17
11	SIK3	rs10892068	117057830	T	C	0.0978877	-0.0474409	0.0057631	2.4E-17

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAf	BETA	SE	P
11	SIK3	rs9943680	117058538	C	T	0.1872150	-0.0242946	0.0044985	3.0E-08
11	SIK3	rs34992009	117059421	G	GC	0.2063350	-0.0265627	0.0042473	1.6E-10
11	SIK3	rs4938331	117059966	A	C	0.2062100	-0.0262907	0.0042474	2.3E-10
11	SIK3	rs4938332	117060082	G	A	0.2063280	-0.0265219	0.0042473	1.7E-10
11	SIK3	rs4938333	117060172	G	A	0.0499107	0.0575991	0.0078571	4.0E-14
11	SIK3	rs4938334	117060326	C	G	0.2065420	-0.0262444	0.0042474	2.5E-10
11	SIK3	rs61903394	117061182	A	G	0.0499023	0.0576213	0.0078578	4.0E-14
11	SIK3	rs6589590	117065365	C	A	0.2074510	-0.0257347	0.0042359	4.8E-10
11	SIK3	rs56751865	117066155	T	C	0.1170780	-0.0410691	0.0053604	3.4E-15
11	SIK3	rs112895963	117066443	T	A	0.0493737	0.0585469	0.0079013	2.5E-14
11	SIK3	rs79955870	117066645	T	C	0.0986742	-0.0482630	0.0057582	5.2E-18
11	SIK3	rs35187263	117067811	AC	A	0.2057280	-0.0276448	0.0042479	2.9E-11
11	SIK3	rs368388328	117069182	T	TTTG	0.0405144	0.0514163	0.0087371	1.0E-09
11	SIK3	rs11216261	117069494	C	T	0.0976804	-0.0475295	0.0057698	2.2E-17
11	SIK3	rs12280210	117069733	C	T	0.1360070	-0.0391062	0.0049950	6.5E-16
11	SIK3	rs9971421	117070824	T	C	0.0962682	-0.0473714	0.0058162	6.8E-17
11	SIK3	rs61903398	117070897	T	C	0.0497942	0.0576693	0.0078669	4.3E-14
11	SIK3	rs144942164	117071184	C	T	0.0391407	0.0570006	0.0088844	4.1E-11
11	SIK3	rs202154722	117071196	AT	A	0.0975615	-0.0472166	0.0057784	4.7E-17
11	SIK3	rs17120280	117071416	A	G	0.0510515	0.0555414	0.0077869	2.0E-13
11	SIK3	rs77182215	117071650	A	C	0.0853256	0.0453554	0.0061560	2.6E-14
11	SIK3	rs61903399	117071759	T	A	0.0493913	0.0588936	0.0078988	1.7E-14
11	SIK3	chr11:117071926_G_GTGTT	117071926	GTGTT	G	0.2011560	-0.0267893	0.0043082	2.0E-10
11	SIK3	rs116582417	117072350	A	G	0.0975047	-0.0478802	0.0057758	1.4E-17
11	SIK3	rs1351452	117072638	C	A	0.4742420	-0.0293466	0.0034415	1.5E-18
11	SIK3	rs17120293	117074130	C	T	0.0975318	-0.0477670	0.0057745	1.6E-17
11	SIK3	rs12274725	117076137	T	C	0.0975047	-0.0478802	0.0057758	1.4E-17
11	SIK3	rs11216265	117076464	C	T	0.0975047	-0.0478802	0.0057758	1.4E-17
11	SIK3	rs12418036	117076590	A	G	0.0975047	-0.0478802	0.0057758	1.4E-17
11	SIK3	rs4938335	117076645	C	A	0.4738250	-0.0291632	0.0034420	2.3E-18
11	SIK3	rs4938336	117077726	G	A	0.0497775	0.0574505	0.0078684	5.4E-14
11	SIK3	rs10736487	117079516	G	A	0.4753610	-0.0289819	0.0034400	3.2E-18
11	SIK3	rs10892070	117080817	A	G	0.2209570	-0.0263319	0.0041669	7.5E-11
11	SIK3	rs10082561	117080868	C	A	0.0922132	-0.0447300	0.0059210	5.9E-15
11	SIK3	rs4936362	117081484	T	C	0.0497608	0.0573144	0.0078706	6.3E-14
11	SIK3	rs11216267	117081676	T	C	0.2084450	-0.0252036	0.0042269	8.3E-10
11	SIK3	rs11216270	117082928	A	C	0.0974963	-0.0479296	0.0057760	1.3E-17
11	SIK3	rs2368149	117085218	A	G	0.0974080	-0.0480338	0.0057788	1.2E-17
11	SIK3	rs61903417	117085441	G	T	0.0497536	0.0572703	0.0078705	6.5E-14
11	SIK3	rs61903418	117085949	A	G	0.0497432	0.0573176	0.0078712	6.3E-14
11	SIK3	rs12281358	117086274	C	T	0.0973976	-0.0480612	0.0057790	1.1E-17
11	SIK3	rs6589592	117087191	C	G	0.3079590	0.0432720	0.0037224	1.3E-32
11	SIK3	rs111901638	117089132	A	G	0.0497817	0.0574081	0.0078686	5.7E-14
11	SIK3	rs10892072	117089597	A	G	0.2080660	-0.0253702	0.0042330	6.4E-10
11	SIK3	rs11823918	117089781	C	G	0.0497910	0.0573301	0.0078679	6.3E-14
11	SIK3	rs77431162	117090820	T	C	0.0684907	0.0420520	0.0067702	1.6E-10
11	SIK3	rs61903421	117091086	T	A	0.0497910	0.0573301	0.0078679	6.3E-14
11	SIK3	rs116861530	117091945	A	G	0.0960022	-0.0493801	0.0058225	2.7E-18
11	SIK3	rs74420345	117092561	A	C	0.0960082	-0.0493817	0.0058225	2.7E-18
11	SIK3	rs7950381	117093181	A	C	0.0497400	0.0576293	0.0078721	4.8E-14
11	SIK3	rs7950501	117093249	T	C	0.0497400	0.0576293	0.0078721	4.8E-14
11	SIK3	rs57383565	117093678	AG	A	0.0501514	0.0574989	0.0078513	4.7E-14
11	SIK3	rs900012	117095719	A	G	0.4711490	-0.0291024	0.0034510	2.9E-18
11	SIK3	rs1320668	117096950	T	C	0.4762350	-0.0277146	0.0034475	7.0E-17
11	SIK3	rs61903426	117097552	T	C	0.0541463	0.0599315	0.0075827	6.2E-16
11	SIK3	rs7128071	117098082	A	G	0.0526332	0.0600050	0.0076976	1.4E-15
11	SIK3 *	rs10892073	117098674	T	C	0.2037910	-0.0248466	0.0042746	1.6E-09
11	SIK3 *	rs76567973	117100045	G	C	0.0971742	-0.0482599	0.0057863	9.2E-18
11	SIK3 *	chr11:117100110_GT_G	117100110	G	GT	0.4794390	-0.0271462	0.0034521	3.3E-16
11	SIK3 *	rs78135964	117100961	T	G	0.0972170	-0.0483290	0.0057836	7.9E-18
11	SIK3 *	rs148233183	117101511	A	G	0.0972944	-0.0480509	0.0057810	1.2E-17
11	SIK3 *	rs4938338	117102178	A	C	0.0543356	0.0598180	0.0075646	6.2E-16
11	SIK3 *	rs4936363	117102219	T	C	0.0543368	0.0598159	0.0075646	6.2E-16
11	SIK3 *	rs76942203	117102531	A	G	0.0973054	-0.0480848	0.0057802	1.2E-17
11	SIK3 *	chr11:117103138_A_AAAT	117103138	AAAT	A	0.0970611	-0.0478846	0.0057911	2.5E-17
11	SIK3 *	rs149576335	117104420	A	G	0.0972592	-0.0481339	0.0057816	1.1E-17
11	SIK3 *	rs142395187	117105293	G	A	0.0965743	-0.0480291	0.0058033	1.7E-17
11	SIK3 *	chr11:117105573_A_AT	117105573	AT	A	0.2033580	-0.0291788	0.0043302	4.5E-12
11	SIK3 *	rs145671645	117106195	A	G	0.0294584	-0.0569209	0.0101479	4.6E-09
11	SIK3 *	rs10160799	117107172	A	G	0.4766990	-0.0266424	0.0034483	1.1E-15
11	SIK3 *	rs181104223	117107559	C	A	0.0296540	0.0787698	0.0100411	6.7E-16
11	SIK3 *	rs12416941	117108647	A	G	0.0978347	-0.0459988	0.0057703	2.1E-16

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	SIK3 *	rs113784559	117108649	G	C	0.0566181	0.0528949	0.0074120	3.4E-13
11	SIK3 *	rs10750101	117108973	C	T	0.4768450	-0.0269376	0.0034455	5.5E-16
11	SIK3 *	rs4938339	117109878	T	C	0.0566273	0.0529562	0.0074115	3.2E-13
11	SIK3 *	rs4938340	117109906	A	G	0.0570281	0.0524733	0.0074067	5.4E-13
11	SIK3 *	rs10892074	117109925	T	G	0.2035530	-0.0239285	0.0042737	6.1E-09
11	SIK3 *	rs114221654	117109963	T	C	0.0978347	-0.0459988	0.0057703	2.1E-16
11	SIK3 *	rs35172278	117110063	CCTG	C	0.4884240	-0.0275413	0.0034514	8.5E-17
11	SIK3 *	rs61903427	117110070	C	G	0.0566273	0.0529562	0.0074115	3.2E-13
11	SIK3 *	rs4635117	117110285	A	G	0.2975250	0.0395383	0.0037817	6.6E-27
11	SIK3 *	rs6589595	117110619	A	G	0.0566273	0.0529562	0.0074115	3.2E-13
11	SIK3 *	rs116770907	117110799	T	C	0.0978367	-0.0459887	0.0057704	2.1E-16
11	SIK3 *	rs2127907	117110864	G	A	0.4912330	-0.0275999	0.0034465	7.0E-17
11	SIK3 *	rs111677878	117111718	T	C	0.0978259	-0.0459957	0.0057711	2.1E-16
11	SIK3 *	rs59700451	117112212	A	G	0.0566067	0.0529430	0.0074132	3.3E-13
11	SIK3 *	rs113979111	117112300	A	G	0.0566055	0.0529469	0.0074132	3.3E-13
11	SIK3 *	rs111560312	117112840	A	G	0.0566055	0.0529469	0.0074132	3.3E-13
11	SIK3 *	rs55703909	117114150	A	G	0.0565987	0.0529996	0.0074139	3.2E-13
11	SIK3 *	rs74882651	117114475	A	G	0.0978111	-0.0460698	0.0057716	1.9E-16
11	SIK3 *	rs60834024	117115141	A	C	0.0978299	-0.0460956	0.0057705	1.7E-16
11	SIK3 *	rs61903429	117115968	A	C	0.0565930	0.0532095	0.0074145	2.6E-13
11	SIK3 *	rs11216277	117116330	A	G	0.2957200	-0.0246351	0.0037579	8.7E-12
11	SIK3 *	rs61903430	117116626	C	G	0.0565930	0.0532095	0.0074145	2.6E-13
11	SIK3 *	rs75904569	117117597	G	A	0.0565837	0.0532246	0.0074150	2.5E-13
11	SIK3 *	rs80197460	117118074	G	C	0.0978467	-0.0463194	0.0057693	1.2E-16
11	SIK3 *	rs10892076	117118220	A	G	0.2946140	-0.0247610	0.0037647	7.7E-12
11	SIK3 *	rs74428560	117119266	T	C	0.0565930	0.0532353	0.0074145	2.4E-13
11	SIK3 *	rs117300172	117119795	C	A	0.0155332	0.0792963	0.0138419	6.4E-09
11	SIK3 *	chr11:117120044_G_GAAAC	117120044	GAAAC	G	0.4325980	-0.0391040	0.0034723	1.9E-31
11	SIK3 *	rs200802441	117120056	C	A	0.4176010	-0.0371870	0.0035342	1.3E-27
11	SIK3 *	rs12366015	117120135	G	A	0.4322640	-0.0389020	0.0034710	3.5E-31
11	SIK3 *	rs138720977	117120356	ATAAG	A	0.2906680	-0.0236887	0.0037928	8.2E-11
11	SIK3 *	rs142756367	117120357	TAAGA	T	0.2954660	-0.0245876	0.0037584	9.8E-12
11	PAFAH1B2 *	rs74955808	117121969	A	G	0.0980913	-0.0461927	0.0057628	1.4E-16
11	PAFAH1B2 *	rs71037454	117122203	3GAGAAAGA	G	0.4898510	-0.0274442	0.0034377	9.2E-17
11	PAFAH1B2 *	rs6589596	117122465	C	T	0.4899890	-0.0274228	0.0034377	9.7E-17
11	PAFAH1B2 *	rs76868258	117122576	T	C	0.0566020	0.0534906	0.0074132	1.9E-13
11	PAFAH1B2 *	rs12420361	117123072	A	G	0.0979273	-0.0464722	0.0057660	9.4E-17
11	PAFAH1B2 *	rs10892078	117123213	T	A	0.2041870	-0.0239982	0.0042629	4.9E-09
11	PAFAH1B2 *	rs11344600	117123743	C	CA	0.4899890	-0.0272384	0.0034345	1.3E-16
11	PAFAH1B2 *	rs35722128	117124277	C	CA	0.0566354	0.0534631	0.0074109	1.9E-13
11	PAFAH1B2 *	chr11:117125062_TAA_T	117125062	T	TAA	0.4902030	-0.0270005	0.0034300	2.2E-16
11	PAFAH1B2 *	rs17120344	117125629	A	G	0.0981940	-0.0460864	0.0057563	1.6E-16
11	PAFAH1B2 *	rs17120347	117125823	A	G	0.0567423	0.0526286	0.0074036	4.4E-13
11	PAFAH1B2 *	rs12419454	117125915	T	C	0.0982024	-0.0461288	0.0057561	1.5E-16
11	PAFAH1B2 *	rs12419459	117125995	T	C	0.0991357	-0.0448903	0.0057301	6.4E-16
11	PAFAH1B2 *	rs12416691	117126067	T	A	0.0982358	-0.0463081	0.0057552	1.1E-16
11	PAFAH1B2 *	rs6589597	117127082	T	C	0.4910120	-0.0270595	0.0034265	1.7E-16
11	PAFAH1B2 *	rs78302396	117127400	G	A	0.0842343	0.0380240	0.0061662	1.3E-10
11	PAFAH1B2 *	rs12420200	117127590	A	G	0.0982525	-0.0464014	0.0057548	9.7E-17
11	PAFAH1B2 *	rs182980806	117127672	T	G	0.0154145	0.0805221	0.0138868	4.0E-09
11	PAFAH1B2 *	rs145802214	117128196	C	A	0.0982525	-0.0464014	0.0057548	9.7E-17
11	PAFAH1B2 *	rs141250514	117128309	C	T	0.0982525	-0.0464014	0.0057548	9.7E-17
11	PAFAH1B2 *	rs4516002	117128343	G	A	0.4910120	-0.0270781	0.0034265	1.6E-16
11	PAFAH1B2 *	rs7131536	117128730	T	C	0.4912470	-0.0269042	0.0034275	2.6E-16
11	PAFAH1B2 *	rs7131686	117128843	T	C	0.4910230	-0.0270531	0.0034264	1.7E-16
11	PAFAH1B2 *	rs138039720	117128884	T	C	0.0982769	-0.0464008	0.0057552	9.9E-17
11	PAFAH1B2 *	chr11:117129006_TA_T	117129006	T	TA	0.4474680	-0.0275260	0.0034691	1.4E-16
11	PAFAH1B2 *	rs146067038	117129463	G	A	0.0982537	-0.0464999	0.0057568	9.0E-17
11	PAFAH1B2 *	rs10400366	117130239	A	G	0.2955510	-0.0240229	0.0037444	2.6E-11
11	PAFAH1B2 *	rs199498085	117130739	G	A	0.0917654	-0.0480142	0.0059582	1.2E-16
11	PAFAH1B2 *	rs12421425	117131244	T	C	0.0982684	-0.0465215	0.0057564	8.6E-17
11	PAFAH1B2 *	chr11:117131317_A_AT	117131317	AT	A	0.4451330	-0.0249929	0.0034927	7.3E-14
11	PAFAH1B2 *	rs142848583	117131334	AC	A	0.0110852	0.0890887	0.0163095	1.5E-08
11	PAFAH1B2 *	rs191044888	117131336	T	G	0.0110850	0.0890747	0.0163095	1.5E-08
11	PAFAH1B2 *	rs4938341	117131880	A	G	0.0571280	0.0514492	0.0073748	1.3E-12
11	PAFAH1B2 *	rs17120367	117132112	T	C	0.0982767	-0.0466062	0.0057562	7.4E-17
11	PAFAH1B2 *	chr11:117132474_CA_C	117132474	C	CA	0.4913010	-0.0270426	0.0034320	1.9E-16
11	PAFAH1B2 *	rs17120370	117132672	C	T	0.0982767	-0.0466062	0.0057562	7.4E-17
11	PAFAH1B2 *	rs74735277	117132702	T	C	0.0982747	-0.0466092	0.0057562	7.4E-17
11	PAFAH1B2 *	rs4938342	117132704	G	C	0.0572632	0.0512327	0.0073506	1.4E-12
11	PAFAH1B2 *	rs17120373	117132743	G	A	0.1365510	-0.0374698	0.0049920	9.1E-15
11	PAFAH1B2 *	rs4938343	117132812	C	G	0.4529540	-0.0261659	0.0034334	2.0E-15

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PAFAH1B2 *	rs75208249	117132907	C	G	0.0984771	-0.0466785	0.0057498	6.4E-17
11	PAFAH1B2 *	rs114945429	117133485	T	G	0.0983310	-0.0475153	0.0057542	2.0E-17
11	PAFAH1B2 *	rs12417098	117134137	A	G	0.0977969	-0.0474392	0.0057701	2.6E-17
11	PAFAH1B2 *	rs141936239	117134911	C	T	0.1032910	-0.0462876	0.0056807	5.9E-17
11	PAFAH1B2 *	rs143261386	117135035	C	T	0.1032930	-0.0463075	0.0056808	5.7E-17
11	PAFAH1B2 *	rs2735181	117139073	T	C	0.2839520	-0.0248211	0.0038466	2.0E-11
11	PAFAH1B2 *	rs115991973	117139375	A	G	0.0977949	-0.0471694	0.0057694	3.6E-17
11	PAFAH1B2 *	rs116384608	117139407	G	A	0.0977949	-0.0471694	0.0057694	3.6E-17
11	PAFAH1B2 *	rs2471884	117139604	C	T	0.4906610	-0.0270776	0.0034317	1.9E-16
11	PAFAH1B2 *	rs77661993	117139758	C	A	0.0978032	-0.0471604	0.0057692	3.7E-17
11	PAFAH1B2 *	rs7934690	117140583	A	T	0.0570093	0.0519166	0.0073876	8.6E-13
11	PAFAH1B2 *	rs1555026168	117143445	AAG	A	0.4874210	-0.0247215	0.0034442	4.7E-14
11	PAFAH1B2 *	rs2622934	117144146	T	G	0.2964210	-0.0239789	0.0037459	3.0E-11
11	PAFAH1B2 *	rs76904522	117144147	A	G	0.0574257	0.0516318	0.0037630	9.6E-13
11	PAFAH1B2	rs113560866	117144473	C	G	0.0577068	0.0511989	0.0073549	1.5E-12
11	PAFAH1B2	rs2735183	117144479	T	C	0.2979740	-0.0235925	0.0037529	6.7E-11
11	PAFAH1B2	rs12419227	117144522	A	C	0.1003470	-0.0401008	0.0057011	2.7E-13
11	PAFAH1B2	rs149188200	117144559	T	G	0.0369668	0.0567300	0.0091419	2.1E-10
11	PAFAH1B2	rs11420191	117145447	CG	C	0.4986360	-0.0253583	0.0034277	8.8E-15
11	PAFAH1B2	rs2306471	117145734	T	C	0.1019300	-0.0407616	0.0056591	7.8E-14
11	PAFAH1B2	rs78270178	117146132	G	T	0.3180830	-0.0217359	0.0037518	1.1E-09
11	PAFAH1B2	rs12419436	117146739	G	T	0.1017120	-0.0406804	0.0056649	9.5E-14
11	PAFAH1B2	rs12420725	117146814	G	A	0.1021780	-0.0402104	0.0056527	1.4E-13
11	PAFAH1B2	rs117592676	117146994	T	C	0.0191647	0.0992315	0.0125087	2.1E-16
11	PAFAH1B2	rs12417984	117146998	A	G	0.1019790	-0.0406725	0.0056579	8.7E-14
11	PAFAH1B2	rs139864910	117147046	C	A	0.1019790	-0.0406725	0.0056579	8.7E-14
11	PAFAH1B2	rs139146464	117149151	G	A	0.1011210	-0.0401235	0.0056835	2.6E-13
11	PAFAH1B2	rs71037463	117149256	A	AT	0.4974810	-0.0256132	0.0034272	4.6E-15
11	PAFAH1B2	rs7115562	117149754	G	A	0.4610830	-0.0246810	0.0034279	5.2E-14
11	PAFAH1B2	rs7116454	117150418	T	A	0.4610830	-0.0246810	0.0034279	5.2E-14
11	PAFAH1B2	rs45625638	117150710	C	G	0.0576815	0.0514680	0.0073476	1.0E-12
11	PAFAH1B2	chr11:117150989_GAA_G	117150989	G	GAA	0.1018730	-0.0398130	0.0056795	4.3E-13
11	PAFAH1B2	rs4938347	117151043	A	T	0.4593210	-0.0247227	0.0034440	6.4E-14
11	PAFAH1B2	rs4938348	117151161	C	G	0.4581120	-0.0237329	0.0034373	4.8E-13
11	PAFAH1B2	rs4938350	117151560	G	A	0.4580420	-0.0238408	0.0034378	3.9E-13
11	PAFAH1B2	rs79831695	117151612	G	A	0.0294179	-0.0675142	0.0101706	1.3E-11
11	PAFAH1B2	rs4938351	117151636	C	A	0.2980570	-0.0233586	0.0037420	9.5E-11
11	PAFAH1B2	rs7128382	117152771	C	A	0.4581300	-0.0237283	0.0034338	4.7E-13
11	PAFAH1B2	rs143494314	117152990	T	C	0.1019790	-0.0406725	0.0056579	8.7E-14
11	PAFAH1B2	rs7950633	117153586	T	C	0.4973630	-0.0244636	0.0034295	6.8E-14
11	PAFAH1B2	rs7940310	117153765	C	T	0.4963050	-0.0247401	0.0034266	3.8E-14
11	PAFAH1B2	chr11:117154119_G_GA	117154119	GA	G	0.4563760	-0.0246349	0.0034425	7.1E-14
11	PAFAH1B2	rs35500922	117154603	AT	A	0.0983955	-0.0393263	0.0057672	1.6E-12
11	PAFAH1B2	rs68137714	117154641	G	A	0.0576815	0.0514680	0.0073476	1.0E-12
11	PAFAH1B2	rs12418349	117155216	G	A	0.1019790	-0.0406725	0.0056579	8.7E-14
11	PAFAH1B2	rs2127905	117155658	C	A	0.5022320	-0.0252604	0.0034224	9.4E-15
11	PAFAH1B2	rs4936366	117156169	A	G	0.4611060	-0.0246805	0.0034278	5.1E-14
11	PAFAH1B2	rs4938352	117156765	A	G	0.4611060	-0.0246805	0.0034278	5.1E-14
11	PAFAH1B2	rs199763004	117157038	A	AG	0.5036730	-0.0248683	0.0034479	4.4E-14
11	PAFAH1B2	rs7123517	117157039	A	G	0.5040180	-0.0247555	0.0034461	5.1E-14
11	PAFAH1B2	rs117588325	117157577	T	A	0.0282620	0.0773419	0.0102966	2.0E-14
11	PAFAH1B2	rs12420250	117158011	A	G	0.1016830	-0.0411205	0.0056674	5.3E-14
11	PAFAH1B2	rs78166985	117159069	T	A	0.1018710	-0.0408793	0.0056607	6.9E-14
11	PAFAH1B2	rs1871757	117159865	A	T	0.4609250	-0.0246065	0.0034287	6.2E-14
11	PAFAH1B2	rs200545029	117159917	C	T	0.1018490	-0.0407753	0.0056604	7.8E-14
11	PAFAH1B2	rs142017584	117160647	A	G	0.1019880	-0.0406850	0.0056577	8.5E-14
11	PAFAH1B2	rs12281009	117162243	G	A	0.1019880	-0.0406850	0.0056577	8.5E-14
11	PAFAH1B2	rs71037468	117163187	3GCTGAGTGT	C	0.4587710	-0.0243964	0.0034388	1.2E-13
11	PAFAH1B2	rs7122944	117163903	T	G	0.4977970	-0.0261936	0.0034240	1.2E-15
11	PAFAH1B2	rs150984554	117164300	A	G	0.1010210	-0.0413063	0.0056842	5.6E-14
11	PAFAH1B2	rs12420127	117164603	G	A	0.1019880	-0.0406850	0.0056577	8.5E-14
11	PAFAH1B2	rs10892080	117164786	G	A	0.2992870	-0.0240109	0.0037361	2.4E-11
11	PAFAH1B2	rs149378955	117164863	A	G	0.0457935	0.0591169	0.0081989	1.8E-13
11	PAFAH1B2	rs7931335	117166089	T	C	0.4611170	-0.0246825	0.0034278	5.1E-14
11	PAFAH1B2	rs6589602	117166349	C	T	0.3004970	-0.0238894	0.0037278	2.9E-11
11	PAFAH1B2	rs7112513	117166645	G	A	0.4987130	-0.0255398	0.0034216	5.3E-15
11	PAFAH1B2	rs77171490	117168025	A	T	0.1019880	-0.0406850	0.0056577	8.5E-14
11	PAFAH1B2	rs190482111	117168438	A	G	0.1019790	-0.0407308	0.0056579	8.1E-14
11	PAFAH1B2	rs10892082	117168609	G	T	0.4985980	-0.0256572	0.0034234	4.2E-15
11	PAFAH1B2	rs116773440	117168745	C	A	0.1015040	-0.0419432	0.0056811	1.7E-14
11	PAFAH1B2	rs1060211	117169081	A	G	0.4610830	-0.0246632	0.0034280	5.4E-14
11	PAFAH1B2	rs45628435	117169482	GT	G	0.3004890	-0.0239551	0.0037280	2.5E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PAFAH1B2	rs77678768	117169789	C	G	0.1019790	-0.0407308	0.0056579	8.1E-14
11	PAFAH1B2	rs10750103	117171522	T	C	0.2998520	-0.0238912	0.0037323	3.0E-11
11	PAFAH1B2	rs4936367	117171661	A	G	0.4987240	-0.0254936	0.0034219	5.8E-15
11	PAFAH1B2	rs10892083	117171864	C	G	0.2088310	-0.0234243	0.0042205	8.2E-09
11	PAFAH1B2	rs7120309	117172100	A	T	0.4611250	-0.0246465	0.0034279	5.5E-14
11	PAFAH1B2	rs7120449	117172183	C	T	0.4608550	-0.0247038	0.0034281	5.1E-14
11	PAFAH1B2	rs7120565	117172233	C	T	0.3005010	-0.0239269	0.0037281	2.6E-11
11	PAFAH1B2	rs56371319	117172251	A	C	0.0576827	0.0514729	0.0073476	1.0E-12
11	PAFAH1B2	rs4604928	117173487	A	C	0.4987240	-0.0254936	0.0034219	5.8E-15
11	PAFAH1B2	chr11:117174484_A_AT	117174484	AT	A	0.0968717	-0.0382752	0.0058143	4.8E-12
11	PAFAH1B2	chr11:117174494_CT_C	117174494	C	CT	0.2987290	-0.0237799	0.0037462	4.2E-11
11	PAFAH1B2	rs7925256	117174619	T	C	0.2847340	0.0384612	0.0038235	6.4E-25
11	PAFAH1B2	rs10535646	117175444	T	TTGC	0.3006290	-0.0239647	0.0037289	2.5E-11
11	PAFAH1B2	rs4938353	117175481	A	G	0.4611100	-0.0246310	0.0034280	5.8E-14
11	PAFAH1B2	rs10790176	117177136	T	G	0.4611250	-0.0246465	0.0034279	5.5E-14
11	PAFAH1B2	rs80353869	117177406	A	G	0.1017930	-0.0406039	0.0056636	1.0E-13
11	SIDT2	rs12419178	117180202	T	C	0.1016810	-0.0405663	0.0056676	1.0E-13
11	SIDT2	rs34783152	117180423	A	AG	0.1016810	-0.0405663	0.0056676	1.0E-13
11	SIDT2	rs76883864	117181009	T	C	0.1016810	-0.0405663	0.0056676	1.0E-13
11	SIDT2	rs35248926	117181353	G	GTCTCT	0.4610080	-0.0246985	0.0034332	5.2E-14
11	SIDT2	rs2046150	117182717	A	C	0.1039890	-0.0392679	0.0056095	2.6E-13
11	SIDT2	rs4938355	117182959	G	A	0.0561241	0.0522853	0.0074441	1.1E-12
11	SIDT2	rs34033077	117183654	CT	C	0.0970939	-0.0378450	0.0058213	8.8E-12
11	SIDT2	rs2046149	117183993	G	C	0.1039970	-0.0392631	0.0056093	2.7E-13
11	SIDT2	rs6589603	117185123	C	T	0.4983890	-0.0255976	0.0034375	4.8E-15
11	SIDT2	rs11606672	117185343	T	C	0.1038610	-0.0388026	0.0056134	5.2E-13
11	SIDT2	rs2306472	117187346	T	C	0.1017200	-0.0402572	0.0056660	1.6E-13
11	SIDT2	rs546506427	117188416	C	T	0.1038810	-0.0388857	0.0056128	4.6E-13
11	SIDT2	rs775148500	117188417	TCA	T	0.1018760	-0.0407242	0.0056611	8.3E-14
11	SIDT2	rs90192	117188631	T	C	0.4635900	-0.0239235	0.0034316	2.7E-13
11	SIDT2	rs7933134	117189078	C	G	0.1040260	-0.0393369	0.0056082	2.4E-13
11	SIDT2	rs12419470	117191059	T	C	0.1038750	-0.0388932	0.0056127	4.6E-13
11	SIDT2	rs61703672	117191109	T	C	0.1038750	-0.0388932	0.0056127	4.6E-13
11	SIDT2	rs140056851	117191110	G	T	0.0458628	0.0590484	0.0081902	1.8E-13
11	SIDT2	rs499713	117191245	C	T	0.4613960	-0.0247068	0.0034364	4.3E-14
11	SIDT2	rs1242230	117191467	C	T	0.5008720	-0.0253737	0.0034231	6.4E-15
11	SIDT2	rs1242229	117191654	C	T	0.5011730	-0.0253609	0.0034223	7.0E-15
11	SIDT2	rs3213459	117191773	C	T	0.1040270	-0.0393379	0.0056080	2.4E-13
11	SIDT2	rs2301174	117192993	G	C	0.1038960	-0.0387606	0.0056117	5.3E-13
11	SIDT2	rs11605883	117194060	G	C	0.1018690	-0.0407316	0.0056611	8.2E-14
11	SIDT2	rs73008568	117194291	G	C	0.0560525	0.0517192	0.0074512	2.0E-12
11	SIDT2	rs3781985	117194350	C	G	0.1018690	-0.0407316	0.0056611	8.2E-14
11	SIDT2	rs80183569	117194437	A	G	0.1018690	-0.0407316	0.0056611	8.2E-14
11	SIDT2	rs1784042	117194760	A	G	0.2101280	-0.0235555	0.0042128	7.8E-09
11	SIDT2	rs11606480	117194817	A	G	0.1018690	-0.0407316	0.0056611	8.2E-14
11	SIDT2	rs112712475	117195056	A	C	0.1005750	-0.0411390	0.0057033	6.0E-14
11	LOC100652768, SIDT2	rs2269399	117195637	C	G	0.1018690	-0.0407316	0.0056611	8.2E-14
11	LOC100652768	rs74385934	117197728	A	G	0.1018730	-0.0407450	0.0056609	8.1E-14
11	LOC100652768	rs588534	117197788	G	A	0.4608490	-0.0248103	0.0034285	3.9E-14
11	LOC100652768	rs2075547	117197818	A	C	0.0560525	0.0517192	0.0074512	2.0E-12
11	LOC100652768	rs147581841	117197929	T	C	0.0244824	0.0604012	0.0110835	2.2E-08
11	LOC100652768	rs474488	117198261	G	A	0.4608260	-0.0248482	0.0034286	3.6E-14
11	LOC100652768	rs7112573	117198307	C	T	0.1040440	-0.0394735	0.0056069	2.1E-13
11	LOC100652768	rs2269398	117199072	T	C	0.1019240	-0.0407450	0.0056605	8.2E-14
11	LOC100652768	rs17523113	117199185	A	G	0.0439729	0.0583007	0.0083670	1.3E-12
11	LOC100652768, TAGLN	rs2239678	117199880	T	C	0.1018930	-0.0408485	0.0056608	7.3E-14
11	LOC100652768, TAGLN	rs2170317	117200024	C	A	0.1019350	-0.0409466	0.0056611	6.6E-14
11	LOC100652768, TAGLN	rs494356	117201254	C	T	0.4723080	-0.0229287	0.0034493	2.2E-12
11	TAGLN	rs145613978	117202393	A	G	0.0295738	0.0752893	0.0100732	2.3E-14
11	TAGLN	rs12970	117203393	A	G	0.1021380	-0.0402985	0.0056528	1.3E-13
11	TAGLN	rs641620	117203513	T	C	0.4395740	-0.0209691	0.0034806	2.5E-10
11	TAGLN	rs2269397	117203583	C	T	0.1082730	-0.0372853	0.0055068	1.5E-12
11	PCSK7	rs659955	117209663	T	A	0.5018440	-0.0240840	0.0034377	1.4E-13
11	PCSK7	rs11216315	117209924	G	C	0.1039810	-0.0381253	0.0056081	1.2E-12
11	PCSK7	rs11216316	117210784	A	C	0.4996140	-0.0235587	0.0034312	4.2E-13
11	PCSK7	rs12417682	117211393	A	G	0.1043670	-0.0381820	0.0055973	9.8E-13
11	PCSK7	rs76169968	117212250	A	G	0.1046000	-0.0383598	0.0055894	7.3E-13
11	PCSK7	rs67201490	117212288	G	T	0.0549712	0.0520521	0.0075177	1.6E-12
11	PCSK7	rs4938357	117213324	A	G	0.0549724	0.0520437	0.0075178	1.7E-12
11	PCSK7	rs12418705	117213680	T	C	0.1021980	-0.0396054	0.0056507	3.2E-13
11	PCSK7	rs139694434	117213935	TTTTTC	T	0.4983610	-0.0237380	0.0034317	3.0E-13
11	PCSK7	rs77683187	117214494	C	A	0.1044440	-0.0382840	0.0055927	8.1E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
11	PCSK7	rs236911	117214554	A	C	0.4988330	-0.0237431	0.0034290	2.9E-13
11	PCSK7	rs56081989	117214589	A	G	0.0550531	0.0518076	0.0075152	2.1E-12
11	PCSK7	rs36028244	117215198	C	CTTA	0.1042330	-0.0382743	0.0056005	9.2E-13
11	PCSK7	rs56061158	117216402	C	G	0.0550993	0.0521969	0.0075133	1.5E-12
11	PCSK7	rs150159690	117217269	AGTCACTGC	A	0.1042270	-0.0379043	0.0056017	1.3E-12
11	PCSK7	rs2238005	117217366	T	C	0.1044580	-0.0383314	0.0055951	7.8E-13
11	PCSK7	rs236915	117217734	A	G	0.3000400	-0.0223101	0.0037380	6.6E-10
11	PCSK7	rs236916	117218912	G	A	0.4627980	-0.0225828	0.0034346	4.0E-12
11	PCSK7	rs2239009	117219006	C	G	0.1043040	-0.0377086	0.0056016	1.9E-12
11	PCSK7	rs74830	117219842	C	T	0.3048020	-0.0219177	0.0037284	8.3E-10
11	PCSK7	rs35590772	117220535	TG	T	0.4654010	-0.0225367	0.0034369	4.2E-12
11	PCSK7	rs236918	117220893	G	C	0.5012350	-0.0232324	0.0034232	6.7E-13
11	PCSK7	rs7941150	117221105	A	G	0.0551179	0.0520770	0.0075114	1.7E-12
11	PCSK7	rs78628783	117221335	T	C	0.1043650	-0.0377950	0.0056013	1.7E-12
11	PCSK7	rs80351364	117221678	T	A	0.1046470	-0.0380915	0.0055937	1.1E-12
11	PCSK7	rs6589606	117222170	T	C	0.1043670	-0.0378018	0.0056014	1.7E-12
11	PCSK7	rs146871029	117225450	T	C	0.0112604	0.0873735	0.0161856	3.0E-08
11	PCSK7	chr11:117226836_T_TGGGA	117226836	TGGGAGCTG	T	0.4918890	0.0197546	0.0034431	9.8E-10
11	PCSK7	rs2306473	117227236	T	C	0.0596819	0.0458887	0.0072311	9.1E-11
11	PCSK7	rs111809212	117228821	C	T	0.0544422	0.0464655	0.0076204	3.6E-10
11	PCSK7	rs4938361	117229225	C	G	0.0574442	0.0469762	0.0074114	8.2E-11
11	PCSK7	rs4938362	117229313	A	G	0.0580421	0.0461875	0.0073745	1.4E-10
11	PCSK7	rs11542139	117229541	T	C	0.0432338	0.0497257	0.0085154	1.5E-09
11	RNF214	rs200694867	117244658	C	CTTTA	0.0256557	0.0688644	0.0108585	1.4E-10
11	RNF214	rs144580263	117253710	T	C	0.0481813	-0.0444512	0.0080220	3.5E-08
11	BACE1	rs3741288	117315499	T	C	0.0308751	-0.0585728	0.0099573	3.7E-09
11	CEP164	rs73014327	117325867	C	T	0.0327233	-0.0569493	0.0096795	5.0E-09
11	CEP164	rs11216357	117330037	G	T	0.0340845	-0.0549397	0.0094373	1.0E-08
11	CEP164	rs144584200	117332064	G	A	0.0306544	0.0694551	0.0100145	3.7E-12
11	CEP164	rs11216360	117342473	A	G	0.0354327	-0.0535833	0.0092567	1.2E-08
11	CEP164	rs10892095	117343177	G	A	0.0341773	-0.0526134	0.0094005	3.8E-08
11	CEP164	rs490262	117351876	A	G	0.1384900	0.0272704	0.0050120	4.9E-08
11	CEP164	rs11216364	117355903	T	C	0.0860919	0.0423233	0.0061933	3.9E-12
11	CEP164	rs12221818	117357803	G	A	0.0345561	-0.0534777	0.0093466	1.8E-08
11	CEP164	rs11606575	117366491	G	C	0.0349472	-0.0544732	0.0092951	8.2E-09
11	CEP164	rs2279013	117412375	T	C	0.4783570	-0.0192349	0.0034714	3.2E-08
11	CEP164 *	rs74523946	117420199	A	G	0.0334952	-0.0553606	0.0095021	9.8E-09
11	CEP164 *	rs11603208	117420247	T	G	0.0349203	-0.0538780	0.0093159	1.5E-08
11	DSCAML1 *	rs11216379	117421040	G	A	0.0553661	-0.0494638	0.0075950	1.8E-10
11	DSCAML1 *	rs11607141	117423306	G	T	0.0329422	-0.0596693	0.0096412	1.1E-09
11	DSCAML1 *	chr11:117423756_AAAAC_?	117423756	AAAAC	A	0.0111104	0.0964696	0.0164485	4.6E-09
11	DSCAML1 *	rs7115491	117424434	G	T	0.0316251	-0.0613931	0.0098718	8.3E-10
12	PTPN11	chr12:112469069_C_CA	112469069	CA	C	0.2873020	-0.0208702	0.0038170	3.0E-08
15	LIPC *	rs62001736	58381852	A	G	0.1865650	0.0237888	0.0044020	3.5E-08
15	LIPC *	rs4775041	58382496	C	G	0.1876360	0.0242970	0.0043867	1.6E-08
15	LIPC *	rs80123226	58383833	T	A	0.1904300	0.0234203	0.0043636	3.6E-08
15	LIPC *	rs11858759	58384622	A	G	0.1871680	0.0237582	0.0043927	3.2E-08
15	LIPC *	rs10468017	58386313	T	C	0.1810480	0.0244533	0.0044578	2.1E-08
15	LIPC *	rs7350789	58387469	A	G	0.3214800	0.0197582	0.0036666	4.0E-08
15	LIPC *	rs58719229	58387608	C	CAGA	0.3215070	0.0197059	0.0036679	4.3E-08
15	LIPC *	rs261291	58387979	C	T	0.4137710	0.0186139	0.0034791	2.9E-08
15	LIPC *	rs7177289	58387985	T	C	0.3216770	0.0197816	0.0036675	3.8E-08
15	LIPC *	rs35980001	58430391	GC	G	0.3417140	0.0241845	0.0036722	4.5E-12
15	LIPC *	rs1077835	58431227	G	A	0.3829370	0.0229778	0.0035407	1.0E-11
15	LIPC *	rs1077834	58431280	C	T	0.3829190	0.0230526	0.0035399	7.8E-12
15	LIPC *	rs1800588	58431476	T	C	0.3590240	0.0225131	0.0035827	9.1E-11
15	LIPC *	rs2070895	58431740	A	G	0.3815810	0.0229534	0.0035418	1.1E-11
15	LIPC	rs261334	58434545	G	C	0.3421010	0.0213063	0.0036087	3.5E-10
15	LIPC	rs71116564	58434769	C	TCCAAAGA	0.3442740	0.0211973	0.0036182	5.4E-10
15	TLE3 *	rs12593720	69868843	T	C	0.2390260	-0.0220534	0.0040439	8.9E-09
15	TLE3 *	rs10162636	69875502	T	G	0.2425890	-0.0224246	0.0040486	6.9E-09
15	TLE3 *	rs78943073	69876104	A	G	0.2394520	-0.0230637	0.0040571	2.4E-09
15	TLE3 *	rs78385799	69878325	A	G	0.2713440	-0.0220264	0.0039049	2.3E-09
15	TLE3 *	rs6494835	69879436	A	T	0.2722090	-0.0231742	0.0038849	3.6E-10
15	TLE3 *	rs8035009	69879649	G	C	0.2726210	-0.0233529	0.0038800	2.5E-10
15	TLE3 *	rs75327024	69880728	A	G	0.2404300	-0.0236575	0.0040467	1.0E-09
15	TLE3 *	rs7166273	69881625	C	T	0.2402550	-0.0238017	0.0040366	7.6E-10
15	TLE3 *	rs80287865	69889112	T	G	0.2304880	-0.0237985	0.0040806	1.1E-09
15	TLE3 *	rs77648222	69890512	G	A	0.2354910	-0.0249314	0.0040368	1.3E-10
15	TLE3 *	rs17756181	69891852	G	A	0.2449630	-0.0251947	0.0039795	6.7E-11
15	TLE3 *	rs28521935	69892800	C	A	0.2399600	-0.0241827	0.0040208	4.4E-10
15	TLE3 *	rs12591142	69897251	C	A	0.2311880	-0.0237066	0.0040711	1.1E-09

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
15	TLE3 *	rs80039904	69901814	T	C	0.2299420	-0.0230218	0.0041011	3.2E-09
15	TLE3 *	rs2601883	69903678	C	G	0.2379260	-0.0223981	0.0040669	8.0E-09
19	HAPLN4	rs150641967	19259531	T	CGACA	0.0596697	-0.0706090	0.0072636	1.8E-23
19	TM6SF2	rs58542926	19268740	T	C	0.0653262	-0.0717974	0.0069406	9.4E-27
19	SUGP1	rs8107974	19277691	T	A	0.0942816	-0.0429184	0.0058406	2.1E-14
19	SUGP1	rs200210321	19283081	AG	A	0.1008860	-0.0418766	0.0056861	3.6E-14
19	SUGP1	rs10401969	19296909	C	T	0.0945786	-0.0433141	0.0058335	1.2E-14
19	SUGP1	rs739846	19308262	A	G	0.0943939	-0.0429013	0.0058354	2.7E-14
19	SUGP1	rs57962361	19314216	T	C	0.1635380	-0.0274259	0.0046153	6.7E-10
19	SUGP1	rs11668104	19315372	A	G	0.1635380	-0.0274259	0.0046153	6.7E-10
19	MAU2	rs111234557	19325420	G	C	0.1632150	-0.0275968	0.0046205	5.6E-10
19	MAU2	rs11411903	19329255	TA	T	0.1664970	-0.0283891	0.0045835	1.6E-10
19	MAU2	rs58489806	19346108	T	C	0.1637960	-0.0281212	0.0046161	2.6E-10
19	MAU2	rs11672355	19351893	C	G	0.1616120	-0.0276075	0.0046625	7.5E-10
19	MAU2	rs2285626	19356736	T	C	0.1738840	-0.0297849	0.0045122	5.5E-12
19	MAU2	rs117970794	19357846	T	C	0.0894499	-0.0382564	0.0059782	3.6E-11
19	MAU2 *	rs56255430	19367068	C	A	0.0648308	-0.0535248	0.0069621	5.8E-15
19	GATAD2A *	rs59148799	19373199	G	A	0.1352590	-0.0279394	0.0050064	8.6E-09
19	GATAD2A *	rs12052117	19374296	T	C	0.1352430	-0.0282178	0.0050061	5.3E-09
19	GATAD2A	rs10408875	19392764	C	T	0.1355900	-0.0281054	0.0050015	5.7E-09
19	GATAD2A	rs56241616	19395283	T	C	0.1355900	-0.0281054	0.0050015	5.7E-09
19	GATAD2A	rs10408596	19401848	T	A	0.1355830	-0.0282161	0.0050016	5.1E-09
19	GATAD2A	rs34324111	19402759	G	T	0.1406520	-0.0286765	0.0049985	2.1E-09
19	GATAD2A	rs113460678	19402771	G	T	0.1283230	-0.0271587	0.0051290	4.5E-08
19	GATAD2A	rs188552254	19406360	G	A	0.1333680	-0.0274295	0.0050476	1.8E-08
19	GATAD2A	rs2965185	19414983	C	T	0.1599020	-0.0316800	0.0046741	3.0E-12
19	GATAD2A	rs11668386	19421101	G	A	0.1357390	-0.0278600	0.0049960	7.7E-09
19	GATAD2A	rs8182472	19429082	C	T	0.1358090	-0.0278899	0.0049944	7.2E-09
19	GATAD2A	rs79954596	19437834	G	T	0.1357430	-0.0278668	0.0049966	7.5E-09
19	GATAD2A	rs28720066	19461411	T	G	0.1350230	-0.0278990	0.0050111	7.9E-09
19	GATAD2A	rs73002956	19467934	G	A	0.0688838	-0.0502112	0.0067583	2.8E-14
19	GATAD2A	rs145702982	19468917	T	A	0.0652097	-0.0478821	0.0069263	1.6E-12
19	GATAD2A	rs73002960	19472183	T	C	0.1387970	-0.0269039	0.0049542	1.8E-08
19	GATAD2A	rs3794991	19499787	T	C	0.0719148	-0.0542665	0.0066205	4.3E-17
19	GATAD2A	rs57009615	19502813	G	A	0.1479740	-0.0323661	0.0048184	3.1E-12
19	GATAD2A *	rs56273306	19510195	C	T	0.1381880	-0.0282080	0.0049640	4.2E-09
19	GATAD2A *	rs113365218	19510388	A	G	0.1376000	-0.0280099	0.0049772	6.4E-09
19	YJEFN3	rs56397647	19531986	T	C	0.1358100	-0.0272988	0.0050056	1.6E-08
19	CILP2 *	rs16996148	19547663	T	G	0.0683870	-0.0571514	0.0067789	6.0E-18
19	CILP2 *	rs17216525	19551411	T	C	0.0743427	-0.0553672	0.0065176	4.4E-18
19	CILP2 *	rs17216588	19553268	T	C	0.0726135	-0.0479853	0.0066299	2.6E-13
19	PBX4 *	rs143988316	19556445	T	C	0.0748744	-0.0504527	0.0065258	4.9E-15
19	PBX4 *	rs78916915	19558399	A	G	0.0743686	-0.0462077	0.0065313	1.1E-12
19	PBX4 *	rs150824230	19559801	A	G	0.0733205	-0.0472724	0.0065776	3.6E-13
19	PBX4 *	rs73004926	19560457	T	C	0.0733205	-0.0472724	0.0065776	3.6E-13
19	PBX4	rs73004933	19564887	T	C	0.0728045	-0.0485524	0.0065935	9.8E-14
19	PBX4	rs141756246	19574661	GT	G	0.0692553	-0.0520190	0.0067913	1.7E-14
19	PBX4	rs73004951	19584419	T	C	0.0928173	-0.0467585	0.0059338	3.4E-15
19	PBX4	rs12608729	19589743	T	C	0.0903446	-0.0485848	0.0059904	6.2E-16
19	PBX4	rs73004959	19600330	T	C	0.0904066	-0.0477730	0.0059859	2.0E-15
19	PBX4	rs73004962	19602260	T	A	0.0827051	-0.0450954	0.0062209	3.9E-13
19	PBX4	rs73004966	19605749	T	C	0.0788040	-0.0509374	0.0063554	1.0E-15
19	PBX4	rs57504626	19609590	T	C	0.0823705	-0.0474247	0.0062334	2.5E-14
19	PBX4	rs16996185	19609979	G	T	0.0839507	-0.0466657	0.0061698	3.6E-14
19	PBX4	rs12610185	19610913	A	G	0.0838522	-0.0465575	0.0061734	4.0E-14
19	PBX4	rs12610191	19611167	T	C	0.0838609	-0.0465967	0.0061743	3.9E-14
19	PBX4	rs10500212	19612406	T	C	0.0841322	-0.0461774	0.0061707	5.7E-14
19	PBX4	rs58847337	19615213	A	G	0.0773381	-0.0527839	0.0064088	1.1E-16
19	PBX4	rs73004975	19616343	G	A	0.0956278	-0.0448530	0.0058318	1.1E-14
19	GMIP	rs2304128	19635342	T	G	0.0532516	-0.0515592	0.0076632	4.5E-12
19	PVRL2	rs12610605	44867581	G	A	0.4830560	0.0249068	0.0034316	3.0E-13
19	PVRL2	rs4803766	44867911	A	G	0.3694000	0.0194103	0.0035494	1.9E-08
19	PVRL2	rs34165484	44868428	A	AT	0.4835140	0.0240789	0.0034680	2.2E-12
19	PVRL2	rs200149544	44868448	T	TTTTTTC	0.4847510	0.0241376	0.0034704	2.0E-12
19	PVRL2	rs148251724	44872787	GTATTTAT	G	0.4649290	0.0255904	0.0034631	7.7E-14
19	PVRL2	rs412776	44876259	A	G	0.1299680	0.0297735	0.0051140	1.9E-09
19	PVRL2	rs3865427	44877704	A	C	0.1252640	0.0277230	0.0051969	3.6E-08
19	PVRL2	rs11668861	44877713	G	T	0.2074280	0.0361958	0.0042548	9.3E-18
19	PVRL2	rs6859	44878777	A	G	0.2979210	0.0258716	0.0037456	3.3E-12
19	PVRL2	rs406456	44879460	G	A	0.1041470	0.0342961	0.0056280	1.5E-09
19	PVRL2	rs3852860	44879709	C	T	0.2118570	0.0436299	0.0042252	3.2E-25
19	PVRL2	rs71352237	44879822	C	T	0.1179070	0.0342069	0.0053459	5.4E-11

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	BETA	SE	P
19	PVRL2	rs71171301	44879834	AC	A	0.1179070	0.0342069	0.0053459	5.4E-11
19	PVRL2	rs34224078	44879858	G	A	0.1179070	0.0342069	0.0053459	5.4E-11
19	PVRL2	rs35879138	44879882	A	A	0.1179110	0.0342336	0.0053455	5.3E-11
19	PVRL2	rs11083749	44880848	C	T	0.0906539	0.0428933	0.0060307	2.7E-12
19	PVRL2	rs406315	44880859	G	A	0.0846111	0.0413607	0.0062120	7.9E-11
19	PVRL2	rs34994196	44881075	GC	G	0.0899154	0.0427742	0.0060427	2.8E-12
19	PVRL2	rs142042446	44883210	GTAA	G	0.0842734	0.0567875	0.0061659	3.1E-21
19	PVRL2	rs283808	44883777	C	A	0.0853129	0.0525124	0.0061684	2.9E-18
19	PVRL2	rs283809	44883800	G	A	0.0858774	0.0536300	0.0061470	4.5E-19
19	PVRL2	rs12972156	44884202	G	C	0.0797905	0.0617752	0.0063438	1.3E-23
19	PVRL2	rs12972970	44884339	A	G	0.0798030	0.0617626	0.0063431	1.3E-23
19	PVRL2	rs34342646	44884873	A	G	0.0799354	0.0615151	0.0063337	1.8E-23
19	PVRL2	rs283810	44884984	G	T	0.0872584	0.0536984	0.0060941	2.2E-19
19	PVRL2	rs283811	44885243	G	A	0.1681880	0.0640255	0.0045905	1.9E-46
19	PVRL2	rs283813	44885917	A	T	0.0879572	0.0558190	0.0060498	3.7E-21
19	PVRL2	rs7254892	44886339	A	G	0.0614507	0.0715398	0.0071631	4.8E-24
19	PVRL2	rs283815	44887076	G	A	0.1728300	0.0618414	0.0045261	1.6E-44
19	PVRL2	rs6857	44888997	T	C	0.0821046	0.0613135	0.0062369	4.3E-24
19	TOMM40 *	rs71352238	44891079	C	T	0.0819545	0.0614906	0.0062444	4.0E-24
19	TOMM40	rs184017	44891712	G	T	0.1748560	0.0605595	0.0045122	4.7E-43
19	TOMM40	rs157580	44892009	A	G	0.4319970	0.0389185	0.0034551	3.1E-30
19	TOMM40	rs2075650	44892362	G	A	0.0824877	0.0601970	0.0062240	1.9E-23
19	TOMM40	rs34404554	44892652	G	C	0.0816905	0.0614081	0.0062496	4.9E-24
19	TOMM40	rs11556505	44892887	T	C	0.0816572	0.0619779	0.0062532	2.0E-24
19	TOMM40	rs157582	44892962	T	C	0.1730020	0.0635521	0.0045255	5.7E-47
19	TOMM40	rs157584	44893642	C	T	0.3150590	0.0267301	0.0036846	4.6E-13
19	TOMM40	rs1160983	44893972	A	G	0.0662415	0.0684000	0.0069314	3.3E-23
19	TOMM40	rs157585	44894255	C	A	0.3199930	0.0272804	0.0036748	9.9E-14
19	TOMM40	rs157588	44895007	T	C	0.3152510	0.0269534	0.0036830	2.3E-13
19	TOMM40	rs157590	44895459	C	A	0.3224080	0.0275239	0.0036568	3.6E-14
19	TOMM40	rs61679753	44897490	A	T	0.0741640	0.0774318	0.0065630	7.3E-33
19	TOMM40	rs111784051	44899005	G	T	0.0732155	0.0767887	0.0066051	6.3E-32
19	TOMM40	chr19:44899618_ATT_A	44899618	A	ATT	0.3138820	0.0253329	0.0036949	6.9E-12
19	TOMM40	rs1160985	44900155	T	C	0.3128490	0.0250474	0.0036929	1.1E-11
19	TOMM40	rs760136	44900601	G	A	0.3128800	0.0249988	0.0036930	1.2E-11
19	TOMM40	rs741780	44901174	C	T	0.3131650	0.0248726	0.0036930	1.4E-11
19	TOMM40	rs405697	44901434	G	A	0.3999670	0.0452077	0.0035080	2.8E-39
19	TOMM40	rs1038025	44901715	C	T	0.3124400	0.0251665	0.0036980	9.2E-12
19	TOMM40	rs1038026	44901805	G	A	0.3131250	0.0249317	0.0036932	1.3E-11
19	TOMM40	rs34215622	44903281	CG	C	0.2916720	0.0255281	0.0037728	1.4E-11
19	TOMM40	rs10119	44903416	A	G	0.0858784	0.0689448	0.0061416	3.4E-31
19	TOMM40 *	rs7259620	44904531	A	G	0.3114320	0.0250152	0.0036991	1.3E-11
19	APOE *	rs769446	44905371	C	T	0.0706252	0.0766274	0.0067680	8.6E-31
19	APOE *	rs405509	44905579	G	T	0.2964270	0.0335676	0.0037520	3.7E-19
19	APOE	rs440446	44905910	G	C	0.3881240	0.0518902	0.0035268	1.4E-50
19	APOE	rs769449	44906745	A	G	0.0754574	0.0707946	0.0064829	3.2E-29
19	APOE	rs429358	44908684	C	T	0.0852088	0.0726652	0.0061440	3.7E-34
19	APOE	rs7412	44908822	T	C	0.0728206	0.0796228	0.0066114	3.5E-34
19	APOE *	rs1065853	44909976	T	G	0.0727813	0.0793910	0.0066156	6.0E-34
19	APOE *	rs376097536	44909977	G	GGT	0.0848112	0.0668945	0.0062116	1.5E-28
19	APOE *	rs75627662	44910319	T	C	0.1668790	0.0709432	0.0046116	4.5E-55
19	APOE *	rs72654473	44911142	A	C	0.0761924	0.0769373	0.0064692	2.0E-33
19	APOE *	rs439401	44911194	C	T	0.4063060	0.0491576	0.0034919	5.1E-46
19	APOC1 *	rs445925	44912383	A	G	0.0831310	0.0787600	0.0062093	5.3E-38
19	APOC1 *	rs10414043	44912456	A	G	0.0895276	0.0585230	0.0059961	3.2E-23
19	APOC1 *	rs7256200	44912678	T	G	0.0897871	0.0589414	0.0059928	1.7E-23
19	APOC1 *	rs483082	44912921	T	G	0.1727910	0.0754332	0.0045351	5.5E-64
19	APOC1 *	rs584007	44913221	G	A	0.4052820	0.0491732	0.0034994	5.3E-46
19	APOC1 *	rs438811	44913484	T	C	0.1728180	0.0753213	0.0045359	8.4E-64
19	APOC1 *	rs390082	44913574	G	T	0.0828364	0.0784894	0.0062253	1.4E-37
19	APOC1 *	rs11568822	44914381	CTTCG	C	0.1674610	0.0732315	0.0045970	1.2E-58
19	APOC1	rs5117	44915533	C	T	0.1683040	0.0740985	0.0046028	8.4E-60
19	APOC1	rs3826688	44915704	C	T	0.4101150	0.0501215	0.0035084	1.9E-47
19	APOC1	rs73052335	44916825	C	A	0.0916432	0.0594697	0.0059872	3.8E-24
19	APOC1	rs12721046	44917997	A	G	0.0998648	0.0584475	0.0057236	1.7E-25
19	APOC1	rs484195	44918620	G	A	0.4050960	0.0489140	0.0035336	9.1E-45
19	APOC1	rs12721051	44918903	G	C	0.1005460	0.0579573	0.0056981	2.4E-25
19	APOC1 *	rs56131196	44919589	A	G	0.1007390	0.0578008	0.0056919	2.6E-25
19	APOC1 *	rs4420638	44919689	G	A	0.1008110	0.0579260	0.0056900	2.0E-25
19	APOC1 *	rs117569256	44920073	G	A	0.0344557	0.0798615	0.0094545	2.2E-17
19	APOC1 *	chr19:44920730_C_CA	44920730	CA	C	0.0866564	0.0597373	0.0061932	3.7E-22
19	APOC1 *	rs199769815	44921765	A	G	0.0230061	0.0820042	0.0115288	5.3E-13

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAf	BETA	SE	P
19	APOC1 *	rs190712692	44921921	A	G	0.0725798	0.0812875	0.0066573	6.3E-35
19	APOC1 *	rs141622900	44923535	A	G	0.0727712	0.0801727	0.0066305	3.3E-34
19	APOC1P1	rs114448690	44928196	A	G	0.2193790	0.0494802	0.0042288	4.0E-32
19	APOC1P1	rs113345881	44928379	G	A	0.2300170	0.0496837	0.0041453	1.1E-33
19	APOC1P1	rs112871012	44928640	A	G	0.2276640	0.0478499	0.0041544	2.8E-31
19	APOC1P1	rs111271293	44928832	C	T	0.2311170	0.0477667	0.0041076	6.7E-32
19	APOC1P1	chr19:44928869_AAAAAC_.	44928869	A	AAAAAC	0.2302320	0.0470912	0.0041132	4.6E-31
19	APOC1P1	rs7259350	44929021	C	T	0.2408610	0.0459526	0.0040107	5.0E-31
19	APOC1P1	rs7259004	44929300	C	G	0.2419640	0.0462808	0.0039970	1.1E-31
19	APOC1P1	chr19:44930070_T_TA	44930070	TA	T	0.2227130	0.0449149	0.0041849	1.2E-27
20	PLTP	rs148753678	45907567	C	CACA	0.0662768	0.0369698	0.0069547	3.7E-08

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error

Supplementary Table 20. Summary of sex-differentiated analysis for variants exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
1	SFPQ *	rs79395015	35,170,115	T	C	0.376865	0.011096	0.0021	2.90E-08	0.010257	0.003562	0.003993	0.010888	0.002635	3.64E-05	3.11E-06	0.886735	
1	SFPQ *	rs77686522	35,171,992	T	A	0.392116	0.011195	0.00207	1.20E-08	0.011944	0.003518	0.000689	0.010167	0.002594	8.97E-05	1.45E-06	0.684369	
1	SFPQ *	rs80099351	35,177,518	G	A	0.392388	0.011126	0.002067	1.60E-08	0.011265	0.003511	0.001342	0.010412	0.002591	5.90E-05	1.81E-06	0.844932	
1	SFPQ	rs3768339	35,184,401	C	T	0.390551	0.011028	0.002071	2.30E-08	0.011783	0.003518	0.000815	0.009999	0.002596	0.000119	2.20E-06	0.683175	
1	SFPQ	rs3738696	35,186,666	C	A	0.389461	0.011583	0.00207	4.10E-09	0.011952	0.003518	0.000684	0.010701	0.002594	3.74E-05	6.27E-07	0.774671	
1	SFPQ	rs12075530	35,188,306	T	C	0.389494	0.011564	0.00207	4.30E-09	0.011912	0.003519	0.000715	0.010688	0.002594	3.83E-05	6.68E-07	0.779407	
1	SFPQ *	rs12075169	35,193,419	G	C	0.410141	0.011518	0.002063	4.90E-09	0.012317	0.003504	0.000443	0.010447	0.002587	5.43E-05	5.96E-07	0.667774	
1	SFPQ *	rs77084091	35,194,249	T	C	0.408525	0.01097	0.002077	2.50E-08	0.01223	0.003531	0.000536	0.00966	0.002602	0.000207	2.52E-06	0.557889	
1	SFPQ *	rs77086052	35,197,007	G	A	0.410591	0.011373	0.00207	7.60E-09	0.012648	0.003516	0.000324	0.010072	0.002595	0.000105	8.29E-07	0.555465	
1	SFPQ *	rs12083658	35,198,902	A	C	0.413097	0.010941	0.00208	3.00E-08	0.012098	0.003532	0.000618	0.009836	0.002607	0.000163	2.30E-06	0.660404	
1	SFPQ *	rs80332318	35,199,001	G	A	0.404779	0.010837	0.002091	4.60E-08	0.012288	0.003548	0.000537	0.009461	0.002622	0.00031	3.70E-06	0.521733	
1	SFPQ *	rs11264116	35,200,158	T	C	0.396434	0.011143	0.002075	1.70E-08	0.011699	0.003527	0.000914	0.010278	0.0026	7.78E-05	1.65E-06	0.7458	
1	SFPQ *	rs12081295	35,200,520	A	G	0.396548	0.011151	0.002076	1.60E-08	0.011653	0.003528	0.000961	0.010313	0.002601	7.41E-05	1.65E-06	0.7599	
1	SFPQ *	rs7542630	35,202,061	C	T	0.408871	0.011057	0.002071	2.10E-08	0.011333	0.003518	0.001282	0.010443	0.002595	5.77E-05	1.70E-06	0.838651	
1	SFPQ *	rs35520620	35,207,155	T	C	0.498113	-0.1139	0.002059	8.70E-09	-0.012459	0.003495	0.000366	-0.010648	0.002581	3.74E-05	3.50E-07	0.676813	
1	SFPQ *	rs28673907	35,207,726	T	C	0.411009	0.011442	0.002081	7.20E-09	0.013266	0.003533	0.000175	0.009853	0.002608	0.00016	6.92E-07	0.436977	
1	SFPQ *	rs7512559	35,212,152	T	C	0.483345	-0.010723	0.002052	3.70E-08	-0.011662	0.003484	0.00082	-0.010217	0.002572	7.19E-05	1.38E-06	0.738531	
1	SFPQ *	rs7520747	35,212,538	G	T	0.483316	-0.010733	0.002052	3.60E-08	-0.01169	0.003484	0.000797	-0.010229	0.002572	7.05E-05	1.32E-06	0.735869	
1	SFPQ *	rs10752602	35,212,644	G	A	0.484273	-0.010825	0.002054	3.10E-08	-0.011856	0.00349	0.000685	-0.01027	0.002575	6.71E-05	1.09E-06	0.714558	
1	SFPQ *	rs10796919	35,213,148	T	C	0.394521	0.011304	0.002087	9.50E-09	0.012055	0.003543	0.000671	0.010296	0.002616	8.39E-05	1.33E-06	0.689617	
1	SFPQ *	rs60037734	35,213,586	T	G	0.488546	0.010729	0.002048	3.60E-08	0.011025	0.003482	0.001554	0.010537	0.002566	4.07E-05	1.46E-06	0.910142	
1	SFPQ *	rs58482098	35,213,593	G	T	0.39411	0.011273	0.002087	1.10E-08	0.011923	0.003543	0.000771	0.010334	0.002616	7.88E-05	1.42E-06	0.718387	
1	SFPQ *	rs12096175	35,215,884	C	T	0.413794	0.011439	0.00209	8.90E-09	0.012724	0.003546	0.000335	0.010126	0.002621	0.000113	9.17E-07	0.555703	
1	SFPQ *	rs12568606	35,216,695	A	C	0.412996	0.011635	0.002087	4.10E-09	0.0133	0.00354	0.000173	0.010186	0.002619	0.000101	4.46E-07	0.479508	
1	SFPQ *	rs72424909	35,218,456	G	A	0.415165	0.011469	0.002079	5.40E-09	0.013026	0.003528	0.000224	0.010025	0.002608	0.000122	6.78E-07	0.493961	
1	SFPQ *	rs58534131	35,220,920	T	C	0.394636	0.011368	0.002086	7.70E-09	0.011805	0.003543	0.000867	0.010434	0.002615	6.65E-05	1.35E-06	0.755564	
1	SFPQ *	rs78157661	35,221,488	C	T	0.394805	0.011441	0.002086	6.40E-09	0.01165	0.003543	0.001015	0.010627	0.002615	4.86E-05	1.16E-06	0.816456	
1	SFPQ *	rs11264122	35,224,074	A	G	0.41958	0.010746	0.002066	2.80E-08	0.010749	0.003506	0.002178	0.010258	0.00259	7.57E-05	3.58E-06	0.91044	
1	SFPQ *	rs75178217	35,226,309	A	G	0.421557	0.010797	0.002064	2.60E-08	0.010512	0.003502	0.002692	0.010488	0.002588	5.13E-05	3.00E-06	0.995655	
1	ZMYM4 *	rs72910977	35,233,068	A	G	0.45075	0.010574	0.002062	3.70E-08	0.010574	0.003499	0.002518	0.01006	0.002586	0.000101	5.37E-06	0.905968	
1	ZMYM4 *	rs72893303	35,233,650	T	C	0.45216	0.010638	0.002061	3.20E-08	0.010335	0.003496	0.003124	0.010312	0.002585	6.71E-05	4.44E-06	0.995648	
1	ZMYM4 *	rs77968776	35,235,523	G	A	0.442374	0.010757	0.002066	3.40E-08	0.011321	0.003503	0.001237	0.010072	0.002592	0.000103	2.84E-06	0.774429	
1	ZMYM4 *	rs74791659	35,236,875	G	A	0.442685	0.010874	0.002068	2.70E-08	0.011477	0.003507	0.00107	0.010136	0.002595	9.46E-05	2.29E-06	0.758621	
1	ZMYM4 *	rs59854554	35,237,683	G	A	0.442225	0.01092	0.002071	2.60E-08	0.011702	0.003512	0.000868	0.010064	0.002598	0.000108	2.14E-06	0.707701	
1	MACF1	rs61779308	39,472,585	T	C	0.145936	0.016507	0.002849	7.00E-09	0.018697	0.004832	0.00011	0.014624	0.003575	4.34E-05	1.30E-07	0.498031	
1	MACF1	rs61779309	39,474,827	C	T	0.144566	0.016324	0.002869	1.30E-08	0.017946	0.004866	0.000227	0.01466	0.003599	4.70E-05	2.58E-07	0.587144	
1	MACF1	rs61779313	39,478,577	C	T	0.147876	0.015559	0.002846	3.50E-08	0.014695	0.004837	0.002389	0.015135	0.003567	2.23E-05	1.22E-06	0.94148	
1	MACF1	rs61779314	39,482,667	T	C	0.148174	0.015513	0.002843	3.70E-08	0.014424	0.004829	0.002831	0.015156	0.003563	2.13E-05	1.36E-06	0.902839	
1	BMP8A	rs72663503	39,503,387	T	C	0.148374	0.015498	0.002835	3.90E-08	0.014596	0.004818	0.002458	0.01504	0.003553	2.33E-05	1.31E-06	0.940881	
1	BMP8A	rs61779331	39,505,256	A	C	0.148005	0.015488	0.002842	4.60E-08	0.014717	0.00483	0.00232	0.014967	0.003562	2.68E-05	1.41E-06	0.966651	
1	BMP8A, PPIEL	rs755249	39,529,402	T	C	0.136293	0.015755	0.002937	4.70E-08	0.014926	0.004991	0.002792	0.015521	0.00368	2.50E-05	1.57E-06	0.923575	
1	PPIEL	rs12141058	39,534,682	T	C	0.141249	0.016115	0.0029	2.50E-08	0.01592	0.004926	0.001236	0.015652	0.003634	1.68E-05	5.06E-07	0.965078	
1	PPIEL	rs72663520	39,537,738	T	C	0.123151	0.018009	0.003071	2.30E-09	0.017683	0.005209	0.000691	0.017866	0.003852	3.57E-06	6.70E-08	0.977454	
1	PPIEL	rs72663521	39,540,231	A	G	0.112513	0.017911	0.003187	1.00E-08	0.01905	0.005417	0.000439	0.016807	0.003993	2.59E-05	2.93E-07	0.738876	
1	PPIEL	rs61779359	39,544,563	C	T	0.112879	0.017426	0.003182	2.40E-08	0.018109	0.005406	0.000813	0.016615	0.003987	3.12E-05	6.21E-07	0.823977	
1	PPIEL	rs41270829	39,546,018	T	G	0.112822	0.017808	0.003181	1.20E-08	0.018856	0.005406	0.00049	0.016824	0.003986	2.46E-05	3.09E-07	0.762267	
1	PPIEL	rs61781362	39,546,558	T	C	0.11332	0.017539	0.003174	1.80E-08	0.018741	0.005394	0.000515	0.016482	0.003979	3.47E-05	4.48E-07	0.736055	
1	PPIEL	rs61781363	39,546,761	T	C	0.113184	0.017524	0.003175	1.90E-08	0.018672	0.005395	0.000541	0.016482	0.00398	3.49E-05	4.72E-07	0.743936	
1	PPIEL	rs4660808	39,552,837	T	C	0.11325	0.017539	0.003175	1.90E-08	0.018659	0.005395	0.000546	0.016532	0.003979	3.30E-05	4.51E-07	0.750926	
1	PPIEL	rs61781364	39,553,919	G	A	0.104384	0.018542	0.003315	1.00E-08	0.018223	0.005625	0.001202	0.01847	0.004158	9.04E-06	2.73E-07	0.971841	
1	PPIEL	rs1180333	39,554,832	T	C	0.114994	0.017155	0.003155	3.60E-08	0.020848	0.005373	0.000105	0.014793	0.00395	0.000182	4.85E-07	0.363884	
1	PPIEL	rs76207570	39,556,810	T	C	0.112065	0.017506	0.003192	2.20E-08	0.018016	0.005422	0.000895	0.016837	0.004001	2.60E-05	5.70E-07	0.861114	
1	PPIEL	rs17264866	39,557,105	G	C	0.113184	0.017524	0.003175	1.90E-08	0.018672	0.005395	0.000541	0.016482	0.00398	3.49E-05	4.72E-07	0.743936	
1	PABPC4	rs4660293	39,562,508	G	A	0.113566	0.017593	0.003171	1.40E-08	0.018791	0.005388	0.00049	0.016596	0.003974	3.00E-05	3.73E-07	0.742986	
1	PABPC4	rs58302493	39,568,233	A	G	0.110637	0.017509	0.003208	3.10E-08	0.018289	0.00545	0.000796	0.016528	0.004021	3.99E-05	7.68E-07	0.794859	
1	PABPC4	rs17513135	39,570,014	T	C	0.110803	0.017462	0.003206	3.30E-08	0.018231	0.005446	0.000819	0.0165	0.004019	4.07E-05	8.05E-07	0.798189	
1	PABPC4	rs3768																

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
1	PABPC4 *	rs11206387	39,587,326	A	G	0.118416	0.017041	0.003116	2.80E-08	0.017329	0.005306	0.001096	0.016487	0.003902	2.41E-05	6.40E-07	0.898259	
1	PABPC4 *	rs61781373	39,587,421	C	A	0.104168	0.017983	0.003321	3.50E-08	0.017947	0.00564	0.001468	0.017459	0.004163	2.77E-05	9.57E-07	0.94449	
1	PABPC4 *	rs2695324	39,587,969	A	G	0.118428	0.017123	0.003116	2.40E-08	0.017357	0.005306	0.001077	0.01659	0.003902	2.14E-05	5.63E-07	0.907244	
1	PABPC4 *	rs11206390	39,588,827	G	A	0.118428	0.01712	0.003116	2.40E-08	0.017353	0.005306	0.00108	0.016587	0.003902	2.15E-05	5.66E-07	0.907365	
1	PABPC4 *	rs2695319	39,591,028	C	G	0.117244	0.017477	0.003133	1.50E-08	0.017506	0.005335	0.001039	0.016969	0.003922	1.53E-05	3.95E-07	0.935246	
1	PABPC4 *	rs113825410	39,591,871	G	A	0.111155	0.017855	0.003201	1.40E-08	0.018079	0.005441	0.000896	0.017283	0.004012	1.67E-05	3.74E-07	0.906348	
1	PABPC4 *	rs76841360	39,594,353	A	G	0.111153	0.017844	0.003201	1.50E-08	0.018122	0.005441	0.000871	0.017237	0.004012	1.76E-05	3.83E-07	0.895822	
1	PABPC4 *	rs4660303	39,594,801	A	G	0.111148	0.017855	0.003202	1.40E-08	0.01815	0.005441	0.000855	0.01725	0.004012	1.74E-05	3.72E-07	0.894036	
1	PABPC4 *	rs12037222	39,599,289	A	G	0.108696	0.017491	0.00323	4.60E-08	0.018042	0.005484	0.001008	0.016623	0.004049	4.08E-05	9.77E-07	0.835186	
1	PABPC4 *	rs74504886	39,599,944	A	G	0.108118	0.018153	0.003237	1.50E-08	0.018754	0.005499	0.000653	0.017182	0.004058	2.32E-05	3.81E-07	0.818149	
1	HEYL *	rs3916164	39,604,267	A	G	0.108798	0.018042	0.003227	1.40E-08	0.018272	0.00548	0.000861	0.017194	0.004045	2.15E-05	4.59E-07	0.874159	
1	HEYL *	rs113879410	39,607,339	C	G	0.108149	0.017856	0.003237	2.30E-08	0.018474	0.005497	0.000781	0.016837	0.004058	3.37E-05	6.43E-07	0.810675	
1	HEYL *	rs61781377	39,609,786	T	C	0.111734	0.017882	0.003194	1.20E-08	0.017661	0.005428	0.001145	0.017427	0.004002	1.35E-05	3.84E-07	0.972237	
1	HEYL *	rs61781390	39,610,222	A	G	0.111784	0.017834	0.003192	1.40E-08	0.01775	0.005421	0.001065	0.017304	0.004002	1.55E-05	4.09E-07	0.94722	
1	HEYL *	rs61781391	39,611,865	A	G	0.111827	0.017732	0.003193	1.70E-08	0.017554	0.005423	0.001215	0.017238	0.004003	1.68E-05	5.00E-07	0.962583	
1	HEYL *	rs61781392	39,617,969	A	C	0.113111	0.017892	0.003178	1.00E-08	0.017254	0.005388	0.001369	0.01759	0.003988	1.04E-05	3.53E-07	0.959591	
1	HEYL *	rs61232586	39,620,685	T	G	0.112655	0.017867	0.003187	1.20E-08	0.017402	0.005413	0.001312	0.01749	0.003995	1.21E-05	3.92E-07	0.989600	
1	HEYL *	rs61781393	39,622,092	A	G	0.112032	0.017678	0.003195	1.80E-08	0.016269	0.005428	0.002736	0.017696	0.004005	1.01E-05	6.45E-07	0.832451	
1	HEYL *	rs17343290	39,622,371	A	G	0.112476	0.017872	0.003188	1.20E-08	0.017182	0.005415	0.001517	0.017546	0.003995	1.14E-05	4.22E-07	0.956812	
1	USP1 *	rs1334806	62,409,642	A	G	0.446147	0.012921	0.00206	1.50E-10	0.007572	0.003509	0.030931	0.015938	0.002579	6.57E-10	4.93E-10	0.054716	
1	USP1 *	rs72929768	62,416,932	T	C	0.449834	0.01373	0.002065	1.10E-11	0.007605	0.003518	0.030671	0.017084	0.002583	3.89E-11	3.08E-11	0.029906	F
1	USP1 *	rs12406266	62,426,154	A	G	0.336307	-0.018225	0.002133	2.40E-18	-0.015423	0.003639	2.28E-05	-0.020422	0.002668	2.04E-14	2.39E-17	0.267963	
1	USP1 *	rs13375306	62,426,411	A	G	0.32568	-0.017956	0.002157	1.30E-17	-0.015043	0.003678	4.37E-05	-0.020229	0.002698	6.81E-14	1.46E-16	0.255584	
1	USP1 *	rs584998	62,426,557	G	A	0.409825	-0.013849	0.00205	5.40E-12	-0.008619	0.0035	0.013825	-0.017298	0.002562	1.51E-11	6.07E-12	0.045436	F
1	USP1 *	rs11207965	62,427,445	A	C	0.336515	-0.018556	0.002129	4.30E-19	-0.015807	0.003633	1.37E-05	-0.020565	0.002663	1.18E-14	8.61E-18	0.29076	
1	USP1 *	rs12023351	62,427,860	T	C	0.40758	-0.01452	0.002049	4.90E-13	-0.009055	0.003499	0.009673	-0.017941	0.00256	2.53E-12	7.66E-13	0.040436	F
1	USP1 *	rs12045548	62,429,211	T	A	0.336589	-0.018473	0.002128	5.40E-19	-0.015598	0.003631	1.76E-05	-0.020587	0.002661	1.08E-14	9.96E-18	0.267799	
1	USP1 *	rs12025429	62,430,113	T	C	0.334186	-0.018936	0.002132	8.60E-20	-0.015691	0.003638	1.63E-05	-0.021194	0.002665	1.93E-15	1.70E-18	0.222382	
1	USP1 *	rs635897	62,430,748	C	A	0.407859	-0.01461	0.002047	3.30E-13	-0.00925	0.003496	0.008171	-0.018013	0.002557	1.96E-12	5.11E-13	0.043126	F
1	USP1 *	rs662723	62,432,105	G	A	0.40958	-0.014098	0.002045	1.90E-12	-0.008882	0.003494	0.011048	-0.017416	0.002555	9.61E-12	3.19E-12	0.048687	F
1	USP1 *	rs10493324	62,432,471	T	C	0.324072	-0.020402	0.00217	7.50E-22	-0.016694	0.003699	6.47E-06	-0.022985	0.002715	2.71E-17	1.04E-20	0.170331	
1	USP1 *	rs60500353	62,433,313	T	C	0.211408	-0.028577	0.002507	4.80E-32	-0.026234	0.004274	8.64E-10	-0.030687	0.003136	1.37E-22	1.05E-29	0.400913	
1	USP1 *	rs624698	62,435,140	G	A	0.260173	-0.030297	0.002303	6.60E-43	-0.030927	0.00392	3.15E-15	-0.030795	0.002884	1.39E-26	5.27E-39	0.978332	
1	USP1 *	rs624700	62,435,141	C	G	0.260173	-0.030297	0.002303	6.60E-43	-0.030927	0.00392	3.15E-15	-0.030795	0.002884	1.39E-26	5.27E-39	0.978332	
1	USP1 *	rs626787	62,435,572	G	C	0.259766	-0.030527	0.002295	1.20E-43	-0.031479	0.003908	8.31E-16	-0.030786	0.002872	8.96E-27	9.13E-40	0.886355	
1	USP1 *	rs631106	62,436,136	A	C	0.25962	-0.030431	0.002295	2.00E-43	-0.031407	0.003908	9.63E-16	-0.030703	0.002873	1.25E-26	1.47E-39	0.884583	
1	USP1	rs646179	62,437,203	G	A	0.382925	-0.022791	0.002079	3.90E-30	-0.022708	0.003537	1.41E-10	-0.023763	0.002604	7.64E-20	9.38E-28	0.810157	
1	USP1	rs9436221	62,437,688	C	T	0.254188	-0.030218	0.00231	3.10E-42	-0.031446	0.003933	1.35E-15	-0.030418	0.002891	7.74E-26	1.25E-38	0.833153	
1	USP1	rs9436222	62,437,692	G	C	0.254188	-0.030218	0.00231	3.10E-42	-0.031446	0.003933	1.35E-15	-0.030418	0.002892	7.74E-26	1.25E-38	0.833153	
1	USP1	rs9436223	62,437,876	T	C	0.254182	-0.030291	0.00231	1.90E-42	-0.031448	0.003932	1.32E-15	-0.030561	0.002892	4.48E-26	7.15E-39	0.855742	
1	USP1	rs12029068	62,438,624	T	C	0.254182	-0.030291	0.00231	1.90E-42	-0.031448	0.003932	1.32E-15	-0.030561	0.002892	4.48E-26	7.15E-39	0.855742	
1	USP1	rs9436661	62,438,904	G	T	0.254184	-0.030288	0.00231	1.90E-42	-0.031439	0.003932	1.35E-15	-0.030561	0.002892	4.48E-26	7.28E-39	0.857174	
1	USP1	rs11588261	62,439,265	A	G	0.254186	-0.030288	0.00231	1.90E-42	-0.031439	0.003932	1.35E-15	-0.030561	0.002892	4.47E-26	7.26E-39	0.857172	
1	USP1	rs10493322	62,440,222	T	C	0.212511	-0.033275	0.002456	1.00E-44	-0.034546	0.004188	1.68E-16	-0.033685	0.003071	5.88E-28	1.26E-41	0.868364	
1	USP1	rs187325430	62,440,427	T	C	0.051831	-0.026165	0.004556	8.50E-09	-0.025715	0.007805	0.00099	-0.027106	0.005685	1.89E-06	5.08E-08	0.88539	
1	USP1	rs638714	62,440,818	T	G	0.253764	-0.030448	0.002311	9.40E-43	-0.031652	0.003934	9.05E-16	-0.03068	0.002893	3.11E-26	3.41E-39	0.842133	
1	USP1	rs638305	62,440,866	T	G	0.253438	-0.030356	0.002308	1.40E-42	-0.031603	0.00393	9.36E-16	-0.030569	0.00289	4.10E-26	4.65E-39	0.832087	
1	USP1	rs637723	62,441,057	T	C	0.251645	-0.030884	0.002323	2.40E-43	-0.032289	0.003958	3.57E-16	-0.031104	0.002907	1.11E-26	4.89E-40	0.809358	
1	USP1	rs656297	62,441,924	G	A	0.254348	-0.030356	0.002308	1.40E-42	-0.031603	0.00393	9.36E-16	-0.030569	0.00289	4.10E-26	4.65E-39	0.832087	
1	USP1	rs642845	62,442,564	C	T	0.261748	-0.028901	0.002296	3.60E-39	-0.029827	0.003904	2.27E-14	-0.029192	0.002876	3.52E-24	8.93E-36	0.895742	
1	USP1	rs641540	62,442,867	G	A	0.254348	-0.030356	0.002308	1.40E-42	-0.031603	0.00393	9.36E-16	-0.030569	0.00289	4.10E-26	4.65E-39	0.832087	
1	USP1	rs598253	62,445,070	C	T	0.254332	-0.030369	0.002309	1.30E-42	-0.031585	0.003931	9.76E-16	-0.030595	0.00289	3.72E-26	4.40E-39	0.839217	
1	USP1	rs11207969	62,446,080	G	A	0.254332	-0.030369	0.002309	1.30E-42	-0.031585	0.003931	9.76E-16	-0.030595	0.00289	3.72E-26	4.40E-39	0.839217	
1	USP1	rs659656	62,446,449	G	C	0.254332	-0.030369	0.002309	1.30E-42	-0.031585	0.003931	9.76E-16	-0.030595	0.00289	3.72E-26	4.40E-39	0.839217	
1	USP1	rs150910573	62,447,199	G	A	0.023553	-0.038285	0.006659	1.80E-09	-0.036664	0.011465	0.001391	-0.041654	0.008287	5.09E-07	1.96E-08	0.724326	
1	USP1	rs10158897	62,447,248	T	C	0.212528	-0.033332	0.002456	9.40E-45	-0.034741	0.004188	1.14E-16	-0.033636	0.003072	7.36E-28	1.08E-41	0.831466	
1	USP1	rs783291	62,449,307	A	G	0.25435	-0.030373	0.										

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
1	DOCK7	rs1167996	62,462,126	T	G	0.251997	-0.030638	0.002317	4.70E-43	-0.031594	0.003944	1.20E-15	-0.031085	0.002902	9.61E-27	1.40E-39	0.917251	
1	DOCK7	rs998403	62,462,878	A	G	0.210694	-0.033659	0.002463	2.50E-45	-0.035275	0.004203	4.97E-17	-0.033937	0.00308	3.39E-28	2.20E-42	0.797398	
1	DOCK7	rs1177541	62,464,221	G	A	0.253005	-0.03066	0.002314	3.50E-43	-0.03212	0.00394	3.74E-16	-0.030807	0.002897	2.22E-26	1.02E-39	0.788335	
1	DOCK7	rs77083979	62,464,435	A	G	0.202337	-0.033182	0.002501	6.50E-43	-0.036228	0.004266	2.15E-17	-0.032702	0.003127	1.46E-25	3.94E-40	0.505128	
1	DOCK7	rs1207972	62,464,553	G	A	0.253023	-0.030644	0.002314	3.80E-43	-0.032106	0.00394	3.86E-16	-0.030788	0.002897	2.36E-26	1.12E-39	0.787542	
1	DOCK7	rs1167998	62,465,961	C	A	0.259674	-0.029711	0.002293	9.70E-42	-0.030858	0.00389	2.27E-15	-0.029844	0.002875	3.32E-25	8.86E-38	0.833855	
1	DOCK7	rs77907749	62,466,449	T	C	0.202368	-0.033068	0.0025	1.10E-42	-0.036186	0.004266	2.34E-17	-0.032553	0.003126	2.33E-25	6.83E-40	0.492252	
1	DOCK7	rs1168001	62,468,087	G	A	0.253041	-0.030581	0.002314	5.20E-43	-0.032147	0.00394	3.53E-16	-0.03067	0.002896	3.61E-26	1.56E-39	0.762664	
1	DOCK7	rs12124284	62,468,356	A	G	0.210957	-0.033691	0.002462	1.90E-45	-0.035564	0.004201	2.70E-17	-0.033826	0.003079	4.82E-28	1.70E-42	0.738563	
1	DOCK7	rs1168002	62,468,637	A	G	0.253915	-0.030757	0.002316	1.90E-43	-0.0322	0.003942	3.31E-16	-0.03094	0.002899	1.48E-26	6.06E-40	0.796728	
1	DOCK7	rs1168003	62,469,175	G	A	0.253041	-0.030581	0.002314	5.20E-43	-0.032147	0.00394	3.53E-16	-0.03067	0.002896	3.61E-26	1.56E-39	0.762664	
1	DOCK7	rs12043877	62,469,328	T	C	0.202369	-0.03308	0.0025	1.00E-42	-0.036277	0.004266	1.94E-17	-0.032522	0.003126	2.60E-25	6.33E-40	0.477752	
1	DOCK7	rs1007205	62,471,241	T	C	0.252975	-0.030578	0.002315	5.50E-43	-0.032124	0.003941	3.81E-16	-0.030712	0.002898	3.26E-26	1.52E-39	0.772801	
1	DOCK7	rs10889330	62,473,795	C	G	0.253039	-0.03057	0.002314	5.40E-43	-0.032139	0.00394	3.60E-16	-0.030666	0.002896	3.67E-26	1.62E-39	0.763196	
1	DOCK7	rs1979722	62,474,426	A	G	0.210736	-0.033562	0.002463	4.10E-45	-0.035304	0.004202	4.67E-17	-0.03377	0.00308	6.02E-28	3.66E-42	0.768487	
1	DOCK7	rs182487886	62,477,264	C	T	0.020717	-0.038907	0.007079	7.50E-09	-0.035834	0.012093	0.003055	-0.043458	0.008846	9.15E-07	7.12E-08	0.610862	
1	DOCK7	rs10889331	62,477,336	G	T	0.253039	-0.030558	0.002314	5.80E-43	-0.032125	0.00394	3.71E-16	-0.030662	0.002897	3.74E-26	1.70E-39	0.764837	
1	DOCK7	rs1168009	62,478,283	G	A	0.253249	-0.030567	0.002315	5.50E-43	-0.032096	0.003941	4.04E-16	-0.030654	0.002898	4.10E-26	2.03E-39	0.768202	
1	DOCK7	rs1168010	62,478,308	G	A	0.253322	-0.03053	0.002315	7.00E-43	-0.032059	0.003942	4.39E-16	-0.030605	0.002898	4.92E-26	2.64E-39	0.766312	
1	DOCK7	rs1183260	62,479,747	A	G	0.252796	-0.030489	0.002314	9.10E-43	-0.032046	0.003941	4.45E-16	-0.030606	0.002897	4.68E-26	2.54E-39	0.76854	
1	DOCK7	rs6587976	62,479,960	T	C	0.252796	-0.030489	0.002314	9.10E-43	-0.032046	0.003941	4.45E-16	-0.030606	0.002897	4.68E-26	2.54E-39	0.76854	
1	DOCK7	rs1305521	62,483,363	A	G	0.254021	-0.030485	0.002314	1.20E-42	-0.03167	0.003939	9.49E-16	-0.030829	0.002897	2.04E-26	2.35E-39	0.86335	
1	DOCK7	rs1207974	62,484,289	C	T	0.252752	-0.030524	0.002314	7.70E-43	-0.032036	0.003941	4.56E-16	-0.030665	0.002897	3.80E-26	2.12E-39	0.779149	
1	DOCK7	rs10889332	62,485,187	T	C	0.252708	-0.030576	0.002316	7.40E-43	-0.032085	0.003943	4.23E-16	-0.030692	0.0029	3.77E-26	1.95E-39	0.775881	
1	DOCK7	rs2489835	62,489,300	T	C	0.252698	-0.030582	0.002315	5.20E-43	-0.03205	0.003941	4.45E-16	-0.030742	0.002898	2.90E-26	1.58E-39	0.789269	
1	DOCK7	rs1690761	62,490,191	C	T	0.252689	-0.03053	0.002315	6.80E-43	-0.032034	0.003941	4.59E-16	-0.030664	0.002898	3.90E-26	2.19E-39	0.779501	
1	DOCK7	rs10889333	62,491,359	A	G	0.210685	-0.033686	0.002463	2.10E-45	-0.035507	0.004203	3.13E-17	-0.033838	0.00308	4.80E-28	1.97E-42	0.748739	
1	DOCK7	rs10889334	62,491,528	G	C	0.210675	-0.033684	0.002463	2.00E-45	-0.035473	0.004203	3.36E-17	-0.033855	0.00308	4.52E-28	1.95E-42	0.756144	
1	DOCK7	rs10789112	62,492,087	C	T	0.210679	-0.033701	0.002464	2.00E-45	-0.035499	0.004204	3.21E-17	-0.033885	0.003081	4.14E-28	1.74E-42	0.75684	
1	DOCK7	rs1183851	62,492,987	T	C	0.37824	-0.023056	0.002083	7.40E-31	-0.023341	0.003545	4.76E-11	-0.023816	0.002608	7.24E-20	3.06E-28	0.913898	
1	DOCK7	rs10889335	62,494,430	G	A	0.202695	-0.032492	0.002513	1.00E-40	-0.033604	0.004287	4.77E-15	-0.032709	0.003143	2.48E-25	1.38E-37	0.866303	
1	DOCK7	rs1168041	62,494,579	T	C	0.21749	-0.029252	0.002437	1.20E-35	-0.030217	0.004161	3.96E-13	-0.029645	0.003046	2.35E-22	9.55E-33	0.911561	
1	DOCK7	rs1168040	62,494,904	T	C	0.252588	-0.031099	0.002315	2.20E-44	-0.032613	0.003942	1.38E-16	-0.031281	0.002899	4.04E-27	7.05E-41	0.785594	
1	DOCK7	rs1168036	62,497,063	A	G	0.251242	-0.030796	0.002317	2.60E-43	-0.032519	0.003945	1.77E-16	-0.030838	0.002902	2.38E-26	5.23E-40	0.731429	
1	DOCK7	rs1002687	62,498,066	G	A	0.252803	-0.030615	0.002316	5.40E-43	-0.03219	0.003942	3.38E-16	-0.030728	0.0029	3.38E-26	1.40E-39	0.765161	
1	DOCK7	rs1168034	62,498,243	G	C	0.251423	-0.030834	0.002317	1.90E-43	-0.032677	0.003943	1.23E-16	-0.030807	0.002901	2.57E-26	7.02E-40	0.702487	
1	DOCK7	rs35529421	62,499,950	A	T	0.204911	-0.033955	0.002502	1.50E-44	-0.03575	0.004271	6.05E-17	-0.034242	0.003127	7.16E-28	5.61E-42	0.775694	
1	DOCK7	rs1168032	62,502,076	A	G	0.251234	-0.030859	0.002317	1.80E-43	-0.033088	0.003946	5.33E-17	-0.030628	0.002901	5.10E-26	3.41E-40	0.615497	
1	DOCK7	rs1168031	62,502,316	C	T	0.251423	-0.030834	0.002317	1.90E-43	-0.032677	0.003943	1.23E-16	-0.030807	0.002901	2.57E-26	3.93E-40	0.702487	
1	DOCK7	rs1168030	62,502,820	C	T	0.251563	-0.030895	0.002317	1.40E-43	-0.032798	0.003944	9.59E-17	-0.030804	0.002902	2.69E-26	3.24E-40	0.683822	
1	DOCK7	rs1168029	62,503,731	G	A	0.252371	-0.030533	0.002316	8.90E-43	-0.032661	0.003943	1.26E-16	-0.030412	0.0029	1.06E-25	1.64E-39	0.645863	
1	DOCK7	rs1168028	62,503,760	G	A	0.251421	-0.030829	0.002317	1.90E-43	-0.032677	0.003943	1.23E-16	-0.0308	0.002901	2.63E-26	4.03E-40	0.701472	
1	DOCK7	rs1168027	62,504,513	T	C	0.25124	-0.030792	0.002317	2.70E-43	-0.032519	0.003945	1.77E-16	-0.030831	0.002902	2.44E-26	5.35E-40	0.7304	
1	DOCK7	rs1168026	62,505,325	T	C	0.251421	-0.030829	0.002317	1.90E-43	-0.032677	0.003943	1.23E-16	-0.0308	0.002901	2.63E-26	4.03E-40	0.701472	
1	DOCK7	rs7527004	62,506,557	G	A	0.251473	-0.030824	0.002317	2.20E-43	-0.032676	0.003945	1.27E-16	-0.030786	0.002901	2.86E-26	4.51E-40	0.699508	
1	DOCK7	rs12027778	62,507,642	G	C	0.192586	-0.033649	0.002547	2.60E-42	-0.037744	0.004342	3.72E-18	-0.032734	0.003186	9.78E-25	4.60E-40	0.352251	
1	DOCK7	rs1184865	62,508,124	A	G	0.251417	-0.030831	0.002317	1.90E-43	-0.032694	0.003943	1.18E-16	-0.030792	0.002901	2.72E-26	4.01E-40	0.697602	
1	DOCK7	rs1168042	62,508,479	A	T	0.251236	-0.0308	0.002317	2.50E-43	-0.032562	0.003945	1.61E-16	-0.030819	0.002902	2.55E-26	5.12E-43	0.721943	
1	DOCK7	rs11207976	62,511,080	A	G	0.251234	-0.030794	0.002317	2.60E-43	-0.032562	0.003945	1.61E-16	-0.030808	0.002902	2.66E-26	5.33E-40	0.720277	
1	DOCK7	rs11207977	62,511,636	T	C	0.209683	-0.033711	0.002469	5.00E-45	-0.0358	0.004214	2.07E-17	-0.033775	0.003088	8.18E-28	2.22E-42	0.698319	
1	DOCK7	rs1781212	62,511,748	G	A	0.253481	-0.030311	0.002326	6.10E-42	-0.032344	0.003961	3.37E-16	-0.030135	0.002911	4.42E-25	1.80E-38	0.653268	
1	DOCK7	rs1168044	62,511,887	A	C	0.2545	-0.030474	0.002319	1.80E-42	-0.032804	0.003949	1.03E-16	-0.030249	0.002903	2.20E-25	2.78E-39	0.602067	
1	DOCK7	rs1690755	62,514,490	A	G	0.251509	-0.030841	0.002317	1.70E-43	-0.032738	0.003943	1.08E-16	-0.03077	0.0029	2.92E-26	3.94E-40	0.687652	
1	DOCK7	rs10889336	62,514,739	C	T	0.209613	-0.033943	0.002468	1.20E-45	-0.036093	0.004212	1.10E-17	-0.033976	0.003086	3.77E-28	5.52E-43	0.685083	
1	DOCK7	rs10889337	62,514,936	A	G	0.251417	-0.030831	0.002317	1.90E-43	-0.032694	0.003943	1.18E-16	-0.030792	0.002901	2.72E-26	4.01E-40	0.697602	
1	DOCK7	rs12090886	62,515,769	G	A	0.251417	-0.030831	0.002317	1.90E-43	-0.032694	0.003943	1.18E-16	-0.030792	0.002901	2.72E-26	4.01E-40	0.697602	
1	DOCK7	rs11207979	62,517,323	A	G	0.25124	-0.030757	0.00231										

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
1	DOCK7	rs1168017	62,536,880	A	G	0.251242	-0.03073	0.002317	3.70E-43	-0.032564	0.003945	1.60E-16	-0.030701	0.002901	3.90E-26	7.72E-40	0.70364	
1	DOCK7	rs76176236	62,538,722	C	T	0.121218	-0.029502	0.003094	3.50E-23	-0.038557	0.005267	2.58E-13	-0.025485	0.003873	4.85E-11	9.12E-22	0.045581	M
1	DOCK7	rs56115463	62,540,080	A	C	0.200015	-0.033345	0.002514	9.70E-43	-0.036866	0.004292	9.22E-18	-0.032562	0.003142	3.94E-25	4.58E-40	0.418369	
1	DOCK7	rs7548877	62,540,279	T	C	0.251258	-0.030709	0.002318	4.30E-43	-0.032563	0.003945	1.61E-16	-0.03067	0.002902	4.42E-26	6.89E-40	0.699215	
1	DOCK7	rs11207981	62,540,416	C	A	0.251467	-0.030827	0.002319	2.50E-43	-0.032684	0.003947	1.29E-16	-0.030796	0.002903	2.94E-26	4.71E-40	0.69997	
1	DOCK7	rs1168023	62,540,924	A	T	0.25126	-0.030704	0.002318	4.40E-43	-0.032563	0.003945	1.61E-16	-0.030664	0.002902	4.52E-26	9.02E-40	0.698323	
1	DOCK7	rs1781221	62,541,171	A	C	0.251295	-0.030705	0.002318	4.30E-43	-0.032561	0.003945	1.62E-16	-0.030659	0.002902	4.65E-26	9.35E-40	0.69774	
1	DOCK7	rs11207982	62,541,511	T	C	0.209307	-0.033833	0.002469	2.10E-45	-0.035976	0.004213	1.43E-17	-0.033877	0.003087	5.50E-28	1.04E-42	0.687842	
1	DOCK7	rs1184547	62,541,557	G	A	0.25126	-0.030704	0.002318	4.40E-43	-0.032563	0.003945	1.61E-16	-0.030664	0.002902	4.52E-26	9.02E-40	0.698323	
1	DOCK7	rs1168022	62,542,050	A	T	0.251253	-0.030711	0.002318	4.30E-43	-0.032583	0.003945	1.55E-16	-0.030669	0.002902	4.44E-26	8.52E-40	0.695994	
1	DOCK7	rs76755357	62,542,503	A	G	0.052743	-0.026124	0.004515	4.60E-09	-0.026373	0.007724	0.000643	-0.026678	0.005637	2.25E-06	4.03E-08	0.974551	
1	DOCK7	rs1168021	62,544,229	A	G	0.252147	-0.030476	0.002317	1.80E-42	-0.032186	0.003944	3.49E-16	-0.030575	0.0029	5.97E-26	2.55E-39	0.74218	
1	DOCK7	rs1168020	62,544,285	C	T	0.252352	-0.03048	0.002319	2.30E-42	-0.032401	0.003947	2.36E-16	-0.030431	0.002903	1.11E-25	3.22E-39	0.687724	
1	DOCK7	rs1179765	62,544,439	G	C	0.25126	-0.030725	0.002318	3.80E-43	-0.032628	0.003945	1.40E-16	-0.030669	0.002902	4.44E-26	7.72E-40	0.689144	
1	DOCK7	rs12074528	62,545,200	T	C	0.25126	-0.030725	0.002318	3.80E-43	-0.032628	0.003945	1.40E-16	-0.030669	0.002902	4.44E-26	7.72E-40	0.689144	
1	DOCK7	rs10889399	62,546,385	A	G	0.251494	-0.030768	0.002318	2.80E-43	-0.032664	0.003946	1.33E-16	-0.030749	0.002903	3.42E-26	5.64E-40	0.695858	
1	DOCK7	rs10889340	62,546,400	A	C	0.251374	-0.030732	0.002318	3.50E-43	-0.032639	0.003946	1.38E-16	-0.030673	0.002902	4.47E-26	7.67E-40	0.688133	
1	DOCK7	rs11207983	62,546,436	C	T	0.25126	-0.030725	0.002318	3.80E-43	-0.032628	0.003945	1.40E-16	-0.030669	0.002902	4.44E-26	7.72E-40	0.689144	
1	DOCK7	rs2029763	62,547,463	G	A	0.209307	-0.033857	0.002469	1.80E-45	-0.036054	0.004213	1.22E-17	-0.033884	0.003087	5.37E-28	8.68E-43	0.677868	
1	DOCK7	rs11207984	62,547,725	C	T	0.25126	-0.030725	0.002318	3.80E-43	-0.032628	0.003945	1.40E-16	-0.030669	0.002902	4.44E-26	7.72E-40	0.689144	
1	DOCK7	rs11207985	62,548,115	A	G	0.251308	-0.030711	0.002318	4.20E-43	-0.032498	0.003945	1.85E-16	-0.030728	0.002902	3.58E-26	8.18E-40	0.717761	
1	DOCK7	rs10789113	62,549,528	T	A	0.209325	-0.03386	0.002469	1.80E-45	-0.036066	0.004213	1.19E-17	-0.033883	0.003087	5.41E-28	8.55E-43	0.676016	
1	DOCK7	rs11207986	62,552,499	T	C	0.251275	-0.030732	0.002318	3.80E-43	-0.032662	0.003945	1.31E-16	-0.030667	0.002902	4.49E-26	7.31E-40	0.683769	
1	DOCK7	rs10889342	62,553,181	T	C	0.207182	-0.034033	0.002482	1.70E-45	-0.036315	0.004237	1.08E-17	-0.03399	0.003103	6.78E-28	9.65E-43	0.658075	
1	DOCK7	rs11207988	62,553,316	T	A	0.188948	-0.03182	0.002606	2.20E-36	-0.029809	0.004453	2.25E-11	-0.034081	0.003256	1.31E-25	3.01E-34	0.438735	
1	DOCK7	rs7519785	62,554,248	G	A	0.251299	-0.030689	0.002317	5.10E-43	-0.032566	0.003945	1.60E-16	-0.030641	0.002902	4.90E-26	9.72E-40	0.69429	
1	DOCK7	rs10159255	62,555,145	A	C	0.209355	-0.033821	0.002469	2.40E-45	-0.035993	0.004213	1.38E-17	-0.033848	0.003087	6.04E-28	1.10E-42	0.681271	
1	DOCK7	rs2131925	62,560,271	G	T	0.252434	-0.030614	0.002316	7.00E-43	-0.032797	0.003942	9.25E-17	-0.03038	0.002899	1.16E-25	1.32E-39	0.621354	
1	DOCK7	rs2131926	62,560,340	C	T	0.251466	-0.030761	0.002316	3.20E-43	-0.032745	0.003943	1.06E-16	-0.03065	0.0029	4.49E-26	5.92E-40	0.668747	
1	DOCK7	rs10889343	62,560,758	T	G	0.251466	-0.030761	0.002316	3.20E-43	-0.032745	0.003943	1.06E-16	-0.03065	0.0029	4.49E-26	5.92E-40	0.668747	
1	DOCK7	rs4329540	62,561,353	C	T	0.252096	-0.030593	0.002315	8.70E-43	-0.03231	0.003941	2.55E-16	-0.03066	0.002898	4.05E-26	1.27E-39	0.735844	
1	DOCK7	rs4915621	62,563,762	A	G	0.251415	-0.030767	0.002317	3.20E-43	-0.032861	0.003945	8.52E-17	-0.030618	0.0029	5.05E-26	5.36E-40	0.646887	
1	DOCK7	rs12025714	62,565,940	A	C	0.197041	-0.032605	0.002532	3.40E-40	-0.036355	0.004321	4.17E-17	-0.031622	0.003166	1.82E-23	9.13E-38	0.376893	
1	DOCK7	rs6693353	62,565,945	A	C	0.251404	-0.030794	0.002317	2.70E-43	-0.032841	0.003945	8.91E-17	-0.030674	0.0029	4.14E-26	4.61E-40	0.65813	
1	DOCK7	rs10889344	62,568,270	T	C	0.251403	-0.0308	0.002317	2.60E-43	-0.032841	0.003945	8.91E-17	-0.030683	0.0029	4.00E-26	4.45E-40	0.659519	
1	DOCK7	rs10789114	62,568,551	C	T	0.208125	-0.033851	0.002477	3.80E-45	-0.036402	0.004228	7.78E-18	-0.033679	0.003097	1.66E-27	1.70E-42	0.603522	
1	DOCK7	rs7555577	62,568,692	A	C	0.251261	-0.030747	0.002322	4.20E-43	-0.032223	0.003953	3.76E-16	-0.030877	0.002907	2.55E-26	1.18E-39	0.783758	
1	DOCK7	rs10789115	62,570,458	A	G	0.251397	-0.030809	0.002317	2.40E-43	-0.032864	0.003945	8.52E-17	-0.030688	0.0029	3.93E-26	4.19E-40	0.656827	
1	DOCK7	rs12735272	62,571,136	G	A	0.251397	-0.030809	0.002317	2.40E-43	-0.032864	0.003945	8.52E-17	-0.030688	0.0029	3.93E-26	4.19E-40	0.656827	
1	DOCK7	rs12116574	62,572,166	T	C	0.205699	-0.033309	0.002491	4.20E-43	-0.035866	0.004251	3.41E-17	-0.032994	0.003114	3.38E-26	1.46E-40	0.65719	
1	DOCK7	rs6696502	62,573,862	C	T	0.251392	-0.03083	0.002317	2.20E-43	-0.032921	0.003945	7.56E-17	-0.030688	0.0029	3.93E-26	3.72E-40	0.648359	
1	DOCK7	rs12038768	62,575,057	T	G	0.209509	-0.033889	0.002468	1.60E-45	-0.036251	0.004212	7.90E-18	-0.033806	0.003085	6.60E-28	6.93E-43	0.63951	
1	DOCK7	rs11207990	62,575,415	T	C	0.251386	-0.030839	0.002317	2.10E-43	-0.032921	0.003945	7.56E-17	-0.030697	0.0029	3.81E-26	3.60E-40	0.649712	
1	DOCK7	rs11207992	62,576,129	G	T	0.209509	-0.033889	0.002468	1.60E-45	-0.036251	0.004212	7.90E-18	-0.033806	0.003085	6.60E-28	6.93E-43	0.63951	
1	DOCK7	rs1472257	62,576,455	A	G	0.251381	-0.030837	0.002317	2.10E-43	-0.032921	0.003945	7.56E-17	-0.030697	0.0029	3.83E-26	3.63E-40	0.649613	
1	DOCK7	rs10789116	62,577,067	G	A	0.209509	-0.033889	0.002468	1.60E-45	-0.036251	0.004212	7.90E-18	-0.033806	0.003085	6.60E-28	6.93E-43	0.63951	
1	DOCK7	rs1748201	62,579,835	A	C	0.250203	-0.030956	0.002322	1.70E-43	-0.033179	0.003954	5.11E-17	-0.030717	0.002907	4.63E-26	2.98E-40	0.616052	
1	DOCK7	rs1748200	62,580,368	T	C	0.251559	-0.030849	0.002317	2.00E-43	-0.032804	0.003945	9.68E-17	-0.030773	0.0029	2.87E-26	3.48E-40	0.678322	
1	DOCK7	rs1629122	62,580,907	C	A	0.251656	-0.030746	0.002317	3.60E-43	-0.032802	0.003945	9.74E-17	-0.03061	0.002901	5.28E-26	6.41E-40	0.654424	
1	DOCK7	rs9436224	62,582,604	C	A	0.229541	-0.030208	0.002444	1.90E-37	-0.032505	0.004164	6.22E-15	-0.029746	0.003059	2.51E-22	1.71E-34	0.593374	
1	DOCK7	rs34465969	62,582,605	C	A	0.227121	-0.030087	0.002446	3.00E-37	-0.032676	0.004168	4.73E-15	-0.029496	0.00306	5.86E-22	3.02E-34	0.538676	
1	DOCK7	rs35194512	62,582,606	C	A	0.185915	-0.034011	0.002629	2.00E-40	-0.036343	0.004498	6.82E-16	-0.033789	0.003283	8.27E-25	6.69E-38	0.64645	
1	DOCK7	rs11207995	62,583,880	C	A	0.211869	-0.033735	0.002466	2.40E-45	-0.036187	0.004208	8.46E-18	-0.033586	0.003083	1.31E-27	1.46E-42	0.61809	
1	DOCK7	rs1748195	62,583,922	G	C	0.243851	-0.02975	0.002342	1.60E-39	-0.032229	0.004004	8.82E-16	-0.029319	0.002924	1.26E-23	1.29E-36	0.557246	
1	DOCK7	rs12042319	62,584,148	A	G	0.20949	-0.03392	0.002468	1.30E-45	-0.036114	0.004212	1.05E-17	-0.033947	0.003086	4.04E-28	5.66E-43	0.678138	
1	DOCK7	rs3850634	62,584,927	G	T	0.209567	-0.033793	0.002467	2.50E-45	-0.036102	0.004211	1.05E-17	-0.033755	0.003085	7.80E-28	1.09E-42	0.653028	
1	DOCK7	rs12030293	62,586,017	T	C	0.201082	-0.033329											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
1	DOCK7	rs10889350	62,619,595	T	C	0.2532	-0.030459	0.002313	1.30E-42	-0.032456	0.003936	1.73E-16	-0.030388	0.002897	1.04E-25	2.20E-39	0.672108	
1	DOCK7	rs12239736	62,620,326	A	T	0.208492	-0.033779	0.002478	4.00E-45	-0.036324	0.004228	9.12E-18	-0.033616	0.003098	2.15E-27	2.58E-42	0.605399	
1	DOCK7	rs12239737	62,620,330	A	T	0.153624	-0.032393	0.002846	1.70E-31	-0.034585	0.004849	1.03E-12	-0.032377	0.003561	1.04E-19	1.01E-29	0.713612	
1	DOCK7	rs6587980	62,625,187	T	C	0.251259	-0.030729	0.002319	3.40E-43	-0.032569	0.003946	1.62E-16	-0.030732	0.002903	3.73E-26	7.49E-40	0.707679	
1	DOCK7	rs11207998	62,625,800	C	G	0.200879	-0.033245	0.002507	1.10E-42	-0.036861	0.004278	7.34E-18	-0.032509	0.003135	3.63E-25	3.37E-40	0.411933	
1	DOCK7	rs10157265	62,627,946	T	C	0.252908	-0.030546	0.002312	7.60E-43	-0.0324	0.003935	1.91E-16	-0.030566	0.002896	5.18E-26	1.22E-39	0.707449	
1	DOCK7	rs11485618	62,628,536	G	A	0.209264	-0.033768	0.002469	3.30E-45	-0.036056	0.004213	1.22E-17	-0.033719	0.003088	9.84E-28	1.58E-42	0.654682	
1	DOCK7	rs10789118	62,629,021	G	A	0.209257	-0.033753	0.002469	3.50E-45	-0.036051	0.004214	1.24E-17	-0.033693	0.003087	1.08E-27	1.75E-42	0.651776	
1	DOCK7	rs7520810	62,630,040	T	C	0.252813	-0.030519	0.002313	8.30E-43	-0.032449	0.003936	1.76E-16	-0.030502	0.002897	6.81E-26	1.48E-39	0.690325	
1	DOCK7	rs12025800	62,631,110	G	C	0.252912	-0.030555	0.002313	7.20E-43	-0.0324	0.003935	1.91E-16	-0.030581	0.002896	4.92E-26	1.16E-39	0.709597	
1	DOCK7	rs10789119	62,632,564	A	G	0.209276	-0.033756	0.002469	3.40E-45	-0.03606	0.004214	1.21E-17	-0.033698	0.003087	1.06E-27	1.69E-42	0.651162	
1	DOCK7	rs11207999	62,632,970	C	A	0.252912	-0.030555	0.002313	7.20E-43	-0.0324	0.003935	1.91E-16	-0.030581	0.002896	4.92E-26	1.16E-39	0.709597	
1	DOCK7	rs10889352	62,633,352	C	T	0.209257	-0.033753	0.002469	3.50E-45	-0.036051	0.004214	1.24E-17	-0.033693	0.003087	1.08E-27	1.75E-42	0.651776	
1	DOCK7	rs2366638	62,633,906	A	G	0.252912	-0.030554	0.002313	7.30E-43	-0.032399	0.003935	1.92E-16	-0.030581	0.002896	4.92E-26	1.17E-39	0.709706	
1	DOCK7	rs10789120	62,635,452	A	G	0.208696	-0.033509	0.002473	1.60E-44	-0.036088	0.004422	1.27E-17	-0.033301	0.003092	5.06E-27	8.36E-42	0.59421	
1	DOCK7	rs1570694	62,637,546	G	A	0.209241	-0.033701	0.002469	4.70E-45	-0.036069	0.004214	1.19E-17	-0.033603	0.003087	1.49E-27	2.33E-42	0.636853	
1	DOCK7	rs6657050	62,639,582	G	A	0.252043	-0.030476	0.002317	1.40E-42	-0.032539	0.003943	1.63E-16	-0.030412	0.002901	1.10E-25	2.19E-39	0.663837	
1	DOCK7	rs12047226	62,639,867	C	T	0.209234	-0.033709	0.002469	4.40E-45	-0.036077	0.004214	1.17E-17	-0.033608	0.003087	1.46E-27	2.25E-42	0.63651	
1	DOCK7	rs7538689	62,640,577	A	G	0.385976	-0.022667	0.002068	5.40E-30	-0.023631	0.003516	1.87E-11	-0.023202	0.002592	3.68E-19	6.13E-28	0.921687	
1	DOCK7	rs7539035	62,641,096	A	G	0.252893	-0.030557	0.002313	6.80E-43	-0.032448	0.003935	1.73E-16	-0.030559	0.002896	5.34E-26	1.14E-39	0.699099	
1	DOCK7	rs995000	62,641,855	T	C	0.208334	-0.033423	0.002474	3.20E-44	-0.036257	0.004223	9.60E-18	-0.033066	0.003092	1.16E-26	1.45E-41	0.542112	
1	DOCK7	rs10789121	62,642,348	C	T	0.385878	-0.022777	0.002069	3.00E-30	-0.023841	0.003517	1.26E-11	-0.023254	0.002592	3.08E-19	3.48E-28	0.893154	
1	DOCK7	rs11208000	62,642,703	G	A	0.249548	-0.030866	0.002329	3.80E-43	-0.032956	0.003966	1.02E-16	-0.030631	0.002916	8.87E-26	1.12E-39	0.636748	
1	DOCK7	rs993013	62,645,398	G	T	0.254192	-0.030577	0.00231	5.20E-43	-0.032301	0.003931	2.19E-16	-0.030746	0.002893	2.42E-26	6.59E-40	0.750175	
1	DOCK7	rs1168085	62,646,649	C	G	0.252908	-0.030577	0.002313	6.30E-43	-0.032468	0.003935	1.65E-16	-0.030573	0.002896	5.07E-26	1.04E-39	0.698145	
1	DOCK7	rs1168086	62,646,718	A	G	0.252908	-0.030577	0.002313	6.30E-43	-0.032468	0.003935	1.65E-16	-0.030573	0.002896	5.07E-26	1.04E-39	0.698145	
1	DOCK7	rs746735	62,647,840	C	A	0.2532	-0.030473	0.002314	1.10E-42	-0.032567	0.003937	1.39E-16	-0.030348	0.002898	1.25E-25	2.14E-39	0.649966	
1	DOCK7	rs1168089	62,648,048	T	C	0.25184	-0.030232	0.002316	5.80E-42	-0.032593	0.003943	1.47E-16	-0.029956	0.002899	5.45E-25	9.71E-39	0.590004	
1	DOCK7	rs1168093	62,650,556	G	A	0.251877	-0.030279	0.002315	4.00E-42	-0.032496	0.003941	1.72E-16	-0.030046	0.002899	3.82E-25	8.02E-39	0.616513	
1	DOCK7	rs112957492	62,651,339	C	T	0.208197	-0.033484	0.002473	1.90E-44	-0.036237	0.004223	9.88E-18	-0.033115	0.003091	9.64E-27	1.24E-41	0.550745	
1	DOCK7	rs10889353	62,652,525	C	A	0.208908	-0.033255	0.002472	6.80E-44	-0.036027	0.004219	1.43E-17	-0.032859	0.00309	2.22E-26	4.04E-43	0.544634	
1	DOCK7	rs1168097	62,654,700	C	T	0.256311	-0.029851	0.00231	4.90E-41	-0.031347	0.003931	1.60E-15	-0.030121	0.002893	2.38E-25	4.51E-38	0.801599	
1	DOCK7	rs1168098	62,655,623	G	A	0.252816	-0.0307	0.002315	3.40E-43	-0.032487	0.003938	1.69E-16	-0.030715	0.002899	3.37E-26	7.06E-40	0.717167	
1	DOCK7	rs1168099	62,657,188	C	A	0.253144	-0.030577	0.002313	5.80E-43	-0.032542	0.003935	1.41E-16	-0.030547	0.002896	5.68E-26	9.94E-40	0.683028	
1	DOCK7	rs4495740	62,658,794	G	T	0.208222	-0.033508	0.002473	1.60E-44	-0.03636	0.004223	7.66E-18	-0.033093	0.003091	1.04E-26	1.03E-41	0.532452	
1	DOCK7	rs1168100	62,658,871	T	C	0.451796	-0.019479	0.002037	5.20E-23	-0.019339	0.003468	2.51E-08	-0.020308	0.002551	1.80E-15	3.06E-21	0.821797	
1	DOCK7	rs1168102	62,662,034	C	T	0.251886	-0.030294	0.002315	3.90E-42	-0.032533	0.003941	1.61E-16	-0.030058	0.002898	3.64E-25	7.14E-39	0.612948	
1	DOCK7	rs1168103	62,662,410	C	T	0.251982	-0.030241	0.002315	5.60E-42	-0.032435	0.003941	1.98E-16	-0.03003	0.002899	4.09E-25	9.82E-39	0.623027	
1	DOCK7	rs1168104	62,662,654	A	G	0.25188	-0.030275	0.002315	4.50E-42	-0.032533	0.003941	1.61E-16	-0.030031	0.002899	4.02E-25	7.89E-39	0.609127	
1	DOCK7	rs10889354	62,663,411	C	T	0.208282	-0.033575	0.002474	1.20E-44	-0.036276	0.004224	9.31E-18	-0.03324	0.003093	6.48E-27	7.87E-42	0.562034	
1	DOCK7	rs11208001	62,664,760	T	C	0.251171	-0.0298	0.002332	5.00E-40	-0.031765	0.00397	1.30E-15	-0.029607	0.002921	4.04E-24	6.08E-37	0.66156	
1	DOCK7	rs12024419	62,664,854	A	G	0.180849	-0.032287	0.002615	4.00E-37	-0.036865	0.00446	1.47E-16	-0.030904	0.00327	3.56E-21	5.86E-35	0.28108	
1	DOCK7	rs2479464	62,665,320	G	A	0.251893	-0.030184	0.002316	9.10E-42	-0.032503	0.003944	1.80E-16	-0.029932	0.0029	6.00E-25	5.59E-39	0.599529	
1	DOCK7	rs1168132	62,667,797	T	A	0.251856	-0.03019	0.002316	9.60E-42	-0.032306	0.003944	2.72E-16	-0.030029	0.0029	4.27E-25	1.40E-38	0.641816	
1	DOCK7	rs4587594	62,668,259	A	G	0.20821	-0.033428	0.002474	3.10E-44	-0.036098	0.004224	1.36E-17	-0.03312	0.003092	9.66E-27	1.69E-41	0.569526	
1	DOCK7	rs28399032	62,669,953	C	G	0.20816	-0.033521	0.002474	2.00E-44	-0.036067	0.004225	1.47E-17	-0.033266	0.003093	5.96E-27	1.14E-41	0.592675	
1	DOCK7	rs1168128	62,670,175	C	G	0.251922	-0.030326	0.002318	4.70E-42	-0.032504	0.003948	1.91E-16	-0.030113	0.002902	3.38E-25	7.87E-39	0.625626	
1	DOCK7	rs181835401	62,670,284	A	G	0.250533	-0.030297	0.002324	8.10E-42	-0.032307	0.003957	3.38E-16	-0.030255	0.00291	2.77E-25	1.13E-38	0.676247	
1	DOCK7	rs1168124	62,674,059	C	T	0.251723	-0.030347	0.002317	3.80E-42	-0.03238	0.003945	2.38E-16	-0.030216	0.002901	2.24E-25	6.47E-39	0.658613	
1	DOCK7	rs138271600	62,679,499	A	G	0.052311	-0.026413	0.004533	3.40E-09	-0.026696	0.007762	0.000587	-0.027077	0.005658	1.73E-06	2.87E-08	0.968304	
1	DOCK7	rs11208004	62,679,768	A	G	0.208465	-0.0332	0.002476	9.10E-44	-0.035756	0.004225	2.73E-17	-0.032944	0.003095	2.03E-26	7.06E-41	0.591243	
1	DOCK7	rs4459145	62,680,578	A	C	0.246719	-0.030015	0.002344	1.70E-40	-0.031371	0.003988	3.84E-15	-0.030334	0.002935	5.22E-25	2.33E-37	0.834095	
1	DOCK7	rs7531579	62,681,369	C	A	0.207963	-0.03363	0.002476	1.30E-44	-0.036004	0.004229	1.77E-17	-0.033486	0.003095	3.03E-27	6.96E-42	0.630883	
1	DOCK7	rs4344355	62,688,282	T	C	0.208133	-0.03378	0.002487	9.20E-45	-0.035961	0.004246	2.59E-17	-0.033821	0.00311	1.62E-27	5.44E-42	0.684352	
1	DOCK7 *	rs10889356	62,689,678	A	G	0.207614	-0.033615	0.002486	2.10E-44	-0.035666	0.004243	4.45E-17	-0.03381	0.003107	1.55E-27	8.89E-42	0.724155	
1	DOCK7 *	rs1168114	62,690,372	A	G	0.21611	-0.032565	0.002455	2.20E-42	-0.034704	0.004189	1.24E-16	-0.032563	0.00307	2.93E-26	4.54E-40	0.680105	
1	DOCK7 *	rs1168113	62,690,427	T	C	0.235798	-0.											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
1	DOCK7 *	rs6686331	62,716,464	C	T	0.226492	-0.030359	0.002409	3.00E-38	-0.031487	0.004106	1.82E-14	-0.030815	0.003013	1.61E-24	3.31E-36	0.895069	
1	DOCK7 *	rs6661669	62,720,298	T	C	0.226771	-0.030492	0.002408	1.50E-38	-0.031746	0.004106	1.12E-14	-0.030853	0.003013	1.40E-24	1.77E-36	0.860856	
1	DOCK7 *	rs76609868	62,720,544	C	A	0.183114	-0.033042	0.002611	4.30E-39	-0.038566	0.004462	5.80E-18	-0.031566	0.003263	4.12E-22	2.85E-37	0.205362	
1	DOCK7 *	rs12031537	62,722,415	A	C	0.183609	-0.033218	0.002603	1.50E-39	-0.038741	0.004448	3.20E-18	-0.031685	0.003252	2.12E-22	8.18E-38	0.200302	
1	DOCK7 *	rs7517372	62,723,893	G	A	0.212296	-0.029086	0.002469	6.90E-34	-0.032131	0.004207	2.31E-14	-0.02866	0.003091	1.91E-20	4.54E-32	0.506133	
1	DOCK7 *	rs4915624	62,725,847	G	A	0.215902	-0.029723	0.002448	1.30E-35	-0.032254	0.004176	1.18E-14	-0.02957	0.003062	4.83E-22	6.13E-34	0.604197	
1	DOCK7 *	rs76794398	62,725,894	A	G	0.183769	-0.032886	0.0026	6.10E-39	-0.038034	0.004443	1.18E-17	-0.031635	0.003249	2.22E-22	3.11E-37	0.244937	
1	DOCK7 *	rs4915853	62,725,906	C	A	0.224779	-0.030111	0.002412	1.60E-37	-0.031252	0.004112	3.11E-14	-0.030642	0.003018	3.47E-24	1.19E-35	0.904854	
1	DOCK7 *	rs12029452	62,727,599	C	A	0.183764	-0.032888	0.0026	5.90E-39	-0.038039	0.004443	1.17E-17	-0.031636	0.003249	2.21E-22	3.06E-37	0.244606	
1	DOCK7 *	rs12026283	62,728,242	A	T	0.183764	-0.032888	0.0026	5.90E-39	-0.038039	0.004443	1.17E-17	-0.031636	0.003249	2.21E-22	3.06E-37	0.244606	
1	DOCK7 *	rs2149116	62,728,301	G	A	0.37487	-0.021418	0.00211	2.60E-25	-0.020174	0.003592	2.01E-08	-0.023083	0.002642	2.54E-18	3.78E-24	0.514262	
1	DOCK7 *	rs12023282	62,728,306	A	G	0.183802	-0.032849	0.0026	7.00E-39	-0.037921	0.004443	1.48E-17	-0.031635	0.003249	2.22E-22	3.90E-37	0.253392	
1	DOCK7 *	rs6664692	62,729,989	C	T	0.212797	-0.029448	0.002462	1.10E-34	-0.032217	0.004201	1.82E-14	-0.029077	0.003079	3.85E-21	7.36E-33	0.54665	
1	DOCK7 *	rs11208009	62,730,021	C	T	0.221232	-0.030041	0.002428	6.10E-37	-0.031459	0.00414	3.13E-14	-0.030376	0.003077	1.57E-23	5.39E-35	0.832896	
1	DOCK7 *	rs10889364	62,731,143	T	C	0.183872	-0.032933	0.002599	4.40E-39	-0.038031	0.00444	1.15E-17	-0.031701	0.003248	1.76E-22	2.40E-37	0.249904	
1	DOCK7 *	rs12049254	62,731,481	C	G	0.183897	-0.03294	0.002599	4.20E-39	-0.038053	0.00444	1.09E-17	-0.031689	0.003247	1.81E-22	2.36E-37	0.247268	
1	DOCK7 *	rs76753312	62,733,237	C	G	0.18392	-0.032805	0.002597	6.20E-39	-0.037501	0.004437	3.00E-17	-0.031772	0.003246	1.34E-22	4.75E-37	0.297258	
1	DOCK7 *	rs4630152	62,733,601	C	T	0.213436	-0.029481	0.002456	6.20E-35	-0.031949	0.004192	2.64E-14	-0.029295	0.003071	1.51E-21	4.21E-33	0.609652	
1	DOCK7 *	rs61775961	62,733,677	G	T	0.222533	-0.030072	0.002433	7.60E-37	-0.030748	0.004154	1.40E-13	-0.030781	0.003041	4.78E-24	7.25E-35	0.994883	
1	DOCK7 *	rs61775962	62,733,679	A	G	0.222533	-0.030072	0.002433	7.60E-37	-0.030748	0.004154	1.40E-13	-0.030781	0.003041	4.78E-24	7.25E-35	0.994883	
1	DOCK7 *	rs6679002	62,734,265	G	T	0.222056	-0.030066	0.00242	3.10E-37	-0.031152	0.00413	4.81E-14	-0.030576	0.003026	5.75E-24	3.04E-35	0.91038	
1	DOCK7 *	rs12024044	62,734,645	A	G	0.184479	-0.032891	0.002593	4.50E-39	-0.037866	0.004431	1.34E-17	-0.031733	0.00324	1.29E-22	2.07E-37	0.263808	
1	DOCK7 *	rs12025111	62,735,769	A	G	0.184378	-0.032959	0.002594	3.20E-39	-0.037737	0.004432	1.77E-17	-0.031922	0.003241	7.41E-23	1.57E-37	0.289608	
1	DOCK7 *	rs12028944	62,735,867	A	T	0.184456	-0.032849	0.002594	5.50E-39	-0.037712	0.004431	1.82E-17	-0.031741	0.003241	1.27E-22	2.76E-37	0.276736	
1	ATG4C *	rs12121288	62,736,790	G	A	0.213017	-0.029563	0.002462	5.80E-35	-0.032101	0.004201	2.25E-14	-0.029337	0.003078	1.66E-21	3.94E-33	0.595658	
1	ATG4C *	rs72915166	62,736,922	A	G	0.212678	-0.029727	0.002466	2.90E-35	-0.032348	0.004207	1.55E-14	-0.029479	0.003083	1.23E-21	2.04E-33	0.582272	
1	ATG4C *	rs78731792	62,736,973	A	G	0.183802	-0.033001	0.002606	5.30E-39	-0.038339	0.004451	7.47E-18	-0.031714	0.003256	2.19E-22	1.96E-37	0.229629	
1	ATG4C *	rs10789123	62,737,950	T	A	0.209539	-0.029896	0.002509	2.40E-34	-0.032166	0.004285	6.36E-14	-0.029903	0.003136	1.59E-21	1.05E-32	0.760065	
1	ATG4C *	rs12027341	62,738,235	A	G	0.179391	-0.033157	0.002658	1.40E-37	-0.037482	0.004538	1.53E-16	-0.032477	0.003323	1.54E-22	2.74E-36	0.373503	
1	ATG4C *	rs78770744	62,738,693	C	T	0.181167	-0.03255	0.002653	1.90E-36	-0.036721	0.004529	5.44E-16	-0.032035	0.003317	4.82E-22	2.95E-35	0.403809	
1	ATG4C *	rs10889365	62,744,078	T	A	0.323051	-0.015892	0.002175	1.40E-14	-0.014673	0.003715	7.89E-05	-0.017345	0.002717	1.79E-10	5.81E-13	0.561529	
1	ATG4C *	rs12124310	62,745,143	G	A	0.472345	-0.014078	0.002055	9.50E-13	-0.012041	0.003492	0.000568	-0.016026	0.002575	4.97E-10	1.01E-11	0.358346	
1	ATG4C *	rs12108013	62,745,229	G	T	0.303204	-0.014919	0.002213	9.40E-13	-0.014466	0.003784	0.000133	-0.015818	0.002764	1.08E-08	5.19E-11	0.773012	
1	ATG4C *	rs10889366	62,746,055	C	T	0.303363	-0.014851	0.002212	1.10E-12	-0.014392	0.003782	0.000143	-0.015793	0.002763	1.11E-08	5.74E-11	0.764833	
1	ATG4C *	rs7517722	62,747,351	A	G	0.322981	-0.015801	0.002172	1.50E-14	-0.014755	0.003711	7.09E-05	-0.017261	0.002713	2.07E-10	6.04E-13	0.585721	
1	ATG4C *	rs7546804	62,749,346	C	T	0.303729	-0.014636	0.002207	2.00E-12	-0.014126	0.003775	0.000184	-0.015628	0.002755	1.45E-08	9.42E-11	0.748043	
1	ATG4C *	rs35245250	62,749,539	A	G	0.307233	-0.014672	0.002215	2.00E-12	-0.014465	0.00379	0.000136	-0.015451	0.002765	2.35E-08	1.13E-10	0.833588	
1	ATG4C *	rs61765877	62,749,542	T	C	0.307552	-0.01464	0.002213	2.20E-12	-0.014462	0.003787	0.000135	-0.01541	0.002763	2.52E-08	1.20E-10	0.839772	
1	ATG4C *	rs61765878	62,749,543	T	G	0.307565	-0.014546	0.002216	3.10E-12	-0.014428	0.003792	0.000143	-0.015274	0.002767	3.47E-08	1.74E-10	0.856983	
1	ATG4C *	rs2149115	62,749,703	A	G	0.323849	-0.015649	0.002167	2.30E-14	-0.014449	0.003703	9.62E-05	-0.017136	0.002707	2.52E-10	9.77E-13	0.558023	
1	ATG4C *	rs10789124	62,753,106	A	C	0.305256	-0.014429	0.002193	2.30E-12	-0.013598	0.003752	0.000292	-0.015548	0.002738	1.40E-08	1.40E-10	0.674639	
1	ATG4C *	rs10749734	62,754,277	G	A	0.325344	-0.015291	0.002155	4.80E-14	-0.013611	0.003683	0.000221	-0.016966	0.002692	3.02E-10	2.56E-12	0.462001	
1	ATG4C *	rs6663281	62,755,520	T	C	0.305289	-0.014451	0.002193	2.10E-12	-0.013598	0.003752	0.000292	-0.015586	0.002738	1.28E-08	1.29E-10	0.668613	
1	ATG4C *	rs6702274	62,756,495	C	A	0.325105	-0.015389	0.002155	3.30E-14	-0.013767	0.003683	0.000187	-0.017063	0.002692	2.39E-10	1.74E-12	0.469966	
1	ATG4C *	rs11208019	62,757,051	A	G	0.324993	-0.015402	0.002155	3.30E-14	-0.013963	0.003684	0.000151	-0.016992	0.002692	2.85E-10	1.69E-12	0.506775	
1	ATG4C *	rs12085904	62,758,431	T	C	0.305299	-0.01448	0.002193	1.90E-12	-0.013588	0.003752	0.000294	-0.015637	0.002738	1.15E-08	1.17E-10	0.659157	
1	ATG4C *	rs12567340	62,759,440	T	C	0.325123	-0.015416	0.002154	2.90E-14	-0.013763	0.003682	0.000187	-0.017109	0.002692	2.13E-10	1.56E-12	0.463245	
1	ATG4C *	rs6688416	62,759,580	A	C	0.325577	-0.015299	0.002156	4.60E-14	-0.013541	0.003685	0.00024	-0.017069	0.002693	2.39E-10	2.20E-12	0.439523	
1	ATG4C *	rs6688417	62,759,584	A	G	0.325123	-0.015416	0.002154	2.90E-14	-0.013763	0.003682	0.000187	-0.017109	0.002692	2.13E-10	1.56E-12	0.463245	
1	ATG4C *	rs11810184	62,759,727	A	G	0.470589	-0.013455	0.002049	6.60E-12	-0.011785	0.003488	0.000732	-0.015187	0.002566	3.34E-09	8.20E-11	0.432047	
1	ATG4C *	rs6664372	62,759,780	C	G	0.305434	-0.014398	0.002193	2.50E-12	-0.013451	0.003752	0.000339	-0.015584	0.002738	1.29E-08	1.50E-10	0.646079	
1	ATG4C *	rs11208021	62,759,863	T	C	0.325116	-0.015408	0.002154	3.00E-14	-0.013763	0.003682	0.000187	-0.017095	0.002691	2.20E-10	1.61E-12	0.465156	
1	ATG4C *	rs6664677	62,760,028	C	T	0.325116	-0.015408	0.002154	3.00E-14	-0.013763	0.003682	0.000187	-0.017095	0.002691	2.20E-10	1.61E-12	0.465156	
1	ATG4C *	rs11208023	62,760,152	C	T	0.325116	-0.015408	0.002154	3.00E-14	-0.013763	0.003682	0.000187	-0.017095	0.002691	2.20E-10	1.61E-12	0.465156	
1	ATG4C *	rs11208024	62,760,241	T	C	0.325422	-0.015464	0.002155	2.80E-14	-0.013804	0.003682	0.000179	-0.017016	0.002692	1.90E-10	1.33E-12	0.461908	
1	ATG4C *	rs10889371	62,760,321	T	C	0.305365	-0.014469	0.002193	1.90E-12	-0.013478	0.003752	0.00033	-0.015678	0.002738	1.05E-08	1.20E-10	0.635773	
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CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
1	ATG4C	rs10736399	62,798,112	T	C	0.301206	-0.01493	0.002202	6.30E-13	-0.014947	0.003765	7.28E-05	-0.015631	0.00275	1.34E-08	3.64E-11	0.883266	
1	ATG4C	rs11208032	62,799,494	G	C	0.32216	-0.015653	0.002162	1.90E-14	-0.014669	0.003693	7.21E-05	-0.017009	0.002701	3.14E-10	9.25E-13	0.609065	
1	ATG4C	rs6587990	62,806,788	T	A	0.323454	-0.015392	0.002156	4.20E-14	-0.014036	0.003682	0.000139	-0.016999	0.002694	2.90E-10	1.59E-12	0.516153	
1	ATG4C	rs12752360	62,808,188	C	G	0.323452	-0.015386	0.002156	4.30E-14	-0.014036	0.003682	0.000139	-0.016988	0.002694	2.97E-10	1.63E-12	0.517669	
1	ATG4C	rs11579518	62,808,587	G	A	0.323814	-0.015209	0.002156	8.40E-14	-0.013949	0.003682	0.000153	-0.016761	0.002695	5.16E-10	3.06E-12	0.537752	
1	ATG4C	rs11208035	62,808,867	T	C	0.322459	-0.015551	0.002157	2.10E-14	-0.014439	0.003685	9.00E-05	-0.016985	0.002696	3.05E-10	1.11E-12	0.577053	
1	ATG4C	rs6683832	62,811,233	G	A	0.301554	-0.014806	0.002197	7.80E-13	-0.014653	0.003756	9.67E-05	-0.015621	0.002744	1.28E-08	4.54E-11	0.835206	
1	ATG4C	rs6686232	62,811,426	C	T	0.322436	-0.015561	0.002157	2.10E-14	-0.014484	0.003685	8.56E-05	-0.016978	0.002696	3.10E-10	1.07E-12	0.584968	
1	ATG4C	rs12120847	62,812,209	G	A	0.322235	-0.015559	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016907	0.002697	3.76E-10	1.10E-12	0.620002	
1	ATG4C	rs10749735	62,812,321	A	G	0.322235	-0.015559	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016907	0.002697	3.76E-10	1.10E-12	0.620002	
1	ATG4C	rs11208036	62,812,347	G	A	0.322235	-0.015559	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016907	0.002697	3.76E-10	1.10E-12	0.620002	
1	ATG4C	rs6665932	62,813,093	A	G	0.322237	-0.015557	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016903	0.002697	3.80E-10	1.11E-12	0.620713	
1	ATG4C	rs6657235	62,813,424	T	C	0.322237	-0.015557	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016903	0.002697	3.80E-10	1.11E-12	0.620713	
1	ATG4C	rs6660873	62,814,582	T	A	0.322238	-0.015554	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016898	0.002697	3.84E-10	1.13E-12	0.621487	
1	ATG4C	rs6682286	62,815,748	G	A	0.322238	-0.015554	0.002158	2.20E-14	-0.014642	0.003687	7.22E-05	-0.016898	0.002697	3.84E-10	1.13E-12	0.621487	
1	ATG4C	rs7539616	62,817,334	C	T	0.477165	-0.013415	0.002021	5.50E-12	-0.012382	0.00344	0.000321	-0.014956	0.002531	3.53E-09	4.02E-11	0.546704	
1	ATG4C	rs12134455	62,817,783	A	G	0.322251	-0.015559	0.002158	2.20E-14	-0.014624	0.003687	7.36E-05	-0.016907	0.002697	3.75E-10	1.12E-12	0.617123	
1	ATG4C	rs11208037	62,817,845	A	G	0.322733	-0.015545	0.002159	2.30E-14	-0.014799	0.003687	6.02E-05	-0.016815	0.002698	4.76E-10	1.17E-12	0.659049	
1	ATG4C	rs11208038	62,817,875	A	G	0.322252	-0.015559	0.002158	2.20E-14	-0.014619	0.003687	7.40E-05	-0.016907	0.002697	3.75E-10	1.13E-12	0.616444	
1	ATG4C	rs2366820	62,818,249	C	T	0.322394	-0.01562	0.002159	1.80E-14	-0.014728	0.003688	6.57E-05	-0.016925	0.002698	3.63E-10	9.74E-13	0.630613	
1	ATG4C	rs2366821	62,818,466	G	C	0.323067	-0.015512	0.002159	1.90E-14	-0.014759	0.003688	6.34E-05	-0.016734	0.002699	5.79E-10	1.49E-12	0.665671	
1	ATG4C	rs7528963	62,820,576	G	A	0.497097	0.014733	0.002042	3.30E-14	0.013895	0.003471	6.31E-05	0.015917	0.00256	5.17E-10	1.33E-12	0.639183	
1	ATG4C	rs11208040	62,821,867	T	A	0.322204	-0.015609	0.002159	1.80E-14	-0.014634	0.003687	7.30E-05	-0.016981	0.002698	3.18E-10	9.45E-13	0.607422	
1	ATG4C	rs7519205	62,824,457	G	A	0.332393	-0.014839	0.002142	3.50E-13	-0.013092	0.003662	0.000352	-0.016607	0.002676	5.61E-10	7.27E-12	0.438307	
1	ATG4C	rs6664673	62,824,892	G	C	0.30202	-0.014801	0.002196	8.50E-13	-0.01469	0.003755	9.22E-05	-0.015568	0.002743	1.43E-08	4.83E-11	0.850259	
1	ATG4C	rs6587991	62,825,003	C	A	0.32288	-0.015541	0.002157	2.50E-14	-0.014473	0.003684	8.61E-05	-0.01693	0.002695	3.47E-10	1.21E-12	0.590425	
1	ATG4C	rs7414021	62,826,201	A	G	0.302258	-0.014768	0.002199	1.10E-12	-0.014545	0.003759	0.00011	-0.015656	0.002748	1.24E-08	4.99E-11	0.81135	
1	ATG4C	rs10159426	62,827,199	C	G	0.30945	-0.014498	0.002185	2.50E-12	-0.013894	0.003738	0.000203	-0.015537	0.002728	1.26E-08	9.03E-11	0.722481	
1	ATG4C	rs10789129	62,827,786	T	C	0.300741	-0.01448	0.0022	3.20E-12	-0.014076	0.00376	0.000183	-0.015355	0.002749	2.40E-08	1.53E-10	0.783636	
1	ATG4C	rs7512374	62,828,034	C	T	0.321914	-0.015295	0.002159	7.10E-14	-0.014011	0.003686	0.000145	-0.016796	0.002699	5.00E-10	2.83E-12	0.542176	
1	ATG4C	rs7512529	62,828,075	G	A	0.321491	-0.015236	0.002161	9.20E-14	-0.013902	0.00369	0.000166	-0.016746	0.002701	5.83E-10	3.72E-12	0.533994	
1	ATG4C	rs7524508	62,828,183	T	A	0.321906	-0.015286	0.002159	7.30E-14	-0.013972	0.003686	0.000152	-0.016801	0.002699	4.93E-10	2.90E-12	0.53571	
1	ATG4C	rs6663165	62,829,519	C	T	0.310974	-0.013819	0.002181	2.40E-11	-0.012969	0.003731	0.000512	-0.015016	0.002723	3.60E-08	5.95E-10	0.657787	
1	ATG4C	rs6687943	62,830,098	A	T	0.310598	-0.013772	0.002181	2.90E-11	-0.012758	0.003731	0.000631	-0.015023	0.002723	3.53E-08	7.10E-10	0.623792	
1	ATG4C	rs6679582	62,830,600	T	C	0.310527	-0.013751	0.00218	3.10E-11	-0.012692	0.00373	0.000671	-0.015037	0.002723	3.42E-08	7.29E-10	0.611612	
1	ATG4C	rs10889383	62,831,090	C	T	0.310492	-0.013789	0.002181	2.70E-11	-0.012779	0.003731	0.000618	-0.015037	0.002723	3.42E-08	6.75E-10	0.62499	
1	ATG4C	rs11587081	62,831,444	A	G	0.331406	-0.014541	0.002144	1.10E-12	-0.012533	0.003664	0.000629	-0.016442	0.002679	8.63E-10	1.90E-11	0.389013	
1	ATG4C	rs2366822	62,831,549	G	T	0.310528	-0.01375	0.00218	3.10E-11	-0.012692	0.00373	0.000671	-0.015035	0.002723	3.43E-08	7.31E-10	0.611915	
1	ATG4C	rs7527905	62,832,439	G	A	0.331403	-0.01456	0.002144	1.00E-12	-0.012563	0.003664	0.00061	-0.016456	0.002679	8.34E-10	1.79E-11	0.39095	
1	ATG4C	rs10889384	62,835,981	G	A	0.310544	-0.01378	0.00218	2.80E-11	-0.01272	0.00373	0.000653	-0.015069	0.002723	3.19E-08	6.65E-10	0.610964	
1	ATG4C	rs10889385	62,836,344	T	A	0.331433	-0.014537	0.002144	1.10E-12	-0.012511	0.003663	0.000641	-0.016462	0.002679	8.20E-10	1.84E-11	0.383975	
1	ATG4C	rs11208043	62,836,820	C	T	0.33257	-0.014371	0.002146	1.90E-12	-0.01234	0.003667	0.000769	-0.016282	0.002681	1.29E-09	3.40E-11	0.38552	
1	ATG4C	rs2886770	62,837,115	A	G	0.301073	-0.014528	0.002199	2.40E-12	-0.014176	0.003758	0.000163	-0.015439	0.002747	1.95E-08	1.12E-10	0.786148	
1	ATG4C	rs2886771	62,837,769	A	G	0.321945	-0.015259	0.002159	7.70E-14	-0.013909	0.003686	0.000162	-0.016811	0.002698	4.80E-10	3.01E-12	0.525199	
1	ATG4C	rs12567999	62,837,928	T	C	0.321945	-0.015259	0.002159	7.70E-14	-0.013909	0.003686	0.000162	-0.016811	0.002698	4.80E-10	3.01E-12	0.525199	
1	ATG4C	rs10493327	62,838,174	C	T	0.321945	-0.015259	0.002159	7.70E-14	-0.013909	0.003686	0.000162	-0.016811	0.002698	4.80E-10	3.01E-12	0.525199	
1	ATG4C	rs10889386	62,839,848	C	G	0.301073	-0.014528	0.002199	2.40E-12	-0.014176	0.003758	0.000163	-0.015439	0.002747	1.95E-08	1.12E-10	0.786148	
1	ATG4C	rs6695607	62,840,561	T	G	0.321945	-0.015259	0.002159	7.70E-14	-0.013909	0.003686	0.000162	-0.016811	0.002698	4.80E-10	3.01E-12	0.525199	
1	ATG4C	rs6683423	62,840,983	G	A	0.310557	-0.013749	0.00218	3.10E-11	-0.012689	0.003729	0.000672	-0.015048	0.002722	3.32E-08	7.09E-10	0.609369	
1	ATG4C	rs12743698	62,841,289	C	T	0.331431	-0.014533	0.002144	1.10E-12	-0.012511	0.003663	0.000641	-0.016454	0.002679	8.34E-10	1.87E-11	0.384889	
1	ATG4C	rs3737892	62,841,632	A	G	0.331431	-0.014533	0.002144	1.10E-12	-0.012511	0.003663	0.000641	-0.016454	0.002679	8.34E-10	1.87E-11	0.384889	
1	ATG4C	rs3737893	62,841,713	T	C	0.321941	-0.015257	0.002159	7.80E-14	-0.013909	0.003686	0.000162	-0.016809	0.002698	4.83E-10	3.03E-12	0.525517	
1	ATG4C	rs6665455	62,842,772	A	G	0.301075	-0.014527	0.002199	2.40E-12	-0.014172	0.003758	0.000164	-0.015439	0.002747	1.95E-08	1.12E-10	0.785455	
1	ATG4C	rs4448455	62,843,657	G	A	0.331433	-0.014532	0.002144	1.10E-12	-0.012507	0.003663	0.000644	-0.016454	0.002679	8.34E-10	1.88E-11	0.384362	
1	ATG4C	rs11208045	62,844,194	A	G	0.321947	-0.015258	0.002159	7.80E-14	-0.013905	0.003686	0.000163	-0.016811	0.002698	4.80E-10	3.03E-12	0.524602	
1	ATG4C	rs11208046	62,844,526	C	T	0.321947	-0.015258	0.002159	7.80E-14	-0.013905	0.003686	0.000163	-0.016811	0.002698	4.80E-10	3.03E-12	0.524602	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
1	ATG4C	rs1333736	62,861,764	T	A	0.32196	-0.015302	0.002158	7.10E-14	-0.013969	0.003684	0.000151	-0.01685	0.002697	4.27E-10	2.51E-12	0.528127	
1	ATG4C	rs6670694	62,862,187	G	A	0.32196	-0.015302	0.002158	7.10E-14	-0.013969	0.003684	0.000151	-0.01685	0.002697	4.27E-10	2.51E-12	0.528127	
1	ATG4C	rs6683732	62,862,408	T	C	0.321992	-0.015287	0.002158	7.40E-14	-0.014008	0.003685	0.000145	-0.016801	0.002697	4.81E-10	2.71E-12	0.540735	
1	ATG4C	rs7540205	62,863,117	T	C	0.322433	-0.015368	0.002158	5.30E-14	-0.014233	0.003686	0.000114	-0.016827	0.002697	4.55E-10	2.04E-12	0.570015	
1	ATG4C	rs1360677	62,863,273	T	C	0.301302	-0.014447	0.002198	3.30E-12	-0.013962	0.003758	0.000204	-0.01544	0.002745	1.90E-08	1.35E-10	0.750785	
1	ATG4C	rs1360678	62,863,380	T	C	0.321993	-0.015282	0.002158	7.60E-14	-0.01398	0.003685	0.000149	-0.016814	0.002697	4.67E-10	2.71E-12	0.534885	
1	ATG4C	rs7531329	62,863,788	G	A	0.301294	-0.0145	0.002197	2.90E-12	-0.014042	0.003756	0.000187	-0.015466	0.002745	1.79E-08	1.18E-10	0.759519	
1	ATG4C	rs3211074	62,864,546	G	A	0.331482	-0.014577	0.002143	9.90E-13	-0.01256	0.003662	0.000609	-0.0165	0.002677	7.33E-10	1.57E-11	0.385021	
1	ATG4C *	rs17097064	62,865,621	T	G	0.331482	-0.014577	0.002143	9.90E-13	-0.01256	0.003662	0.000609	-0.0165	0.002677	7.33E-10	1.57E-11	0.385021	
1	ATG4C *	rs1413242	62,866,193	C	T	0.310622	-0.013751	0.002139	3.30E-11	-0.012591	0.003729	0.000738	-0.015102	0.002721	2.91E-08	6.82E-10	0.586384	
1	ATG4C *	rs998096	62,866,234	A	C	0.331412	-0.014566	0.002143	1.00E-12	-0.012576	0.003664	0.000601	-0.016491	0.002677	7.53E-10	1.60E-11	0.388263	
1	ATG4C *	rs12128286	62,866,524	A	C	0.331476	-0.014557	0.002143	1.10E-12	-0.012565	0.003662	0.000605	-0.016468	0.002677	7.92E-10	1.69E-11	0.389595	
1	ATG4C *	rs1931079	62,866,953	G	A	0.33149	-0.014568	0.002143	1.00E-12	-0.012582	0.003662	0.000595	-0.016474	0.002677	7.81E-10	1.64E-11	0.39094	
1	ATG4C *	rs2803245	62,867,539	C	T	0.290972	-0.014237	0.002225	1.40E-11	-0.014663	0.003815	0.000122	-0.014967	0.002776	7.13E-08	3.01E-10	0.94852	
1	ATG4C *	rs11803404	62,867,652	T	C	0.331576	-0.014601	0.002143	8.90E-13	-0.012653	0.003663	0.000555	-0.016492	0.002677	7.51E-10	1.48E-11	0.397354	
1	ATG4C *	rs1333730	62,868,437	G	A	0.331517	-0.014612	0.002143	8.90E-13	-0.012637	0.003662	0.000562	-0.016511	0.002677	7.14E-10	1.43E-11	0.393042	
1	ATG4C *	rs11208049	62,868,614	G	A	0.331579	-0.014535	0.002143	1.20E-12	-0.012592	0.003662	0.000588	-0.01643	0.002677	8.60E-10	1.78E-11	0.397549	
1	ATG4C *	rs7553110	62,869,374	A	G	0.322027	-0.015336	0.002158	6.50E-14	-0.01406	0.003685	0.000137	-0.016841	0.002697	4.38E-10	2.35E-12	0.542533	
1	ATG4C *	rs7555606	62,869,525	A	G	0.322236	-0.015405	0.002158	5.00E-14	-0.014037	0.003685	0.00014	-0.016951	0.002697	3.36E-10	1.86E-12	0.523383	
1	ATG4C *	rs11584363	62,870,392	A	G	0.322027	-0.015336	0.002158	6.50E-14	-0.01406	0.003685	0.000137	-0.016841	0.002697	4.38E-10	2.35E-12	0.542533	
1	ATG4C *	rs11208050	62,870,600	T	C	0.322027	-0.015336	0.002158	6.50E-14	-0.01406	0.003685	0.000137	-0.016841	0.002697	4.38E-10	2.35E-12	0.542533	
1	ATG4C *	rs11208051	62,870,957	C	T	0.331517	-0.014612	0.002143	8.90E-13	-0.012637	0.003662	0.000562	-0.016511	0.002677	7.14E-10	1.43E-11	0.393042	
1	ATG4C *	rs28793284	62,871,200	G	T	0.334125	-0.014561	0.00214	1.00E-12	-0.012332	0.003658	0.000753	-0.016558	0.002674	6.08E-10	1.60E-11	0.35093	
1	ATG4C *	rs12756081	62,871,663	G	A	0.331514	-0.014614	0.002143	8.90E-13	-0.012637	0.003662	0.000562	-0.016513	0.002677	7.10E-10	1.42E-11	0.392738	
1	ATG4C *	rs2050248	62,872,447	A	T	0.310636	-0.013775	0.002179	3.10E-11	-0.01262	0.003729	0.000717	-0.015125	0.002721	2.77E-08	6.33E-10	0.587383	
1	ATG4C *	rs6587997	62,872,515	T	G	0.331492	-0.014568	0.002143	1.00E-12	-0.012534	0.003662	0.000624	-0.016504	0.002677	7.28E-10	1.60E-11	0.381564	
1	ATG4C *	rs11208052	62,873,126	A	G	0.331537	-0.014545	0.002143	1.10E-12	-0.012521	0.003662	0.000633	-0.016488	0.002677	7.57E-10	1.68E-11	0.381976	
1	ATG4C *	rs6657552	62,873,981	T	C	0.310459	-0.013844	0.00218	2.60E-11	-0.012801	0.00373	0.000604	-0.015157	0.002722	2.63E-08	5.12E-10	0.609964	
1	ATG4C *	rs6693530	62,873,985	G	A	0.331312	-0.014621	0.002144	9.00E-13	-0.01274	0.003664	0.00051	-0.016506	0.002678	7.34E-10	1.34E-11	0.40664	
1	ATG4C *	rs10889387	62,875,174	C	T	0.310293	-0.013855	0.00218	2.60E-11	-0.012772	0.003731	0.000622	-0.015169	0.002721	2.55E-08	5.10E-10	0.603777	
1	ATG4C *	rs12725996	62,876,411	T	A	0.33148	-0.014735	0.002146	6.20E-13	-0.012615	0.003668	0.000587	-0.016705	0.002681	4.79E-10	1.00E-11	0.367983	
1	ATG4C *	rs7515960	62,876,535	A	G	0.331156	-0.014629	0.002143	8.80E-13	-0.012689	0.003664	0.000537	-0.01652	0.002678	7.05E-10	1.35E-11	0.398551	
1	ATG4C *	rs6587998	62,876,798	C	T	0.331156	-0.014629	0.002143	8.80E-13	-0.012689	0.003664	0.000537	-0.01652	0.002678	7.05E-10	1.35E-11	0.398551	
1	ATG4C *	rs6685784	62,877,152	C	A	0.331156	-0.014629	0.002143	8.80E-13	-0.012689	0.003664	0.000537	-0.01652	0.002678	7.05E-10	1.35E-11	0.398551	
1	ATG4C *	rs1333734	62,877,305	C	T	0.310295	-0.013851	0.00218	2.60E-11	-0.012772	0.003731	0.000622	-0.015163	0.002721	2.58E-08	5.16E-10	0.604669	
1	ATG4C *	rs12749904	62,877,674	C	A	0.331156	-0.014629	0.002143	8.80E-13	-0.012689	0.003664	0.000537	-0.01652	0.002678	7.05E-10	1.35E-11	0.398551	
1	ATG4C *	rs1537496	62,878,769	A	T	0.33256	-0.014495	0.002146	1.40E-12	-0.012833	0.003668	0.000471	-0.016202	0.002682	1.57E-09	2.61E-11	0.458452	
1	ATG4C *	rs7522726	62,878,835	A	G	0.310295	-0.013851	0.00218	2.60E-11	-0.012772	0.003731	0.000622	-0.015163	0.002721	2.58E-08	5.16E-10	0.604669	
1	ATG4C *	rs7526246	62,880,316	A	T	0.326744	-0.014261	0.00215	3.20E-12	-0.012355	0.003675	0.000779	-0.016117	0.002686	2.03E-09	5.35E-11	0.408584	
1	ATG4C *	rs12728111	62,880,901	C	T	0.326744	-0.014261	0.00215	3.20E-12	-0.012355	0.003675	0.000779	-0.016117	0.002686	2.03E-09	5.35E-11	0.408584	
1	ATG4C *	rs12742537	62,881,305	G	A	0.326483	-0.014231	0.002151	3.50E-12	-0.012398	0.003678	0.000754	-0.016065	0.002687	2.32E-09	5.91E-11	0.420743	
1	ATG4C *	rs11580642	62,882,427	T	A	0.326744	-0.014261	0.00215	3.20E-12	-0.012355	0.003675	0.000779	-0.016117	0.002686	2.03E-09	5.35E-11	0.408584	
1	ATG4C *	rs7535496	62,882,885	A	T	0.306736	-0.013686	0.002187	3.90E-11	-0.012652	0.003742	0.000727	-0.014904	0.002731	4.95E-08	1.12E-09	0.626973	
1	ATG4C *	rs11804568	62,885,930	T	C	0.325758	-0.014062	0.002167	6.20E-12	-0.012437	0.003705	0.000793	-0.015766	0.002707	5.93E-09	1.55E-10	0.468069	
1	ATG4C *	rs11208056	62,887,038	C	T	0.326008	-0.014143	0.002168	4.30E-12	-0.01255	0.003707	0.000715	-0.015795	0.002708	5.60E-09	1.33E-10	0.479662	
1	ATG4C *	rs12564421	62,887,759	G	T	0.291981	-0.015153	0.002245	3.50E-12	-0.011776	0.003829	0.002112	-0.017848	0.002808	2.15E-10	1.50E-11	0.200983	
1	ATG4C *	rs2780871	62,889,202	T	C	0.27874	-0.015588	0.002267	1.00E-12	-0.012954	0.003867	0.000813	-0.017686	0.002835	4.53E-10	1.29E-11	0.323657	
1	ATG4C *	rs7512480	62,893,145	C	T	0.297964	-0.016691	0.002221	1.10E-14	-0.012824	0.003784	0.000705	-0.019647	0.002779	1.61E-12	4.48E-13	0.146132	
1	ATG4C *	rs2803238	62,893,889	G	A	0.284797	-0.014837	0.00224	8.80E-12	-0.011912	0.003826	0.001858	-0.017045	0.002799	1.17E-09	7.00E-11	0.278972	
1	ATG4C *	rs55924040	62,894,308	C	T	0.269218	-0.014819	0.002276	1.40E-11	-0.014141	0.003886	0.000276	-0.015821	0.002845	2.76E-08	2.58E-10	0.727211	
1	SMG5	rs12128955	156,274,030	T	C	0.47516	-0.01142	0.002017	4.20E-08	-0.011782	0.00343	0.000597	-0.010696	0.002526	2.32E-05	3.51E-07	0.798762	
1	SMG5	rs9943105	156,275,454	C	T	0.475269	-0.011443	0.002015	4.00E-08	-0.011642	0.003428	0.000689	-0.010802	0.002524	1.90E-05	3.31E-07	0.843591	
1	SMG5	rs7542045	156,276,682	C	G	0.475269	-0.011443	0.002015	4.00E-08	-0.011642	0.003428	0.000689	-0.010802	0.002524	1.90E-05	3.31E-07	0.843591	
1	SMG5	rs6701440	156,279,714	G	A	0.475445	-0.01145	0.002016	3.90E-08	-0.011699	0.003428	0.000648	-0.010793	0.002524	1.93E-05	3.18E-07	0.831567	
1	VHLL *	rs12072638	156,297,689	G	T	0.474319	-0.011624	0.002018	2.30E-08	-0.012072	0.003431	0.000437	-0.010858	0.002528	1.77E-05	2.02E-07	0.775612	
1	VHLL *	rs949464	156,302,480	T	C	0.473031	-0.011554	0.002022	3.30E-08	-0.012133	0.003439	0.000421	-0.010798	0.002532	2.03E-05	2.23E-07	0.75461	
1	CCT3 *	rs752286																

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
2	C2orf43 *	rs13008369	20,900,678	T	G	0.150463	-0.016012	0.002819	4.80E-10	-0.022022	0.004814	2.74E-05	-0.013841	0.003526	8.75E-05	6.76E-08	0.286379	
2	C2orf43 *	rs7583126	20,901,107	G	A	0.150356	-0.016475	0.002822	2.00E-10	-0.021019	0.004818	1.30E-05	-0.014191	0.00353	5.87E-05	2.27E-08	0.252873	
2	C2orf43 *	rs13015995	20,901,187	T	C	0.15035	-0.016481	0.002822	2.00E-10	-0.021019	0.004818	1.30E-05	-0.014201	0.00353	5.80E-05	2.25E-08	0.253593	
2	C2orf43 *	rs6722139	20,901,622	A	C	0.150175	-0.016478	0.002824	2.00E-10	-0.02127	0.004821	1.04E-05	-0.014059	0.003532	6.96E-05	2.16E-08	0.227575	
2	APOB *	rs113780557	20,920,505	C	T	0.141609	-0.017702	0.002938	7.30E-11	-0.021441	0.004996	1.80E-05	-0.01621	0.003684	1.09E-05	6.25E-09	0.399412	
2	APOB *	rs114851711	20,921,082	A	C	0.139759	-0.017804	0.002957	1.10E-10	-0.023091	0.005025	4.39E-06	-0.015435	0.003709	3.19E-05	4.51E-09	0.22022	
2	APOB *	rs7580543	20,921,560	A	G	0.142194	-0.018024	0.00293	3.00E-11	-0.022505	0.004984	6.40E-06	-0.016223	0.003672	1.01E-05	2.15E-09	0.310112	
2	APOB *	rs7588415	20,923,901	A	G	0.142252	-0.018464	0.00293	1.30E-11	-0.02319	0.004988	3.39E-06	-0.016525	0.003671	6.84E-06	8.07E-10	0.281844	
2	APOB *	rs7586740	20,925,873	C	T	0.142246	-0.018561	0.00293	1.10E-11	-0.02308	0.004987	3.75E-06	-0.01669	0.003671	5.54E-06	7.26E-10	0.302114	
2	APOB *	rs7596102	20,926,088	A	G	0.142217	-0.018519	0.00293	1.10E-11	-0.022924	0.004988	4.38E-06	-0.016693	0.003671	5.53E-06	8.41E-10	0.314328	
2	APOB *	rs7594084	20,927,845	C	T	0.143234	-0.018305	0.002922	1.60E-11	-0.022381	0.00497	6.80E-06	-0.016759	0.003661	4.78E-06	1.12E-09	0.362448	
2	APOB *	rs4479392	20,928,382	T	C	0.143356	-0.018256	0.002923	2.00E-11	-0.022064	0.004972	9.20E-06	-0.016868	0.003664	4.21E-06	1.32E-09	0.400133	
2	APOB *	rs111471227	20,929,266	T	C	0.143599	-0.018149	0.00292	2.60E-11	-0.022663	0.004966	5.10E-06	-0.016298	0.003659	8.56E-06	1.48E-09	0.302077	
2	APOB *	rs6731905	20,929,669	C	T	0.143655	-0.018136	0.002919	2.70E-11	-0.022619	0.004965	5.31E-06	-0.016326	0.003659	8.25E-06	1.48E-09	0.307575	
2	APOB *	rs6732027	20,929,774	G	T	0.143655	-0.018136	0.002919	2.70E-11	-0.022619	0.004965	5.31E-06	-0.016326	0.003659	8.25E-06	1.48E-09	0.307575	
2	APOB *	rs7565511	20,930,030	G	C	0.142595	-0.018386	0.00293	1.60E-11	-0.022904	0.004985	4.41E-06	-0.016477	0.003671	7.29E-06	1.10E-09	0.299291	
2	APOB *	rs72888845	20,931,957	A	C	0.138449	-0.017502	0.002968	2.50E-10	-0.02181	0.005055	1.62E-05	-0.015515	0.003718	3.04E-05	1.50E-08	0.315748	
2	APOB *	rs74358761	20,935,300	A	G	0.139874	-0.016335	0.00296	1.10E-09	-0.019656	0.005031	9.43E-05	-0.015012	0.003711	5.28E-05	1.35E-07	0.457613	
2	APOB *	rs5013879	20,936,353	C	A	0.04622	0.025688	0.004779	1.10E-08	0.023622	0.008037	0.003302	0.027021	0.006027	7.45E-06	7.73E-10	0.735134	
2	APOB *	rs12710748	20,936,567	C	T	0.046217	0.025727	0.004779	1.10E-08	0.023728	0.008038	0.003167	0.027028	0.006027	7.41E-06	5.50E-07	0.742563	
2	APOB *	rs12710749	20,936,790	C	A	0.046138	0.02622	0.004787	5.80E-09	0.023989	0.00805	0.002894	0.027728	0.006037	4.44E-06	3.10E-07	0.7102	
2	APOB *	rs12710750	20,936,804	T	C	0.045729	0.025763	0.004804	1.00E-08	0.024185	0.008073	0.002746	0.026845	0.006062	9.63E-06	6.21E-07	0.792223	
2	APOB *	rs76203970	20,937,176	A	C	0.149616	-0.018034	0.002868	5.20E-12	-0.019689	0.004877	5.48E-05	-0.017539	0.003595	1.09E-06	1.97E-09	0.727787	
2	APOB *	rs9306897	20,938,306	T	C	0.081577	0.031161	0.003718	5.00E-17	0.028924	0.006291	4.34E-06	0.031931	0.004673	8.65E-12	1.87E-15	0.701268	
2	APOB *	rs72888868	20,938,435	A	G	0.150767	-0.01774	0.00286	1.00E-11	-0.019077	0.00486	8.75E-05	-0.017506	0.003586	1.07E-06	3.01E-09	0.794715	
2	APOB *	rs75509845	20,940,759	A	G	0.151021	-0.017923	0.002857	6.90E-12	-0.019058	0.004856	8.76E-05	-0.017788	0.003582	6.96E-07	1.99E-09	0.833221	
2	APOB *	rs11096869	20,940,780	C	T	0.079717	0.032811	0.00375	2.70E-18	0.030934	0.006345	1.11E-06	0.033309	0.004714	1.67E-12	9.97E-17	0.763905	
2	APOB *	rs13414987	20,942,072	A	C	0.146548	-0.018118	0.002898	1.40E-11	-0.018536	0.004926	0.00017	-0.018171	0.003633	5.80E-07	3.12E-09	0.952394	
2	APOB *	rs4072815	20,942,098	T	G	0.146514	-0.018054	0.002898	1.60E-11	-0.018573	0.004927	0.000165	-0.018037	0.003634	7.04E-07	3.66E-09	0.930226	
2	APOB *	rs4296389	20,943,234	C	T	0.095673	0.033556	0.003459	1.20E-22	0.029479	0.005832	4.39E-07	0.035388	0.004358	4.86E-16	1.35E-20	0.417023	
2	APOB *	rs4507059	20,943,569	G	A	0.083641	0.031989	0.003655	8.90E-19	0.029903	0.006161	1.23E-06	0.032853	0.004603	9.93E-13	6.66E-17	0.701314	
2	APOB *	rs10201379	20,943,917	C	A	0.130143	0.030691	0.003023	2.20E-25	0.028364	0.005099	2.73E-08	0.031743	0.003807	7.92E-17	1.52E-22	0.595428	
2	APOB *	rs4426495	20,944,222	C	T	0.130179	0.030683	0.003022	2.30E-25	0.02842	0.005099	2.55E-08	0.031701	0.003805	8.44E-17	1.52E-22	0.60608	
2	APOB *	rs10180633	20,945,069	G	T	0.126882	0.030997	0.003059	2.50E-25	0.028155	0.00516	4.98E-08	0.032378	0.003851	4.41E-17	1.53E-22	0.511918	
2	APOB *	rs13020417	20,945,074	T	G	0.049306	0.039142	0.004664	1.30E-16	0.033801	0.007858	1.72E-05	0.041605	0.005876	1.50E-12	1.25E-15	0.426384	
2	APOB *	rs10183548	20,945,739	G	A	0.125487	0.031582	0.003064	3.30E-26	0.027813	0.005171	7.70E-08	0.033344	0.003857	5.63E-18	3.09E-23	0.391189	
2	APOB *	rs6732011	20,946,761	G	T	0.125454	0.031574	0.003065	2.70E-26	0.028093	0.005169	5.61E-08	0.033259	0.00386	7.28E-18	2.91E-23	0.42322	
2	APOB *	rs35424228	20,947,933	T	C	0.04903	0.039406	0.004676	1.30E-16	0.034371	0.007885	1.32E-05	0.041815	0.005888	1.28E-12	8.35E-16	0.44938	
2	APOB *	rs3293037	20,948,514	A	C	0.123491	0.031362	0.003085	1.50E-25	0.027657	0.005208	1.12E-07	0.033189	0.003882	1.31E-17	1.02E-22	0.394401	
2	APOB *	rs149034253	20,951,648	A	G	0.049396	0.039073	0.004658	1.20E-16	0.033106	0.007859	2.55E-05	0.041931	0.005864	9.02E-13	1.11E-15	0.368083	
2	APOB *	rs4076525	20,952,157	T	C	0.032209	0.029962	0.005739	3.10E-08	0.023151	0.009699	0.017008	0.034365	0.00722	1.97E-06	6.96E-07	0.353644	
2	APOB *	rs141074569	20,952,398	C	G	0.036447	0.029696	0.005402	5.80E-09	0.023586	0.009161	0.010054	0.032893	0.006782	1.26E-06	2.84E-07	0.414225	
2	APOB *	rs148458076	20,955,854	C	T	0.123042	0.033098	0.003079	2.60E-28	0.031611	0.005225	1.49E-09	0.033521	0.003864	4.33E-18	5.07E-25	0.768857	
2	APOB *	rs36145916	20,956,506	T	C	0.122383	0.033468	0.003086	1.00E-28	0.031933	0.005237	1.11E-09	0.033927	0.003872	2.04E-18	1.81E-25	0.759441	
2	APOB *	rs143375141	20,956,554	T	C	0.161621	-0.018738	0.002758	8.60E-14	-0.020605	0.004702	1.19E-05	-0.018212	0.003453	1.35E-07	6.13E-11	0.681678	
2	APOB *	rs36187918	20,958,070	G	A	0.122567	0.033057	0.003082	3.00E-28	0.031348	0.005233	1.84E-09	0.033514	0.003867	4.74E-18	6.83E-25	0.754699	
2	APOB *	rs141232528	20,958,693	T	C	0.040982	0.029135	0.00509	2.70E-09	0.024078	0.008679	0.005548	0.032103	0.006371	4.76E-07	6.52E-08	0.45604	
2	APOB *	rs36190370	20,958,814	A	C	0.046058	0.041423	0.004809	2.20E-17	0.038305	0.008155	2.68E-06	0.041992	0.006037	3.63E-12	5.03E-16	0.716393	
2	APOB *	rs147436013	20,959,450	T	G	0.162746	-0.018757	0.002743	7.50E-14	-0.020405	0.004676	1.30E-05	-0.018466	0.003434	7.73E-08	3.86E-11	0.738151	
2	APOB *	rs36191919	20,960,266	G	A	0.041898	0.028726	0.005032	2.60E-09	0.022961	0.008603	0.007623	0.032016	0.006289	3.64E-07	6.70E-08	0.395461	
2	APOB *	rs13440663	20,961,673	T	C	0.12596	0.032337	0.003041	1.20E-27	0.031757	0.005164	8.01E-10	0.032335	0.003815	2.45E-17	1.53E-24	0.928195	
2	APOB *	rs2337382	20,961,892	A	G	0.089181	0.036792	0.003535	1.40E-25	0.03298	0.006015	4.28E-08	0.038453	0.00443	4.19E-18	1.29E-23	0.463778	
2	APOB *	rs17397667	20,961,975	A	G	0.04197	0.02879	0.005026	2.20E-09	0.023368	0.008583	0.006495	0.031979	0.006286	3.70E-07	5.89E-08	0.418277	
2	APOB *	rs12999441	20,963,235	C	T	0.044423	0.044671	0.004883	2.80E-19	0.042278	0.008267	3.22E-07	0.044838	0.006135	2.82E-13	5.29E-18	0.80361	
2	APOB *	rs2337381	20,963,249	A	C	0.041976	0.028756	0.005026	2.30E-09	0.023372	0.008582	0.00648	0.031913	0.006285	3.90E-07	6.19E-08	0.422066	
2	APOB *	rs4665639	20,964,019	A	G	0.12237	0.033472	0.003073	6.40E-29	0.032057	0.005219	8.41E-10	0.033909	0.003854	1.48E-18	1.01E-25	0.775301	
2	APOB *	rs62120837	20,964,499	A	G	0.042037	0.028785	0.005024	2.20E-									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
2	AOB*	rs10495712	20,973,240	A	G	0.042176	0.028249	0.005013	4.10E-09	0.023334	0.008568	0.006479	0.031136	0.006266	6.86E-07	1.07E-07	0.4623	
2	AOB*	rs34335269	20,973,378	A	G	0.121822	0.033531	0.003077	5.20E-29	0.031886	0.005227	1.09E-09	0.034042	0.003859	1.20E-18	1.06E-25	0.740037	
2	AOB*	rs62120842	20,973,575	A	G	0.042176	0.028249	0.005013	4.10E-09	0.023334	0.008568	0.006479	0.031136	0.006266	6.86E-07	1.07E-07	0.4623	
2	AOB*	rs62120843	20,973,812	G	T	0.042185	0.0284	0.005013	3.40E-09	0.023568	0.008569	0.005967	0.031192	0.006266	6.55E-07	9.47E-08	0.472682	
2	AOB*	rs938848	20,973,975	G	C	0.042499	0.029392	0.004995	9.30E-10	0.024124	0.008535	0.004722	0.032561	0.006245	1.89E-07	2.30E-08	0.425038	
2	AOB*	rs6733447	20,975,264	G	A	0.123005	0.034067	0.003064	4.00E-30	0.032125	0.005206	7.00E-10	0.034776	0.003843	1.52E-19	8.88E-27	0.682026	
2	AOB*	rs55664492	20,975,554	T	C	0.044716	0.044511	0.004869	2.00E-19	0.04232	0.008234	2.81E-07	0.044469	0.006121	3.89E-13	6.36E-18	0.834026	
2	AOB*	rs10495713	20,977,647	A	G	0.121303	0.034231	0.003083	6.70E-30	0.033103	0.005238	2.71E-10	0.03451	0.003867	4.71E-19	1.07E-26	0.828873	
2	AOB*	rs7608123	20,980,007	T	G	0.121285	0.034261	0.003083	6.10E-30	0.033152	0.005238	2.55E-10	0.034529	0.003866	4.49E-19	9.83E-27	0.832496	
2	AOB*	rs121097204	20,980,087	A	C	0.042179	0.028328	0.005012	3.90E-09	0.023567	0.008567	0.005959	0.031134	0.006266	6.85E-07	9.89E-08	0.475875	
2	AOB*	rs7571469	20,981,609	G	C	0.121292	0.034296	0.003082	5.50E-30	0.033121	0.005236	2.61E-10	0.034635	0.003865	3.43E-19	7.55E-27	0.816099	
2	AOB*	rs10172650	20,982,585	A	G	0.156989	-0.020307	0.002768	1.70E-15	-0.023483	0.00472	6.64E-07	-0.019217	0.003464	2.97E-08	8.77E-13	0.466211	
2	AOB*	rs10164442	20,982,691	G	A	0.156705	-0.020311	0.002769	1.60E-15	-0.023479	0.004722	6.73E-07	-0.019218	0.003467	3.03E-08	9.05E-13	0.466994	
2	AOB*	rs35131127	20,983,042	C	T	0.087433	0.038525	0.003564	2.80E-27	0.034348	0.006062	1.50E-08	0.04021	0.004467	2.38E-19	2.73E-25	0.436299	
2	AOB*	rs62120847	20,983,048	C	T	0.042504	0.029261	0.004993	1.10E-09	0.024061	0.008533	0.00482	0.032349	0.006242	2.24E-07	2.77E-08	0.433108	
2	AOB*	rs9789416	20,983,180	A	G	0.121219	0.034316	0.003083	5.90E-30	0.033114	0.005239	2.68E-10	0.034689	0.003865	3.02E-19	6.85E-27	0.808814	
2	AOB*	rs11242942	20,983,403	C	G	0.17376	-0.019347	0.00266	1.50E-15	-0.022699	0.004548	6.11E-07	-0.017841	0.003326	8.29E-08	2.19E-12	0.388576	
2	AOB*	rs56327713	20,983,964	T	G	0.08748	0.038897	0.003567	8.10E-28	0.034755	0.006068	1.04E-08	0.040702	0.00447	9.16E-20	7.49E-26	0.430039	
2	AOB*	rs56403064	20,984,034	C	T	0.121802	0.034812	0.003076	7.10E-31	0.033625	0.005231	1.33E-10	0.035212	0.003856	7.19E-20	8.33E-28	0.807061	
2	AOB*	rs56213756	20,984,123	G	C	0.121442	0.034887	0.003081	5.80E-31	0.03378	0.005237	1.15E-10	0.035229	0.003863	7.96E-20	8.00E-28	0.823803	
2	AOB*	rs67212568	20,985,612	G	T	0.044359	0.044818	0.004885	2.20E-19	0.042487	0.008271	2.85E-07	0.044931	0.006138	2.59E-13	4.33E-18	0.812406	
2	AOB*	rs55938327	20,986,670	C	T	0.042529	0.028841	0.004993	1.90E-09	0.023679	0.008536	0.005551	0.031935	0.006242	3.17E-07	4.41E-08	0.434983	
2	AOB*	rs34059329	20,986,894	T	C	0.087528	0.03809	0.003565	9.20E-27	0.035278	0.006064	6.12E-09	0.039096	0.004469	2.30E-18	1.08E-24	0.612298	
2	AOB*	rs1320143	20,989,476	G	A	0.120226	0.034793	0.003102	2.00E-30	0.034535	0.005267	5.68E-11	0.034671	0.003893	5.55E-19	2.73E-27	0.983436	
2	AOB*	rs6721844	20,989,699	T	G	0.087035	0.037992	0.003579	1.90E-26	0.03442	0.006084	1.58E-08	0.039465	0.004488	1.53E-18	1.81E-24	0.504634	
2	AOB*	rs6722374	20,990,190	T	G	0.119606	0.034812	0.00311	2.50E-30	0.034271	0.005279	8.73E-11	0.034634	0.003903	7.54E-19	9.55E-27	0.955876	
2	AOB*	rs13014683	20,990,254	T	C	0.049359	0.041154	0.004647	3.00E-18	0.037108	0.007895	2.65E-06	0.041617	0.005828	9.66E-13	1.35E-16	0.645909	
2	AOB*	rs4665642	20,990,313	G	A	0.119618	0.034805	0.003111	2.50E-30	0.034277	0.005279	8.70E-11	0.034611	0.003903	7.56E-19	9.59E-27	0.959423	
2	AOB*	rs62120852	20,990,672	T	C	0.042242	0.027177	0.005008	1.60E-08	0.022205	0.008556	0.009471	0.029992	0.006262	1.70E-06	3.60E-07	0.462689	
2	AOB*	rs1318006	20,991,280	G	A	0.120337	0.035241	0.003105	5.10E-31	0.034028	0.005274	1.14E-10	0.035401	0.003896	1.08E-19	1.07E-27	0.834112	
2	AOB*	rs1318005	20,991,336	G	A	0.120041	0.034999	0.00311	1.30E-30	0.033701	0.005281	1.81E-10	0.035204	0.003901	1.93E-19	2.99E-27	0.818886	
2	AOB*	rs1318004	20,991,337	C	T	0.120041	0.034999	0.00311	1.30E-30	0.033701	0.005281	1.81E-10	0.035204	0.003901	1.93E-19	2.99E-27	0.818886	
2	AOB*	rs72780134	20,991,960	A	G	0.167929	-0.020243	0.002708	4.20E-16	-0.02371	0.004625	3.01E-07	-0.018767	0.003387	3.09E-08	4.23E-13	0.388492	
2	AOB*	rs12992267	20,992,773	T	C	0.071282	0.038455	0.003922	1.60E-22	0.03792	0.006649	1.21E-08	0.037405	0.004924	3.19E-14	2.56E-20	0.950341	
2	AOB*	rs34776010	20,993,375	G	C	0.071287	0.03846	0.003922	1.60E-22	0.037987	0.006648	1.13E-08	0.037374	0.004924	3.35E-14	2.53E-20	0.940898	
2	AOB*	rs79823619	20,993,415	C	G	0.164415	-0.019727	0.002735	2.80E-15	-0.022355	0.004672	1.74E-06	-0.0187	0.00342	4.65E-08	3.42E-12	0.52788	
2	AOB*	rs62122481	20,993,943	A	C	0.042315	0.027046	0.005001	2.00E-08	0.021972	0.008547	0.010164	0.029902	0.006253	1.76E-06	3.97E-07	0.453982	
2	AOB*	rs57947200	20,994,357	A	T	0.069202	0.038226	0.003999	2.30E-21	0.037299	0.006771	3.71E-08	0.0373	0.005025	1.20E-13	2.80E-19	0.999848	
2	AOB*	rs56984418	20,994,358	G	A	0.071272	0.038236	0.003923	1.90E-22	0.037555	0.006641	1.60E-08	0.037171	0.00493	4.92E-14	5.14E-20	0.962915	
2	AOB*	rs74580781	20,994,558	A	G	0.038139	0.028004	0.005265	4.50E-08	0.021209	0.009	0.01846	0.031401	0.006581	1.86E-06	7.09E-07	0.36065	
2	AOB*	rs6756501	20,995,933	T	C	0.066624	0.037445	0.004051	2.40E-20	0.036009	0.006864	1.59E-07	0.036951	0.005088	3.97E-13	3.73E-18	0.912161	
2	AOB*	rs6725189	20,996,129	T	G	0.066927	0.037269	0.004043	2.30E-20	0.035786	0.006846	1.75E-07	0.036723	0.005081	5.10E-13	5.26E-18	0.912504	
2	AOB*	rs4665709	20,998,083	A	G	0.071372	0.037695	0.003921	6.40E-22	0.037122	0.006635	2.27E-08	0.036677	0.004928	1.03E-13	1.50E-19	0.957045	
2	AOB*	rs4371387	20,998,261	A	G	0.071285	0.038036	0.003923	2.70E-22	0.037178	0.006638	2.19E-08	0.037105	0.00493	5.44E-14	7.71E-20	0.992942	
2	AOB*	rs952274	20,998,485	T	G	0.066947	0.03715	0.004042	2.80E-20	0.035562	0.006842	2.06E-07	0.036647	0.00508	5.66E-13	6.81E-18	0.898675	
2	AOB*	rs952275	20,998,527	G	T	0.043288	0.029558	0.004948	6.30E-10	0.023696	0.008458	0.0051	0.032614	0.006185	1.37E-07	1.81E-08	0.394761	
2	AOB*	rs62122484	21,000,700	A	C	0.039361	0.044421	0.005183	4.50E-17	0.041537	0.008769	2.21E-06	0.04489	0.006516	5.83E-12	6.64E-16	0.758951	
2	AOB*	rs369226260	21,001,217	A	T	0.036324	0.044911	0.005434	5.70E-16	0.041232	0.00917	7.01E-06	0.045505	0.00684	2.98E-11	9.99E-15	0.708819	
2	AOB*	rs371445178	21,001,218	T	A	0.036329	0.044906	0.005434	5.60E-16	0.041263	0.009169	6.89E-06	0.045505	0.00684	2.98E-11	9.82E-15	0.710736	
2	AOB*	rs51038752	21,001,219	A	T	0.036324	0.044911	0.005434	5.70E-16	0.041232	0.00917	7.01E-06	0.045505	0.00684	2.98E-11	9.99E-15	0.708819	
2	AOB	rs1042031	21,002,881	T	C	0.044415	0.044446	0.004884	5.90E-19	0.041417	0.008266	5.53E-07	0.044897	0.006138	2.70E-13	8.53E-18	0.735328	
2	AOB	rs1800479	21,004,511	G	C	0.042961	0.045179	0.004972	5.00E-19	0.041252	0.008389	8.92E-07	0.045901	0.00626	2.36E-13	1.19E-17	0.656923	
2	AOB	rs693	21,009,323	A	G	0.048642	0.030812	0.004681	6.80E-12	0.031168	0.007996	9.79E-05	0.030855	0.005853	1.38E-07	4.63E-10	0.974798	
2	AOB	rs1041968	21,009,932	A	G	0.048181	0.03005	0.004698	2.40E-11	0.030314	0.008024	0.00016	0.030026	0.005875	3.27E-07	1.69E-09	0.976942	
2	AOB	rs3749054	21,014,366	T	A	0.044515	0.044608	0.00488	3.60E-19	0.041326	0.008255	5.66E-07	0.045153	0.006135	1.91E-13	6.23E-18	0.709842	
2	AOB	rs2854725	21,014,914	G	T	0.155434	-0.021878	0.002787	1.50E-17	-0.025446	0.004744	8.31E-08	-0.020884	0.003492	2.28E-09	9.62E-15	0.438698	
2	AOB	rs12713868	21,016,712	T	C	0.028424	0.035368	0.006083	4.20E-08	0.031865	0.01029							

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
2	AOBP *	rs60857806	21,061,227	G	T	0.17318	-0.020088	0.002699	1.30E-15	-0.02527	0.004581	3.55E-08	-0.017703	0.003387	1.77E-07	2.89E-13	0.184108	
2	AOBP *	rs56885855	21,061,405	T	C	0.173192	-0.020104	0.002699	1.30E-15	-0.025327	0.004581	3.31E-08	-0.017696	0.003387	1.79E-07	2.74E-13	0.180444	
2	AOBP *	rs75953246	21,061,841	A	G	0.173186	-0.020112	0.002699	1.20E-15	-0.025299	0.004581	3.45E-08	-0.017773	0.003387	1.69E-07	2.70E-13	0.184482	
2	AOBP *	rs77225367	21,062,230	T	C	0.172249	-0.020365	0.002707	6.40E-16	-0.025491	0.004589	2.85E-08	-0.017996	0.003398	1.21E-07	1.62E-13	0.189351	
2	AOBP *	rs11894096	21,062,695	G	A	0.171008	-0.020058	0.002716	2.00E-15	-0.02528	0.004613	4.34E-08	-0.017707	0.003408	2.08E-07	4.12E-13	0.186628	
2	AOBP *	rs11894310	21,063,145	G	A	0.173866	-0.019951	0.002694	1.90E-15	-0.025601	0.004568	2.14E-08	-0.017366	0.003382	2.87E-07	2.83E-13	0.147297	
2	AOBP *	rs57024468	21,064,771	C	T	0.173891	-0.019887	0.002693	2.30E-15	-0.025646	0.004567	2.01E-08	-0.017275	0.003381	3.29E-07	3.04E-13	0.140705	
2	AOBP *	rs75207863	21,068,360	A	G	0.17414	-0.019696	0.002692	3.60E-15	-0.02523	0.004565	3.34E-08	-0.017247	0.00338	3.42E-07	5.18E-13	0.159853	
2	AOBP *	rs79662771	21,068,361	G	A	0.17414	-0.019696	0.002692	3.60E-15	-0.02523	0.004565	3.34E-08	-0.017247	0.00338	3.42E-07	5.18E-13	0.159853	
2	AOBP *	rs17041755	21,069,695	A	G	0.174152	-0.019724	0.002692	3.20E-15	-0.025217	0.004565	3.40E-08	-0.017283	0.00338	3.22E-07	4.96E-13	0.162446	
2	AOBP *	rs1897084	21,074,114	G	A	0.173655	-0.019436	0.002684	7.20E-15	-0.024834	0.004556	5.12E-08	-0.017032	0.003368	4.33E-07	9.83E-13	0.166485	
2	AOBP *	rs7422168	21,074,322	C	G	0.173657	-0.019473	0.002684	6.50E-15	-0.024938	0.004555	4.49E-08	-0.017032	0.003367	4.33E-07	8.66E-13	0.162791	
2	AOBP *	rs58420813	21,077,134	C	T	0.173953	-0.019573	0.00268	4.80E-15	-0.024928	0.004546	4.28E-08	-0.017257	0.003364	2.96E-07	5.73E-13	0.174962	
2	AOBP *	rs80196520	21,078,435	A	C	0.174161	-0.019582	0.002678	4.20E-15	-0.0249	0.004544	4.35E-08	-0.017278	0.003361	2.80E-07	5.50E-13	0.177433	
2	AOBP *	rs59263713	21,079,390	T	G	0.174196	-0.019507	0.002677	5.00E-15	-0.024706	0.004543	5.49E-08	-0.017249	0.00336	2.91E-07	7.17E-13	0.186919	
2	AOBP *	rs11886946	21,082,715	C	A	0.17459	-0.019777	0.002673	2.30E-15	-0.025107	0.004536	3.19E-08	-0.017442	0.003355	2.04E-07	3.01E-13	0.17426	
2	AOBP *	rs79721590	21,083,359	C	G	0.174571	-0.019641	0.002673	3.40E-15	-0.024991	0.004537	3.70E-08	-0.017343	0.003354	2.39E-07	4.04E-13	0.175239	
2	AOBP *	rs112680646	21,084,238	A	G	0.174612	-0.019472	0.002672	5.10E-15	-0.024694	0.004534	5.28E-08	-0.017228	0.003353	2.84E-07	6.73E-13	0.185555	
2	AOBP *	rs57666320	21,093,675	T	C	0.175501	-0.019003	0.002651	1.10E-14	-0.024574	0.004502	4.91E-08	-0.016472	0.003326	7.46E-07	1.60E-12	0.147715	
2	AOBP *	rs11899839	21,095,586	A	T	0.17639	-0.018568	0.002642	3.10E-14	-0.023494	0.004486	1.66E-07	-0.016285	0.003314	9.09E-07	6.31E-12	0.196159	
2	AOBP *	rs13019377	21,096,429	A	T	0.133593	-0.015535	0.002962	4.80E-08	0.019721	0.005033	9.00E-05	0.012402	0.003714	0.000844	1.76E-06	0.241911	
2	AOBP *	rs1544977	21,097,940	G	C	0.17642	-0.018659	0.00264	2.20E-14	-0.023569	0.004483	1.49E-07	-0.016393	0.003312	7.60E-07	4.77E-12	0.197942	
2	AOBP *	rs76234631	21,101,118	A	C	0.17657	-0.018467	0.002639	3.70E-14	-0.02345	0.00448	1.69E-07	-0.016126	0.003311	1.13E-06	7.95E-12	0.188594	
2	AOBP *	rs77449706	21,104,188	T	C	0.176568	-0.018556	0.002641	3.10E-14	-0.023233	0.004483	2.24E-07	-0.016399	0.003313	7.55E-07	7.04E-12	0.220152	
2	AOBP *	rs77809614	21,105,146	A	C	0.176388	-0.018641	0.00264	2.40E-14	-0.023631	0.004484	1.39E-07	-0.016319	0.003312	8.48E-07	4.97E-12	0.189566	
2	AOBP *	rs6757883	21,107,738	G	A	0.176504	-0.018593	0.002639	2.50E-14	-0.02339	0.004482	1.84E-07	-0.016344	0.003311	8.11E-07	6.25E-12	0.206047	
2	AOBP *	rs2337384	21,110,978	G	A	0.176518	-0.018555	0.002639	2.80E-14	-0.023322	0.004482	2.00E-07	-0.016326	0.003311	8.34E-07	6.93E-12	0.209281	
2	AOBP *	rs78943787	21,111,867	A	T	0.176518	-0.018555	0.002639	2.80E-14	-0.023322	0.004482	2.00E-07	-0.016326	0.003311	8.34E-07	6.93E-12	0.209281	
2	AOBP *	rs74367604	21,112,857	C	T	0.176518	-0.018555	0.002639	2.80E-14	-0.023322	0.004482	2.00E-07	-0.016326	0.003311	8.34E-07	6.93E-12	0.209281	
2	AOBP *	rs61086479	21,114,871	T	C	0.17646	-0.018511	0.00264	3.20E-14	-0.023318	0.004482	2.01E-07	-0.016276	0.003311	9.03E-07	7.52E-12	0.206316	
2	AOBP *	rs12172886	21,116,332	G	C	0.176458	-0.0185	0.00264	3.30E-14	-0.023318	0.004482	2.01E-07	-0.016257	0.003311	9.29E-07	7.73E-12	0.205121	
2	AOBP *	rs11892095	21,116,651	G	A	0.176478	-0.018482	0.00264	3.60E-14	-0.023272	0.004482	2.12E-07	-0.016257	0.003311	9.31E-07	8.18E-12	0.208104	
2	AOBP *	rs74957119	21,118,017	C	T	0.176478	-0.018509	0.00264	3.30E-14	-0.023257	0.004482	2.16E-07	-0.016308	0.003312	8.61E-07	7.72E-12	0.212448	
2	AOBP *	rs312955	21,119,021	G	A	0.272353	0.014531	0.002267	1.30E-11	0.019844	0.003867	2.93E-07	0.011736	0.002836	3.54E-05	3.66E-10	0.090889	
2	AOBP *	rs79542263	21,121,389	G	A	0.176515	-0.018571	0.002639	2.70E-14	-0.023307	0.004482	2.03E-07	-0.016359	0.003311	7.94E-07	6.72E-12	0.212404	
2	AOBP *	rs76885666	21,121,682	C	A	0.176515	-0.018571	0.002639	2.70E-14	-0.023307	0.004482	2.03E-07	-0.016359	0.003311	7.94E-07	6.72E-12	0.212404	
2	AOBP *	rs78051902	21,122,133	A	G	0.171404	-0.018568	0.002676	6.60E-14	-0.023777	0.004547	1.74E-07	-0.016038	0.003357	1.80E-06	1.27E-11	0.170885	
2	AOBP *	rs2059972	21,123,923	G	T	0.083985	-0.022791	0.003685	3.10E-11	-0.027647	0.006245	9.69E-06	-0.020146	0.004627	1.35E-05	4.25E-09	0.334543	
2	AOBP *	rs61517696	21,126,306	C	T	0.176546	-0.01855	0.002639	2.80E-14	-0.023259	0.004481	2.14E-07	-0.016355	0.003311	7.96E-07	7.10E-12	0.2153	
2	AOBP *	rs74582026	21,127,869	C	T	0.176646	-0.018633	0.002639	2.20E-14	-0.023231	0.004482	2.23E-07	-0.016483	0.003311	6.54E-07	6.09E-12	0.225898	
2	AOBP *	rs61142046	21,129,214	C	T	0.175983	-0.018506	0.002644	3.70E-14	-0.023126	0.004489	2.64E-07	-0.016326	0.003317	8.71E-07	9.48E-12	0.22315	
2	AOBP *	rs77258720	21,129,410	A	G	0.176541	-0.018545	0.002639	2.90E-14	-0.023254	0.004481	2.15E-07	-0.016351	0.003311	8.01E-07	7.18E-12	0.215358	
2	AOBP *	rs79909173	21,129,857	C	T	0.176541	-0.018545	0.002639	2.90E-14	-0.023254	0.004481	2.15E-07	-0.016351	0.003311	8.01E-07	7.18E-12	0.215358	
2	AOBP *	rs61437001	21,131,249	A	G	0.176645	-0.018436	0.002639	3.80E-14	-0.023154	0.00448	2.42E-07	-0.016219	0.00331	9.75E-07	9.70E-12	0.213178	
2	AOBP *	rs11903814	21,133,608	C	T	0.176205	-0.018326	0.002642	6.10E-14	-0.023159	0.004487	2.50E-07	-0.016047	0.003315	1.31E-06	1.33E-11	0.202314	
2	AOBP *	rs59537367	21,134,007	A	T	0.175902	-0.018571	0.002644	3.30E-14	-0.023273	0.004488	2.19E-07	-0.016396	0.003317	7.83E-07	7.15E-12	0.217767	
2	AOBP *	rs79538365	21,136,575	G	C	0.176349	-0.018551	0.002641	3.10E-14	-0.02333	0.004484	2.00E-07	-0.016323	0.003313	8.51E-07	7.09E-12	0.208814	
2	AOBP *	rs312966	21,137,711	A	G	0.283629	0.013796	0.002244	5.80E-11	0.01941	0.003834	4.21E-07	0.010877	0.002805	0.000106	1.47E-09	0.072427	
2	AOBP *	rs58411268	21,145,373	A	G	0.07801	-0.024374	0.003817	6.00E-12	-0.028995	0.006458	7.24E-06	-0.02182	0.004797	5.49E-06	1.35E-09	0.372493	
2	AOBP *	rs79783818	21,147,375	A	T	0.171215	-0.018762	0.002689	4.50E-14	-0.022398	0.004568	9.59E-07	-0.017247	0.003373	3.23E-07	1.26E-11	0.364359	
2	AOBP *	rs78059021	21,148,150	T	C	0.176318	-0.018598	0.002641	2.80E-14	-0.023454	0.004485	1.73E-07	-0.016322	0.003314	8.55E-07	6.18E-12	0.200848	
2	AOBP *	rs11685909	21,149,673	T	C	0.042795	0.032298	0.004995	2.80E-10	0.032868	0.008457	0.000103	0.032524	0.006276	2.24E-07	7.73E-10	0.973968	
2	AOBP *	rs11689541	21,149,675	C	T	0.042707	0.032426	0.005	2.70E-10	0.032447	0.008464	0.000127	0.032939	0.006283	1.62E-07	6.93E-10	0.962749	
2	AOBP *	rs140043113	21,149,823	T	G	0.176354	-0.018594	0.002641	2.80E-14	-0.023443	0.004485	1.76E-07	-0.016329	0.003314	8.47E-07	6.23E-12	0.202037	
2	AOBP *	rs11900335	21,150,887	C	T	0.176328	-0.018559	0.002641	3.10E-14	-0.023386	0.004485	1.88E-07	-0.016299	0.003314	8.88E-07	6.96E-12	0.20369	
2	AOBP *	rs113725991	21,151,946	T	C	0.174824	-0.01815	0.002653	1.40E-13	-0.023209	0.004504	2.62E-07	-0.015822	0.003329	2.04E-06	2.14E-11	0.187209	
2	AOBP *	rs35112647	21,152,185	A	G	0.044608	0.031113	0.004891	4.70E-1									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	APOB *	rs75249613	21,191,561	G	T	0.156032	-0.017003	0.002807	1.10E-10	-0.019401	0.004749	4.44E-05	-0.016293	0.003528	3.93E-06	5.55E-09	0.59943	
2	DPYSL5	rs3769134	26,928,023	A	G	0.324564	0.011178	0.002163	3.90E-08	0.007159	0.003678	0.051624	0.013559	0.002712	5.84E-07	5.60E-07	0.161335	
2	DPYSL5	rs7579579	26,928,974	T	C	0.324657	0.011175	0.002162	3.90E-08	0.007197	0.003676	0.050258	0.013548	0.002711	5.91E-07	5.54E-07	0.164332	
2	DPYSL5	rs6547317	26,929,051	A	G	0.324654	0.011177	0.002162	3.90E-08	0.007199	0.003676	0.050171	0.013548	0.002711	5.91E-07	5.54E-07	0.164506	
2	DPYSL5	rs7599286	26,929,530	T	C	0.325164	0.011204	0.002162	3.70E-08	0.007337	0.003676	0.045955	0.013498	0.00271	6.48E-07	5.62E-07	0.177273	
2	DPYSL5	rs2384511	26,929,867	G	A	0.325281	0.011264	0.002162	3.20E-08	0.007119	0.003674	0.052716	0.013726	0.00271	4.18E-07	4.13E-07	0.147869	
2	DPYSL5	rs6547318	26,930,613	A	C	0.331827	0.011229	0.002154	4.00E-08	0.00719	0.00366	0.049451	0.013487	0.002701	6.06E-07	5.60E-07	0.166256	
2	DPYSL5	rs3820821	26,932,980	C	T	0.331496	0.012055	0.002155	4.30E-09	0.007877	0.00366	0.031382	0.01452	0.002703	7.99E-08	5.35E-08	0.144292	
2	DPYSL5	rs4665929	26,932,981	T	G	0.332583	0.011812	0.002152	7.50E-09	0.007506	0.003657	0.040153	0.014354	0.002698	1.06E-07	8.70E-08	0.131803	
2	DPYSL5	rs3820822	26,932,994	A	G	0.332558	0.011812	0.002152	7.60E-09	0.007531	0.003658	0.039519	0.014344	0.002699	1.09E-07	8.79E-08	0.133387	
2	DPYSL5	rs4665363	26,933,548	G	T	0.332707	0.011989	0.002154	4.90E-09	0.00769	0.003659	0.03564	0.014543	0.002702	7.54E-08	5.64E-08	0.131885	
2	DPYSL5	rs920437	26,934,528	A	G	0.332788	0.011999	0.002155	5.00E-09	0.007733	0.003661	0.034651	0.014553	0.002703	7.44E-08	5.44E-08	0.133938	
2	DPYSL5	rs920435	26,934,920	C	T	0.332029	0.012031	0.002157	4.60E-09	0.007892	0.003662	0.031184	0.014526	0.002706	8.11E-08	5.40E-08	0.145131	
2	DPYSL5	rs12615423	26,935,755	T	G	0.332568	0.012026	0.002156	4.60E-09	0.007797	0.003661	0.033198	0.01454	0.002704	7.72E-08	5.43E-08	0.138423	
2	DPYSL5	rs1992313	26,936,473	G	A	0.332539	0.01207	0.002156	4.20E-09	0.007791	0.003661	0.033338	0.014597	0.002704	6.88E-08	4.88E-08	0.134776	
2	DPYSL5	rs7589627	26,936,918	C	T	0.335545	0.012361	0.002162	1.60E-09	0.008351	0.003671	0.022921	0.014648	0.002712	6.76E-08	3.47E-08	0.167687	
2	DPYSL5	rs6759548	26,938,192	A	G	0.332528	0.012056	0.002156	4.40E-09	0.007838	0.003661	0.032302	0.014574	0.002704	7.23E-08	4.98E-08	0.138865	
2	DPYSL5	rs72804857	26,938,608	C	G	0.166268	0.017104	0.002718	7.80E-11	0.017103	0.004646	0.000234	0.016426	0.003398	1.36E-06	9.60E-09	0.906414	
2	DPYSL5	rs6718978	26,938,723	G	A	0.332503	0.012073	0.002156	4.20E-09	0.007836	0.003662	0.032399	0.014609	0.002704	6.75E-08	4.67E-08	0.136765	
2	DPYSL5	rs3739085	26,940,176	T	C	0.32861	0.011971	0.002164	5.20E-09	0.007646	0.003676	0.037542	0.0145	0.002714	9.33E-08	7.26E-08	0.133586	
2	DPYSL5	rs3820823	26,941,938	G	A	0.32825	0.011993	0.002164	5.50E-09	0.007753	0.003677	0.035008	0.014484	0.002713	9.58E-08	7.01E-08	0.140757	
2	DPYSL5	rs3739086	26,942,334	C	T	0.334977	0.013196	0.002162	1.50E-10	0.008586	0.003676	0.019543	0.015763	0.00271	6.13E-09	2.93E-09	0.116604	
2	DPYSL5	rs6707735	26,943,954	T	C	0.327873	0.012372	0.002164	1.70E-09	0.008229	0.003677	0.025264	0.014904	0.002713	4.02E-08	2.28E-08	0.144044	
2	DPYSL5	rs6708148	26,944,452	A	G	0.328067	0.012289	0.002163	2.20E-09	0.008166	0.003677	0.026363	0.014819	0.002712	4.77E-08	2.79E-08	0.145369	
2	DPYSL5	rs3739088	26,944,916	T	C	0.328668	0.01217	0.002162	3.10E-09	0.007621	0.003675	0.03814	0.014874	0.002711	4.19E-08	3.38E-08	0.112222	
2	MAPRE3 *	rs10181777	26,964,386	A	G	0.191435	0.014424	0.002565	1.20E-08	0.011687	0.004372	0.00754	0.015065	0.00321	2.74E-06	4.65E-04	0.533484	
2	MAPRE3 *	rs62130501	26,966,629	T	C	0.154602	0.015763	0.002787	7.70E-09	0.01453	0.004757	0.002265	0.015448	0.003485	9.46E-06	5.11E-07	0.87635	
2	MAPRE3 *	rs12471037	26,968,343	T	C	0.154595	0.015775	0.002787	8.20E-09	0.014521	0.004759	0.002289	0.015445	0.003487	9.56E-06	5.22E-07	0.875484	
2	MAPRE3 *	rs7564363	26,968,605	A	G	0.154598	0.015771	0.002787	8.20E-09	0.014513	0.004759	0.002301	0.015443	0.003487	9.58E-06	5.25E-07	0.874697	
2	MAPRE3 *	rs12714026	26,969,333	T	C	0.154561	0.015725	0.002788	9.20E-09	0.014335	0.00476	0.002607	0.015477	0.003487	9.16E-06	5.64E-07	0.846454	
2	MAPRE3 *	rs7568733	26,970,140	A	T	0.154614	0.015771	0.002788	8.10E-09	0.014541	0.004759	0.002258	0.015441	0.003487	9.62E-06	5.18E-07	0.878762	
2	MAPRE3	rs17005732	26,976,553	C	A	0.153791	0.015503	0.002795	1.60E-08	0.014085	0.004777	0.003203	0.015252	0.003494	1.29E-05	9.44E-07	0.84361	
2	MAPRE3	rs10207573	27,020,067	C	G	0.155224	0.016002	0.002783	4.00E-09	0.014605	0.004758	0.002153	0.015708	0.003479	6.43E-06	3.37E-07	0.851479	
2	MAPRE3	rs10865456	27,023,417	C	T	0.155495	0.015793	0.002781	6.10E-09	0.013747	0.004752	0.003832	0.015856	0.003476	5.16E-06	4.63E-07	0.720323	
2	TMEM214 *	rs34732613	27,031,928	T	C	0.236641	0.012717	0.002382	4.10E-08	0.011672	0.004055	0.004012	0.012637	0.002984	2.32E-05	2.03E-06	0.84801	
2	TMEM214	rs2304714	27,035,383	G	T	0.161598	0.016952	0.002746	3.60E-10	0.015229	0.004691	0.001175	0.01684	0.003433	9.51E-07	3.07E-08	0.781616	
2	TMEM214	rs2304713	27,035,893	G	C	0.161647	0.016965	0.002745	3.50E-10	0.015209	0.004691	0.001192	0.016859	0.003432	9.19E-07	3.01E-08	0.776432	
2	TMEM214 *	rs7584145	27,044,380	A	C	0.237003	0.012644	0.002375	4.80E-08	0.011182	0.004042	0.00568	0.012815	0.002976	1.68E-05	2.05E-06	0.744931	
2	TMEM214 *	rs4665940	27,046,646	C	G	0.143702	0.016108	0.002923	4.10E-08	0.010728	0.004985	0.031395	0.018377	0.003659	5.20E-07	3.28E-07	0.216085	
2	AGBL5 *	rs11679069	27,047,443	G	A	0.23734	0.012702	0.002374	4.20E-08	0.011301	0.004041	0.005175	0.012852	0.002975	1.58E-05	1.77E-06	0.757237	
2	AGBL5-AS1	rs11126836	27,050,260	C	T	0.237349	0.012724	0.002374	4.00E-08	0.011344	0.00404	0.005006	0.012858	0.002975	1.57E-05	1.71E-06	0.762775	
2	AGBL5 *	rs11680096	27,050,703	T	C	0.235124	0.012846	0.002389	3.70E-08	0.010583	0.004068	0.009308	0.013455	0.002991	6.96E-06	1.37E-06	0.56949	
2	AGBL5	rs3806520	27,053,334	G	A	0.237374	0.012666	0.002374	4.40E-08	0.011317	0.00404	0.005102	0.012792	0.002975	1.73E-05	1.91E-06	0.768836	
2	AGBL5	rs2728593	27,056,145	G	A	0.161732	0.016876	0.002743	4.00E-10	0.014835	0.004681	0.001537	0.016918	0.003432	8.37E-07	3.48E-08	0.71968	
2	AGBL5	rs7560144	27,057,592	A	G	0.23524	0.012764	0.002381	4.10E-08	0.011816	0.004054	0.003576	0.012799	0.002983	1.81E-05	1.44E-06	0.845063	
2	AGBL5	rs6547401	27,061,977	A	G	0.237501	0.012917	0.002376	2.40E-08	0.011661	0.004042	0.003928	0.012986	0.002977	1.30E-05	1.15E-06	0.791787	
2	AGBL5	rs13014240	27,063,530	G	C	0.236944	0.013078	0.002379	1.70E-08	0.012343	0.004048	0.002303	0.012885	0.00298	1.56E-05	8.36E-07	0.914177	
2	AGBL5	rs7078809	27,066,047	C	T	0.236805	0.013004	0.002377	2.10E-08	0.012516	0.004045	0.001983	0.012673	0.002979	2.12E-05	9.80E-07	0.97501	
2	AGBL5	rs35874715	27,068,193	G	A	0.159244	0.017084	0.002761	3.30E-10	0.01622	0.004715	0.000586	0.016667	0.003453	1.41E-06	2.35E-08	0.938919	
2	AGBL5	rs7575465	27,068,793	G	A	0.234801	0.012996	0.002384	2.40E-08	0.01263	0.004058	0.001866	0.012726	0.002986	2.06E-05	9.00E-07	0.984791	
2	AGBL5	rs10865461	27,069,783	T	C	0.234751	0.013018	0.002384	2.30E-08	0.012671	0.004059	0.001808	0.012738	0.002987	2.03E-05	8.61E-07	0.989467	
2	AGBL5	rs1053609	27,070,282	G	T	0.236808	0.013032	0.002377	1.90E-08	0.012545	0.004045	0.001937	0.012698	0.002979	2.05E-05	9.26E-07	0.975725	
2	OST4 *	rs4665943	27,073,017	T	C	0.234667	0.013152	0.002385	1.80E-08	0.012862	0.00406	0.001544	0.012853	0.002987	1.71E-05	6.33E-07	0.998575	
2	OST4 *	rs11126857	27,074,889	A	G	0.234891	0.013025	0.002384	2.30E-08	0.012743	0.004058	0.001698	0.012708	0.002986	2.11E-05	8.43E-07	0.994518	
2	EMILIN1 *	rs11679681	27,075,611	C	A	0.241172	0.01324	0.002382	1.20E-08	0.011596	0.004053	0.00423	0.013573	0.002984	5.49E-06	5.37E-07	0.694426	
2	EMILIN1 *	rs3754734	27,076,730	G	T	0.237305	0.013075	0.002377	1.80E-08	0.012381	0.004046	0.00222	0.012866	0.002978	1.58E-05	8.18E-07	0.922987	
2	EMILIN1	rs2011616	27,07															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	CGREF1	rs13423359	27,112,032	T	G	0.243004	0.014948	0.002373	1.10E-10	0.014314	0.004038	0.000395	0.014792	0.002974	6.68E-07	7.92E-09	0.924024	
2	CGREF1	rs1866559	27,112,718	C	T	0.241207	0.015242	0.002377	5.70E-11	0.014669	0.004046	0.000291	0.01513	0.002978	3.85E-07	3.49E-09	0.926968	
2	CGREF1	rs7582361	27,113,508	C	T	0.241428	0.015116	0.002377	8.20E-11	0.014351	0.004046	0.000392	0.015117	0.002979	3.95E-07	4.73E-09	0.878737	
2	CGREF1	rs12174094	27,113,564	C	A	0.241432	0.015115	0.002377	8.30E-11	0.01435	0.004046	0.000392	0.015116	0.002979	3.96E-07	4.75E-09	0.878895	
2	CGREF1	rs12617392	27,113,959	A	C	0.239056	0.01509	0.002391	1.10E-10	0.013772	0.004067	0.000713	0.015456	0.002996	2.53E-07	5.38E-09	0.738926	
2	CGREF1	rs6749216	27,117,951	C	T	0.239331	0.01566	0.002389	2.70E-11	0.01485	0.004065	0.000261	0.015737	0.002994	1.51E-07	1.27E-09	0.860621	
2	CGREF1	rs6746337	27,118,195	T	A	0.239347	0.0157	0.00239	2.60E-11	0.014888	0.004065	0.000252	0.015784	0.002995	1.39E-07	1.14E-09	0.85903	
2	CGREF1 *	rs7560633	27,119,199	C	G	0.239393	0.015518	0.002392	3.90E-11	0.014683	0.004068	0.000309	0.015644	0.002998	1.84E-07	1.81E-09	0.849169	
2	ABHD1 *	rs11126871	27,121,589	A	T	0.238658	0.015965	0.002396	1.60E-11	0.015225	0.004075	0.000189	0.016018	0.003003	9.84E-08	6.19E-10	0.875585	
2	ABHD1 *	rs7605526	27,122,616	A	G	0.236931	0.016001	0.002415	2.10E-11	0.014628	0.004111	0.000375	0.016364	0.003026	6.52E-08	7.93E-10	0.733855	
2	ABHD1	rs4665946	27,125,063	A	C	0.299935	0.020584	0.002211	2.30E-21	0.020765	0.00376	3.41E-08	0.019712	0.002772	1.20E-12	2.49E-18	0.821545	
2	ABHD1	rs4665947	27,125,161	C	T	0.301075	0.020724	0.002216	2.30E-21	0.020647	0.003767	4.33E-08	0.019996	0.002777	6.27E-13	1.66E-18	0.889354	
2	ABHD1	rs6741646	27,125,330	T	C	0.307646	0.020331	0.002187	3.10E-21	0.020377	0.003723	4.52E-08	0.019446	0.00274	1.34E-12	3.64E-18	0.840374	
2	ABHD1	rs12467319	27,125,819	C	T	0.299538	0.019646	0.002198	9.00E-20	0.019512	0.003745	1.93E-07	0.019082	0.002753	4.31E-12	4.69E-17	0.926254	
2	ABHD1	rs1866561	27,128,411	G	A	0.299587	0.020194	0.002195	6.80E-21	0.020062	0.003741	8.41E-08	0.019698	0.002749	8.03E-13	4.03E-18	0.937555	
2	ABHD1	rs2304678	27,130,639	C	G	0.163268	0.021184	0.002735	2.50E-15	0.02028	0.004664	1.39E-05	0.021116	0.003423	7.10E-10	4.27E-13	0.885134	
2	PREB	rs11695930	27,132,103	T	C	0.162272	0.021031	0.002745	6.10E-15	0.020163	0.004683	1.69E-05	0.020875	0.003435	1.27E-09	9.06E-13	0.902477	
2	PREB	rs2289358	27,133,123	T	G	0.16272	0.021215	0.002746	2.70E-15	0.019559	0.00468	2.96E-05	0.021503	0.003438	4.13E-10	5.19E-13	0.737885	
2	PREB	rs2289359	27,133,410	C	T	0.162791	0.021284	0.002746	2.10E-15	0.019587	0.00468	2.88E-05	0.021613	0.003439	3.38E-10	4.15E-13	0.72722	
2	PREB *	rs11678061	27,134,751	T	C	0.162779	0.021266	0.002748	2.50E-15	0.019376	0.004682	3.53E-05	0.021705	0.003441	2.93E-10	4.39E-13	0.688544	
2	PRR30	rs11121	27,137,019	C	T	0.294392	0.01754	0.00223	1.30E-15	0.019409	0.003796	3.24E-07	0.01635	0.002794	4.97E-09	7.69E-14	0.516424	
2	PRR30	rs2304680	27,138,378	T	C	0.157753	0.020732	0.002783	3.40E-14	0.01949	0.004741	3.99E-05	0.021176	0.003485	1.27E-09	2.06E-12	0.774478	
2	PRR30	rs3795961	27,139,079	A	G	0.157892	0.020689	0.002784	3.70E-14	0.019533	0.004742	3.85E-05	0.021067	0.003486	1.55E-09	2.42E-12	0.794372	
2	PRR30 *	rs11691585	27,139,503	G	A	0.160123	0.021159	0.002769	6.90E-15	0.019574	0.004714	3.33E-05	0.021673	0.003468	4.25E-10	5.97E-13	0.719769	
2	PRR30 *	rs7574004	27,140,243	C	T	0.295179	0.018123	0.002231	1.50E-16	0.01944	0.003793	3.04E-07	0.017161	0.002796	8.67E-10	1.32E-14	0.628797	
2	PRR30 *	rs2439076	27,142,694	T	C	0.294701	0.018026	0.002228	2.00E-16	0.019027	0.003788	5.20E-07	0.017291	0.002792	6.11E-10	1.57E-14	0.712267	
2	PRR30 *	rs1659677	27,142,747	A	G	0.294752	0.018036	0.002228	1.90E-16	0.01895	0.003788	5.78E-07	0.017337	0.002793	5.52E-10	1.57E-14	0.73178	
2	PRR30 *	rs1659711	27,143,540	C	A	0.298767	0.018142	0.002221	8.70E-17	0.018952	0.003776	5.28E-07	0.017381	0.002785	4.45E-10	1.17E-14	0.737778	
2	TCF23 *	rs1298360	27,144,930	T	C	0.157821	0.020993	0.002784	1.70E-14	0.019499	0.004745	4.01E-05	0.021537	0.003486	6.65E-10	1.10E-12	0.72932	
2	TCF23 *	rs4665950	27,145,435	A	G	0.157818	0.020977	0.002784	1.80E-14	0.019459	0.004745	4.16E-05	0.02155	0.003486	6.50E-10	1.12E-12	0.722602	
2	TCF23 *	rs1275518	27,145,623	G	A	0.16018	0.021388	0.002769	3.70E-15	0.019589	0.004717	3.33E-05	0.021999	0.003468	2.33E-10	3.30E-13	0.68067	
2	TCF23 *	rs1275515	27,147,364	C	T	0.160168	0.021475	0.00277	2.90E-15	0.019701	0.004717	3.00E-05	0.022086	0.003469	1.98E-10	2.56E-13	0.683695	
2	TCF23 *	rs1275514	27,147,662	C	T	0.158784	0.021559	0.002793	2.80E-15	0.020217	0.004758	2.17E-05	0.021853	0.003497	4.26E-10	3.98E-13	0.781687	
2	TCF23 *	rs7606672	27,147,737	C	G	0.160165	0.021429	0.00277	3.40E-15	0.019702	0.004718	3.00E-05	0.022006	0.003469	2.32E-10	2.99E-13	0.69397	
2	TCF23 *	rs1275513	27,148,102	T	C	0.295831	0.018856	0.002228	7.90E-18	0.020133	0.003787	1.08E-07	0.01797	0.002794	1.30E-10	7.59E-16	0.64591	
2	TCF23	rs1275511	27,150,802	T	C	0.305759	0.016661	0.002217	2.90E-14	0.017824	0.003772	2.34E-06	0.015967	0.002778	9.30E-09	7.92E-13	0.691807	
2	TCF23	rs1275510	27,150,871	A	G	0.157043	0.021516	0.002796	6.00E-15	0.019521	0.00477	4.31E-05	0.022345	0.003499	1.75E-10	3.20E-13	0.633091	
2	TCF23	rs1275509	27,151,141	G	A	0.307092	0.016272	0.002213	1.10E-13	0.017315	0.003767	4.37E-06	0.015567	0.002773	2.03E-08	7.70E-08	0.708598	
2	TCF23	rs1275508	27,151,551	C	A	0.156786	0.0215	0.002797	5.80E-15	0.019615	0.004772	3.99E-05	0.022221	0.003499	2.22E-10	3.76E-13	0.659697	
2	SLC5A6 *	rs74684611	27,191,771	C	T	0.104577	-0.030955	0.003361	2.30E-21	-0.039214	0.005666	4.67E-12	-0.025649	0.004233	1.41E-09	4.25E-19	0.055147	
2	CAD *	rs118130043	27,245,399	G	A	0.043899	0.035039	0.004997	3.80E-13	0.02869	0.008552	0.000799	0.038031	0.006242	1.14E-09	3.13E-11	0.377604	
2	TRIM54	rs76147177	27,286,115	C	T	0.042929	0.0297	0.00502	4.40E-09	0.027765	0.008514	0.001116	0.028816	0.006302	4.89E-06	1.41E-07	0.920915	
2	TRIM54	rs189387480	27,292,538	T	A	0.025387	-0.04112	0.006443	5.90E-12	-0.048514	0.010966	9.82E-06	-0.037498	0.008072	3.45E-06	1.16E-09	0.418554	
2	MPV17	rs146502189	27,322,314	T	G	0.031976	-0.039853	0.005727	3.30E-13	-0.043105	0.009709	9.13E-06	-0.039385	0.00719	4.41E-08	1.60E-11	0.758155	
2	GTF3C2	rs201232671	27,348,271	G	A	0.040449	0.038281	0.005205	6.40E-14	0.029389	0.008904	0.000969	0.042456	0.006504	6.90E-11	2.40E-12	0.235967	
2	PPM1G	rs140391935	27,387,603	T	C	0.044801	0.038113	0.004933	1.10E-15	0.030057	0.008502	0.00041	0.041703	0.00614	1.14E-11	1.85E-13	0.266739	
2	PPM1G	rs17060049	27,389,375	A	G	0.070626	0.021476	0.003945	4.10E-08	0.019282	0.006738	0.004228	0.022147	0.004933	7.25E-06	7.01E-07	0.731551	
2	PPM1G	rs79803862	27,399,271	A	T	0.06668	-0.03788	0.004107	4.00E-22	-0.042415	0.006991	1.34E-09	-0.034735	0.005145	1.53E-11	1.29E-18	0.137621	
2	PPM1G *	rs1728918	27,412,596	A	G	0.028816	0.02666	0.002476	5.90E-28	0.025402	0.004216	1.73E-09	0.027564	0.003102	6.69E-19	9.29E-26	0.679507	
2	NRBP1 *	rs147558391	27,427,727	T	A	0.019467	-0.045181	0.007314	6.50E-10	-0.052462	0.012772	4.04E-05	-0.040908	0.009041	6.13E-06	0.640279	0.776E-09	
2	IFT172	rs117414910	27,455,222	T	C	0.047282	0.039239	0.004799	1.80E-17	0.033343	0.008228	5.13E-05	0.041596	0.005988	3.89E-12	9.04E-15	0.417349	
2	IFT172	rs140257887	27,456,289	T	C	0.027198	-0.044315	0.006201	4.90E-14	-0.048389	0.01058	4.86E-06	-0.043251	0.007758	2.54E-08	5.11E-12	0.695336	
2	IFT172	rs141875753	27,478,462	G	A	0.020805	0.044549	0.00706	2.70E-11	0.046499	0.012061	0.000117	0.044131	0.008827	5.86E-07	2.21E-09	0.874105	
2	IFT172	rs150202539	27,489,531	T	A	0.026183	-0.037633	0.006331	8.60E-09	-0.042912	0.010812	7.29E-05	-0.03359	0.007918	2.24E-05	4.69E-08	0.486648	
2	GCKR	rs1260326	27,508,073	T	C	0.492771	0.059432	0.002013	4.30E-204	0.064916	0.003425	4.65E-80	0.056667	0.002522	1.03E-111	2.44E-188	0.052469	
2	GCKR	rs3817588	27,508,345	C	T	0.35755	-0.055891	0.0021	3.70E-165	-0.061368	0.003553	8.79E-67	-0.052613	0.002639	2.24E-88	8.30E-152	0.047933	F
2	GCKR	rs146716184	27,508															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	GCKR *	rs7606605	27,532,849	T	A	0.210882	0.027045	0.002507	2.70E-29	0.028857	0.004277	1.57E-11	0.026594	0.003138	2.46E-17	3.28E-26	0.669758	
2	GCKR *	rs4665987	27,532,958	A	G	0.472462	0.044819	0.002019	1.30E-114	0.051069	0.003431	4.54E-50	0.041091	0.002531	3.37E-59	4.71E-106	0.019283	F
2	GCKR *	rs4665381	27,534,283	A	C	0.148752	-0.015743	0.002829	8.70E-09	-0.014253	0.00482	0.003119	-0.016455	0.003543	3.47E-06	2.62E-07	0.127777	
2	GCKR *	rs10181342	27,534,476	G	A	0.375851	-0.039567	0.00208	2.00E-84	-0.047454	0.003529	3.58E-41	-0.034914	0.00261	9.29E-41	7.85E-79	0.004294	M
2	GCKR *	rs149454845	27,536,953	C	T	0.021761	-0.044969	0.006926	3.40E-11	-0.054809	0.011802	3.47E-06	-0.041302	0.008671	1.94E-06	2.46E-10	0.356385	
2	GCKR *	rs4665988	27,538,569	A	C	0.472629	0.044843	0.002018	9.30E-115	0.051135	0.003431	3.36E-50	0.041082	0.002531	3.25E-59	3.36E-106	0.018387	F
2	GCKR *	rs116443177	27,541,255	T	C	0.377609	-0.039373	0.002078	1.20E-83	-0.046743	0.003526	4.60E-40	-0.034962	0.002608	6.30E-41	6.75E-78	0.007249	F
2	GCKR *	rs62131881	27,541,914	T	G	0.375722	-0.039574	0.00208	1.80E-84	-0.047486	0.003529	3.09E-41	-0.0349	0.00261	9.58E-41	6.99E-79	0.004149	M
2	GCKR *	rs62131882	27,542,613	C	T	0.377298	-0.039402	0.002077	6.70E-84	-0.046877	0.003524	2.46E-40	-0.034986	0.002607	4.94E-41	2.85E-78	0.006688	F
2	GCKR *	rs12473139	27,542,720	C	T	0.473538	0.045119	0.002017	2.80E-116	0.051518	0.00343	5.90E-51	0.041298	0.002529	6.77E-60	1.24E-107	0.01649	F
2	GCKR *	rs4665991	27,543,417	A	G	0.473113	0.04501	0.002019	1.50E-115	0.051388	0.003432	1.25E-50	0.041185	0.002531	1.77E-59	6.88E-107	0.016764	F
2	GCKR *	rs1972669	27,544,240	T	G	0.148798	-0.015684	0.002829	9.80E-09	-0.014268	0.00482	0.003084	-0.016356	0.003542	3.94E-06	2.93E-07	0.72698	
2	GCKR *	rs4493210	27,545,205	G	T	0.150276	-0.015516	0.002819	1.30E-08	-0.013464	0.004803	0.005076	-0.016559	0.003529	2.75E-06	3.26E-07	0.603617	
2	GCKR *	rs62141278	27,545,514	T	C	0.378041	-0.039248	0.002078	2.60E-83	-0.046761	0.003525	3.99E-40	-0.034846	0.002608	1.10E-40	1.02E-77	0.006591	F
2	GCKR *	rs1080060	27,545,941	T	A	0.148802	-0.015688	0.002829	9.70E-09	-0.014271	0.00482	0.003077	-0.016365	0.003542	3.89E-06	2.89E-07	0.726273	
2	GCKR *	rs61185615	27,546,345	C	T	0.146895	-0.015462	0.002848	2.00E-08	-0.013039	0.004857	0.007282	-0.016626	0.003563	3.12E-06	5.51E-07	0.551535	
2	GCKR *	rs59210625	27,546,607	C	A	0.211089	0.027012	0.002506	2.60E-29	0.028924	0.004275	1.37E-11	0.026507	0.003136	3.02E-17	3.51E-26	0.64847	
2	GCKR *	rs62141279	27,548,548	T	C	0.376719	-0.039451	0.002079	6.60E-84	-0.046834	0.003528	3.56E-40	-0.035087	0.002609	3.47E-41	2.90E-78	0.007445	F
2	GCKR *	rs6749052	27,550,012	A	T	0.150348	-0.015058	0.002822	3.30E-08	-0.01415	0.004809	0.003269	-0.015414	0.003533	1.30E-05	9.68E-07	0.832236	
2	C2orf16 *	rs2384626	27,550,781	A	G	0.148825	-0.015722	0.002829	8.80E-09	-0.014294	0.00482	0.003031	-0.016413	0.003542	3.64E-06	2.67E-07	0.723064	
2	C2orf16 *	rs2384627	27,551,582	A	G	0.375911	-0.039106	0.002079	2.50E-82	-0.046622	0.003526	7.28E-40	-0.034687	0.002609	2.74E-40	4.61E-77	0.006529	F
2	C2orf16 *	rs1820297	27,552,057	A	G	0.151051	-0.015206	0.002811	2.60E-08	-0.013897	0.004789	0.003719	-0.015794	0.003519	7.30E-06	6.28E-07	0.749579	
2	C2orf16 *	rs62141281	27,554,784	T	G	0.376692	-0.039208	0.002076	5.40E-83	-0.046797	0.003523	3.21E-40	-0.034722	0.002606	1.81E-40	1.35E-77	0.005874	F
2	C2orf16 *	rs6750943	27,555,037	T	G	0.151329	-0.015012	0.002809	3.80E-08	-0.01345	0.004784	0.004945	-0.015711	0.003518	8.10E-06	8.98E-07	0.70346	
2	C2orf16 *	rs6761095	27,555,143	G	T	0.151095	-0.015195	0.00281	2.60E-08	-0.013937	0.004788	0.003617	-0.015741	0.003519	7.80E-06	6.53E-07	0.761385	
2	C2orf16 *	rs6751087	27,555,149	C	T	0.376693	-0.039208	0.002076	5.30E-83	-0.046797	0.003523	3.21E-40	-0.034723	0.002606	1.80E-40	1.34E-77	0.00588	F
2	C2orf16 *	rs6706610	27,555,224	G	A	0.151098	-0.0152	0.00281	2.60E-08	-0.01395	0.004788	0.003586	-0.015741	0.003519	7.80E-06	6.47E-07	0.762985	
2	C2orf16 *	rs12995461	27,555,300	C	A	0.472051	0.044816	0.002016	1.70E-114	0.051402	0.003427	8.21E-51	0.040844	0.002528	1.17E-58	2.95E-106	0.013183	F
2	C2orf16 *	rs10169065	27,555,693	G	A	0.472051	0.044816	0.002016	1.70E-114	0.051403	0.003427	8.17E-51	0.040844	0.002528	1.17E-58	2.93E-106	0.013174	F
2	C2orf16 *	rs10179872	27,555,705	A	G	0.470849	0.044596	0.002018	2.10E-113	0.050921	0.003429	7.92E-50	0.040797	0.00253	1.82E-58	4.39E-105	0.017527	F
2	C2orf16 *	rs79414972	27,558,930	G	A	0.364267	-0.03797	0.002114	2.90E-75	-0.046041	0.00359	1.31E-37	-0.033205	0.002651	6.10E-36	1.71E-70	0.004037	M
2	C2orf16 *	rs62141288	27,560,331	A	G	0.354775	-0.037243	0.002129	3.40E-71	-0.044522	0.003617	8.76E-35	-0.0329	0.00267	7.49E-35	1.33E-66	0.009749	F
2	C2orf16 *	rs62141290	27,560,525	C	T	0.374975	-0.039162	0.002082	2.30E-82	-0.046848	0.003533	4.43E-40	-0.034683	0.002612	3.36E-40	3.45E-77	0.005647	F
2	C2orf16 *	rs6547709	27,560,551	G	A	0.15122	-0.01531	0.002809	2.10E-08	-0.013948	0.004784	0.003565	-0.015895	0.003518	6.33E-06	5.27E-07	0.743036	
2	C2orf16 *	rs4665382	27,560,934	C	T	0.472066	0.044804	0.002017	2.10E-114	0.05136	0.003427	1.01E-50	0.040843	0.002529	1.22E-58	3.79E-106	0.01356	F
2	C2orf16 *	rs62141291	27,561,167	T	C	0.376712	-0.039137	0.002076	1.10E-82	-0.046756	0.003523	3.67E-40	-0.034642	0.002605	2.65E-40	2.26E-77	0.005711	F
2	C2orf16 *	rs62141292	27,561,433	C	A	0.376707	-0.039142	0.002076	1.10E-82	-0.046772	0.003523	3.44E-40	-0.034642	0.002605	2.65E-40	2.12E-77	0.005646	F
2	C2orf16 *	rs7570476	27,561,791	T	C	0.471999	0.044775	0.002017	3.20E-114	0.051433	0.003427	7.37E-51	0.040754	0.002528	2.12E-58	4.81E-106	0.012189	F
2	C2orf16 *	rs10208529	27,563,321	T	A	0.472007	0.044767	0.002017	3.60E-114	0.051432	0.003427	7.38E-51	0.040742	0.002528	2.29E-58	5.20E-106	0.012093	F
2	C2orf16 *	rs60854669	27,564,062	C	T	0.376686	-0.039144	0.002076	1.00E-82	-0.046736	0.003523	4.03E-40	-0.034668	0.002605	2.32E-40	2.17E-77	0.005901	F
2	C2orf16 *	rs12714204	27,564,673	T	C	0.151183	-0.015167	0.002809	2.80E-08	-0.014077	0.004785	0.003277	-0.015591	0.003518	9.50E-06	7.20E-07	0.798723	
2	C2orf16 *	rs965813	27,566,994	A	T	0.376663	-0.039132	0.002076	1.20E-82	-0.046719	0.003523	4.30E-40	-0.034657	0.002605	2.49E-40	2.48E-77	0.005927	F
2	C2orf16 *	rs4665383	27,568,688	G	C	0.472011	0.044768	0.00217	3.50E-114	0.051432	0.003427	7.38E-51	0.040742	0.002528	2.29E-58	5.19E-106	0.012091	F
2	C2orf16 *	rs59876138	27,569,456	C	A	0.376673	-0.039138	0.002076	1.10E-82	-0.046713	0.003523	4.42E-40	-0.034673	0.002606	2.30E-40	2.36E-77	0.00602	F
2	C2orf16 *	rs7577311	27,571,054	T	G	0.472218	0.04478	0.00217	3.50E-114	0.051403	0.003429	9.30E-51	0.040802	0.002529	1.72E-58	4.91E-106	0.012861	F
2	C2orf16 *	rs4260197	27,571,283	C	G	0.151198	-0.015202	0.002809	2.50E-08	-0.014004	0.004785	0.003436	-0.015678	0.003518	8.47E-06	6.73E-07	0.778011	
2	C2orf16 *	rs10205364	27,571,366	C	T	0.151219	-0.015203	0.002809	2.50E-08	-0.014051	0.004784	0.003326	-0.015666	0.003519	8.61E-06	6.64E-07	0.785616	
2	C2orf16 *	rs10165098	27,573,659	C	T	0.151191	-0.015174	0.002809	2.70E-08	-0.014004	0.004785	0.003436	-0.015638	0.003519	8.93E-06	7.09E-07	0.783207	
2	C2orf16 *	rs6704596	27,574,060	G	A	0.376681	-0.039139	0.002076	1.10E-82	-0.046713	0.003523	4.42E-40	-0.034675	0.002605	2.27E-40	2.33E-77	0.006027	F
2	C2orf16	rs1919125	27,578,536	C	G	0.15156	-0.014975	0.002807	3.80E-08	-0.013686	0.004782	0.004222	-0.015459	0.003516	1.11E-05	1.05E-06	0.765193	
2	C2orf16	rs1919126	27,578,551	C	A	0.151562	-0.014979	0.002807	3.70E-08	-0.013693	0.004782	0.004203	-0.015459	0.003516	1.11E-05	1.05E-06	0.766039	
2	C2orf16	rs1919127	27,578,626	C	T	0.471991	0.04469	0.002016	6.90E-114	0.051277	0.003426	1.33E-50	0.04068	0.002528	3.13E-58	1.27E-105	0.012826	F
2	C2orf16	rs1919128	27,578,892	G	A	0.472037	0.044668	0.002016	8.30E-114	0.051269	0.003426	1.36E-50	0.040663	0.002527	3.38E-58	1.41E-105	0.012744	F
2	C2orf16	rs3811644	27,579,938	G	A	0.376664	-0.039164	0.002076	7.90E-83	-0.046638	0.003523	5.70E-40	-0.034742	0.002605	1.59E-40	2.10E-77	0.00664	F
2	ZNF512	rs62138961	27,584,547	G	C	0.148968	-0.015214	0.002826	3.40E-08	-0.014311	0.004813	0.002959	-0.015588	0.00354	1.08E-05	7.42E-07	0.830729	
2	ZNF512	rs13026621	27,584,757	G	A	0.150497	-0.015045	0.002814	3.70E-08	-0.014524	0.004792	0.002449	-0.015178	0.003524	1.68E-05	9.49E-07	0.9	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
2	ZNF512	rs62138968	27,601,618	G	C	0.376641	-0.039172	0.002076	7.60E-83	-0.046646	0.003523	5.54E-40	-0.034741	0.002605	1.56E-40	2.01E-77	0.006598	F
2	ZNF512	rs7604798	27,602,073	T	C	0.150517	-0.014959	0.002814	4.30E-08	-0.014432	0.004793	0.002615	-0.015083	0.003524	1.89E-05	1.13E-06	0.912792	
2	ZNF512	rs12467476	27,602,848	C	T	0.471495	0.044394	0.002017	2.10E-112	0.050993	0.003429	5.60E-50	0.040415	0.002529	1.93E-57	3.27E-104	0.013052	F
2	ZNF512	rs12464616	27,604,225	T	C	0.472781	0.044648	0.002016	1.10E-113	0.051483	0.003426	5.33E-51	0.040532	0.002528	8.16E-58	1.33E-105	0.010126	F
2	ZNF512	rs2141372	27,604,329	T	G	0.376666	-0.039172	0.002076	8.60E-83	-0.046576	0.003523	7.35E-40	-0.034775	0.002605	1.34E-40	2.28E-77	0.007092	F
2	ZNF512	rs62138969	27,605,425	G	A	0.150514	-0.014996	0.002814	3.90E-08	-0.014391	0.004792	0.002685	-0.015195	0.003524	1.64E-05	1.01E-06	0.892402	
2	ZNF512	rs6719960	27,607,200	G	A	0.376629	-0.039199	0.002076	6.30E-83	-0.046693	0.003523	4.70E-40	-0.034759	0.002605	1.45E-40	1.58E-77	0.006473	F
2	ZNF512	rs6547734	27,608,123	G	T	0.150878	-0.015019	0.002811	3.70E-08	-0.014464	0.004788	0.00253	-0.015149	0.003521	1.71E-05	9.95E-07	0.90811	
2	ZNF512	rs6547735	27,608,740	C	T	0.376625	-0.039224	0.002076	5.10E-83	-0.046707	0.003523	4.50E-40	-0.034793	0.002605	1.23E-40	1.28E-77	0.006561	F
2	ZNF512	rs2384656	27,609,188	G	A	0.472792	0.044691	0.002016	6.40E-114	0.05152	0.003426	4.58E-51	0.040578	0.002528	6.12E-58	8.61E-106	0.010185	F
2	ZNF512	rs1881397	27,609,418	G	A	0.377062	-0.039265	0.002077	4.20E-83	-0.046398	0.003525	1.61E-39	-0.035021	0.002606	4.09E-41	1.53E-77	0.00948	F
2	ZNF512	rs74175068	27,610,635	C	T	0.459228	0.044264	0.00206	2.20E-107	0.050506	0.003498	3.19E-47	0.040436	0.002584	3.64E-55	3.36E-99	0.020594	F
2	ZNF512	rs34016998	27,610,820	T	C	0.472149	0.044629	0.002016	1.30E-113	0.051528	0.003427	4.62E-51	0.040496	0.002527	9.95E-58	1.41E-105	0.009584	F
2	ZNF512	rs12987055	27,611,285	C	T	0.472459	0.044492	0.002016	6.80E-113	0.051092	0.003426	3.00E-50	0.040558	0.002528	6.99E-58	6.38E-105	0.013371	F
2	ZNF512	rs4665999	27,611,577	T	C	0.150896	-0.014932	0.002811	4.40E-08	-0.014413	0.004788	0.00262	-0.015049	0.00352	1.93E-05	1.16E-06	0.914736	
2	ZNF512	rs13405762	27,611,748	C	A	0.374292	-0.038848	0.002084	5.10E-81	-0.046799	0.003536	6.01E-40	-0.034262	0.002615	3.52E-39	4.84E-76	0.004376	M
2	ZNF512	rs78170284	27,612,215	A	G	0.376951	-0.038889	0.002076	1.20E-81	-0.04638	0.003524	1.58E-39	-0.03448	0.002606	6.20E-40	2.25E-76	0.006633	F
2	ZNF512	rs13020949	27,613,738	T	C	0.47227	0.044399	0.002017	2.00E-112	0.051212	0.003428	2.02E-50	0.04032	0.002529	3.53E-57	2.16E-104	0.010574	F
2	ZNF512	rs11127071	27,615,191	C	A	0.150518	-0.014979	0.002817	4.20E-08	-0.014185	0.004798	0.003125	-0.015258	0.003527	1.54E-05	1.09E-06	0.856933	
2	ZNF512	rs1881395	27,615,682	A	G	0.376571	-0.038926	0.002079	1.40E-81	-0.046426	0.003527	1.56E-39	-0.034544	0.002609	5.60E-40	2.01E-76	0.006777	F
2	ZNF512	rs6737921	27,616,240	T	C	0.150446	-0.014986	0.002818	4.20E-08	-0.014253	0.0048	0.002996	-0.015219	0.003528	1.63E-05	1.11E-06	0.871099	
2	ZNF512	rs4666000	27,616,502	C	T	0.472148	0.044367	0.002018	2.80E-112	0.050947	0.003429	6.69E-50	0.0404	0.00253	2.44E-57	4.93E-104	0.013335	F
2	ZNF512	rs2068834	27,616,672	C	T	0.471784	0.044424	0.002018	1.90E-112	0.051132	0.003429	3.01E-50	0.040395	0.002531	2.62E-57	2.39E-104	0.011765	F
2	ZNF512	rs7571558	27,616,965	G	C	0.376647	-0.03891	0.002079	1.50E-81	-0.046429	0.003527	1.55E-39	-0.034516	0.002609	6.53E-40	2.31E-76	0.006636	F
2	ZNF512	rs4666001	27,617,672	G	A	0.156551	0.02359	0.002774	4.90E-18	0.028448	0.004711	1.60E-09	0.020345	0.00348	5.14E-09	4.56E-16	0.166531	
2	ZNF512	rs4666002	27,617,773	C	G	0.471553	0.044548	0.00202	7.50E-113	0.051319	0.003433	1.77E-50	0.040427	0.002532	2.56E-57	1.38E-104	0.010691	F
2	ZNF512	rs62138971	27,617,887	A	G	0.375501	-0.039175	0.002089	4.40E-82	-0.047545	0.003544	5.47E-41	-0.034262	0.002622	5.67E-39	7.15E-77	0.002599	M
2	ZNF512	rs6756238	27,618,438	G	A	0.150421	-0.014896	0.002018	4.70E-08	-0.014082	0.004804	0.003388	-0.015194	0.003529	1.69E-05	1.28E-06	0.851923	
2	ZNF512	rs1881396	27,621,734	G	T	0.371524	-0.039765	0.002093	8.80E-84	-0.04744	0.003554	1.31E-40	-0.035292	0.002627	4.05E-41	1.25E-78	0.005993	F
2	GNP1	rs3749147	27,629,051	A	G	0.31819	0.036325	0.002172	1.50E-65	0.04086	0.003696	2.24E-28	0.033878	0.002722	1.57E-35	6.53E-61	0.128246	
2	GNP1	rs34502053	27,631,657	A	G	0.316429	0.03684	0.002168	7.90E-68	0.041558	0.003692	2.34E-29	0.034199	0.002716	2.54E-36	1.14E-62	0.108357	
2	GNP1	rs10173720	27,632,530	A	T	0.418805	0.028115	0.002044	1.10E-44	0.031729	0.003485	9.27E-20	0.026243	0.002558	1.16E-24	1.42E-41	0.204456	
2	GNP1	rs6719175	27,636,484	A	T	0.314964	0.036904	0.002179	3.30E-67	0.041634	0.003711	3.57E-29	0.034247	0.002729	4.49E-36	3.04E-62	0.108775	
2	GNP1	rs77350364	27,643,272	A	G	0.418271	0.027855	0.00205	1.80E-43	0.031535	0.003495	1.96E-19	0.025849	0.002566	7.66E-24	1.93E-40	0.189674	
2	GNP1	rs12474585	27,648,726	C	T	0.418299	0.028121	0.002049	1.90E-44	0.031828	0.003494	8.70E-20	0.026113	0.002564	2.51E-24	2.86E-41	0.187221	
2	GNP1	rs8731	27,650,459	C	G	0.417856	0.028189	0.002049	1.30E-44	0.031952	0.003494	6.37E-20	0.026135	0.002564	2.32E-24	1.94E-41	0.179496	
2	SUPT7L	rs10202364	27,652,175	T	A	0.418235	0.027911	0.002053	1.10E-43	0.031236	0.0035	4.68E-19	0.026101	0.00257	3.30E-24	1.98E-40	0.236899	
2	SUPT7L	rs4666010	27,655,819	T	C	0.417773	0.028211	0.002049	9.90E-45	0.032028	0.003494	5.20E-20	0.026131	0.002564	2.34E-24	1.60E-41	0.173652	
2	SLC4A1AP	rs2722406	27,669,156	T	A	0.335271	0.032828	0.002139	9.00E-56	0.036811	0.003644	5.87E-24	0.030698	0.002679	2.29E-30	2.14E-51	0.17655	
2	SLC4A1AP	rs76586169	27,674,968	G	A	0.417473	0.02816	0.002048	1.50E-44	0.031991	0.003494	5.68E-20	0.026091	0.002564	2.70E-24	2.01E-41	0.173322	
2	SLC4A1AP	rs13021208	27,678,861	T	C	0.335345	0.033421	0.00214	1.60E-57	0.037309	0.003646	1.50E-24	0.031331	0.00268	1.53E-31	3.78E-53	0.18644	
2	SLC4A1AP	rs72613829	27,680,120	C	T	0.416616	0.028528	0.00205	1.60E-45	0.032225	0.003497	3.33E-20	0.026506	0.002565	5.33E-25	2.38E-42	0.187265	
2	SLC4A1AP	rs13023094	27,687,839	C	A	0.335411	0.03279	0.002138	9.60E-56	0.036842	0.003643	5.14E-24	0.030604	0.002678	3.24E-30	2.65E-51	0.167658	
2	SLC4A1AP	rs12998770	27,690,321	C	T	0.335627	0.032793	0.002139	9.50E-56	0.036921	0.003643	4.16E-24	0.030563	0.002678	3.91E-30	2.59E-51	0.159651	
2	SLC4A1AP *	rs80322731	27,697,569	G	A	0.208356	0.026665	0.002519	3.70E-28	0.027414	0.004289	1.70E-10	0.026604	0.003155	3.59E-17	4.91E-25	0.879027	
2	SLC4A1AP *	rs13030973	27,705,930	C	T	0.332559	0.032915	0.002139	4.50E-56	0.036319	0.003643	2.23E-23	0.031016	0.002678	5.60E-31	1.99E-51	0.24084	
2	SLC4A1AP *	rs4665385	27,707,970	C	T	0.413128	0.028202	0.002048	1.10E-44	0.031489	0.003496	2.26E-19	0.026417	0.002561	6.44E-25	1.91E-41	0.241864	
2	SLC4A1AP *	rs6727388	27,709,720	G	A	0.331812	0.033213	0.00214	6.80E-57	0.036369	0.003647	2.14E-23	0.031426	0.00268	1.02E-31	3.52E-52	0.274669	
2	SLC4A1AP *	rs4616435	27,710,775	T	C	0.332519	0.032919	0.002139	4.60E-56	0.036333	0.003644	2.19E-23	0.031005	0.002678	5.92E-31	2.06E-51	0.238789	
2	SLC4A1AP *	rs58199976	27,711,657	T	C	0.412244	0.028559	0.002048	1.00E-45	0.031734	0.003497	1.22E-19	0.026844	0.002562	1.16E-25	1.89E-42	0.259273	
2	SLC4A1AP *	rs6727215	27,711,864	A	G	0.331778	0.033223	0.00214	6.20E-57	0.036436	0.003647	1.79E-23	0.031412	0.00268	1.09E-31	3.15E-52	0.266978	
2	SLC4A1AP *	rs4665386	27,712,485	C	A	0.413698	0.028443	0.002047	2.40E-45	0.032105	0.003496	4.39E-20	0.026492	0.002561	4.68E-25	2.74E-42	0.195102	
2	SLC4A1AP *	rs6742571	27,719,021	G	A	0.419392	0.028207	0.002048	7.50E-45	0.032116	0.003493	4.04E-20	0.026186	0.002563	1.82E-24	9.73E-42	0.171115	
2	SLC4A1AP *	rs1881394	27,726,185	G	A	0.41547	0.027977	0.002065	1.70E-43	0.031323	0.00352	6.02E-19	0.026141	0.002585	5.26E-24	4.03E-40	0.235494	
2	SLC4A1AP *	rs143611256	27,726,613	A	G	0.034079	0.032108	0.005561	8.30E-09	0.035227	0.009495	0.000209	0.28923	0.006955	3.23E-05	1.80E-07	0.592239	
2	SLC4A1AP *	rs10432705	27,727,970	A	G	0.331615	0.033487	0.002163	1.80E-56	0.03665	0.003681	2.56E-23	0.031675	0.00271	1.56E-31	6.38E-52	0.276476	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	MRPL33 *	rs77154381	27,759,252	A	G	0.408163	0.025699	0.002052	1.30E-37	0.027876	0.003497	1.64E-15	0.024346	0.002569	2.78E-21	4.97E-34	0.415972	
2	MRPL33 *	rs12477908	27,764,179	C	A	0.411035	0.025437	0.002048	6.90E-37	0.027807	0.003489	1.68E-15	0.023897	0.002564	1.24E-20	2.23E-33	0.366551	
2	MRPL33 *	rs13006480	27,764,354	G	C	0.326285	0.028651	0.002166	1.40E-41	0.031021	0.003687	4.20E-17	0.02713	0.002714	1.72E-23	8.64E-38	0.395408	
2	MRPL33 *	rs140124512	27,764,951	T	A	0.042755	-0.035544	0.00509	4.20E-12	-0.052827	0.008603	8.48E-10	-0.026077	0.006401	4.68E-05	1.62E-12	0.012629	M
2	MRPL33 *	rs13013484	27,765,954	A	G	0.410004	0.025618	0.002048	2.20E-37	0.028193	0.003492	7.18E-16	0.024001	0.002564	8.45E-21	6.62E-34	0.333291	
2	MRPL33 *	rs146796793	27,766,610	G	A	0.053044	-0.041	0.004552	4.80E-21	-0.037428	0.00774	1.35E-06	-0.043549	0.005707	2.43E-14	1.89E-18	0.524428	
2	MRPL33 *	rs4665390	27,767,042	C	T	0.411047	0.025378	0.002049	1.20E-36	0.027608	0.003491	2.74E-15	0.023906	0.002566	1.26E-20	3.69E-33	0.39279	
2	MRPL33 *	rs74429612	27,770,976	C	T	0.411139	0.025417	0.002048	8.20E-37	0.027794	0.003489	1.72E-15	0.023867	0.002564	1.38E-20	2.54E-33	0.364485	
2	MRPL33 *	rs3736594	27,772,914	C	A	0.411138	0.02554	0.002048	3.30E-37	0.027875	0.003489	1.42E-15	0.024029	0.002564	7.61E-21	1.17E-33	0.374369	
2	MRPL33 *	rs3792252	27,773,064	A	G	0.409967	0.025607	0.002048	2.20E-37	0.02814	0.003492	8.09E-16	0.024015	0.002564	8.01E-21	7.05E-34	0.341028	
2	MRPL33	rs139682392	27,776,317	A	G	0.029487	0.03511	0.005949	2.80E-09	0.040477	0.009982	5.07E-05	0.029531	0.007512	8.54E-05	1.19E-07	0.380906	
2	MRPL33	rs35463245	27,777,857	C	G	0.408066	0.025376	0.002054	1.40E-36	0.027756	0.003503	2.40E-15	0.023914	0.002571	1.48E-20	3.78E-33	0.376594	
2	MRPL33	rs17006242	27,778,184	C	A	0.410985	0.025472	0.002048	5.20E-37	0.027865	0.00349	1.47E-15	0.023934	0.002564	1.08E-20	1.72E-33	0.363955	
2	MRPL33	rs3792253	27,779,135	T	C	0.409868	0.025619	0.002049	2.30E-37	0.028192	0.003493	7.29E-16	0.024002	0.002564	8.53E-21	6.78E-34	0.333615	
2	MRPL33 *	rs13030345	27,780,307	T	G	0.306598	0.027149	0.002203	5.30E-36	0.029706	0.003744	2.21E-15	0.025292	0.002762	5.58E-20	1.30E-32	0.342595	
2	RBKS	rs74327441	27,784,205	G	A	0.403848	0.024941	0.002081	2.20E-34	0.027492	0.003544	9.10E-15	0.023433	0.002606	2.54E-19	3.56E-186	0.324E31	
2	RBKS	rs192918024	27,787,093	T	A	0.029314	-0.040147	0.006037	1.10E-12	-0.031134	0.010367	0.002683	-0.045777	0.007527	1.23E-09	1.02E-10	0.253044	
2	RBKS	rs7596967	27,789,917	T	G	0.38996	0.022991	0.002087	4.80E-29	0.025186	0.003553	1.42E-12	0.021601	0.002614	1.48E-16	1.82E-26	0.416364	
2	RBKS	rs7593136	27,794,925	A	G	0.411352	0.025012	0.002048	1.00E-35	0.027443	0.00349	3.93E-15	0.023617	0.002564	3.40E-20	1.40E-32	0.377003	
2	RBKS	rs6744348	27,795,158	A	C	0.411367	0.025017	0.002048	1.00E-35	0.027436	0.00349	3.98E-15	0.02363	0.002563	3.21E-20	1.34E-32	0.37943	
2	RBKS	rs36035825	27,795,264	T	G	0.411364	0.025021	0.002048	9.80E-36	0.027436	0.00349	3.98E-15	0.023637	0.002563	3.13E-20	1.31E-32	0.380231	
2	RBKS	rs4666012	27,795,426	A	G	0.411362	0.025021	0.002048	9.70E-36	0.027436	0.00349	3.98E-15	0.023635	0.002563	3.15E-20	1.31E-32	0.380041	
2	RBKS	rs4666013	27,796,239	C	T	0.411364	0.025023	0.002047	9.10E-36	0.027499	0.00349	3.44E-15	0.0236	0.002563	3.55E-20	1.29E-32	0.367895	
2	RBKS	rs4666014	27,796,308	G	A	0.411459	0.024926	0.002047	1.50E-35	0.027322	0.003489	5.12E-15	0.023556	0.002563	4.19E-20	2.23E-32	0.384387	
2	RBKS	rs4666015	27,796,500	G	A	0.411384	0.02501	0.002047	9.70E-36	0.027458	0.00349	3.76E-15	0.023597	0.002563	3.60E-20	1.42E-32	0.372578	
2	RBKS	rs34181670	27,796,989	T	C	0.411384	0.025012	0.002047	9.60E-36	0.027458	0.00349	3.76E-15	0.023599	0.002563	3.57E-20	1.41E-32	0.372863	
2	RBKS	rs35679500	27,797,099	T	C	0.411384	0.025012	0.002047	9.60E-36	0.027458	0.00349	3.76E-15	0.023599	0.002563	3.57E-20	1.41E-32	0.372863	
2	RBKS	rs12623170	27,797,290	C	T	0.41181	0.02469	0.002047	7.60E-35	0.027231	0.003489	6.18E-15	0.023311	0.002562	9.85E-20	6.28E-32	0.368E2	
2	RBKS	rs3935148	27,798,099	T	A	0.408517	0.025201	0.002051	3.70E-36	0.027883	0.003493	1.51E-15	0.023755	0.002569	2.42E-20	3.89E-33	0.340988	
2	RBKS	rs13027427	27,798,176	G	T	0.379866	0.022703	0.00208	3.80E-29	0.025976	0.003541	2.29E-13	0.021214	0.002606	4.12E-16	8.34E-27	0.278742	
2	RBKS	rs6745545	27,798,978	C	G	0.379798	0.022687	0.00208	4.20E-29	0.025926	0.003542	2.57E-13	0.021221	0.002606	4.05E-16	9.20E-27	0.284578	
2	RBKS	rs7570730	27,799,808	G	A	0.379735	0.022628	0.002082	7.20E-29	0.025426	0.003545	7.68E-13	0.021408	0.002608	2.38E-16	1.60E-26	0.361261	
2	RBKS	rs11127125	27,800,253	T	C	0.379006	0.022521	0.002084	1.40E-28	0.025502	0.003548	6.82E-13	0.021245	0.002611	4.22E-16	2.50E-26	0.333822	
2	RBKS	rs11127126	27,800,417	C	T	0.379756	0.022553	0.002083	1.10E-28	0.025238	0.003546	1.14E-12	0.021389	0.002609	2.57E-16	2.53E-26	0.38195	
2	RBKS	rs12473340	27,800,930	G	A	0.379693	0.022535	0.002083	1.20E-28	0.025401	0.003547	8.30E-13	0.0213	0.002609	3.44E-16	2.48E-26	0.351737	
2	RBKS	rs12473400	27,801,157	G	T	0.380546	0.022516	0.002083	1.50E-28	0.025273	0.003547	1.09E-12	0.021322	0.00261	3.24E-16	3.05E-26	0.369605	
2	RBKS	rs4630723	27,801,464	T	C	0.389752	0.021126	0.0021	4.60E-25	0.024284	0.003577	1.18E-11	0.019536	0.002629	1.13E-13	1.01E-22	0.284846	
2	RBKS	rs13019037	27,801,775	C	T	0.379812	0.02242	0.002085	2.20E-28	0.025328	0.00355	1.01E-12	0.021156	0.002612	5.74E-16	4.98E-26	0.34383	
2	RBKS	rs4632296	27,802,117	T	C	0.380991	0.022344	0.002091	4.50E-28	0.024886	0.00356	2.86E-12	0.021223	0.00262	5.70E-16	1.37E-25	0.407208	
2	RBKS	rs13001060	27,802,194	T	C	0.382657	0.0221	0.00209	1.50E-27	0.025281	0.003557	1.23E-12	0.020585	0.002618	3.91E-15	4.02E-25	0.287622	
2	RBKS	rs12995865	27,802,199	A	C	0.382657	0.0221	0.00209	1.50E-27	0.025281	0.003557	1.23E-12	0.020585	0.002618	3.91E-15	4.02E-25	0.287643	
2	RBKS	rs11891769	27,802,713	G	C	0.379895	0.022339	0.002085	3.90E-28	0.024792	0.00355	3.01E-12	0.021301	0.002611	3.58E-16	9.13E-26	0.428364	
2	RBKS	rs12465012	27,805,324	C	T	0.359118	0.019771	0.002109	1.00E-21	0.022645	0.003592	2.98E-10	0.018336	0.002641	4.00E-12	7.98E-20	0.33377	
2	RBKS	rs4665392	27,806,782	A	G	0.358937	0.019534	0.002109	2.70E-21	0.022588	0.003592	3.31E-10	0.018038	0.002641	8.80E-12	1.92E-19	0.307485	
2	RBKS	rs12986980	27,807,570	A	G	0.358156	0.019736	0.002109	1.10E-21	0.022658	0.003592	2.92E-10	0.018286	0.002641	4.56E-12	8.92E-20	0.326864	
2	RBKS	rs13023003	27,809,270	G	C	0.358541	0.019712	0.002107	1.10E-21	0.022423	0.003588	4.24E-10	0.018398	0.002639	3.23E-12	9.15E-20	0.366006	
2	RBKS	rs4233716	27,811,517	C	T	0.379153	0.017365	0.002085	2.10E-17	0.020282	0.00355	1.13E-08	0.016341	0.002612	4.05E-10	2.57E-16	0.371203	
2	RBKS	rs4233717	27,811,813	A	T	0.379153	0.017365	0.002085	2.10E-17	0.020282	0.00355	1.13E-08	0.016341	0.002612	4.05E-10	2.57E-16	0.371203	
2	RBKS	rs4666016	27,814,273	T	A	0.377551	0.017465	0.002086	1.40E-17	0.020438	0.003551	8.86E-09	0.016466	0.002613	3.04E-10	1.53E-16	0.367629	
2	RBKS	rs4464229	27,815,213	C	T	0.379228	0.017321	0.002087	2.50E-17	0.020515	0.003554	8.02E-09	0.016192	0.002615	6.11E-10	2.74E-16	0.372261	
2	RBKS	rs12617171	27,815,932	C	T	0.378183	0.017285	0.002085	2.70E-17	0.020275	0.00355	1.15E-08	0.01625	0.002612	5.09E-10	3.27E-16	0.361128	
2	RBKS	rs4420671	27,816,433	G	C	0.378268	0.017368	0.002085	2.00E-17	0.020336	0.003549	1.03E-08	0.01634	0.002612	4.05E-10	2.34E-16	0.364502	
2	RBKS	rs4493211	27,816,605	G	T	0.37874	0.017349	0.002086	2.30E-17	0.020381	0.003551	9.72E-09	0.016293	0.002613	4.63E-10	2.52E-16	0.353722	
2	RBKS	rs4665393	27,817,409	G	A	0.378278	0.017362	0.002085	2.00E-17	0.020325	0.003549	1.05E-08	0.01634	0.002612	4.06E-10	2.39E-16	0.365744	
2	RBKS	rs4666017	27,817,658	C	A	0.378278	0.017362	0.002085	2.00E-17	0.020325	0.003549	1.05E-08	0.01634	0.002612	4.06E-10	2.39E-16	0.365744	
2	RBKS	rs12478766	27,818,333	T	C	0.378241	0.017299	0.002085	2.70E-17	0.02034	0.00355	1.03E-08	0.016256	0.002612	5.00E-10	2.88E-16	0.354097	
2	RBKS	rs13026758	27,818,406	A	G	0.378261	0.01734	0.002085	2.3									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	RBKS	rs4462754	27,841,127	C	T	0.381897	0.017545	0.002075	1.10E-17	0.020036	0.003536	1.49E-08	0.0169	0.002599	8.12E-11	6.95E-17	0.474742	
2	RBKS	rs9678336	27,842,537	A	G	0.381357	0.017348	0.002076	2.60E-17	0.019735	0.003536	2.46E-08	0.016754	0.0026	1.20E-10	1.65E-16	0.497048	
2	RBKS	rs74446114	27,843,255	C	T	0.300086	0.020525	0.002213	5.00E-21	0.023583	0.003755	3.49E-10	0.019419	0.002777	2.78E-12	6.52E-20	0.372572	
2	RBKS	rs4233718	27,843,493	A	G	0.381417	0.017341	0.002076	2.70E-17	0.019703	0.003536	2.59E-08	0.016774	0.0026	1.14E-10	1.66E-16	0.504469	
2	RBKS	rs11127127	27,844,037	G	T	0.382009	0.017528	0.002075	1.10E-17	0.019966	0.003536	1.68E-08	0.016914	0.002599	7.83E-11	7.53E-17	0.486721	
2	RBKS	rs11127128	27,844,103	T	A	0.381417	0.017341	0.002076	2.70E-17	0.019703	0.003536	2.59E-08	0.016774	0.0026	1.14E-10	1.66E-16	0.504469	
2	RBKS	rs77853892	27,844,692	A	C	0.165512	0.023859	0.002759	3.10E-19	0.022313	0.004681	1.90E-06	0.025304	0.003463	2.87E-13	2.99E-17	0.607471	
2	RBKS	rs4564736	27,846,676	A	T	0.381322	0.017351	0.002076	2.50E-17	0.019759	0.003536	2.36E-08	0.016748	0.0026	1.22E-10	1.61E-16	0.492701	
2	RBKS	rs11901133	27,846,846	T	G	0.381351	0.017352	0.002076	2.50E-17	0.019804	0.003537	2.20E-08	0.01673	0.0026	1.27E-10	1.58E-16	0.483832	
2	RBKS	rs4555299	27,848,323	A	G	0.381322	0.017351	0.002076	2.50E-17	0.019759	0.003536	2.36E-08	0.016748	0.0026	1.22E-10	1.61E-16	0.492701	
2	RBKS	rs35841453	27,849,835	T	C	0.381402	0.017353	0.002076	2.60E-17	0.019727	0.003536	2.49E-08	0.016779	0.0026	1.12E-10	1.57E-16	0.501929	
2	RBKS	rs4666024	27,850,112	C	G	0.379054	0.017395	0.00208	2.30E-17	0.019342	0.003542	4.87E-08	0.017073	0.002605	5.79E-11	1.58E-16	0.605971	
2	RBKS	rs4666025	27,851,027	C	T	0.381402	0.017353	0.002076	2.60E-17	0.019727	0.003536	2.49E-08	0.016779	0.0026	1.12E-10	1.57E-16	0.501929	
2	RBKS	rs4313931	27,851,834	C	T	0.381402	0.017353	0.002076	2.60E-17	0.019727	0.003536	2.49E-08	0.016779	0.0026	1.12E-10	1.57E-16	0.501929	
2	RBKS	rs4583413	27,851,957	C	T	0.381322	0.017351	0.002076	2.50E-17	0.019759	0.003536	2.36E-08	0.016748	0.0026	1.22E-10	1.61E-16	0.492701	
2	RBKS	rs4419196	27,852,431	A	G	0.381322	0.017351	0.002076	2.50E-17	0.019759	0.003536	2.36E-08	0.016748	0.0026	1.22E-10	1.61E-16	0.492701	
2	RBKS	rs4447576	27,853,381	T	C	0.384953	0.017256	0.002085	3.90E-17	0.019491	0.00355	4.09E-08	0.016739	0.002612	1.51E-10	3.41E-16	0.532324	
2	RBKS	rs11127129	27,853,841	C	G	0.381683	0.017646	0.00208	8.50E-18	0.020036	0.003544	1.60E-08	0.017104	0.002605	5.31E-11	4.93E-17	0.504967	
2	RBKS	rs7426295	27,856,127	G	A	0.375981	0.017264	0.002083	8.60E-17	0.017473	0.003545	8.43E-07	0.017907	0.00261	7.05E-12	3.17E-16	0.921407	
2	RBKS	rs4233719	27,856,477	C	A	0.375981	0.017264	0.002083	8.60E-17	0.017473	0.003545	8.43E-07	0.017907	0.00261	7.05E-12	3.17E-16	0.921407	
2	RBKS	rs4233720	27,856,908	A	G	0.376072	0.017177	0.002083	1.30E-16	0.017372	0.003545	9.75E-07	0.017834	0.00261	8.56E-12	4.41E-16	0.916356	
2	RBKS	rs13025314	27,857,347	G	A	0.376072	0.017177	0.002083	1.30E-16	0.017372	0.003545	9.75E-07	0.017834	0.00261	8.56E-12	4.41E-16	0.916356	
2	RBKS	rs4578808	27,858,763	G	T	0.376072	0.017177	0.002083	1.30E-16	0.017372	0.003545	9.75E-07	0.017834	0.00261	8.56E-12	4.41E-16	0.916356	
2	RBKS	rs4578809	27,859,627	G	A	0.376072	0.017177	0.002083	1.30E-16	0.017372	0.003545	9.75E-07	0.017834	0.00261	8.56E-12	4.41E-16	0.916356	
2	RBKS	rs6714106	27,860,977	C	T	0.37868	0.017226	0.002085	1.50E-16	0.01742	0.003549	9.37E-07	0.01772	0.002613	1.07E-11	5.27E-16	0.936358	
2	RBKS	rs7595986	27,862,444	A	G	0.375919	0.017294	0.002083	7.50E-17	0.0176	0.003545	6.98E-07	0.017884	0.002609	7.54E-12	2.82E-16	0.949312	
2	RBKS	rs13021285	27,862,480	T	C	0.37601	0.017207	0.002083	1.10E-16	0.017499	0.003545	8.08E-07	0.017807	0.002609	9.15E-12	3.93E-16	0.944264	
2	RBKS	rs77353560	27,862,677	A	C	0.284816	0.019235	0.002252	9.20E-18	0.02077	0.003818	5.46E-08	0.018983	0.002827	1.96E-11	6.10E-17	0.706904	
2	RBKS	rs11902158	27,863,898	A	G	0.37601	0.017207	0.002083	1.10E-16	0.017499	0.003545	8.08E-07	0.017807	0.002609	9.15E-12	3.93E-16	0.944264	
2	RBKS	rs13004096	27,864,338	C	T	0.37601	0.017207	0.002083	1.10E-16	0.017499	0.003545	8.08E-07	0.017807	0.002609	9.15E-12	3.93E-16	0.944264	
2	RBKS	rs1973116	27,865,051	C	T	0.375044	0.017599	0.002088	3.10E-17	0.017672	0.003553	6.66E-07	0.018342	0.002616	2.44E-12	8.79E-274	0.89274	
2	RBKS	rs4666028	27,865,713	T	A	0.377126	0.016971	0.002082	2.70E-16	0.017305	0.003544	1.06E-06	0.017554	0.002609	1.78E-11	9.81E-16	0.954825	
2	RBKS	rs71441095	27,866,981	A	G	0.471656	-0.026153	0.00204	2.10E-38	-0.028125	0.003463	4.84E-16	-0.025508	0.00256	2.38E-23	1.33E-36	0.543363	
2	RBKS	rs10171517	27,867,192	T	C	0.471815	-0.026146	0.00204	2.10E-38	-0.028196	0.003463	4.06E-16	-0.025452	0.00256	2.92E-23	1.37E-36	0.524018	
2	RBKS	rs898034	27,867,953	T	C	0.471922	-0.026189	0.00204	1.50E-38	-0.028308	0.003462	3.10E-16	-0.025461	0.00256	2.76E-23	9.95E-37	0.508621	
2	RBKS	rs2337373	27,870,055	C	T	0.375985	0.017238	0.002083	9.40E-17	0.017406	0.003545	9.29E-07	0.017899	0.00261	7.21E-12	3.56E-16	0.910741	
2	RBKS	rs13016573	27,871,403	C	G	0.377268	0.017372	0.002086	6.80E-17	0.017683	0.00355	6.45E-07	0.017925	0.002614	7.22E-12	2.50E-16	0.956133	
2	RBKS	rs4665398	27,871,903	A	T	0.376069	0.017185	0.002083	1.20E-16	0.01736	0.003545	9.91E-07	0.017857	0.00261	8.06E-12	4.22E-16	0.910157	
2	RBKS	rs12466687	27,873,840	C	A	0.377013	0.01735	0.002085	7.30E-17	0.017628	0.003548	6.90E-07	0.017884	0.002613	7.97E-12	2.94E-16	0.953601	
2	RBKS	rs12466717	27,873,925	G	A	0.37591	0.017309	0.002083	7.10E-17	0.01759	0.003545	7.10E-07	0.017906	0.002609	7.04E-12	2.68E-16	0.942731	
2	RBKS	rs4666030	27,874,355	C	T	0.375907	0.017312	0.002083	7.00E-17	0.01759	0.003545	7.10E-07	0.01791	0.002609	6.96E-12	2.65E-16	0.942043	
2	RBKS	rs13411592	27,875,857	A	G	0.375909	0.017316	0.002083	6.90E-17	0.01759	0.003545	7.10E-07	0.017914	0.002609	6.88E-12	2.62E-16	0.941302	
2	RBKS	rs6706209	27,879,071	T	C	0.375853	0.017441	0.002082	4.10E-17	0.017687	0.003545	6.16E-07	0.018042	0.002609	4.82E-12	1.61E-16	0.935766	
2	RBKS	rs12620151	27,879,837	T	A	0.375932	0.017441	0.002082	4.30E-17	0.017658	0.003545	6.43E-07	0.018067	0.002609	4.50E-12	1.57E-16	0.925291	
2	RBKS	rs6547814	27,880,131	G	A	0.375853	0.01744	0.002082	4.10E-17	0.017683	0.003545	6.21E-07	0.018042	0.002609	4.82E-12	1.62E-16	0.934917	
2	RBKS	rs11886463	27,881,670	C	T	0.375939	0.017361	0.002082	5.90E-17	0.017627	0.003545	6.73E-07	0.017965	0.002609	5.93E-12	2.15E-16	0.938855	
2	RBKS	rs13413962	27,881,699	A	G	0.375851	0.017446	0.002082	4.00E-17	0.017683	0.003545	6.21E-07	0.01805	0.002609	4.71E-12	1.59E-16	0.933417	
2	RBKS	rs6708889	27,884,825	T	C	0.37584	0.017367	0.002082	5.40E-17	0.017624	0.003545	6.75E-07	0.017964	0.002608	5.90E-12	2.15E-16	0.938507	
2	BABAM2	rs7607546	27,895,795	A	G	0.375681	0.017257	0.002079	6.40E-17	0.017418	0.003539	8.71E-07	0.017955	0.002604	5.60E-12	2.61E-16	0.90279	
2	BABAM2	rs141361525	27,896,053	G	C	0.055586	-0.036713	0.004461	8.70E-18	-0.031551	0.00755	2.97E-05	-0.039705	0.005606	1.47E-12	2.07E-15	0.385854	
2	BABAM2	rs7592580	27,898,323	C	T	0.37661	0.017035	0.002078	2.00E-16	0.01725	0.003538	1.10E-06	0.017679	0.002603	1.15E-11	6.64E-16	0.922011	
2	BABAM2	rs17006365	27,900,507	G	T	0.37655	0.017233	0.002079	6.70E-17	0.017688	0.003539	5.91E-07	0.01782	0.002605	8.14E-12	2.59E-16	0.975916	
2	BABAM2	rs6709765	27,900,893	T	A	0.375807	0.01725	0.002078	6.10E-17	0.017449	0.003538	8.28E-07	0.017894	0.002603	6.47E-12	2.86E-16	0.919318	
2	BABAM2	rs10177845	27,901,304	A	G	0.375883	0.017211	0.002078	7.30E-17	0.017483	0.003537	7.86E-07	0.017826	0.002603	7.76E-12	3.25E-16	0.937692	
2	BABAM2	rs34483784	27,906,524	G	A	0.389669	0.015239	0.002068	2.60E-13	0.014967	0.003521	2.15E-05	0.01589	0.002591	7.17E-10	6.56E-13	0.816834	
2	BABAM2	rs10201105	27,908,366	C	G	0.389677	0.015228	0.002068	2.70E-13	0.014962	0.003521	2.17E-05	0.015964	0.002591	7.45E-10	6.86E-13	0.818739	
2	BABAM2	rs10190494	27,908,376	G	A	0.389918	0.015029	0.002068	5.40E-13	0.014772	0.00352	2.74E-						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	BABAM2	rs4390729	27,939,994	C	T	0.390424	0.015341	0.002065	2.00E-13	0.014847	0.003517	2.46E-05	0.016192	0.002587	4.00E-10	4.22E-13	0.758111	
2	BABAM2	rs10170872	27,941,686	T	C	0.387043	0.015755	0.002066	3.70E-14	0.015551	0.003518	9.99E-06	0.016463	0.002588	2.05E-10	9.28E-14	0.834661	
2	BABAM2	rs57403744	27,942,131	A	G	0.158298	0.022079	0.002788	4.50E-16	0.018023	0.004722	0.000136	0.025191	0.003503	6.69E-13	4.05E-15	0.222747	
2	BABAM2	rs13399709	27,944,583	T	C	0.387209	0.015655	0.002065	5.20E-14	0.015435	0.003518	1.16E-05	0.016376	0.002587	2.52E-10	1.31E-13	0.829363	
2	BABAM2	rs7577437	27,945,548	G	A	0.387404	0.015644	0.002065	5.00E-14	0.01545	0.003518	1.14E-05	0.016367	0.002587	2.58E-10	1.31E-13	0.833752	
2	BABAM2	rs6547816	27,946,730	C	T	0.388758	0.015361	0.002071	1.80E-13	0.015191	0.003527	1.67E-05	0.01618	0.002594	4.61E-10	3.35E-13	0.821271	
2	BABAM2	rs12165240	27,949,258	T	A	0.389334	0.015556	0.002069	8.70E-14	0.015113	0.003523	1.81E-05	0.016485	0.002591	2.06E-10	1.65E-13	0.753716	
2	BABAM2	rs13382482	27,949,426	C	T	0.389711	0.015682	0.002067	5.50E-14	0.015109	0.00352	1.79E-05	0.016646	0.002589	1.33E-10	1.06E-13	0.725125	
2	BABAM2	rs7595847	27,950,176	A	T	0.389894	0.015643	0.002067	5.90E-14	0.015136	0.00352	1.73E-05	0.016592	0.00259	1.53E-10	1.18E-13	0.738956	
2	BABAM2	rs1506535	27,951,214	G	A	0.390009	0.015624	0.002067	6.40E-14	0.0151	0.00352	1.81E-05	0.01659	0.002589	1.52E-10	1.23E-13	0.732993	
2	BABAM2	rs13008539	27,951,540	A	C	0.390009	0.015624	0.002067	6.40E-14	0.0151	0.00352	1.81E-05	0.01659	0.002589	1.52E-10	1.23E-13	0.732993	
2	BABAM2	rs7584462	27,953,189	T	A	0.390423	0.015413	0.002067	1.50E-13	0.014704	0.00352	2.98E-05	0.016506	0.002589	1.89E-10	2.43E-13	0.680082	
2	BABAM2	rs7587180	27,953,242	G	A	0.390826	0.015303	0.002067	2.10E-13	0.014647	0.00352	3.20E-05	0.016404	0.002588	2.41E-10	3.29E-13	0.687698	
2	BABAM2	rs10205313	27,953,660	C	A	0.389178	0.014989	0.002073	8.60E-13	0.014413	0.003529	4.48E-05	0.016057	0.002596	6.38E-10	1.18E-12	0.707429	
2	BABAM2	rs188363080	27,953,699	T	A	0.035855	0.032359	0.005442	3.00E-09	0.036316	0.009177	7.66E-05	0.027574	0.006853	5.78E-05	1.21E-07	0.445312	
2	BABAM2	rs1506537	27,959,034	C	G	0.387492	0.015508	0.002067	9.90E-14	0.015048	0.003519	1.93E-05	0.016422	0.002589	2.32E-10	1.96E-13	0.753099	
2	BABAM2	rs1506536	27,959,139	C	T	0.390123	0.015349	0.002068	2.00E-13	0.014568	0.003521	3.56E-05	0.016472	0.00259	2.09E-10	3.18E-13	0.663168	
2	BABAM2	rs2012704	27,961,899	A	T	0.387151	0.015391	0.002068	1.40E-13	0.015235	0.003522	1.54E-05	0.016067	0.002591	5.77E-10	3.86E-13	0.849039	
2	BABAM2	rs1350481	27,962,941	C	G	0.386783	0.015336	0.002068	1.70E-13	0.015141	0.003521	1.73E-05	0.016072	0.00259	5.61E-10	4.19E-13	0.831283	
2	BABAM2	rs1902966	27,966,413	A	G	0.384347	0.015475	0.002071	1.00E-13	0.014803	0.003528	2.74E-05	0.016387	0.002594	2.76E-10	3.25E-13	0.717538	
2	BABAM2	rs1841068	27,968,762	T	C	0.387106	0.015703	0.002066	4.30E-14	0.015465	0.003518	1.12E-05	0.016422	0.002587	2.26E-10	1.13E-13	0.826503	
2	BABAM2	rs10188108	27,969,688	G	C	0.387558	0.015485	0.002065	8.90E-14	0.01533	0.003517	1.33E-05	0.0162	0.002586	3.86E-10	2.26E-13	0.841996	
2	BABAM2	rs10198257	27,973,444	C	T	0.375985	0.01498	0.002108	3.20E-12	0.013787	0.003586	0.000122	0.016081	0.002642	1.19E-09	5.55E-12	0.606422	
2	BABAM2	rs12465000	27,976,557	A	G	0.387375	0.015654	0.002065	4.90E-14	0.015468	0.003517	1.11E-05	0.016368	0.002587	2.57E-10	1.28E-13	0.83663	
2	BABAM2	rs12465103	27,976,869	C	G	0.3874	0.015632	0.002065	5.20E-14	0.015421	0.003517	1.18E-05	0.016355	0.002587	2.66E-10	1.40E-13	0.830659	
2	BABAM2	rs2337374	27,977,285	A	G	0.387399	0.015628	0.002065	5.30E-14	0.015421	0.003517	1.18E-05	0.016349	0.002587	2.70E-10	1.42E-13	0.831712	
2	BABAM2	rs898032	27,980,069	G	C	0.38791	0.015356	0.002065	1.60E-13	0.014997	0.003517	2.03E-05	0.016195	0.002586	3.93E-10	3.46E-13	0.783689	
2	BABAM2	rs898031	27,980,427	T	C	0.246737	0.015477	0.002357	1.70E-11	0.010956	0.004004	0.006227	0.018753	0.002956	2.31E-10	4.31E-11	0.11717	
2	BABAM2	rs7577342	27,982,714	T	C	0.388157	0.015621	0.002066	6.10E-14	0.014734	0.003518	2.85E-05	0.016649	0.002588	1.30E-10	1.61E-13	0.660973	
2	BABAM2	rs28662360	27,986,053	G	A	0.387395	0.015603	0.002065	5.80E-14	0.015423	0.003518	1.18E-05	0.016306	0.002587	3.01E-10	1.58E-13	0.839851	
2	BABAM2	rs10209126	27,986,416	T	C	0.387096	0.015661	0.002066	5.00E-14	0.015436	0.003518	1.16E-05	0.016361	0.002587	2.63E-10	1.37E-13	0.832195	
2	BABAM2	rs13029008	27,990,023	A	G	0.386876	0.015448	0.002066	1.10E-13	0.01541	0.003519	1.21E-05	0.016096	0.002587	5.08E-10	2.69E-13	0.875081	
2	BABAM2	rs10175508	27,990,557	T	C	0.386971	0.015583	0.002066	6.90E-14	0.015464	0.003519	1.13E-05	0.01624	0.002588	3.59E-10	1.80E-13	0.858853	
2	BABAM2	rs12470614	27,994,460	C	T	0.387907	0.015344	0.002065	1.70E-13	0.014997	0.003517	2.03E-05	0.016175	0.002586	4.13E-10	3.63E-13	0.787728	
2	BABAM2	rs1458397	27,996,741	C	T	0.389157	0.015257	0.002065	2.40E-13	0.015222	0.003519	1.54E-05	0.015942	0.002586	7.31E-10	4.86E-13	0.86903	
2	BABAM2	rs1458398	27,997,074	G	A	0.388579	0.015342	0.002064	1.70E-13	0.014962	0.003516	2.11E-05	0.016215	0.002585	3.66E-10	3.33E-13	0.774059	
2	BABAM2	rs10204513	27,998,058	C	G	0.388726	0.01517	0.002064	3.20E-13	0.014789	0.003515	2.62E-05	0.016049	0.002584	5.44E-10	6.04E-13	0.772636	
2	BABAM2	rs10196483	27,998,315	T	A	0.388726	0.01517	0.002064	3.20E-13	0.014789	0.003515	2.62E-05	0.016049	0.002584	5.44E-10	6.04E-13	0.772636	
2	BABAM2	rs11127131	28,001,249	T	G	0.136358	0.017266	0.002941	2.70E-09	0.021385	0.00499	1.84E-05	0.014293	0.003691	0.000109	5.69E-08	0.253172	
2	BABAM2	rs10204832	28,005,541	A	T	0.388728	0.015163	0.002064	3.30E-13	0.014789	0.003515	2.62E-05	0.01604	0.002585	5.57E-10	6.18E-13	0.77425	
2	BABAM2	rs10168171	28,009,220	G	A	0.388734	0.015169	0.002064	3.20E-13	0.014799	0.003515	2.58E-05	0.016042	0.002584	5.54E-10	6.07E-13	0.775773	
2	BABAM2	rs2839791	28,009,412	C	A	0.38829	0.015399	0.002064	1.50E-13	0.014983	0.003516	2.05E-05	0.016264	0.002585	3.26E-10	2.90E-13	0.7691	
2	BABAM2	rs145058190	28,010,531	T	C	0.040653	-0.037779	0.005168	6.70E-14	-0.026186	0.00873	0.002713	-0.044364	0.006501	9.18E-12	8.59E-13	0.094895	
2	BABAM2	rs56046821	28,011,834	A	T	0.388729	0.015169	0.002064	3.20E-13	0.014803	0.003515	2.57E-05	0.016042	0.002584	5.54E-10	6.05E-13	0.776392	
2	BABAM2	rs7602328	28,012,317	A	G	0.388583	0.015339	0.002064	1.80E-13	0.014977	0.003516	2.07E-05	0.016205	0.002585	3.75E-10	3.36E-13	0.778343	
2	BABAM2	rs13003383	28,012,896	C	T	0.388517	0.015112	0.002064	4.10E-13	0.014441	0.003517	4.06E-05	0.016115	0.002585	4.69E-10	7.94E-13	0.701245	
2	BABAM2	rs10495971	28,013,088	T	C	0.388184	0.015196	0.002064	3.10E-13	0.014952	0.003516	2.13E-05	0.015978	0.002585	6.56E-10	5.97E-13	0.814107	
2	BABAM2	rs11127132	28,013,253	C	T	0.388456	0.01522	0.002064	2.90E-13	0.014826	0.003516	2.50E-05	0.01609	0.002585	4.96E-10	5.29E-13	0.772089	
2	BABAM2	rs6547817	28,015,118	T	C	0.388289	0.015391	0.002064	1.60E-13	0.014987	0.003516	2.05E-05	0.016251	0.002585	3.37E-10	2.99E-13	0.772066	
2	BABAM2	rs10180107	28,017,658	C	T	0.387626	0.015543	0.002064	8.50E-14	0.015287	0.003516	1.39E-05	0.01627	0.002585	3.21E-10	1.98E-13	0.821794	
2	BABAM2	rs4616436	28,019,441	A	G	0.387477	0.015705	0.002065	4.80E-14	0.015424	0.003517	1.17E-05	0.016437	0.002586	2.14E-10	1.13E-13	0.816534	
2	BABAM2	rs6725627	28,019,585	G	T	0.387646	0.015546	0.002064	8.60E-14	0.015298	0.003516	1.38E-05	0.016278	0.002586	3.15E-10	1.92E-13	0.8223	
2	BABAM2	rs12997202	28,027,522	A	G	0.386848	0.015561	0.002065	7.80E-14	0.0157	0.003518	8.20E-06	0.016068	0.002586	5.35E-10	1.96E-13	0.932922	
2	BABAM2	rs6727432	28,028,123	G	T	0.387685	0.015426	0.002065	1.30E-13	0.015278	0.003517	1.41E-05	0.016086	0.002586	5.12E-10	3.16E-13	0.853132	
2	BABAM2	rs17006439	28,031,825	A	G	0.182471	0.018335	0.00266	7.50E-13	0.013669	0.00452	0.002504	0.021624	0.003336	9.40E-11	7.81E-12	0.156752	
2	BABAM2	rs4666032	28,031,902	C	T	0.148544	0.018979	0.002852	8.30E-12	0.023693	0.004831	9.56E-07	0.015596	0.003583	1.36E-05	4.62E-10	0.17825	
2	BABAM2	rs937812	28,032,435	T	C	0.387411												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
2	BABAM2	rs13409819	28,070,432	A	C	0.386002	0.016033	0.002101	4.20E-14	0.016299	0.003578	5.30E-06	0.016516	0.002632	3.60E-10	8.74E-14	0.961053	
2	BABAM2	rs11691385	28,076,117	G	A	0.469986	0.017101	0.002058	1.10E-16	0.019497	0.003508	2.81E-08	0.016533	0.002576	1.42E-10	2.23E-16	0.4959	
2	BABAM2	rs6737313	28,076,400	G	A	0.470819	0.017171	0.002058	8.50E-17	0.019634	0.003507	2.22E-08	0.016628	0.002577	1.13E-10	1.42E-16	0.48975	
2	BABAM2	rs2337699	28,080,846	T	C	0.444895	0.016835	0.002024	1.90E-16	0.018209	0.003448	1.31E-07	0.016798	0.002536	3.60E-11	2.59E-16	0.741602	
2	BABAM2	rs11682011	28,081,194	A	G	0.293343	0.016755	0.002225	3.20E-14	0.014673	0.003786	0.000107	0.018245	0.002788	6.15E-11	2.73E-13	0.447434	
2	BABAM2	rs13415164	28,082,796	T	C	0.293895	0.016335	0.002224	1.40E-13	0.014427	0.003783	0.000138	0.017728	0.002786	2.05E-10	1.13E-12	0.482355	
2	BABAM2	rs2337700	28,084,076	G	A	0.4616	0.014987	0.002015	1.50E-13	0.017345	0.003437	4.59E-07	0.014561	0.002522	7.95E-09	1.70E-13	0.513797	
2	BABAM2	rs12614949	28,084,924	A	G	0.442716	0.016692	0.002025	4.20E-16	0.018689	0.003447	6.06E-08	0.016343	0.002537	1.21E-10	4.02E-16	0.583661	
2	BABAM2	rs10173426	28,086,710	G	A	0.312538	0.014228	0.002184	3.50E-11	0.013481	0.003717	0.000289	0.015096	0.002737	3.54E-08	3.44E-10	0.72639	
2	BABAM2	rs13402525	28,091,991	T	G	0.295683	0.016252	0.002217	1.40E-13	0.014855	0.003773	8.32E-05	0.017452	0.002777	3.39E-10	1.14E-12	0.579378	
2	BABAM2	rs13405377	28,092,277	T	G	0.29457	0.01696	0.002222	1.20E-14	0.015523	0.003782	4.10E-05	0.018167	0.002783	6.91E-11	1.23E-13	0.57345	
2	BABAM2	rs13431542	28,092,278	T	C	0.29457	0.01696	0.002222	1.20E-14	0.015523	0.003782	4.10E-05	0.018167	0.002783	6.91E-11	1.23E-13	0.57345	
2	BABAM2	rs11678963	28,092,691	G	A	0.312599	0.014313	0.002184	2.40E-11	0.013762	0.003717	0.000215	0.015103	0.002736	3.49E-08	2.56E-10	0.771429	
2	BABAM2	rs6710214	28,094,574	G	A	0.321553	0.015073	0.002169	1.30E-12	0.013906	0.00369	0.000166	0.016128	0.002717	3.01E-09	1.84E-11	0.627784	
2	BABAM2	rs10182585	28,094,942	G	A	0.318961	0.01592	0.002178	1.30E-13	0.014424	0.003708	0.000101	0.017039	0.002729	4.42E-10	1.78E-12	0.570073	
2	BABAM2	rs7578052	28,096,012	G	A	0.304343	0.016842	0.002196	1.00E-14	0.014424	0.003738	0.000115	0.018501	0.00275	1.80E-11	8.74E-14	0.379672	
2	BABAM2	rs6757405	28,096,049	T	C	0.303246	0.01708	0.0022	5.20E-15	0.014614	0.003746	9.64E-05	0.01875	0.002756	1.05E-11	4.38E-14	0.373789	
2	BABAM2	rs3863	28,096,267	G	A	0.302894	0.016905	0.0022	8.40E-15	0.014736	0.003745	8.43E-05	0.018414	0.002756	2.47E-11	8.89E-14	0.429027	
2	BABAM2	rs13395259	28,096,429	T	C	0.452127	0.017453	0.002027	1.90E-17	0.019026	0.003451	3.61E-08	0.017254	0.002539	1.12E-11	2.37E-17	0.679237	
2	BABAM2	rs11679638	28,096,872	T	C	0.304808	0.016924	0.002191	6.10E-15	0.014382	0.003733	0.000118	0.018565	0.002744	1.37E-11	6.87E-14	0.366536	
2	BABAM2	rs7581813	28,097,094	G	T	0.451406	0.017252	0.002019	2.80E-17	0.018671	0.003438	5.76E-08	0.017125	0.002529	1.32E-11	4.37E-17	0.71719	
2	BABAM2	rs7572644	28,097,166	T	C	0.451208	0.017188	0.002019	3.60E-17	0.018441	0.003439	8.39E-08	0.017152	0.002529	1.23E-11	5.88E-17	0.762747	
2	BABAM2	rs7558946	28,097,314	T	C	0.450371	0.017321	0.002021	1.90E-17	0.018597	0.003441	6.63E-08	0.017253	0.002532	9.77E-12	7.750353		
2	BABAM2	rs10209559	28,099,593	A	G	0.293978	0.016843	0.002217	1.90E-14	0.015015	0.003777	7.10E-05	0.018177	0.002775	5.97E-11	1.79E-13	0.499988	
2	BABAM2	rs10187665	28,101,263	G	A	0.319035	0.01576	0.002171	1.50E-13	0.014517	0.003699	8.76E-05	0.016885	0.002719	5.48E-10	1.92E-12	0.606018	
2	BABAM2	rs80259585	28,101,619	T	C	0.030715	0.032512	0.005846	3.40E-08	0.030479	0.010078	0.002502	0.034627	0.002724	1.96E-06	1.24E-07	0.738626	
2	BABAM2	rs118163881	28,101,775	C	A	0.027665	0.035568	0.006161	3.40E-09	0.03373	0.018082	0.0018	0.039411	0.0076	2.20E-07	1.11E-08	0.667108	
2	BABAM2	rs6705961	28,102,334	T	C	0.441347	0.0167	0.002031	4.60E-16	0.01846	0.003456	9.45E-08	0.016344	0.002545	1.39E-10	7.08E-16	0.622091	
2	BABAM2	rs9309659	28,103,391	C	G	0.451981	0.017467	0.002032	1.80E-17	0.019333	0.003459	2.33E-08	0.01708	0.002546	2.04E-11	2.78E-17	0.599889	
2	BABAM2	rs10186196	28,104,963	G	C	0.293469	0.01574	0.002232	1.10E-12	0.014708	0.003801	0.00011	0.016548	0.002796	3.34E-09	1.39E-11	0.696673	
2	BABAM2	rs55796876	28,107,028	G	A	0.459192	0.014552	0.002054	1.60E-12	0.019643	0.003495	1.96E-08	0.012594	0.002573	1.00E-06	8.70E-13	0.104388	
2	BABAM2	rs13000292	28,112,486	C	T	0.450987	0.013808	0.002049	1.30E-11	0.017895	0.003485	2.89E-07	0.012179	0.002567	2.13E-06	2.45E-11	0.186633	
2	BABAM2	rs1948922	28,119,286	A	G	0.441606	0.012787	0.00205	4.00E-10	0.016796	0.003489	1.50E-06	0.011257	0.002569	1.19E-05	0.201053	0.166630	
2	BABAM2	rs13030032	28,125,303	A	T	0.478688	0.010939	0.002044	4.20E-08	0.015493	0.003484	8.81E-06	0.008933	0.002559	0.000485	1.15E-07	0.129104	
2	BABAM2	rs56115343	28,125,617	C	T	0.33231	0.012971	0.00216	6.20E-10	0.015564	0.003675	2.31E-05	0.01207	0.002707	8.38E-06	6.16E-09	0.443965	
2	BABAM2	rs6707054	28,127,353	T	C	0.321352	0.012513	0.00217	3.50E-09	0.015404	0.003693	3.06E-05	0.011527	0.00272	2.28E-05	2.10E-08	0.397872	
2	BABAM2	rs7559383	28,127,876	T	C	0.321238	0.011957	0.002171	1.50E-08	0.01424	0.003692	0.000116	0.011272	0.00272	3.46E-05	1.10E-07	0.517446	
2	BABAM2	rs7585476	28,128,055	A	G	0.323308	0.011733	0.002167	2.80E-08	0.014406	0.003686	9.38E-05	0.010826	0.002716	6.80E-05	1.71E-07	0.434251	
2	BABAM2	rs6712135	28,129,014	T	C	0.323658	0.011979	0.002164	1.40E-08	0.014785	0.00368	5.93E-05	0.010966	0.002713	5.35E-05	8.82E-08	0.403434	
2	BABAM2	rs6720961	28,132,428	G	A	0.324171	0.012035	0.002162	1.10E-08	0.014895	0.003677	5.15E-05	0.010995	0.002711	5.05E-05	7.31E-08	0.393183	
2	BABAM2	rs11692928	28,133,519	T	G	0.324095	0.012061	0.002162	1.10E-08	0.014857	0.003676	5.37E-05	0.011056	0.002711	4.59E-05	6.94E-08	0.405301	
2	BABAM2	rs7581912	28,134,403	G	T	0.323588	0.011976	0.002163	1.40E-08	0.014773	0.003678	5.96E-05	0.010963	0.002712	5.34E-05	8.87E-08	0.40442	
2	BABAM2	rs7579101	28,134,460	G	A	0.323586	0.011964	0.002163	1.40E-08	0.014773	0.003678	5.96E-05	0.010948	0.002712	5.48E-05	9.08E-08	0.402485	
2	BABAM2	rs11689563	28,134,841	G	A	0.323583	0.011967	0.002163	1.40E-08	0.014785	0.003678	5.88E-05	0.010951	0.002712	5.45E-05	8.91E-08	0.401556	
2	BABAM2	rs10189434	28,135,884	T	C	0.324361	0.011768	0.002162	2.50E-08	0.014423	0.003676	8.79E-05	0.01085	0.002711	6.33E-05	1.51E-07	0.433935	
2	BABAM2	rs13431389	28,137,361	C	T	0.324506	0.011821	0.002163	1.90E-08	0.014639	0.003677	6.93E-05	0.010781	0.002712	7.10E-05	1.34E-07	0.398442	
2	BABAM2	rs7594162	28,138,594	G	A	0.323691	0.012023	0.002163	1.20E-08	0.014868	0.003677	5.31E-05	0.010982	0.002711	5.17E-05	7.71E-08	0.394903	
2	BABAM2	rs13384961	28,139,127	C	T	0.322979	0.011974	0.002165	1.60E-08	0.014925	0.003681	5.07E-05	0.010876	0.002715	6.22E-05	8.78E-08	0.375966	
2	BABAM2	rs7581221	28,139,135	A	C	0.323714	0.012167	0.002164	8.50E-09	0.015065	0.003678	4.25E-05	0.011094	0.002713	4.38E-05	5.33E-08	0.385015	
2	BABAM2	rs13393848	28,139,147	A	G	0.322474	0.012252	0.002169	7.00E-09	0.015059	0.003686	4.45E-05	0.011196	0.002719	3.87E-05	4.94E-08	0.398971	
2	BABAM2	rs11691530	28,139,451	G	C	0.32369	0.012029	0.002163	1.10E-08	0.014871	0.003677	5.29E-05	0.010989	0.002711	5.12E-05	7.60E-08	0.39536	
2	BABAM2	rs10170879	28,140,730	T	A	0.324298	0.011948	0.002162	1.40E-08	0.014656	0.003675	6.74E-05	0.01101	0.00271	4.89E-05	9.16E-08	0.42451	
2	BABAM2	rs7575930	28,142,797	T	C	0.324587	0.011603	0.002148	3.00E-08	0.014227	0.003653	9.91E-05	0.010661	0.002692	7.56E-05	1.99E-07	0.431861	
2	BABAM2	rs141106979	28,145,437	A	T	0.020655	-0.046571	0.007108	2.20E-11	-0.057716	0.012122	1.96E-06	-0.042335	0.008894	1.97E-06	1.44E-10	0.306323	
2	BABAM2	rs6741499	28,146,569	T	C	0.324613	0.011535	0.002147	3.20E-08	0.014094	0.003652	0.000115	0.010634	0.002691	7.82E-05	2.37E-07	0.445721	
2	BABAM2	rs11886621	28,150,033	T	C	0.323807	0.012112	0.002149	6.80E-09	0.014918	0.003656	4.55E-05	0.011125	0.002693	3.66E-05	4.79E-08	0.403653	
2	BABAM2	rs60751755	28,155,692	C	T	0.324567	0.0118											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	GRB14 *	rs12692735	164,648,055	T	G	0.102874	-0.02087	0.00331	7.10E-10	-0.012657	0.005637	0.003938	-0.023242	0.004146	2.12E-08	2.34E-09	0.318121	
2	GRB14 *	rs10930133	164,650,214	A	T	0.106432	-0.019742	0.003264	4.50E-09	-0.01588	0.005561	0.004305	-0.021901	0.004088	8.63E-08	9.92E-09	0.383011	
2	COBLL1 *	rs6754919	164,651,333	T	C	0.103165	-0.021192	0.003305	3.20E-10	-0.016446	0.005626	0.003473	-0.023673	0.004141	1.11E-08	1.11E-09	0.300888	
2	COBLL1 *	rs6713419	164,651,790	C	T	0.103175	-0.021175	0.003305	3.30E-10	-0.016379	0.005625	0.003607	-0.023696	0.004141	1.08E-08	1.12E-09	0.294791	
2	COBLL1 *	rs10184004	164,651,879	T	C	0.103064	-0.021037	0.003305	4.60E-10	-0.01642	0.005627	0.003533	-0.023419	0.004141	1.59E-08	1.60E-09	0.316406	
2	COBLL1 *	rs10179126	164,655,284	G	C	0.103144	-0.021014	0.003304	4.80E-10	-0.016414	0.005623	0.003524	-0.023399	0.004139	1.62E-08	1.63E-09	0.31713	
2	COBLL1 *	rs10195252	164,656,581	C	T	0.103295	-0.020767	0.003302	8.20E-10	-0.0161	0.005621	0.004189	-0.02319	0.004138	2.14E-08	2.50E-09	0.309719	
2	COBLL1 *	rs36105243	164,668,241	G	C	0.10314	-0.021111	0.003304	3.90E-10	-0.016483	0.005623	0.003388	-0.023517	0.004139	1.37E-08	1.34E-09	0.313748	
2	COBLL1 *	rs7592412	164,669,828	C	T	0.10313	-0.021119	0.003304	3.90E-10	-0.016522	0.005624	0.003314	-0.023497	0.004139	1.41E-08	1.35E-09	0.317879	
2	COBLL1 *	rs13432797	164,670,077	C	G	0.080572	-0.022336	0.003693	5.50E-09	-0.019349	0.006277	0.002061	-0.024197	0.00463	1.77E-07	1.01E-08	0.534265	
2	COBLL1 *	rs1128249	164,672,114	T	G	0.103276	-0.02107	0.003302	4.40E-10	-0.01636	0.005622	0.003627	-0.023525	0.004137	1.33E-08	1.38E-09	0.30459	
2	COBLL1 *	rs13389219	164,672,366	T	C	0.10338	-0.021424	0.003304	2.10E-10	-0.017213	0.005624	0.002218	-0.023605	0.00414	1.22E-08	8.07E-10	0.360074	
2	COBLL1 *	rs10187501	164,675,944	G	A	0.080271	-0.022269	0.003701	6.50E-09	-0.019595	0.006286	0.001832	-0.023848	0.004642	2.85E-07	1.44E-08	0.58631	
2	COBLL1	rs6717858	164,683,151	C	T	0.103859	-0.02108	0.003297	3.50E-10	-0.017842	0.005614	0.001489	-0.02262	0.004129	4.40E-08	1.95E-09	0.493026	
2	COBLL1	rs6753142	164,687,561	C	T	0.103551	-0.020863	0.0033	5.50E-10	-0.01723	0.005618	0.002171	-0.022655	0.004134	4.35E-08	2.73E-09	0.43676	
2	COBLL1	rs6738627	164,687,940	A	G	0.103819	-0.02102	0.003296	3.90E-10	-0.017482	0.005613	0.001848	-0.022742	0.004128	3.70E-08	2.01E-09	0.450284	
2	COBLL1	rs12692737	164,697,799	A	C	0.078247	-0.021173	0.003743	3.80E-08	-0.016707	0.006348	0.008511	-0.023771	0.004699	4.29E-07	8.67E-08	0.371092	
2	COBLL1	rs9653282	164,698,148	T	A	0.078042	-0.020983	0.003747	4.80E-08	-0.016705	0.006355	0.00859	-0.023497	0.004705	6.02E-07	1.21E-07	0.390404	
2	COBLL1	rs7609045	164,698,697	A	G	0.078038	-0.021	0.003748	4.60E-08	-0.016705	0.006355	0.00859	-0.023523	0.004705	5.85E-07	1.18E-07	0.388582	
2	COBLL1	rs2198550	164,700,250	C	A	0.077915	-0.021111	0.003752	4.10E-08	-0.016815	0.006369	0.008299	-0.023635	0.004709	5.29E-07	1.04E-07	0.389224	
2	COBLL1	rs6712203	164,700,808	T	C	0.114206	-0.01833	0.003168	1.10E-08	-0.014581	0.005399	0.006933	-0.019924	0.003966	5.18E-07	8.65E-08	0.425139	
2	NOSTRIN	rs2947934	168,839,020	G	A	0.322658	0.011433	0.002195	4.50E-08	0.01392	0.003728	0.00019	0.01067	0.002753	0.000107	5.13E-07	0.483037	
2	NOSTRIN	rs560952	168,847,977	T	C	0.417743	0.011145	0.002077	1.70E-08	0.015403	0.003538	1.35E-05	0.009035	0.0026	0.000515	1.83E-07	0.146957	
2	NOSTRIN	rs497808	168,848,527	T	G	0.420476	0.010949	0.002068	2.30E-08	0.015489	0.003521	1.10E-05	0.008773	0.002591	0.000714	2.04E-07	0.124474	
2	NOSTRIN	rs566465	168,848,594	A	T	0.354392	0.011325	0.002136	1.40E-08	0.015628	0.003627	1.66E-05	0.009828	0.00268	0.000247	1.12E-07	0.198428	
2	NOSTRIN	rs540652	168,850,918	C	T	0.418174	0.011089	0.00207	1.30E-08	0.016116	0.003523	4.85E-06	0.008712	0.002593	0.000784	1.01E-07	0.090531	
2	NOSTRIN	rs488621	168,851,042	A	G	0.418015	0.011017	0.00207	1.60E-08	0.016076	0.003524	5.13E-06	0.00863	0.002593	0.00088	1.19E-07	0.088806	
2	NOSTRIN	rs546146	168,852,687	C	G	0.352872	0.011453	0.002137	8.90E-09	0.016041	0.00363	1.00E-05	0.009859	0.002681	0.000238	6.66E-08	0.170726	
2	NOSTRIN	rs527393	168,853,247	G	A	0.418179	0.011146	0.002069	1.10E-08	0.016015	0.003521	5.50E-06	0.008849	0.002592	0.000644	9.49E-08	0.101233	
2	NOSTRIN	rs2685799	168,854,794	T	C	0.414609	0.011304	0.002073	7.60E-09	0.015695	0.003529	8.80E-06	0.009229	0.002597	0.000383	9.17E-08	0.139993	
2	NOSTRIN	rs2632380	168,857,840	T	C	0.413523	0.011498	0.002074	4.30E-09	0.016092	0.003531	5.25E-06	0.009252	0.002599	0.000373	5.45E-08	0.118711	
2	NOSTRIN	rs569997	168,858,383	T	C	0.41521	0.011571	0.002072	3.50E-09	0.015949	0.003527	6.21E-06	0.009423	0.002595	0.000284	4.97E-08	0.136089	
2	NOSTRIN	rs576062	168,859,176	A	G	0.413886	0.011628	0.002073	3.00E-09	0.016091	0.003529	5.21E-06	0.009485	0.002597	0.000262	3.90E-08	0.131644	
2	NOSTRIN	rs2632372	168,861,031	T	C	0.350509	0.011519	0.002118	4.40E-09	0.016433	0.003599	5.05E-06	0.009702	0.002656	0.000261	3.76E-08	0.132358	
2	SPC25 *	rs9751269	168,869,393	A	G	0.419279	0.011241	0.002054	5.70E-09	0.016181	0.0035	3.85E-06	0.008869	0.002571	0.000566	5.98E-08	0.092264	
2	SPC25	rs6734923	168,871,220	G	C	0.418551	0.011197	0.002055	6.20E-09	0.016015	0.003502	4.87E-06	0.008873	0.002572	0.000565	7.49E-08	0.100261	
2	SPC25	rs554494	168,873,053	G	A	0.419605	0.011196	0.002054	5.90E-09	0.016071	0.003501	4.50E-06	0.008824	0.002572	0.000605	7.39E-08	0.09529	
2	SPC25	rs506273	168,875,025	T	C	0.412971	0.011191	0.00206	6.70E-09	0.015251	0.00351	1.41E-05	0.009259	0.00258	0.000334	1.26E-07	0.168863	
2	SPC25	rs453727	168,879,788	A	T	0.437139	0.011576	0.002066	2.80E-09	0.014522	0.003516	3.66E-05	0.010158	0.002588	8.77E-05	8.92E-08	0.317505	
2	SPC25	rs524586	168,881,341	A	G	0.373724	0.011845	0.002108	1.70E-09	0.015317	0.003582	1.92E-05	0.01061	0.002644	6.08E-05	3.42E-08	0.29046	
2	SPC25	rs493816	168,881,727	C	T	0.44058	0.011825	0.002066	1.00E-09	0.015449	0.003516	1.13E-05	0.010072	0.002588	1.00E-04	3.31E-08	0.218154	
2	G6PC2 *	rs34177044	168,897,975	A	G	0.407277	0.012501	0.002072	1.30E-09	0.012139	0.003524	0.000575	0.012728	0.002597	9.72E-07	1.61E-08	0.892925	
2	G6PC2 *	rs13387347	168,898,336	C	T	0.45441	0.012588	0.002045	2.30E-10	0.013035	0.003467	0.000171	0.012526	0.002593	1.09E-06	5.80E-09	0.906203	
2	G6PC2 *	rs1402837	168,900,844	T	C	0.403825	0.012391	0.002055	1.10E-09	0.012484	0.003494	0.000355	0.012551	0.002576	1.13E-06	1.19E-08	0.987642	
2	G6PC2	rs2232326	168,907,981	C	T	0.404031	-0.033658	0.005155	3.80E-11	-0.032331	0.008699	0.000203	-0.035115	0.006489	6.40E-08	4.38E-10	0.797599	
2	G6PC2 *	rs12053049	168,910,638	C	T	0.289853	0.016296	0.002254	6.90E-14	0.018552	0.003822	1.23E-06	0.01522	0.002829	7.65E-08	3.99E-12	0.483532	
2	G6PC2 *	rs16856187	168,913,876	C	A	0.293402	0.016413	0.002249	7.20E-14	0.018277	0.003811	1.64E-06	0.015397	0.002825	5.14E-08	3.57E-12	0.543682	
2	G6PC2 *	rs60415045	168,914,614	C	A	0.288613	0.015823	0.002258	7.30E-13	0.018218	0.003827	1.97E-06	0.014605	0.002835	2.64E-07	0.448158		
2	G6PC2 *	rs10497347	168,914,704	C	T	0.284481	0.015981	0.002269	7.30E-13	0.01765	0.003842	4.42E-06	0.015131	0.00285	1.12E-07	1.98E-11	0.598507	
2	G6PC2 *	rs13419326	168,914,910	C	A	0.282965	0.015886	0.002271	9.20E-13	0.017554	0.003848	5.15E-06	0.015098	0.002853	1.23E-07	2.51E-11	0.608164	
2	G6PC2 *	rs4144857	168,914,996	C	G	0.282988	0.01587	0.002271	9.80E-13	0.017611	0.003848	4.79E-06	0.015042	0.002852	1.37E-07	2.59E-11	0.591737	
2	G6PC2 *	rs4144858	168,915,008	T	C	0.283	0.0159	0.002271	8.80E-13	0.017641	0.003848	4.62E-06	0.015075	0.002852	1.28E-07	2.35E-11	0.592137	
2	G6PC2 *	rs504979	168,915,349	T	C	0.345693	0.012827	0.002149	5.60E-10	0.016986	0.003638	3.08E-06	0.010788	0.002699	6.49E-05	6.30E-09	0.171289	
2	ABC811 *	rs73972707	168,919,250	G	A	0.288752	0.016897	0.002245	1.20E-14	0.01991	0.00381	1.77E-07	0.015428	0.002818	4.47E-08	3.62E-13	0.344227	
2	ABC811 *	rs28819151	168,919,319	G	A	0.288751	0.016889	0.002245	1.20E-14	0.019865	0.00381	1.88E-07	0.015436	0.002818	4.40E-08	3.80E-13	0.349973	
2	ABC811 *	rs74870851	168,919,713	G	A	0.288831	0.016913	0.002245	1.20E-14	0.019908	0.00381	1.77E-07	0.015449	0.002817	4.26E-08	3.46E-13	0.346655	
2	ABC811 *	rs78529720	1															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
2	ABCB11	rs3755158	168,935,678	G	C	0.344791	0.012492	0.002119	5.90E-10	0.014181	0.003594	8.05E-05	0.011938	0.00266	7.30E-06	1.77E-08	0.615985	
2	ABCB11	rs472614	168,935,911	A	G	0.372266	0.012038	0.002084	1.90E-09	0.015971	0.003533	6.27E-06	0.010218	0.002616	9.45E-05	1.78E-08	0.190637	
2	ABCB11	rs565412	168,937,773	A	G	0.372117	0.012004	0.002089	2.20E-09	0.015618	0.003543	1.05E-05	0.010419	0.002623	7.18E-05	2.25E-08	0.238126	
2	ABCB11	rs567074	168,937,921	T	C	0.372074	0.011973	0.002089	2.60E-09	0.015692	0.003543	9.58E-06	0.010344	0.002623	8.10E-05	2.30E-08	0.224973	
2	ABCB11	rs479682	168,938,177	T	C	0.369879	0.012076	0.002095	2.20E-09	0.015838	0.003553	8.41E-06	0.010419	0.002629	7.48E-05	1.89E-08	0.220165	
2	ABCB11	rs480562	168,938,261	T	A	0.371933	0.011942	0.00209	2.90E-09	0.015716	0.003545	9.39E-06	0.010287	0.002624	8.95E-05	2.48E-08	0.218284	
2	ABCB11	rs482508	168,938,473	A	G	0.370294	0.012122	0.002093	1.80E-09	0.015552	0.003549	1.19E-05	0.010652	0.002628	5.09E-05	1.83E-08	0.26718	
2	ABCB11	rs508743	168,938,777	C	G	0.370673	0.012212	0.002096	1.40E-09	0.014995	0.003555	2.49E-05	0.011114	0.002632	2.44E-05	1.84E-08	0.38021	
2	ABCB11	rs58512362	168,938,957	G	A	0.344633	0.012343	0.002129	1.00E-09	0.01298	0.003611	0.000327	0.012416	0.002673	3.45E-06	3.23E-08	0.900167	
2	ABCB11	rs2544360	168,939,677	T	C	0.357876	0.012111	0.00211	1.80E-09	0.013524	0.003576	0.000157	0.011741	0.00265	9.53E-06	4.28E-08	0.688706	
2	ABCB11	rs2685803	168,939,775	A	G	0.371788	0.012096	0.002097	1.90E-09	0.014795	0.003555	3.20E-05	0.011012	0.002633	2.92E-05	2.77E-08	0.392591	
2	ABCB11	rs2544367	168,939,778	T	C	0.371788	0.012096	0.002097	1.90E-09	0.014795	0.003555	3.20E-05	0.011012	0.002633	2.92E-05	2.77E-08	0.392591	
2	ABCB11	rs2685804	168,940,262	A	G	0.37137	0.012111	0.002095	1.70E-09	0.014794	0.003552	3.15E-05	0.010996	0.00263	2.93E-05	2.73E-08	0.390091	
2	ABCB11	rs2685805	168,940,550	A	G	0.371401	0.01209	0.002096	1.80E-09	0.014842	0.003554	2.99E-05	0.010951	0.002631	3.18E-05	2.82E-08	0.378868	
2	ABCB11	rs2685806	168,940,794	A	G	0.371313	0.012098	0.002095	1.80E-09	0.014882	0.003553	2.84E-05	0.010948	0.00263	3.19E-05	2.68E-08	0.373473	
2	ABCB11	rs2685807	168,941,016	C	T	0.371297	0.012089	0.002095	1.80E-09	0.014871	0.003553	2.88E-05	0.010937	0.002631	3.25E-05	2.77E-08	0.373554	
2	ABCB11	rs2685808	168,941,130	G	T	0.371445	0.012028	0.002096	2.20E-09	0.014792	0.003554	3.19E-05	0.01088	0.002631	3.59E-05	3.35E-08	0.376312	
2	ABCB11	rs1581397	168,941,142	T	C	0.371529	0.011991	0.002096	2.50E-09	0.014857	0.003554	2.95E-05	0.010789	0.002632	4.18E-05	3.60E-08	0.357729	
2	ABCB11	rs2685810	168,941,222	T	C	0.371312	0.012064	0.002095	1.90E-09	0.014844	0.003553	2.98E-05	0.010908	0.002631	3.41E-05	3.00E-08	0.373348	
2	ABCB11	rs2685811	168,941,417	A	G	0.371298	0.012094	0.002096	1.80E-09	0.014896	0.003553	2.80E-05	0.010934	0.002631	3.27E-05	2.71E-08	0.370242	
2	ABCB11	rs77601801	168,941,523	G	A	0.321801	0.012895	0.002173	4.30E-10	0.013663	0.003682	0.000208	0.012844	0.002729	2.57E-06	1.59E-08	0.858083	
2	ABCB11	rs2685812	168,941,661	A	G	0.372662	0.012176	0.002096	1.20E-09	0.014621	0.003555	3.94E-05	0.01125	0.002631	1.93E-05	2.27E-08	0.445862	
2	ABCB11	rs2685813	168,941,929	T	C	0.372662	0.012193	0.002096	1.10E-09	0.014681	0.003555	3.67E-05	0.011236	0.002631	1.98E-05	2.17E-08	0.436036	
2	ABCB11	rs2685814	168,942,109	T	C	0.372633	0.012193	0.002097	1.10E-09	0.014643	0.003556	3.86E-05	0.011265	0.002632	1.89E-05	2.18E-08	0.445103	
2	ABCB11	rs2250677	168,942,778	C	T	0.37283	0.012171	0.002097	1.30E-09	0.014764	0.003557	3.36E-05	0.011178	0.002633	2.21E-05	2.21E-08	0.417177	
2	ABCB11	rs853791	168,943,918	A	G	0.372867	0.012084	0.002098	1.60E-09	0.014548	0.003559	4.41E-05	0.011166	0.002634	2.27E-05	2.95E-08	0.444916	
2	ABCB11	rs853790	168,943,931	A	T	0.374251	0.012038	0.0021	1.80E-09	0.014801	0.003563	3.30E-05	0.010981	0.002636	3.13E-05	3.04E-08	0.38874	
2	ABCB11	rs860510	168,945,118	A	C	0.372863	0.012102	0.002099	1.50E-09	0.014663	0.00356	3.85E-05	0.011149	0.002635	2.36E-05	2.69E-08	0.427658	
2	ABCB11	rs853788	168,945,395	T	C	0.372835	0.012086	0.002099	1.60E-09	0.014614	0.00356	4.09E-05	0.011152	0.002636	2.35E-05	2.84E-08	0.434513	
2	ABCB11	rs853786	168,945,800	G	A	0.373099	0.012051	0.002101	1.80E-09	0.014728	0.003563	3.61E-05	0.011046	0.002638	2.85E-05	3.03E-08	0.406267	
2	ABCB11	rs862662	168,945,819	C	A	0.373083	0.012044	0.002101	1.90E-09	0.014732	0.003563	3.59E-05	0.01103	0.002638	2.93E-05	3.09E-08	0.403656	
2	ABCB11	rs853785	168,946,084	C	T	0.37304	0.012084	0.002104	1.70E-09	0.014519	0.003567	4.75E-05	0.011153	0.002641	2.44E-05	3.39E-08	0.448261	
2	ABCB11	rs16856261	168,947,058	T	C	0.310459	0.015038	0.002206	1.80E-12	0.015624	0.003734	2.90E-05	0.014983	0.002771	6.59E-08	7.13E-11	0.890249	
2	ABCB11	rs853784	168,947,164	C	T	0.37259	0.011721	0.00212	7.20E-09	0.014488	0.003589	5.49E-05	0.010708	0.002664	5.88E-05	8.97E-08	0.397816	
2	ABCB11	rs853783	168,949,001	A	C	0.368074	0.011123	0.002128	3.30E-08	0.014124	0.003602	8.89E-05	0.009915	0.002675	0.000212	4.76E-07	0.348149	
2	ABCB11	rs55700007	168,949,511	G	T	0.342056	0.01198	0.002165	3.80E-09	0.01212	0.003662	0.000938	0.012407	0.002721	5.19E-06	1.27E-07	0.949905	
2	ABCB11	rs853782	168,949,788	C	T	0.370232	0.011423	0.002127	1.50E-08	0.014137	0.0036	8.68E-05	0.010412	0.002673	9.89E-05	2.27E-07	0.406039	
2	ABCB11	rs853781	168,949,811	A	G	0.367993	0.011363	0.002131	2.00E-08	0.014283	0.003607	7.59E-05	0.010229	0.002678	0.000134	0.366919	0.267E-07	
2	ABCB11	rs139014876	168,950,218	A	G	0.037205	-0.031902	0.005393	1.90E-09	-0.029351	0.009086	0.001243	-0.033882	0.006795	6.26E-07	2.16E-08	0.689685	
2	ABCB11	rs72886761	168,950,228	A	G	0.341076	0.012092	0.002166	2.80E-09	0.01244	0.003664	0.000689	0.012394	0.002722	5.36E-06	9.88E-08	0.991972	
2	ABCB11	rs853780	168,950,972	C	G	0.370211	0.011452	0.002129	1.40E-08	0.014409	0.003603	6.41E-05	0.010289	0.002676	0.000121	2.07E-07	0.358629	
3	SYN2 *	rs7615580	11,985,766	C	T	0.036049	-0.031118	0.005409	1.20E-09	-0.040668	0.009068	7.40E-06	-0.028503	0.006824	2.99E-05	6.98E-09	0.283734	
3	SYN2 *	rs2623897	11,989,795	G	A	0.0347	-0.032378	0.005506	8.30E-10	-0.043366	0.009247	2.78E-06	-0.028656	0.006938	3.67E-05	3.31E-09	0.203179	
3	SYN2 *	rs2600268	11,991,338	G	A	0.0347	-0.032378	0.005506	8.30E-10	-0.043366	0.009247	2.78E-06	-0.028656	0.006938	3.67E-05	3.31E-09	0.203179	
3	SYN2 *	rs2600269	11,992,486	C	T	0.03471	-0.032437	0.005505	7.60E-10	-0.043478	0.009242	2.58E-06	-0.028686	0.006938	3.59E-05	3.03E-09	0.200516	
3	SYN2 *	rs2600271	11,994,702	T	C	0.034627	-0.032594	0.00551	7.20E-10	-0.043698	0.009251	2.36E-06	-0.02877	0.006945	3.47E-05	2.68E-09	0.196877	
3	SYN2 *	rs199870642	11,995,302	A	T	0.034718	-0.03236	0.005505	8.30E-10	-0.04325	0.009245	2.94E-06	-0.028675	0.006938	3.62E-05	3.45E-09	0.207287	
3	SYN2 *	rs2600229	11,996,979	A	T	0.034707	-0.032459	0.005505	7.30E-10	-0.043472	0.009243	2.60E-06	-0.028697	0.006938	3.57E-05	3.03E-09	0.201045	
3	SYN2 *	rs2600230	11,997,155	T	A	0.034707	-0.032459	0.005505	7.30E-10	-0.043472	0.009243	2.60E-06	-0.028697	0.006938	3.57E-05	3.03E-09	0.201045	
3	SYN2 *	rs2618404	11,997,191	A	C	0.034707	-0.032459	0.005505	7.30E-10	-0.043472	0.009243	2.60E-06	-0.028697	0.006938	3.57E-05	3.03E-09	0.201045	
3	SYN2 *	rs2618403	11,997,989	C	T	0.034711	-0.032647	0.005505	5.80E-10	-0.043472	0.009243	2.60E-06	-0.029005	0.006937	2.93E-05	2.51E-09	0.210596	
3	SYN2 *	rs2618402	11,998,325	C	A	0.034768	-0.031994	0.0055	1.10E-09	-0.042714	0.009234	3.79E-06	-0.028313	0.006931	4.46E-05	5.38E-09	0.212301	
3	SYN2	rs2923857	12,004,864	G	C	0.034486	-0.033011	0.005522	4.00E-10	-0.043676	0.009271	2.50E-06	-0.029501	0.00696	2.28E-05	1.90E-09	0.221391	
3	SYN2	rs2600235	12,004,945	T	G	0.034486	-0.033011	0.005522	4.00E-10	-0.043676	0.009271	2.50E-06	-0.029501	0.00696	2.28E-05	1.90E-09	0.221391	
3	SYN2	rs2623879	12,004,946	T	C	0.034503	-0.033098	0.005521	3.70E-10	-0.0437	0.00927	2.47E-06	-0.029658	0.006959	2.05E-05	1.70E-09	0.225708	
3	SYN2	rs2618389	12,007,234	C	T	0.034476	-0.0329	0.005523	4.50E-10	-0.043676	0.009271	2.50E-06	-0.029322	0.006962	2.56E-05	2.13E-09	0.21566	
3	SYN2	rs261																

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
3	SYN2	rs184262	12,093,240	A	G	0.034392	-0.032772	0.005528	5.30E-10	-0.043738	0.009277	2.46E-06	-0.029045	0.006697	3.12E-05	2.52E-09	0.205397	
3	SYN2	rs13061425	12,095,404	G	T	0.034392	-0.032777	0.005528	5.30E-10	-0.043731	0.009277	2.47E-06	-0.029045	0.006697	3.12E-05	2.53E-09	0.205604	
3	SYN2	rs6798755	12,097,592	T	C	0.033051	-0.034383	0.005639	2.00E-10	-0.04322	0.009453	4.90E-06	-0.031591	0.007113	9.08E-06	1.51E-09	0.325614	
3	SYN2	rs58683249	12,098,765	C	T	0.034392	-0.032766	0.005528	5.30E-10	-0.043731	0.009277	2.47E-06	-0.029038	0.006697	3.13E-05	2.54E-09	0.205388	
3	SYN2	rs453131	12,099,453	C	G	0.034391	-0.032757	0.005528	5.40E-10	-0.043731	0.009277	2.47E-06	-0.029024	0.006697	3.16E-05	2.56E-09	0.204953	
3	SYN2	rs6442307	12,101,855	C	A	0.034391	-0.032757	0.005528	5.40E-10	-0.043731	0.009277	2.47E-06	-0.029024	0.006697	3.16E-05	2.56E-09	0.204953	
3	SYN2	rs160113	12,103,739	T	C	0.115525	-0.018138	0.003165	1.60E-09	-0.026364	0.005359	8.83E-07	-0.01482	0.003971	0.000191	5.25E-09	0.0835	
3	SYN2	rs34206487	12,103,849	G	A	0.034391	-0.032754	0.005528	5.40E-10	-0.043731	0.009277	2.47E-06	-0.02902	0.006697	3.17E-05	2.57E-09	0.204833	
3	SYN2	rs11715886	12,105,736	G	C	0.03439	-0.032758	0.005528	5.40E-10	-0.04374	0.009277	2.46E-06	-0.02902	0.006697	3.17E-05	2.56E-09	0.204574	
3	SYN2	rs73813125	12,106,763	C	T	0.03439	-0.032758	0.005528	5.40E-10	-0.04374	0.009277	2.46E-06	-0.02902	0.006697	3.17E-05	2.56E-09	0.204574	
3	SYN2	rs13079332	12,107,348	A	G	0.03439	-0.032758	0.005528	5.40E-10	-0.04374	0.009277	2.46E-06	-0.02902	0.006697	3.17E-05	2.56E-09	0.204574	
3	SYN2	rs117621918	12,108,368	C	T	0.028273	-0.033131	0.006084	1.70E-08	-0.046704	0.010198	4.73E-06	-0.02767	0.007675	0.000314	4.20E-08	0.135888	
3	SYN2	rs13064800	12,110,157	A	C	0.032997	-0.031352	0.005639	4.20E-09	-0.041912	0.009451	9.35E-06	-0.027866	0.007114	9.05E-05	2.50E-08	0.235049	
3	SYN2	rs11720130	12,114,816	A	G	0.115864	-0.018027	0.00316	1.90E-09	-0.026668	0.005353	6.41E-07	-0.014399	0.003963	0.000282	5.55E-09	0.065476	
3	SYN2	rs71628736	12,115,035	A	C	0.034401	-0.032657	0.005527	6.10E-10	-0.043785	0.009274	2.38E-06	-0.02886	0.006968	3.49E-05	2.73E-09	0.198228	
3	SYN2	rs71624931	12,125,648	A	G	0.034318	-0.032614	0.005534	6.80E-10	-0.044415	0.009283	1.74E-06	-0.028514	0.006979	4.44E-05	2.54E-09	0.170911	
3	SYN2	rs13064956	12,128,751	C	T	0.115809	-0.017734	0.003162	2.40E-09	-0.027002	0.005351	4.60E-07	-0.013808	0.003967	0.000503	6.93E-09	0.047634	M
3	SYN2	rs34831171	12,132,155	C	T	0.115969	-0.018217	0.003159	1.10E-09	-0.026939	0.005348	4.82E-07	-0.01456	0.003963	0.00024	3.63E-09	0.062961	
3	SYN2	rs7647950	12,139,096	T	G	0.034325	-0.032723	0.005535	5.90E-10	-0.044532	0.009283	1.64E-06	-0.028625	0.00698	4.16E-05	2.24E-09	0.170786	
3	SYN2	rs71304088	12,139,633	C	T	0.034325	-0.032723	0.005535	5.90E-10	-0.044532	0.009283	1.64E-06	-0.028625	0.00698	4.16E-05	2.24E-09	0.170786	
3	SYN2	rs4488811	12,140,528	T	C	0.034357	-0.032779	0.00554	5.70E-10	-0.044739	0.00929	1.49E-06	-0.028593	0.006987	4.32E-05	2.13E-09	0.164827	
3	SYN2	rs7621569	12,143,057	G	A	0.115202	-0.018258	0.00317	9.20E-10	-0.027588	0.005364	2.76E-07	-0.014239	0.003978	0.000347	2.97E-09	0.045629	M
3	SYN2	rs11721223	12,143,660	G	A	0.034247	-0.032628	0.005541	6.70E-10	-0.044642	0.009291	1.58E-06	-0.028389	0.006988	4.91E-05	2.53E-09	0.162107	
3	SYN2	rs1039247	12,144,804	G	T	0.034247	-0.032628	0.005541	6.70E-10	-0.044642	0.009291	1.58E-06	-0.028389	0.006988	4.91E-05	2.53E-09	0.162107	
3	SYN2	rs1867012	12,146,743	C	T	0.034243	-0.032842	0.005541	5.40E-10	-0.04455	0.009293	1.66E-06	-0.028748	0.006989	3.94E-05	2.16E-09	0.174108	
3	SYN2	rs11708978	12,146,995	G	A	0.034243	-0.032842	0.005541	5.40E-10	-0.04455	0.009293	1.66E-06	-0.028748	0.006989	3.94E-05	2.16E-09	0.174108	
3	SYN2	rs35252627	12,147,066	A	C	0.034243	-0.032842	0.005541	5.40E-10	-0.04455	0.009293	1.66E-06	-0.028748	0.006989	3.94E-05	2.16E-09	0.174108	
3	SYN2	rs6768568	12,148,318	A	G	0.034126	-0.031853	0.005551	1.80E-09	-0.043673	0.009313	2.78E-06	-0.027775	0.006999	7.31E-05	6.38E-09	0.172332	
3	SYN2	rs6792867	12,148,400	C	A	0.034126	-0.031853	0.005551	1.80E-09	-0.043673	0.009313	2.78E-06	-0.027775	0.006999	7.31E-05	6.38E-09	0.172332	
3	SYN2	rs7629805	12,150,894	G	A	0.034212	-0.033233	0.005544	3.50E-10	-0.044688	0.009294	1.55E-06	-0.029295	0.006993	2.83E-05	1.47E-09	0.185642	
3	SYN2	rs117082374	12,150,945	C	T	0.02807	-0.033901	0.006107	9.30E-09	-0.047989	0.010228	2.75E-06	-0.028151	0.007708	0.000262	1.21E-08	0.12138	
3	SYN2	rs7652520	12,151,127	C	G	0.034212	-0.033233	0.005544	3.50E-10	-0.044688	0.009294	1.55E-06	-0.029295	0.006993	2.83E-05	1.47E-09	0.185642	
3	SYN2, TIMP4	rs17035945	12,153,128	T	C	0.11474	-0.018163	0.003178	1.60E-09	-0.026937	0.005374	5.48E-07	-0.014379	0.00399	0.000316	5.31E-09	0.060641	
3	SYN2, TIMP4	rs71304089	12,155,463	T	C	0.034213	-0.033162	0.005543	3.80E-10	-0.04425	0.009294	1.96E-06	-0.029429	0.006992	2.59E-05	1.70E-09	0.202535	
3	SYN2, TIMP4	rs71304090	12,155,999	G	A	0.034209	-0.033202	0.005543	3.60E-10	-0.044321	0.009295	1.89E-06	-0.029443	0.006992	2.57E-05	1.63E-09	0.200814	
3	SYN2, TIMP4	rs10433537	12,156,985	T	A	0.034209	-0.033198	0.005543	3.60E-10	-0.044321	0.009295	1.89E-06	-0.029436	0.006992	2.58E-05	1.64E-09	0.200614	
3	SYN2	rs18627553	12,165,221	A	G	0.028471	-0.033786	0.006064	7.80E-09	-0.048348	0.010158	1.97E-06	-0.027924	0.007653	0.000265	1.55E-08	0.108313	
3	SYN2	rs78518024	12,165,961	C	T	0.034661	-0.033264	0.005508	2.60E-10	-0.0461	0.009231	6.02E-07	-0.028692	0.006948	3.68E-05	7.60E-10	0.131866	
3	SYN2	rs13064273	12,174,631	A	G	0.034664	-0.033228	0.005507	2.80E-10	-0.046004	0.009229	6.33E-07	-0.028693	0.006948	3.68E-05	7.98E-10	0.133988	
3	SYN2	rs6781687	12,174,760	G	A	0.050799	-0.029168	0.004621	2.10E-11	-0.040438	0.007757	1.89E-07	-0.024337	0.005824	2.97E-05	2.03E-10	0.096932	
3	SYN2	rs13070993	12,176,297	T	C	0.03494	-0.033383	0.005487	2.10E-10	-0.044861	0.009209	1.13E-06	-0.02957	0.006917	1.94E-05	7.56E-10	0.184263	
3	SYN2	rs6805092	12,179,924	T	C	0.044783	-0.032513	0.004877	4.20E-12	-0.039803	0.008191	1.20E-06	-0.030334	0.006146	8.14E-07	3.83E-11	0.355144	
3	SYN2	rs310763	12,189,204	T	C	0.116495	-0.01798	0.003154	1.60E-09	-0.027431	0.005333	2.75E-07	-0.013803	0.00396	0.000494	4.13E-09	0.040224	M
3	SYN2 *	rs71304092	12,195,065	A	G	0.044799	-0.032117	0.004878	6.40E-12	-0.039447	0.008196	1.51E-06	-0.029833	0.006145	1.23E-06	7.13E-11	0.348	
3	SYN2 *	rs13077227	12,200,266	G	A	0.044804	-0.032101	0.004878	6.90E-12	-0.039653	0.008197	1.34E-06	-0.029767	0.006145	1.29E-06	6.65E-11	0.334505	
3	SYN2 *	rs7637403	12,200,988	A	G	0.116268	-0.018169	0.003157	1.10E-09	-0.028184	0.005337	1.31E-07	-0.013657	0.003963	0.000573	2.32E-09	0.028889	M
3	SYN2 *	rs13079837	12,209,346	A	T	0.117316	-0.017763	0.003143	1.70E-09	-0.027502	0.00532	2.39E-07	-0.013471	0.003944	0.00064	4.60E-09	0.034127	M
3	SYN2 *	rs13099882	12,209,388	G	A	0.117406	-0.017856	0.003142	1.40E-09	-0.027621	0.005318	2.10E-07	-0.013559	0.003942	0.000586	3.74E-09	0.033666	M
3	SYN2 *	rs11718525	12,213,765	T	C	0.034001	-0.034028	0.005566	1.20E-10	-0.047079	0.009338	4.71E-07	-0.029377	0.007018	2.88E-05	4.75E-10	0.129669	
3	SYN2 *	rs34562457	12,214,750	C	T	0.033395	-0.0349	0.005616	5.00E-11	-0.045773	0.009426	1.22E-06	-0.031468	0.007079	8.91E-06	0.224908	0.332417	
3	SYN2 *	rs74280642	12,221,434	A	G	0.033318	-0.036371	0.005624	6.90E-12	-0.045972	0.009441	1.14E-06	-0.033635	0.007088	2.11E-06	9.15E-11	0.296028	
3	SYN2 *	rs6786675	12,223,962	C	G	0.033442	-0.036556	0.005611	4.80E-12	-0.045955	0.009413	1.07E-06	-0.033994	0.007074	1.57E-06	6.47E-11	0.309713	
3	SYN2 *	rs35355828	12,225,005	A	G	0.046238	-0.035198	0.004814	1.00E-14	-0.038682	0.008113	1.89E-06	-0.034645	0.006055	1.08E-08	8.99E-13	0.690047	
3	SYN2 *	rs11720578	12,225,584	T	G	0.046274	-0.034667	0.004813	2.30E-14	-0.038176	0.008114	2.58E-06	-0.034126	0.006053	1.76E-08	1.95E-12	0.689122	
3	SYN2 *	rs35146940	12,229,787	T	A	0.033321	-0.035968	0.00562	1.10E-11	-0.045737	0.009408	1.18E-06	-0.033116	0.007095	3.10E-06	0.284084	0.332417	
3	SYN2 *	rs310749	12,232,268	G	T	0.13663	-0.016411	0.002954	4.20E-09	-0.027134	0.004998	5.80E-08	-0.011397	0.003708	0.002123	3.54E-09	0.011462	M
3	SYN2 *	rs13065423	12,233,															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
3	PPARG *	rs1596417	12,249,399	T	A	0.034679	-0.033899	0.005503	4.80E-11	-0.042681	0.009235	3.86E-06	-0.031656	0.006937	5.11E-06	6.91E-10	0.339834	
3	PPARG *	rs34881099	12,250,003	A	C	0.034608	-0.034411	0.005508	2.80E-11	-0.043253	0.009241	2.91E-06	-0.032069	0.006944	3.93E-06	4.09E-10	0.333275	
3	PPARG *	rs35577339	12,254,847	A	G	0.034536	-0.03445	0.005517	2.70E-11	-0.042956	0.009255	3.52E-06	-0.032208	0.006955	3.70E-06	4.64E-10	0.353238	
3	PPARG *	rs71304095	12,255,014	A	G	0.034537	-0.034455	0.005518	2.70E-11	-0.042972	0.009255	3.49E-06	-0.032207	0.006955	3.71E-06	4.60E-10	0.352464	
3	PPARG *	rs35252428	12,255,654	T	C	0.03454	-0.034462	0.005517	2.70E-11	-0.042981	0.009255	3.47E-06	-0.032212	0.006955	3.69E-06	4.57E-10	0.352282	
3	PPARG *	rs773846047	12,256,287	G	A	0.034493	-0.032276	0.005528	3.00E-10	-0.040409	0.009264	1.31E-05	-0.03038	0.006975	1.34E-05	5.61E-09	0.387103	
3	PPARG *	rs66615477	12,256,815	T	G	0.03206	-0.032347	0.005777	9.70E-09	-0.041472	0.009722	2.02E-05	-0.030111	0.007272	3.50E-05	2.11E-08	0.349374	
3	PPARG *	rs35316189	12,257,068	A	G	0.034531	-0.034364	0.005518	2.90E-11	-0.042902	0.009257	3.63E-06	-0.032107	0.006957	3.99E-06	5.14E-10	0.351214	
3	PPARG *	rs71304096	12,257,866	G	A	0.034527	-0.034415	0.005518	2.70E-11	-0.043054	0.009258	3.36E-06	-0.032113	0.006958	3.98E-06	4.76E-10	0.34477	
3	PPARG *	rs71304097	12,258,116	A	C	0.034527	-0.034414	0.005518	2.70E-11	-0.043054	0.009258	3.36E-06	-0.032112	0.006958	3.98E-06	4.76E-10	0.34473	
3	PPARG *	rs35877199	12,258,161	A	G	0.034527	-0.034414	0.005518	2.70E-11	-0.043054	0.009258	3.36E-06	-0.032112	0.006958	3.98E-06	4.76E-10	0.34473	
3	PPARG *	rs35057507	12,258,223	A	G	0.034859	-0.033949	0.005501	4.10E-11	-0.04369	0.009229	2.24E-06	-0.031155	0.006936	7.16E-06	5.64E-10	0.277524	
3	PPARG *	rs13067702	12,258,446	C	G	0.034521	-0.034445	0.005519	2.60E-11	-0.043175	0.00926	3.17E-06	-0.0321	0.006958	4.02E-06	4.54E-10	0.338947	
3	PPARG *	rs34685612	12,258,484	A	G	0.034521	-0.034445	0.005519	2.60E-11	-0.043175	0.00926	3.17E-06	-0.0321	0.006958	4.02E-06	4.54E-10	0.338947	
3	PPARG *	rs71304098	12,258,559	A	G	0.034521	-0.03444	0.005519	2.60E-11	-0.043188	0.00926	3.15E-06	-0.032086	0.006958	4.05E-06	4.55E-10	0.337828	
3	PPARG *	rs13088598	12,259,564	T	C	0.034443	-0.034689	0.005527	2.20E-11	-0.04272	0.009279	4.21E-06	-0.032627	0.006966	2.86E-06	4.30E-10	0.384372	
3	PPARG *	rs13088608	12,259,617	G	A	0.034443	-0.034689	0.005527	2.20E-11	-0.04272	0.009279	4.21E-06	-0.032627	0.006966	2.86E-06	4.30E-10	0.384372	
3	PPARG *	rs13089415	12,259,861	T	G	0.034438	-0.034788	0.005528	2.00E-11	-0.042772	0.009279	4.10E-06	-0.032751	0.006967	2.63E-06	3.87E-10	0.387781	
3	PPARG *	rs6771792	12,259,973	T	C	0.034438	-0.034789	0.005528	2.00E-11	-0.042772	0.009279	4.10E-06	-0.032751	0.006967	2.63E-06	3.87E-10	0.387786	
3	PPARG *	rs44430055	12,260,072	C	T	0.034438	-0.034789	0.005528	2.00E-11	-0.042772	0.009279	4.10E-06	-0.032751	0.006967	2.63E-06	3.87E-10	0.387786	
3	PPARG *	rs35541642	12,260,763	T	C	0.034439	-0.034803	0.005528	1.90E-11	-0.04279	0.009279	4.06E-06	-0.032762	0.006967	2.61E-06	3.81E-10	0.387451	
3	PPARG *	rs11715261	12,275,733	C	G	0.035786	-0.032597	0.005421	1.00E-10	-0.041382	0.009095	5.45E-06	-0.030113	0.006835	1.07E-05	1.95E-09	0.321905	
3	PPARG *	rs11715234	12,275,811	A	C	0.035787	-0.032598	0.005421	1.00E-10	-0.041389	0.009095	5.43E-06	-0.030112	0.006835	1.07E-05	1.94E-09	0.32155	
3	PPARG *	rs2920502	12,287,696	G	C	0.219171	-0.014498	0.002478	9.70E-10	-0.014956	0.004194	0.000365	-0.014248	0.003109	4.65E-06	4.75E-08	0.892147	
3	PPARG	rs17036160	12,288,284	T	C	0.038518	-0.033821	0.005239	5.90E-12	-0.037385	0.008774	2.06E-05	-0.034414	0.006612	1.99E-07	1.50E-10	0.786843	
3	PPARG	rs11709077	12,295,008	A	G	0.03099	-0.034881	0.005147	6.00E-13	-0.037722	0.008641	1.29E-05	-0.036125	0.006488	2.64E-08	1.35E-11	0.882487	
3	PPARG	rs11712037	12,303,231	G	C	0.037132	-0.032911	0.005333	6.10E-11	-0.037805	0.008965	2.51E-05	-0.032982	0.006715	9.20E-07	7.96E-10	0.666769	
3	PPARG	rs117937053	12,305,918	G	A	0.033441	-0.030776	0.00563	3.50E-09	-0.036016	0.009476	0.000145	-0.029516	0.007085	3.14E-05	1.24E-07	0.582825	
3	PPARG	rs35000407	12,310,022	G	T	0.039628	-0.033903	0.005163	3.00E-12	-0.036891	0.008668	2.11E-05	-0.035009	0.006508	7.64E-08	6.06E-11	0.862144	
3	PPARG	rs2067819	12,317,550	A	G	0.039691	-0.03339	0.00516	5.30E-12	-0.036369	0.008664	2.73E-05	-0.034605	0.006502	1.05E-07	1.05E-10	0.870649	
3	PPARG	rs13083375	12,323,809	T	G	0.039608	-0.034035	0.005164	2.50E-12	-0.0372	0.008671	1.81E-05	-0.03509	0.006509	7.15E-08	7.15E-10	0.845642	
3	PPARG	rs13064760	12,327,902	T	C	0.039608	-0.034035	0.005164	2.50E-12	-0.0372	0.008671	1.81E-05	-0.03509	0.006509	7.15E-08	7.15E-10	0.845642	
3	PPARG	rs2012444	12,334,457	T	C	0.039601	-0.033936	0.005165	3.40E-12	-0.037093	0.008674	1.92E-05	-0.035116	0.006509	7.01E-08	7.01E-10	0.855333	
3	PPARG	rs35240997	12,337,852	G	A	0.039697	-0.033159	0.00516	8.30E-12	-0.036238	0.008665	2.92E-05	-0.034451	0.006502	1.19E-07	1.28E-10	0.868922	
3	PPARG	rs13085211	12,341,766	A	G	0.040154	-0.034193	0.00513	1.40E-12	-0.037595	0.008631	1.34E-05	-0.035078	0.006458	5.72E-08	2.98E-11	0.815448	
3	PPARG	rs7638903	12,342,215	A	G	0.039554	-0.034365	0.005166	1.60E-12	-0.038291	0.00868	1.04E-05	-0.035132	0.006509	6.91E-08	2.80E-11	0.770916	
3	PPARG	rs11128603	12,344,329	G	A	0.039602	-0.034073	0.005163	2.30E-12	-0.037832	0.008677	1.32E-05	-0.034977	0.006504	7.70E-08	3.90E-11	0.79236	
3	PPARG	rs4684847	12,344,838	T	C	0.039409	-0.034318	0.005175	1.80E-12	-0.038389	0.008696	1.03E-05	-0.034949	0.006519	8.46E-08	3.37E-11	0.751648	
3	PPARG	rs7610055	12,346,910	A	G	0.037419	-0.032441	0.00531	8.10E-11	-0.036884	0.008935	3.70E-05	-0.032931	0.006683	8.46E-07	1.06E-09	0.723147	
3	PPARG	rs17036326	12,347,814	G	A	0.039762	-0.03359	0.005153	4.30E-12	-0.037345	0.00866	1.64E-05	-0.034451	0.006491	1.14E-07	7.01E-11	0.789154	
3	PPARG	rs17036328	12,348,985	C	T	0.039667	-0.034009	0.005159	2.40E-12	-0.037843	0.008664	1.27E-05	-0.034846	0.006501	8.49E-08	4.14E-11	0.781982	
3	PPARG	rs6802898	12,349,708	T	C	0.039693	-0.033939	0.005156	2.60E-12	-0.037851	0.008657	1.25E-05	-0.034674	0.006498	9.70E-08	4.63E-11	0.769208	
3	PPARG	rs2197423	12,350,084	A	G	0.039712	-0.034037	0.005156	2.30E-12	-0.03784	0.008657	1.25E-05	-0.034829	0.006498	8.52E-08	4.11E-11	0.780843	
3	PPARG	rs7647481	12,350,314	A	C	0.039627	-0.033894	0.005161	2.80E-12	-0.037332	0.00867	1.69E-05	-0.034929	0.006502	7.97E-08	5.11E-11	0.824459	
3	PPARG	rs7649970	12,350,773	T	C	0.039742	-0.034036	0.005153	2.20E-12	-0.037984	0.00865	1.14E-05	-0.034776	0.006495	8.79E-08	3.88E-11	0.766772	
3	PPARG	rs1801282	12,351,626	G	C	0.039741	-0.03367	0.005153	3.60E-12	-0.037351	0.008649	1.59E-05	-0.034585	0.006496	1.04E-07	6.23E-11	0.798118	
3	PPARG	rs17036352	12,352,183	G	A	0.039604	-0.033652	0.005162	4.30E-12	-0.037138	0.008666	1.85E-05	-0.034636	0.006506	1.04E-07	7.21E-11	0.817339	
3	PPARG	rs1899951	12,353,341	T	C	0.039641	-0.033764	0.00516	3.50E-12	-0.037447	0.008663	1.56E-05	-0.034616	0.006502	1.04E-07	7.19E-11	0.793865	
3	PPARG	rs4684848	12,354,146	A	G	0.0396	-0.033647	0.005162	4.30E-12	-0.03707	0.008666	1.91E-05	-0.03466	0.006506	1.02E-07	7.29E-11	0.824035	
3	PPARG	rs4135250	12,355,346	G	A	0.039599	-0.033652	0.005162	4.30E-12	-0.037078	0.008666	1.90E-05	-0.034661	0.006506	1.02E-07	7.26E-11	0.823453	
3	PPARG	rs71304101	12,355,414	A	G	0.039599	-0.033652	0.005162	4.30E-12	-0.037078	0.008666	1.90E-05	-0.034661	0.006506	1.02E-07	7.26E-11	0.823453	
3	PPARG	rs2881654	12,355,456	A	G	0.039599	-0.033652	0.005162	4.30E-12	-0.037078	0.008666	1.90E-05	-0.034661	0.006506	1.02E-07	7.26E-11	0.823453	
3	PPARG	rs2120825	12,371,840	G	T	0.030319	-0.031433	0.005902	2.00E-08	-0.040777	0.009841	3.46E-05	-0.029123	0.007467	9.70E-05	9.31E-08	0.345512	
3	KBTBD8 *	rs13078428	66,802,660	T	C	0.377766	-0.010979	0.002126	7.90E-09	-0.011401	0.003603	0.001561	-0.009826	0.002666	0.00023	7.52E-06	0.725353	
3	KBTBD8 *	rs9813067	66,812,220	T	C	0.470648	-0.011274	0.002035	3.30E-09	-0.012096	0.003454	0.000465	-0.010128	0.002549	7.17E-05	6.46E-08	0.64668	
3	KBTBD8 *	rs7638057	66,812,294	C	T	0.471142	-0.011305	0.002035	3.00E-09	-0.012216	0.003453	0.000407	-0.010094	0.002549	7.60E-05	7.57E-07	0.62103	
3	KBTBD8 *	rs7645370	66,812,469	T	G	0.470692	-0.01132	0.002035	2.60E-09	-0.012								

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
4	RGS12 *	rs73193354	3,298,808	G	T	0.3365	0.013564	0.00215	1.20E-09	0.01524	0.003658	3.13E-05	0.01224	0.00269	5.45E-06	5.44E-09	0.50871	
4	RGS12 *	rs3129310	3,299,661	T	G	0.377188	-0.012684	0.002089	1.60E-09	-0.015516	0.003551	1.26E-05	-0.011099	0.002616	2.24E-05	8.84E-09	0.316547	
4	RGS12 *	rs2239725	3,304,012	C	T	0.347773	-0.012345	0.002122	7.70E-09	-0.016508	0.0036	4.60E-06	-0.01018	0.00266	0.000131	1.80E-08	0.157398	
4	RGS12 *	rs910568	3,305,646	A	G	0.34615	-0.012465	0.002124	6.00E-09	-0.016695	0.003604	3.67E-06	-0.010282	0.002661	0.000113	1.26E-08	0.152738	
4	RGS12 *	rs3135446	3,305,911	C	G	0.347473	-0.012481	0.002121	6.10E-09	-0.016794	0.003599	3.13E-06	-0.010247	0.002659	0.000117	1.12E-08	0.14347	
4	RGS12 *	rs73193357	3,306,228	G	C	0.333971	-0.012979	0.002141	5.10E-09	0.015053	0.003646	3.70E-05	0.011499	0.002679	1.79E-05	1.99E-08	0.432188	
4	RGS12 *	rs3129308	3,307,545	G	A	0.381445	-0.012597	0.002078	1.50E-09	-0.015573	0.003532	1.05E-05	-0.010995	0.002602	2.41E-05	7.95E-09	0.296607	
4	RGS12 *	rs2749786	3,313,239	C	T	0.336225	-0.013269	0.002134	2.20E-09	0.015261	0.003631	2.66E-05	0.011787	0.00267	1.03E-05	8.57E-09	0.440813	
4	RGS12	rs2236052	3,316,686	A	G	0.348366	-0.012809	0.002114	2.20E-09	-0.016941	0.003589	2.40E-06	-0.010639	0.002649	5.99E-05	4.58E-09	0.157755	
4	RGS12	rs2281470	3,317,826	T	C	0.333789	0.012909	0.002136	5.60E-09	0.01504	0.003636	3.58E-05	0.011332	0.002673	2.27E-05	2.42E-08	0.411327	
4	RGS12	rs12643903	3,319,967	A	G	0.336224	0.012963	0.002134	4.20E-09	0.015105	0.003631	3.22E-05	0.011468	0.002671	1.78E-05	1.74E-08	0.419834	
4	RGS12	rs2857859	3,320,413	T	C	0.334997	0.012979	0.002136	4.70E-09	0.015234	0.003634	2.80E-05	0.011385	0.002672	2.07E-05	1.75E-08	0.393645	
4	RGS12	rs2857861	3,322,040	C	T	0.440888	-0.012409	0.002037	1.80E-09	-0.015644	0.003462	6.30E-06	-0.010486	0.002551	4.00E-05	7.89E-09	0.230301	
4	RGS12	rs2051558	3,323,159	G	A	0.408335	-0.014196	0.002051	8.00E-12	-0.015716	0.003489	6.74E-06	-0.013152	0.002567	3.07E-07	7.85E-11	0.553956	
4	RGS12	rs2749785	3,323,452	G	C	0.34939	-0.012658	0.002115	2.90E-09	-0.0169	0.003591	2.57E-06	-0.01045	0.00265	8.10E-05	6.52E-09	0.148419	
4	RGS12	rs2749783	3,324,371	A	C	0.382146	-0.012963	0.002075	5.50E-10	-0.016136	0.003529	4.88E-06	-0.011264	0.002597	1.46E-05	2.37E-09	0.266052	
4	RGS12	rs2857860	3,328,062	G	A	0.328715	0.013372	0.002155	2.90E-09	0.01621	0.00367	1.02E-05	0.011535	0.002697	1.91E-05	6.18E-09	0.304646	
4	RGS12	rs3129336	3,333,174	T	C	0.326069	0.013285	0.002165	3.20E-09	0.015838	0.003687	1.77E-05	0.011641	0.002709	1.75E-05	9.63E-09	0.358885	
4	RGS12	rs2748447	3,336,104	G	A	0.351616	-0.012727	0.002118	2.30E-09	-0.017226	0.003596	1.70E-06	-0.010421	0.002655	8.74E-05	4.70E-09	0.127892	
4	RGS12	rs12640526	3,338,001	T	C	0.334035	0.012886	0.002139	6.20E-09	0.015328	0.003642	2.59E-05	0.011158	0.002675	3.08E-05	2.38E-08	0.356131	
4	RGS12	rs2749782	3,338,034	T	C	0.350448	-0.012573	0.002121	4.00E-09	-0.016911	0.003601	2.70E-06	-0.010339	0.002658	0.000101	8.42E-09	0.142045	
4	RGS12	rs2073286	3,343,164	C	T	0.337133	0.013004	0.002133	4.70E-09	0.015174	0.003633	2.99E-05	0.01153	0.002669	1.58E-05	1.44E-08	0.418951	
4	RGS12	rs2749781	3,344,890	T	C	0.350959	-0.012522	0.002121	4.90E-09	-0.016953	0.003601	2.54E-06	-0.010245	0.002658	0.000117	9.16E-09	0.13394	
4	RGS12	rs2749780	3,347,365	T	A	0.380918	-0.012855	0.00208	9.30E-10	-0.016181	0.003538	4.86E-06	-0.011108	0.002603	2.00E-05	3.18E-09	0.248061	
4	RGS12	rs2749779	3,348,521	G	A	0.336954	-0.013073	0.002133	3.70E-09	0.015187	0.003632	2.92E-05	0.011627	0.002669	1.34E-05	1.21E-08	0.429561	
4	RGS12	rs2749778	3,349,978	T	C	0.349403	-0.012687	0.002119	2.60E-09	-0.017117	0.003598	1.99E-06	-0.010429	0.002656	8.67E-05	5.44E-09	0.13476	
4	RGS12	rs2749776	3,353,308	G	A	0.334881	0.012946	0.002138	6.00E-09	0.015313	0.003639	2.60E-05	0.011326	0.002675	2.33E-05	1.83E-08	0.377343	
4	RGS12	rs2749775	3,353,811	T	C	0.334844	0.012957	0.002138	5.00E-09	0.015257	0.003639	2.79E-05	0.011372	0.002675	2.16E-05	1.82E-08	0.389746	
4	RGS12	rs2857982	3,356,938	G	A	0.357461	-0.012445	0.002107	4.80E-09	-0.016724	0.003579	3.01E-06	-0.010274	0.00264	1.00E-04	9.30E-09	0.146901	
4	RGS12	rs60181496	3,362,661	C	G	0.362227	-0.011651	0.002124	4.50E-08	-0.0156	0.00361	1.57E-05	-0.009602	0.002661	0.00031	1.31E-07	0.181052	
4	RGS12	rs60208975	3,362,803	A	G	0.393267	-0.012184	0.002091	7.00E-09	-0.014945	0.003559	2.70E-05	-0.010738	0.002616	4.10E-05	3.25E-08	0.340792	
4	RGS12	rs881817	3,363,654	A	G	0.388538	-0.01249	0.002085	3.00E-09	-0.015781	0.003548	8.78E-06	-0.010749	0.002609	3.84E-05	1.04E-08	0.253189	
4	RGS12	rs881818	3,363,680	C	G	0.322925	0.012676	0.002174	1.90E-08	0.015304	0.003705	3.66E-05	0.010845	0.002719	6.73E-05	6.93E-08	0.331871	
4	RGS12	rs16844197	3,364,833	G	T	0.325017	0.012747	0.002169	1.50E-08	0.015211	0.003697	3.92E-05	0.011051	0.002713	4.68E-05	5.26E-08	0.364348	
4	RGS12	rs62274923	3,365,109	G	A	0.32573	0.0124	0.002168	3.20E-08	0.014955	0.003692	5.16E-05	0.010521	0.002712	0.000106	1.47E-07	0.333063	
4	RGS12	rs16844201	3,365,141	C	G	0.325728	0.012397	0.002168	3.20E-08	0.014955	0.003692	5.16E-05	0.010518	0.002712	0.000106	1.48E-07	0.332714	
4	RGS12	rs13104157	3,365,223	T	C	0.355633	-0.01181	0.002123	3.50E-08	-0.01617	0.003606	7.44E-06	-0.009562	0.00266	0.000327	6.74E-08	0.140334	
4	RGS12	rs13150241	3,365,554	A	G	0.354992	-0.012014	0.00212	1.80E-08	-0.016515	0.003601	4.57E-06	-0.009652	0.002656	0.000281	3.67E-08	0.125073	
4	RGS12	rs6819202	3,366,537	G	A	0.356022	-0.012097	0.002122	1.20E-08	-0.016622	0.003603	4.02E-06	-0.009694	0.002659	0.000268	3.10E-08	0.121853	
4	RGS12	rs3129334	3,366,799	T	C	0.354627	-0.012194	0.002123	1.00E-08	-0.016538	0.003604	4.51E-06	-0.009912	0.00266	0.000195	2.57E-08	0.129021	
4	RGS12	rs10155132	3,367,773	A	G	0.352755	-0.012662	0.002127	3.10E-09	-0.017533	0.003611	1.23E-06	-0.010131	0.002665	0.000145	5.55E-09	0.099091	
4	RGS12	rs7435601	3,367,918	T	C	0.35178	-0.012663	0.00213	3.60E-09	-0.017391	0.003615	1.53E-06	-0.010244	0.002668	0.000125	5.95E-09	0.111715	
4	RGS12	rs12640721	3,372,448	G	A	0.337239	0.013034	0.002147	6.10E-09	0.015013	0.003652	3.98E-05	0.011618	0.002688	1.56E-05	1.87E-08	0.454006	
4	RGS12	rs12640186	3,372,812	T	C	0.334239	0.01268	0.002152	1.90E-08	0.014863	0.003659	4.90E-05	0.011084	0.002694	3.93E-05	5.50E-08	0.405465	
4	RGS12	rs10937924	3,373,171	T	C	0.373483	-0.014071	0.002107	4.80E-11	-0.017472	0.003578	1.06E-06	-0.012385	0.00264	2.75E-06	1.10E-10	0.252578	
4	RGS12	rs73193372	3,373,261	T	C	0.333572	0.01274	0.002153	1.60E-08	0.014904	0.003661	4.74E-05	0.011162	0.002696	3.51E-05	4.79E-08	0.410499	
4	RGS12	rs3129333	3,373,271	A	G	0.334107	0.012672	0.002153	2.00E-08	0.014952	0.003661	4.47E-05	0.011005	0.002696	4.52E-05	5.75E-08	0.385417	
4	RGS12	rs3129332	3,374,041	A	G	0.336249	0.012967	0.002152	9.60E-09	0.015071	0.003659	3.86E-05	0.01144	0.002695	2.21E-05	4.24E-08	0.424262	
4	RGS12	rs2343799	3,375,007	C	T	0.334162	0.012679	0.002163	2.10E-08	0.014621	0.003674	6.97E-05	0.011102	0.002709	4.21E-05	8.21E-08	0.44077	
4	RGS12	rs3129331	3,375,947	A	G	0.333232	0.012873	0.00217	1.40E-08	0.014861	0.003685	5.56E-05	0.011183	0.002719	3.94E-05	6.22E-08	0.421813	
4	RGS12	rs3129330	3,377,653	T	C	0.332022	0.012985	0.002182	1.40E-08	0.014485	0.003705	9.32E-05	0.011569	0.002735	2.36E-05	6.23E-08	0.526544	
4	RGS12	rs1894442	3,384,588	T	C	0.45955	-0.02636	0.002039	5.50E-37	-0.021595	0.003466	4.79E-10	-0.029753	0.002554	2.51E-31	1.26E-38	0.058124	
4	RGS12	rs16844249	3,385,421	T	C	0.120197	0.017573	0.003149	2.50E-09	0.013959	0.005373	0.009396	0.019486	0.003936	7.51E-07	1.63E-07	0.406572	
4	RGS12	rs12644442	3,385,844	A	G	0.495182	0.025747	0.002048	1.80E-35	0.021126	0.003484	1.36E-09	0.02861	0.002563	6.71E-29	9.03E-36	0.083561	
4	RGS12	rs4690090	3,387,800	T	C	0.441754	-0.025372	0.002058	4.20E-34	-0.020544	0.003492	4.15E-09	-0.028835	0.00258	5.74E-29	2.29E-35	0.056188	
4	RGS12	rs6828057	3,388,084	A	G	0.444263	-0.025577	0.002059	2.10E-34	-0.02093	0.003494	2.16E-09	-0.028956	0.00258	3.36E-29	7.13E-36	0.064639	
4	RGS12	rs2269496	3,388,419	C	T	0.287228	0.019854	0.002279	1.90E-17	0.017959	0.003868	3.49E-06						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
4	RGS12	rs3748037	3,418,544	A	G	0.265152	0.022676	0.002336	4.20E-21	0.018777	0.00397	2.28E-06	0.024791	0.002925	2.49E-17	3.52E-21	0.222644	
4	RGS12	rs3748036	3,418,644	T	C	0.473269	-0.026314	0.002059	1.20E-36	-0.020339	0.00349	5.78E-09	-0.030129	0.002583	2.07E-31	1.19E-37	0.024168	F
4	RGS12	rs4690095	3,419,582	C	T	0.487297	0.025991	0.002065	8.30E-36	0.021571	0.003505	7.79E-10	0.02927	0.002588	1.25E-29	9.87E-37	0.077223	
4	RGS12	rs3088231	3,420,484	A	G	0.263768	0.022518	0.002346	1.10E-20	0.018333	0.003989	4.37E-06	0.02479	0.002938	3.37E-17	8.87E-21	0.192922	
4	RGS12	rs3789739	3,421,715	T	C	0.475474	-0.026397	0.002066	1.80E-36	-0.020875	0.003504	2.64E-09	-0.03	0.00259	5.33E-31	1.41E-37	0.036249	F
4	RGS12	rs16844330	3,422,504	T	C	0.105435	0.021649	0.003302	2.30E-11	0.019049	0.005629	0.000719	0.02394	0.004128	6.86E-09	1.63E-10	0.483509	
4	RGS12	rs58143210	3,423,303	T	C	0.472041	-0.026112	0.002068	8.70E-36	-0.020287	0.003509	7.63E-09	-0.029807	0.002592	1.47E-30	1.09E-36	0.029131	F
4	RGS12	rs3804388	3,429,615	A	G	0.104082	0.020853	0.003328	1.30E-10	0.01896	0.005688	0.000862	0.022733	0.004156	4.62E-08	1.23E-09	0.592229	
4	HGFAC	rs2073505	3,442,776	A	C	0.092945	0.025872	0.003488	2.70E-14	0.020938	0.005988	0.000474	0.029427	0.004345	1.31E-11	2.43E-13	0.251252	
4	HGFAC *	rs28766336	3,452,024	T	G	0.474155	-0.025939	0.002062	2.40E-36	-0.019981	0.003508	1.26E-08	-0.029392	0.002581	5.14E-30	6.15E-36	0.030697	F
4	HGFAC *	rs4690099	3,452,727	T	C	0.464836	-0.025265	0.002063	1.60E-34	-0.019745	0.00351	1.90E-08	-0.028487	0.002582	2.91E-28	5.04E-34	0.044838	F
4	DOK7 *	rs2091626	3,460,173	T	G	0.466697	-0.025333	0.002064	9.90E-35	-0.020092	0.003511	1.07E-08	-0.028547	0.002584	2.41E-28	2.41E-34	0.052436	
4	DOK7 *	rs1076903	3,460,467	G	A	0.466729	-0.025435	0.002064	5.30E-35	-0.020175	0.003511	9.38E-09	-0.028649	0.002584	1.58E-28	1.39E-34	0.051959	
4	DOK7 *	rs28478452	3,461,750	A	G	0.465547	-0.02552	0.002068	4.80E-35	-0.020243	0.003516	8.74E-09	-0.028729	0.002589	1.40E-28	1.15E-34	0.051968	
4	DOK7	rs36205397	3,468,877	G	A	0.380466	0.019116	0.002089	1.50E-20	0.016595	0.00355	2.98E-06	0.020955	0.002616	1.19E-15	2.07E-19	0.322824	
4	DOK7	rs10007119	3,471,339	G	A	0.381509	0.019051	0.002079	1.70E-20	0.016265	0.003534	4.23E-06	0.021008	0.002603	7.36E-16	1.80E-19	0.279794	
4	DOK7	rs6831256	3,471,412	G	A	0.381961	0.018959	0.002077	2.20E-20	0.016317	0.003531	3.87E-06	0.020856	0.0026	1.10E-15	2.47E-19	0.300646	
4	LRPAP1	rs56358267	3,504,455	G	A	0.417099	0.011574	0.002056	2.20E-08	0.013883	0.003499	7.33E-05	0.01081	0.002572	2.67E-05	5.58E-08	0.479216	
4	LRPAP1	rs2093098	3,512,107	C	T	0.421421	0.011652	0.002051	1.50E-08	0.013592	0.003489	9.90E-05	0.011073	0.002567	1.62E-05	4.61E-08	0.560837	
4	LRPAP1	rs6789	3,512,968	G	A	0.417527	0.01127	0.002056	4.90E-08	0.013539	0.003498	0.00011	0.010467	0.002573	4.80E-05	1.43E-07	0.479466	
4	LRPAP1	rs2285088	3,514,721	T	C	0.475089	0.012621	0.002054	8.10E-10	0.013683	0.003498	9.24E-05	0.012871	0.00257	5.60E-07	1.70E-09	0.851545	
4	LRPAP1	rs1741550	3,515,322	C	T	0.420771	0.011562	0.002053	2.00E-08	0.013245	0.003494	0.000152	0.011123	0.00257	1.52E-05	6.47E-08	0.624734	
4	LRPAP1	rs1730778	3,516,720	C	T	0.417109	0.011314	0.002056	4.60E-08	0.013823	0.003499	7.88E-05	0.010432	0.002574	5.11E-05	1.11E-07	0.43496	
4	FAM184B *	rs73096946	17,787,092	C	T	0.352798	0.010944	0.002122	4.50E-08	0.008735	0.003607	0.015451	0.012061	0.002658	5.79E-06	1.80E-06	0.457951	
4	FAM184B *	rs16895735	17,787,560	C	T	0.137156	0.015904	0.002946	4.10E-08	0.009791	0.005003	0.050375	0.019102	0.003691	2.33E-07	2.26E-07	0.134266	
4	DCAF16 *	rs60258355	17,791,257	A	T	0.28403	0.011926	0.002245	1.90E-08	0.007124	0.003808	0.061363	0.014613	0.002815	2.13E-07	2.44E-07	0.113797	
4	DCAF16 *	rs118071982	17,791,701	A	G	0.137931	0.015677	0.002935	4.90E-08	0.009591	0.004982	0.05421	0.018949	0.003678	2.62E-07	2.69E-07	0.130695	
4	DCAF16 *	rs77992809	17,792,298	C	G	0.138295	0.015692	0.002934	4.90E-08	0.009634	0.004982	0.053142	0.018978	0.003677	2.50E-07	2.52E-07	0.131258	
4	DCAF16 *	rs7672919	17,795,832	T	G	0.28386	0.011722	0.002243	3.20E-08	0.007085	0.003804	0.062505	0.014288	0.002812	3.83E-07	4.37E-07	0.127826	
4	DCAF16 *	rs113241654	17,798,521	G	A	0.283061	0.011868	0.002247	2.10E-08	0.007305	0.003811	0.055264	0.014369	0.002817	3.46E-07	3.58E-07	0.136063	
4	DCAF16	rs7690457	17,803,756	A	G	0.137948	0.01577	0.002935	4.20E-08	0.009761	0.004979	0.049965	0.018984	0.003679	2.52E-07	1.36E-07	0.136257	
4	NCAPG	rs11941723	17,810,905	G	A	0.143028	0.017605	0.002885	4.30E-10	0.013378	0.004899	0.006334	0.0195	0.003615	7.01E-08	1.15E-08	0.314607	
4	NCAPG	rs16895792	17,811,173	T	C	0.126844	0.016488	0.003045	2.80E-08	0.011659	0.005173	0.024226	0.019012	0.003814	6.31E-07	3.17E-07	0.252566	
4	NCAPG	rs16895796	17,811,596	A	T	0.142337	0.017298	0.002891	8.80E-10	0.013123	0.004907	0.007501	0.019185	0.003623	1.21E-07	2.27E-08	0.320231	
4	NCAPG	rs16895802	17,814,266	G	C	0.143005	0.017178	0.002881	1.10E-09	0.012848	0.004889	0.008617	0.019128	0.003611	1.20E-07	2.56E-08	0.301457	
4	NCAPG	rs139724825	17,822,441	T	C	0.141607	0.017392	0.002896	6.60E-10	0.013353	0.00492	0.006665	0.019252	0.003628	1.14E-07	1.93E-08	0.334507	
4	LCORL, NCAPG	rs59037741	17,843,847	T	C	0.141216	0.016953	0.002898	2.40E-09	0.012934	0.004922	0.008616	0.018542	0.003631	3.35E-07	6.89E-08	0.359208	
4	LCORL	rs16895882	17,847,141	G	T	0.142788	0.016903	0.002886	1.80E-09	0.012619	0.004898	0.010001	0.01866	0.003618	2.56E-07	6.07E-08	0.321108	
4	LCORL	rs75878186	17,855,630	G	A	0.287564	0.012773	0.002233	1.60E-09	0.008736	0.003783	0.020955	0.014735	0.002801	1.47E-07	6.84E-08	0.202497	
4	LCORL	rs79334166	17,857,843	G	A	0.287804	0.012698	0.002233	1.80E-09	0.008779	0.003784	0.020362	0.014617	0.002802	1.86E-07	8.34E-08	0.21493	
4	LCORL	rs145087631	17,860,695	T	C	0.140742	0.016965	0.002906	1.80E-09	0.012882	0.004933	0.009034	0.01868	0.003642	2.97E-07	6.40E-08	0.344287	
4	LCORL	rs58854324	17,862,391	C	T	0.350955	0.011244	0.002126	2.30E-08	0.00944	0.003613	0.008988	0.012129	0.002663	5.35E-06	1.03E-06	0.549246	
4	LCORL	rs113476736	17,862,651	C	T	0.28712	0.012612	0.002239	2.30E-09	0.008924	0.003794	0.018698	0.014376	0.002809	3.14E-07	1.29E-07	0.248128	
4	LCORL	rs74619517	17,863,938	A	G	0.284534	0.012747	0.002248	2.70E-09	0.008718	0.00381	0.022137	0.014568	0.00282	2.44E-07	1.17E-07	0.217148	
4	LCORL	rs73098804	17,864,242	A	T	0.279887	0.012564	0.002262	4.20E-09	0.008204	0.00383	0.032201	0.014581	0.002839	2.87E-07	1.89E-07	0.18104	
4	LCORL	rs16895917	17,867,611	C	T	0.144979	0.015571	0.002862	1.30E-08	0.010868	0.004854	0.025173	0.01764	0.003589	9.06E-07	4.64E-07	0.261978	
4	LCORL	rs78439738	17,873,012	C	T	0.144874	0.015769	0.002862	8.00E-09	0.011594	0.004853	0.016925	0.017658	0.003589	8.81E-07	3.20E-07	0.315053	
4	LCORL	rs13131350	17,875,864	G	A	0.291497	0.012399	0.00222	2.80E-09	0.008646	0.003762	0.021555	0.014298	0.002784	2.87E-07	1.33E-07	0.227178	
4	LCORL	rs76264386	17,876,967	G	A	0.144336	0.015621	0.002869	1.30E-08	0.011576	0.004865	0.017366	0.017512	0.003598	1.15E-06	4.22E-07	0.326607	
4	LCORL	rs78994908	17,876,968	C	A	0.144336	0.015621	0.002869	1.30E-08	0.011576	0.004865	0.017366	0.017512	0.003598	1.15E-06	4.22E-07	0.326607	
4	LCORL	rs7700107	17,878,793	C	A	0.294009	0.011852	0.002215	1.30E-08	0.008872	0.003752	0.018068	0.013327	0.002778	1.64E-06	6.15E-07	0.339868	
4	LCORL	rs16895971	17,883,363	C	T	0.294387	0.012107	0.002213	6.50E-09	0.009236	0.00375	0.013811	0.013516	0.002777	1.15E-06	3.45E-07	0.359016	
4	LCORL	rs78993313	17,916,447	T	C	0.140435	0.015647	0.002901	2.30E-08	0.011076	0.004922	0.024456	0.017597	0.003637	1.33E-06	6.55E-07	0.286559	
4	LCORL	rs78471813	17,921,045	A	G	0.140422	0.015402	0.0029	3.80E-08	0.011061	0.004919	0.024571	0.017228	0.003635	2.18E-06	1.06E-06	0.313305	
4	LCORL	rs16870149	17,926,197	C	T	0.144593	0.015762	0.002865	1.10E-08	0.011092	0.004859	0.022457	0.017769	0.003593	7.75E-07	3.61E-07	0.269232	
4	LCORL	rs80043981	17,939,923	T	C	0.143909	0.016073	0.002873	5.60E-09	0.011514	0.004872	0.018134	0.017951	0.003602	6.34E-07	2.47E-07	0.288031	
4	LCORL	rs76828425	17,971,670	T	C	0.138707												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
4	UGT2B15 *	rs293438	68,720,647	A	G	0.451849	-0.011404	0.002049	4.00E-08	-0.015502	0.003477	8.36E-06	-0.008875	0.002569	0.000554	1.23E-07	0.125234	
4	UGT2B15 *	rs141200334	68,722,470	A	G	0.451658	-0.011525	0.002048	2.70E-08	-0.015707	0.003476	6.32E-06	-0.008932	0.002568	0.000507	8.69E-08	0.116942	
4	UGT2B15 *	rs139502240	68,726,315	G	T	0.451549	-0.011601	0.002048	2.30E-08	-0.015802	0.003476	5.54E-06	-0.008984	0.002567	0.000468	7.10E-08	0.114594	
4	UGT2B15 *	rs293422	68,726,929	A	G	0.452125	-0.011542	0.002051	2.80E-08	-0.015665	0.003481	6.88E-06	-0.008957	0.002571	0.000498	9.26E-08	0.121094	
4	UGT2B15 *	rs12644441	68,727,085	G	T	0.453878	-0.012149	0.002066	6.90E-09	-0.016901	0.003507	1.46E-06	-0.009153	0.002589	0.000409	1.74E-08	0.075478	
4	UGT2B15 *	rs293420	68,727,115	C	T	0.452502	-0.011873	0.002051	1.10E-08	-0.016218	0.003481	3.23E-06	-0.009144	0.002571	0.000378	3.47E-08	0.102142	
4	UGT2B15 *	rs1708574	68,728,368	T	C	0.451664	-0.011596	0.002049	2.50E-08	-0.015855	0.003478	5.23E-06	-0.008918	0.002568	0.000519	7.40E-08	0.10862	
4	AF11	rs7660883	87,061,724	G	C	0.407389	-0.011589	0.00205	4.70E-09	-0.012748	0.003481	0.000252	-0.011204	0.002569	1.31E-05	9.08E-08	0.721178	
4	AF11	rs28432336	87,063,179	G	A	0.407831	-0.011879	0.002052	2.10E-09	-0.01287	0.003483	0.000222	-0.011568	0.002572	6.95E-06	4.39E-08	0.763611	
4	AF11	rs11946481	87,063,458	T	C	0.407679	-0.011571	0.002051	5.20E-09	-0.012434	0.003482	0.000358	-0.011345	0.002571	1.03E-05	1.00E-07	0.801342	
4	AF11	rs3775228	87,064,014	T	C	0.404093	0.011734	0.002063	4.40E-09	0.016571	0.003501	2.24E-06	0.0095	0.002586	0.000241	1.60E-08	0.104193	
4	AF11	rs17668131	87,064,378	T	G	0.405681	0.011917	0.00206	2.70E-09	0.017258	0.003498	8.20E-07	0.009401	0.002582	0.000274	6.84E-09	0.070715	
4	AF11	rs72877984	87,064,569	A	G	0.407439	-0.011738	0.002051	3.10E-09	-0.012673	0.003482	0.000275	-0.01147	0.00257	8.21E-06	6.29E-08	0.78101	
4	AF11	rs10018904	87,065,054	C	G	0.40579	0.01182	0.002061	3.60E-09	0.017063	0.003499	1.10E-06	0.00937	0.002582	0.000287	9.50E-09	0.076929	
4	AF11	rs28677145	87,065,229	A	G	0.407387	-0.011814	0.002056	2.30E-09	-0.012829	0.00349	0.000238	-0.011596	0.002577	6.90E-06	4.66E-08	0.776132	
4	AF11	rs13120301	87,065,243	T	C	0.405686	0.011851	0.002061	3.30E-09	0.017109	0.0035	1.03E-06	0.009397	0.002583	0.000277	8.65E-09	0.076258	
4	AF11	rs236679	87,065,449	C	A	0.405499	0.01153	0.002063	9.40E-09	0.01718	0.003504	9.58E-07	0.008902	0.002585	0.000576	1.59E-08	0.057268	
4	AF11	rs236681	87,067,356	G	T	0.407414	0.012342	0.002058	7.40E-10	0.017716	0.003495	4.06E-07	0.009785	0.002579	0.00015	1.97E-09	0.067878	
4	AF11	rs2280952	87,067,388	C	T	0.405573	0.012028	0.002058	1.80E-09	0.017238	0.003495	8.25E-07	0.009545	0.002579	0.000217	5.53E-09	0.076551	
4	AF11	rs2280953	87,067,438	T	C	0.405122	0.011942	0.002059	2.40E-09	0.017085	0.003495	1.04E-06	0.009493	0.00258	0.000236	7.45E-09	0.080539	
4	AF11	rs2280954	87,067,710	G	A	0.405192	0.011841	0.002059	3.20E-09	0.016909	0.003495	1.34E-06	0.009428	0.002581	0.000261	1.05E-08	0.085101	
4	AF11	rs3775226	87,068,313	A	G	0.40259	0.011782	0.002065	3.90E-09	0.016681	0.003504	1.97E-06	0.009498	0.002589	0.000246	1.43E-08	0.099187	
4	AF11	rs11097127	87,069,182	T	G	0.407428	-0.011758	0.002057	2.90E-09	-0.012534	0.003491	0.000333	-0.011613	0.002578	6.72E-06	6.22E-08	0.831825	
4	AF11	rs3736668	87,071,058	C	T	0.40356	0.011957	0.002062	2.30E-09	0.017058	0.0035	1.12E-06	0.009567	0.002584	0.000215	7.35E-09	0.085127	
4	AF11	rs3736669	87,071,601	A	G	0.41355	-0.012159	0.002055	8.90E-10	-0.013411	0.003487	0.000121	-0.011761	0.002576	5.04E-06	1.82E-08	0.703447	
4	AF11	rs17012368	87,074,967	G	T	0.415401	-0.012451	0.002054	3.60E-10	-0.013724	0.003483	8.23E-05	-0.012003	0.002575	3.19E-06	8.15E-09	0.691127	
4	AF11	rs1251587	87,075,471	G	A	0.415954	-0.012378	0.00205	3.90E-10	-0.013727	0.003477	7.97E-05	-0.01189	0.00257	3.78E-06	9.29E-09	0.671034	
4	AF11	rs17605615	87,075,593	A	G	0.395778	0.012521	0.002065	4.10E-10	0.017694	0.003504	4.52E-07	0.010051	0.002589	0.000104	1.55E-09	0.079362	
4	AF11	rs998251	87,077,903	A	G	0.414815	-0.012605	0.002047	1.80E-10	-0.014292	0.003473	3.91E-05	-0.011902	0.002566	3.57E-06	4.48E-09	0.580093	
4	AF11	rs236995	87,079,271	G	C	0.416085	-0.012505	0.002044	2.20E-10	-0.014045	0.003468	5.18E-05	-0.011931	0.002563	3.28E-06	5.40E-09	0.624026	
4	AF11	rs3775223	87,079,294	T	A	0.41482	-0.012618	0.002047	1.70E-10	-0.014293	0.003473	3.90E-05	-0.011922	0.002566	3.44E-06	4.51E-09	0.582916	
4	AF11	rs236996	87,084,051	A	G	0.416623	-0.012418	0.002044	3.20E-10	-0.014013	0.003466	5.33E-05	-0.011854	0.002562	3.78E-06	6.36E-09	0.616475	
4	AF11	rs151451	87,085,215	T	C	0.395212	0.012308	0.002065	7.90E-10	0.017671	0.003503	4.64E-07	0.009774	0.002588	0.000161	2.39E-09	0.069799	
4	AF11	rs4693156	87,086,075	C	T	0.415311	-0.012411	0.002047	3.30E-10	-0.014054	0.003472	5.23E-05	-0.011739	0.002566	4.85E-06	7.92E-09	0.591831	
4	AF11	rs236984	87,087,462	A	G	0.416563	-0.012292	0.002044	4.30E-10	-0.013824	0.003468	6.79E-05	-0.011734	0.002563	4.76E-06	9.97E-09	0.628081	
4	AF11	rs236985	87,087,630	A	G	0.416539	-0.012325	0.002044	3.80E-10	-0.013858	0.003469	6.52E-05	-0.011755	0.002563	4.58E-06	9.24E-09	0.625809	
4	AF11	rs236976	87,088,468	A	G	0.395338	0.012358	0.002064	6.80E-10	0.017176	0.003503	4.05E-07	0.009795	0.002588	0.000155	2.02E-09	0.067399	
4	AF11	rs236987	87,088,627	T	C	0.41599	-0.01231	0.002046	4.10E-10	-0.013901	0.003471	6.28E-05	-0.011723	0.002566	4.97E-06	9.65E-09	0.613875	
4	AF11	rs3775221	87,090,641	G	T	0.415313	-0.012434	0.002047	2.90E-10	-0.014163	0.003473	4.59E-05	-0.011711	0.002567	5.12E-06	7.37E-09	0.570169	
4	AF11	rs2045592	87,093,194	G	C	0.414847	-0.012413	0.002049	3.20E-10	-0.014204	0.003475	4.41E-05	-0.011679	0.002568	5.52E-06	7.63E-09	0.558919	
4	AF11	rs3775220	87,093,601	G	A	0.415036	-0.012343	0.002048	3.80E-10	-0.01406	0.003474	5.24E-05	-0.011646	0.002567	5.82E-06	9.45E-09	0.57632	
4	AF11	rs151450	87,095,362	A	G	0.396231	0.012573	0.002063	3.20E-10	0.017838	0.003502	3.58E-07	0.010073	0.002586	9.92E-05	1.18E-09	0.074476	
4	AF11	rs236992	87,095,587	A	G	0.415893	-0.01236	0.002045	3.30E-10	-0.014026	0.00347	5.35E-05	-0.011751	0.002564	4.67E-06	7.81E-09	0.598038	
4	AF11	rs236993	87,095,722	G	T	0.415812	-0.012403	0.002045	2.90E-10	-0.013994	0.00347	5.57E-05	-0.011816	0.002564	4.12E-06	7.19E-09	0.61367	
4	AF11	rs342452	87,097,256	A	G	0.415791	-0.012382	0.002045	3.10E-10	-0.014047	0.003469	5.21E-05	-0.011764	0.002564	4.54E-06	7.41E-09	0.596706	
4	AF11	rs342453	87,097,337	C	G	0.41587	-0.012382	0.002045	3.10E-10	-0.013973	0.00347	5.71E-05	-0.011788	0.002564	4.35E-06	7.75E-09	0.61254	
4	AF11	rs2035403	87,097,839	G	A	0.396451	0.012664	0.002063	2.40E-10	0.017996	0.003502	2.81E-07	0.010108	0.002587	9.40E-05	8.88E-10	0.070003	
4	AF11	rs3775217	87,098,315	G	A	0.414609	-0.012573	0.002048	1.80E-10	-0.014284	0.003475	3.99E-05	-0.011873	0.002568	3.82E-06	4.87E-09	0.576883	
4	AF11	rs342454	87,100,348	T	A	0.415783	-0.012394	0.002046	3.00E-10	-0.013985	0.003472	5.70E-05	-0.011792	0.002565	4.35E-06	7.75E-09	0.611561	
4	AF11	rs60695258	87,101,557	T	C	0.396892	0.012711	0.002078	2.30E-10	0.017868	0.003524	4.05E-07	0.010168	0.002605	9.56E-05	1.28E-09	0.078913	
4	AF11	rs3775214	87,102,147	G	A	0.415566	-0.012366	0.002046	3.20E-10	-0.014047	0.003472	5.28E-05	-0.011708	0.002565	5.10E-06	8.39E-09	0.587975	
4	AF11	rs342456	87,102,718	T	C	0.413764	-0.012378	0.002048	2.90E-10	-0.014425	0.003473	3.31E-05	-0.011495	0.002568	7.68E-06	7.96E-09	0.497477	
4	AF11	rs3755985	87,103,586	G	A	0.399216	0.01274	0.002062	1.60E-10	0.018909	0.003499	6.66E-08	0.009744	0.002585	0.000165	3.74E-10	0.035152	M
4	AF11	rs1674999	87,106,498	G	A	0.414043	-0.012498	0.002047	2.10E-10	-0.014546	0.003471	2.82E-05	-0.011577	0.002567	6.55E-06	5.87E-09	0.491757	
4	AF11	rs3733377	87,108,330	G	C	0.398885	0.012563	0.002062	3.00E-10	0.018505	0.0035	1.27E-07	0.009718	0.002585	0.000172	7.26E-10	0.043455	M
4	AF11	rs42177	87,109,109	G	T	0.414166	-0.012595	0.002045	1.40E-10	-0.014753	0.003469	2.14E-05	-0.01177	0.002564	4.50E-06	3.15E-09	0.489344	
4	AF11	rs75921854	87,110,944	A	T	0.399634	0.012											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
4	AFF1 *	rs10023050	87,143,279	G	A	0.411	-0.014032	0.002058	2.20E-12	-0.017366	0.00349	6.62E-07	-0.012512	0.002258	1.26E-06	3.30E-11	0.263365	
4	AFF1 *	rs10023056	87,143,314	G	A	0.402848	0.013925	0.002075	7.00E-12	0.020414	0.003521	6.93E-09	0.010812	0.002601	3.26E-05	8.92E-12	0.028316	M
4	AFF1 *	rs10032710	87,145,107	A	G	0.387117	0.013811	0.002098	2.50E-11	0.020413	0.003561	1.02E-08	0.010581	0.00263	5.80E-05	2.24E-11	0.026381	M
4	AFF1 *	rs17012512	87,146,352	C	T	0.389361	0.013378	0.002099	1.50E-10	0.020279	0.003561	1.27E-08	0.009962	0.00263	0.000153	6.98E-11	0.019817	M
4	AFF1 *	rs17012517	87,149,332	G	A	0.455027	0.012027	0.002066	1.10E-09	0.018404	0.003507	1.56E-07	0.008859	0.002589	0.000625	2.99E-09	0.028547	M
4	KLHL8 *	rs28734493	87,151,541	T	A	0.451693	0.012305	0.002066	3.90E-10	0.018573	0.003509	1.23E-07	0.00918	0.002588	0.000393	1.54E-09	0.03125	M
4	KLHL8 *	rs28882732	87,154,824	G	A	0.449159	0.012188	0.002074	5.90E-10	0.01853	0.003522	1.46E-07	0.009062	0.002599	0.000491	2.23E-09	0.030562	M
4	KLHL8 *	rs55747890	87,155,474	G	A	0.361847	0.01291	0.002137	2.00E-10	0.020022	0.00363	3.57E-08	0.009466	0.002678	0.000411	4.81E-10	0.019304	M
4	KLHL8 *	rs7437661	87,156,860	C	A	0.451749	0.012348	0.002066	3.30E-10	0.018326	0.003508	1.79E-07	0.009392	0.002588	0.000286	1.64E-09	0.04044	M
4	KLHL8 *	rs10211004	87,157,017	A	G	0.451749	0.012372	0.002066	3.00E-10	0.018325	0.003508	1.79E-07	0.009424	0.002588	0.000273	1.57E-09	0.041177	M
4	KLHL8 *	rs28670747	87,157,327	G	C	0.451732	0.012345	0.002066	3.30E-10	0.018296	0.003508	1.87E-07	0.009405	0.002588	0.000281	1.68E-09	0.041455	M
4	KLHL8 *	rs111686783	87,158,018	A	G	0.450697	0.012325	0.002069	4.10E-10	0.018012	0.003513	3.01E-07	0.009538	0.002592	0.000236	2.25E-09	0.052293	
4	KLHL8 *	rs1481947	87,159,990	T	C	0.450839	0.012351	0.002066	3.30E-10	0.018167	0.003509	2.30E-07	0.00952	0.002587	0.000236	1.74E-09	0.047359	M
4	KLHL8	rs3209390	87,161,300	C	T	0.468849	0.011843	0.00206	1.10E-09	0.017288	0.003499	7.91E-07	0.009137	0.002581	0.000402	9.46E-09	0.060842	
4	KLHL8	rs1393672	87,161,955	C	T	0.450844	0.012048	0.002064	7.10E-10	0.017938	0.003504	3.13E-07	0.009157	0.002585	4.00E-04	3.85E-09	0.043787	M
4	KLHL8	rs10000784	87,166,331	G	A	0.467667	0.010962	0.002059	1.40E-08	0.016417	0.003491	2.62E-06	0.008263	0.002581	0.001375	9.42E-08	0.060397	
4	KLHL8	rs28505236	87,172,309	G	C	0.449813	0.011306	0.002065	5.80E-09	0.016877	0.003501	1.46E-06	0.0086	0.00259	0.000904	3.63E-08	0.057362	
4	KLHL8	rs1552144	87,173,498	T	C	0.450216	0.011176	0.002064	9.10E-09	0.016699	0.003501	1.87E-06	0.008515	0.002589	0.001009	5.12E-08	0.060172	
4	KLHL8	rs66527077	87,188,846	A	G	0.467426	0.010821	0.002061	1.90E-08	0.015827	0.003496	6.05E-06	0.008369	0.002584	0.001207	1.87E-07	0.086223	
4	KLHL8	rs11946293	87,191,788	A	C	0.46775	0.010974	0.002058	1.30E-08	0.016092	0.00349	4.07E-06	0.008459	0.002581	0.001052	1.12E-07	0.078654	
4	KLHL8	rs4577539	87,202,806	G	T	0.467872	0.011136	0.002058	8.90E-09	0.016257	0.003489	3.23E-06	0.008636	0.00258	0.00082	7.13E-08	0.079074	
4	KLHL8	rs10025704	87,207,192	A	G	0.468006	0.01107	0.002057	1.10E-08	0.016186	0.003489	3.56E-06	0.008582	0.00258	0.000884	8.41E-08	0.079725	
4	KLHL8 *	rs35624376	87,237,936	C	T	0.449526	0.011102	0.002049	2.30E-08	0.013526	0.003473	9.93E-05	0.01015	0.00257	7.90E-05	2.08E-07	0.434466	
4	KLHL8 *	rs35844368	87,238,219	T	C	0.447937	0.011252	0.002049	1.80E-08	0.013462	0.003474	0.000107	0.010378	0.002571	5.47E-05	1.58E-07	0.475369	
4	KLHL8 *	rs13137873	87,238,277	T	C	0.448313	0.011101	0.002047	2.50E-08	0.013324	0.003471	0.000125	0.010235	0.002568	6.79E-05	2.24E-07	0.474389	
4	KLHL8 *	rs13113529	87,238,292	C	T	0.448314	0.011101	0.002047	2.50E-08	0.013323	0.003471	0.000125	0.010235	0.002568	6.79E-05	2.24E-07	0.474575	
4	KLHL8 *	rs10006766	87,238,866	G	A	0.448391	0.011146	0.002047	2.30E-08	0.013391	0.00347	0.000115	0.010266	0.002567	6.43E-05	1.97E-07	0.469085	
4	KLHL8 *	rs10029254	87,238,988	T	C	0.448409	0.011142	0.002047	2.30E-08	0.01337	0.00347	0.000118	0.010272	0.002567	6.37E-05	2.00E-07	0.472899	
4	KLHL8 *	rs35469118	87,247,026	T	C	0.355437	0.012875	0.002148	1.00E-09	0.016526	0.003641	5.73E-06	0.011467	0.002694	2.10E-05	3.89E-09	0.26394	
4	KLHL8 *	rs7656630	87,252,540	C	T	0.450907	0.011078	0.002043	2.40E-08	0.012819	0.003466	0.000218	0.010398	0.002561	4.97E-05	2.82E-07	0.574347	
4	TLL1 *	rs17634465	166,206,230	C	T	0.462485	-0.012086	0.00204	3.20E-09	-0.007384	0.00347	0.033331	-0.01484	0.002553	6.34E-09	4.80E-09	0.083514	
4	TLL1 *	rs17691028	166,209,275	G	A	0.433535	-0.012055	0.002043	1.50E-08	-0.007507	0.003477	0.030858	-0.014632	0.002557	1.08E-08	7.57E-09	0.098751	
4	TLL1 *	rs59649146	166,211,072	G	A	0.456809	-0.011379	0.002025	3.30E-08	-0.007417	0.00344	0.03109	-0.013718	0.002537	6.51E-08	4.36E-08	0.140346	
4	TLL1 *	rs74718730	166,225,287	G	T	0.4574	-0.011833	0.002026	1.10E-08	-0.007819	0.003442	0.023112	-0.014185	0.002538	2.33E-08	1.24E-08	0.136567	
4	TLL1 *	rs7889045	166,227,270	A	G	0.434324	-0.012227	0.002037	8.50E-09	-0.007378	0.003466	0.033287	-0.014942	0.00255	4.74E-09	3.61E-09	0.078739	
4	TLL1 *	rs17634553	166,230,796	T	C	0.433333	-0.011938	0.002037	2.00E-08	-0.007093	0.003466	0.04074	-0.014681	0.00255	8.81E-09	7.85E-09	0.077875	
4	TLL1 *	rs10517883	166,232,518	T	C	0.433796	-0.011864	0.002037	2.40E-08	-0.007081	0.003465	0.041029	-0.014518	0.002549	1.26E-08	1.12E-08	0.083825	
4	TLL1 *	rs149723812	166,235,572	G	A	0.456717	-0.011588	0.002026	2.30E-08	-0.007527	0.003442	0.028792	-0.01393	0.002538	4.13E-08	2.62E-08	0.134286	
4	TLL1 *	rs184793585	166,238,504	T	C	0.43279	-0.01193	0.002039	2.00E-08	-0.007148	0.003469	0.039391	-0.014528	0.002552	1.28E-08	1.10E-08	0.0866	
4	TLL1 *	rs11941421	166,239,949	C	G	0.439568	-0.011908	0.00204	2.30E-08	-0.006981	0.00347	0.044247	-0.014647	0.002554	1.00E-08	9.53E-09	0.075179	
4	TLL1 *	rs58933593	166,244,458	G	C	0.43474	-0.012061	0.002036	1.50E-08	-0.007332	0.003465	0.034365	-0.014655	0.002548	9.02E-09	6.95E-09	0.08864	
4	TLL1 *	rs58312036	166,249,069	A	G	0.434166	-0.011974	0.002042	1.90E-08	-0.007293	0.003475	0.035883	-0.014515	0.002556	1.38E-08	1.09E-08	0.09411	
4	TLL1 *	rs7657081	166,252,466	G	A	0.455773	-0.011556	0.002038	3.30E-08	-0.007909	0.003463	0.022404	-0.013672	0.002553	8.78E-08	4.38E-08	0.180455	
4	TLL1 *	rs78510747	166,254,179	T	A	0.454063	-0.012104	0.002043	8.50E-09	-0.008635	0.003468	0.012811	-0.014052	0.002561	4.16E-08	1.30E-08	0.20886	
4	TLL1 *	rs78093495	166,256,202	A	G	0.455842	-0.011724	0.002031	2.00E-08	-0.008347	0.00345	0.015554	-0.01365	0.002545	8.38E-08	3.04E-08	0.2161	
4	TLL1 *	rs76273838	166,256,725	G	A	0.455919	-0.011689	0.002031	2.10E-08	-0.008163	0.003448	0.017948	-0.0137	0.002545	7.46E-08	3.09E-08	0.196332	
4	TLL1 *	rs421948	166,264,239	G	A	0.455021	-0.011406	0.00203	4.80E-08	-0.007848	0.003447	0.022814	-0.013499	0.002544	1.14E-07	5.76E-08	0.187157	
4	TLL1 *	rs143526433	166,269,713	C	T	0.455009	-0.011434	0.00203	4.40E-08	-0.007848	0.003447	0.022826	-0.013536	0.002544	1.05E-07	5.32E-08	0.18422	
4	TLL1 *	rs144318493	166,270,896	G	C	0.455015	-0.011433	0.00203	4.30E-08	-0.007848	0.003447	0.022826	-0.013534	0.002544	1.06E-07	5.33E-08	0.184315	
4	TLL1 *	rs13144379	166,272,560	A	G	0.454894	-0.011525	0.00203	3.40E-08	-0.008108	0.003448	0.018721	-0.013543	0.002544	1.04E-07	4.43E-08	0.204636	
4	TLL1 *	rs59688821	166,274,447	G	A	0.455214	-0.011457	0.002031	4.60E-08	-0.007573	0.003449	0.02815	-0.013721	0.002546	7.19E-08	4.40E-08	0.151517	
4	TLL1 *	rs12511044	166,299,482	A	T	0.440612	-0.011471	0.002058	4.70E-08	-0.007044	0.003497	0.04399	-0.013791	0.002577	8.95E-08	7.97E-08	0.120388	
5	ANKRD55 *	rs157504	56,498,248	C	T	0.293571	-0.012385	0.002267	1.70E-08	-0.010943	0.003853	0.004518	-0.013365	0.002839	2.56E-06	2.74E-07	0.612924	
5	ANKRD55 *	rs151837	56,498,732	T	C	0.294568	-0.01256	0.002257	1.00E-08	-0.011355	0.003836	0.003084	-0.01338	0.002827	2.24E-06	1.71E-07	0.670836	
5	ANKRD55 *	rs151838	56,498,738	T	C	0.294587	-0.01257	0.002257	1.00E-08	-0.011357	0.003835	0.003077	-0.01339	0.002827	2.20E-06	1.67E-07	0.669505	
5	ANKRD55 *	rs157505	56,498,801	T	C	0.294479	-0.012706	0.002257	6.50E-09	-0.011271	0.003834	0.003297	-0.013678	0.002826	1.32E-06	1.09E-07	0.613356	
5	ANKRD55 *	rs30351	56,498,805	A	G	0.23731												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
5	ANKRD55 *	rs25757	56,508,377	G	C	0.298773	-0.013347	0.002205	3.90E-10	-0.011879	0.003753	0.001559	-0.014481	0.002759	1.57E-07	7.00E-09	0.576557	
5	ANKRD55 *	rs467022	56,509,812	T	C	0.237839	-0.013823	0.002371	1.50E-09	0.015091	0.004028	0.00018	0.013787	0.00297	3.50E-06	1.87E-08	0.794431	
5	ANKRD55 *	rs16885608	56,510,081	T	G	0.290119	-0.014545	0.002219	1.90E-11	0.012575	0.003768	0.00085	0.01578	0.00278	1.41E-08	3.83E-10	0.493641	
5	ANKRD55 *	rs459193	56,510,924	A	G	0.470542	-0.022128	0.00202	1.80E-29	-0.021494	0.003434	3.98E-10	-0.023099	0.002528	6.86E-20	2.32E-27	0.706761	
5	C5orf67	rs464605	56,511,543	C	T	0.470819	-0.022198	0.002021	1.10E-29	-0.021754	0.003436	2.50E-10	-0.02308	0.00253	7.69E-20	1.65E-27	0.755991	
5	C5orf67	rs458741	56,512,010	C	T	0.239188	0.013687	0.002366	2.10E-09	0.014872	0.004019	0.000217	0.013667	0.002964	4.05E-06	2.56E-08	0.80939	
5	C5orf67	rs245143	56,512,322	G	A	0.296522	-0.01331	0.00222	4.80E-10	-0.011846	0.003776	0.001713	-0.014417	0.002778	2.15E-07	1.03E-08	0.583528	
5	C5orf67	rs157507	56,512,451	T	C	0.330996	-0.015496	0.002144	7.30E-14	-0.011528	0.003647	0.001581	-0.017867	0.002683	2.85E-11	1.59E-12	0.161498	
5	C5orf67	rs392794	56,512,515	C	T	0.470704	-0.02221	0.002021	9.60E-30	-0.021731	0.003436	2.63E-10	-0.023123	0.00253	6.75E-20	1.52E-27	0.744371	
5	C5orf67	rs465002	56,512,648	C	T	0.470702	-0.02223	0.002021	8.60E-30	-0.021729	0.003436	2.64E-10	-0.023151	0.00253	6.09E-20	1.38E-27	0.738867	
5	C5orf67	rs157510	56,513,139	C	A	0.330932	-0.015486	0.002144	7.70E-14	-0.011571	0.003647	0.001516	-0.017829	0.002683	3.11E-11	1.67E-12	0.166803	
5	C5orf67	rs157512	56,513,300	C	T	0.43599	-0.020025	0.002037	1.70E-24	-0.018226	0.003464	1.46E-07	-0.021569	0.00255	2.84E-17	2.81E-22	0.437059	
5	C5orf67	rs256903	56,513,311	C	A	0.469986	-0.022244	0.002023	8.50E-30	-0.021675	0.00344	3.05E-10	-0.023217	0.002533	5.15E-20	1.35E-27	0.718096	
5	C5orf67	rs173964	56,513,638	A	G	0.469726	-0.022334	0.002024	5.30E-30	-0.021727	0.003441	2.79E-10	-0.023348	0.002533	3.26E-20	7.85E-28	0.704442	
5	C5orf67	rs256904	56,514,478	A	T	0.470266	-0.022156	0.002024	1.60E-29	-0.021605	0.003441	3.52E-10	-0.023141	0.002533	6.96E-20	2.09E-27	0.719278	
5	C5orf67	rs245142	56,514,622	A	G	0.330627	-0.015457	0.002144	9.10E-14	-0.011628	0.003647	0.001438	-0.017776	0.002683	3.56E-11	1.81E-12	0.174408	
5	C5orf67	rs456867	56,515,265	T	C	0.330727	-0.015432	0.002142	1.00E-13	-0.011461	0.003645	0.001672	-0.017825	0.002681	3.08E-11	1.80E-12	0.159543	
5	C5orf67	rs459447	56,515,514	A	G	0.329474	-0.015469	0.002146	9.40E-14	-0.011383	0.00365	0.001827	-0.017976	0.002686	2.28E-11	1.46E-12	0.145755	
5	C5orf67	rs465983	56,516,303	G	A	0.439061	-0.019756	0.002038	7.20E-24	-0.017225	0.003466	6.85E-07	-0.021695	0.002551	1.94E-17	8.62E-22	0.299015	
5	C5orf67	rs61142999	56,516,795	A	G	0.282761	-0.013776	0.002245	2.00E-10	0.011051	0.003815	0.003786	0.015442	0.002811	4.05E-08	4.24E-09	0.35411	
5	C5orf67	rs2448427	56,516,855	T	C	0.295755	-0.011974	0.002227	3.20E-08	-0.009171	0.003795	0.015677	-0.01368	0.002785	9.21E-07	3.12E-07	0.338154	
5	C5orf67	rs405176	56,517,885	G	A	0.369679	-0.016063	0.002096	3.50E-15	-0.011888	0.00357	0.000872	-0.018697	0.002621	1.02E-12	3.49E-14	0.124143	
5	C5orf67	rs60202005	56,518,728	T	C	0.284491	0.013924	0.00224	1.30E-10	0.01083	0.003804	0.004428	0.015814	0.002806	1.79E-08	2.21E-09	0.291659	
5	C5orf67	rs56411612	56,519,256	T	G	0.284529	0.013946	0.00224	1.20E-10	0.010898	0.003805	0.004192	0.015817	0.002806	1.78E-08	2.09E-09	0.298096	
5	C5orf67	rs458356	56,520,065	G	A	0.23749	0.013767	0.002379	1.80E-09	0.014193	0.004041	0.000447	0.014148	0.00298	2.09E-06	2.66E-08	0.992908	
5	C5orf67	rs458036	56,520,254	C	A	0.236888	0.013743	0.002381	2.00E-09	0.013963	0.004045	0.00056	0.014235	0.002983	1.85E-06	2.93E-08	0.956725	
5	C5orf67	rs455660	56,521,061	T	C	0.381592	-0.016641	0.002076	1.00E-16	-0.011914	0.003533	0.000751	-0.019587	0.002597	4.82E-14	1.51E-15	0.080162	
5	C5orf67	rs76721602	56,522,121	A	C	0.282004	0.014056	0.002278	1.50E-10	0.011976	0.003864	0.001949	0.015405	0.002855	7.00E-08	3.92E-09	0.475506	
5	C5orf67	rs76878791	56,522,574	G	A	0.282281	0.013971	0.002287	2.70E-10	0.011801	0.003879	0.002358	0.015492	0.002867	6.68E-08	4.47E-09	0.444277	
5	C5orf67	rs384367	56,560,548	T	G	0.113402	0.018223	0.003182	4.60E-09	0.012404	0.005433	0.02244	0.021256	0.003975	9.12E-08	4.56E-08	0.188503	
5	C5orf67	rs11743303	56,564,125	G	A	0.114468	0.017942	0.003169	5.30E-09	0.011658	0.005411	0.031232	0.021131	0.003957	9.52E-08	6.32E-08	0.157637	
5	C5orf67	rs3936511	56,564,954	G	A	0.114363	0.018051	0.00317	4.30E-09	0.01189	0.005413	0.028073	0.021175	0.003959	9.05E-08	5.49E-08	0.166133	
5	C5orf67	rs3936510	56,565,039	T	G	0.114393	0.018018	0.003169	4.50E-09	0.011758	0.005413	0.02985	0.021204	0.003958	8.65E-08	5.54E-08	0.1589	
5	C5orf67	rs13173241	56,565,532	A	G	0.11447	0.018149	0.003169	3.60E-09	0.01152	0.005411	0.033282	0.021473	0.003957	5.88E-08	4.18E-08	0.137624	
5	C5orf67	rs28650790	56,565,637	T	C	0.114351	0.018209	0.00317	3.50E-09	0.011779	0.005413	0.029587	0.021446	0.003959	6.20E-08	3.98E-08	0.149445	
5	C5orf67	rs9687832	56,565,768	A	G	0.115659	0.017972	0.003154	4.40E-09	0.012863	0.005385	0.016936	0.020594	0.003939	1.75E-07	6.71E-08	0.246566	
5	C5orf67	rs9687833	56,565,774	A	G	0.115702	0.017873	0.003153	5.30E-09	0.012602	0.005384	0.019263	0.020574	0.003939	1.79E-07	7.68E-08	0.232048	
5	C5orf67	rs9687846	56,566,067	A	G	0.115025	0.018082	0.003162	3.80E-09	0.012391	0.005398	0.021719	0.020926	0.00395	1.20E-07	5.77E-08	0.201937	
5	TNFAIP8	rs145778841	119,363,651	T	C	0.03865	-0.030245	0.005246	4.20E-08	-0.005147	0.008931	0.564393	-0.04256	0.006562	9.13E-11	6.22E-10	0.00074	F
5	TNFAIP8	rs143932930	119,364,483	T	G	0.03865	-0.030243	0.005246	4.20E-08	-0.005147	0.008931	0.564393	-0.042556	0.006562	9.17E-11	6.24E-10	0.000741	F
5	TNFAIP8	rs150800682	119,365,445	G	C	0.038664	-0.030661	0.005249	2.80E-08	-0.00538	0.008938	0.547259	-0.043068	0.006567	5.63E-11	3.82E-10	0.000683	F
5	TNFAIP8	rs9327100	119,366,180	G	A	0.039713	-0.029838	0.005184	3.70E-08	-0.005268	0.008827	0.550659	-0.041989	0.006485	9.79E-11	6.58E-10	0.000805	F
5	TNFAIP8	rs143225937	119,370,413	G	C	0.038431	-0.031412	0.005265	1.30E-08	-0.006202	0.008965	0.489094	-0.04339	0.006587	2.93E-11	1.89E-10	0.00072	F
5	TNFAIP8	rs151300053	119,374,385	A	G	0.038188	-0.030807	0.005279	3.20E-08	-0.005855	0.008985	0.514682	-0.043309	0.006606	5.72E-11	3.75E-10	0.000788	F
5	TNFAIP8	rs59406275	119,379,517	A	G	0.038221	-0.031321	0.005277	1.30E-08	-0.005329	0.008998	0.553718	-0.044717	0.006595	1.25E-11	8.74E-11	0.000417	F
5	TNFAIP8	rs140403040	119,381,339	G	A	0.037911	-0.030796	0.005294	2.10E-08	-0.004776	0.009028	0.59683	-0.044478	0.006617	1.86E-11	1.34E-10	0.000393	F
5	TNFAIP8	rs143744864	119,383,503	A	G	0.038078	-0.030015	0.005279	4.10E-08	-0.005102	0.009004	0.571005	-0.04327	0.006597	5.60E-11	3.87E-10	0.000631	F
5	TNFAIP8	rs12332329	119,385,999	A	G	0.144573	-0.02048	0.002872	8.60E-13	-0.008961	0.004899	0.067394	-0.027007	0.003588	5.44E-14	9.38E-14	0.002973	F
5	TNFAIP8	rs6882000	119,387,339	A	G	0.039204	-0.029648	0.005205	3.40E-08	-0.005159	0.008885	0.561472	-0.042745	0.006502	5.07E-11	3.48E-10	0.000644	F
5	TNFAIP8	rs6595187	119,387,914	G	A	0.159791	-0.020012	0.002753	5.80E-13	-0.00909	0.004685	0.052365	-0.026184	0.003453	3.52E-14	4.96E-14	0.003324	F
5	TNFAIP8	rs139299785	119,389,092	C	T	0.0381	-0.029868	0.005277	4.70E-08	-0.004781	0.009001	0.595328	-0.043205	0.006596	5.93E-11	4.18E-10	0.000578	F
5	TNFAIP8	rs9764678	119,390,967	C	T	0.158996	-0.01982	0.002762	9.80E-13	-0.00857	0.004693	0.067856	-0.026132	0.003458	4.33E-14	7.54E-14	0.002601	F
5	TNFAIP8	rs7720409	119,392,561	A	G	0.157548	-0.019539	0.002767	2.60E-12	-0.00854	0.004702	0.069341	-0.025801	0.003465	1.00E-13	1.75E-13	0.003133	F
5	TNFAIP8	rs3203922	119,393,258	C	G	0.157555	-0.019549	0.002767	2.60E-12	-0.008627	0.004702	0.066527	-0.025786	0.003465	1.03E-13	1.75E-13	0.003315	F
5	TNFAIP8	rs1045241	119,393,591	T	C	0.157669	-0.019515	0.002765	2.90E-12	-0.008713	0.004699	0.063706	-0.025654	0.003463	1.34E-13	2.17E-13	0.003717	F
5	TNFAIP8	rs1045242	119,393,632	G	A	0.157721	-0.019789	0.002768	1.40E-12	-0.00885	0.004703	0.059896	-0.026018	0.003466	6.37E-14	9.93E-14	0.003311	F
5																		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
5	TIMD4 *	rs17054099	156,963,969	A	G	0.05716	-0.0249	0.004387	1.80E-09	-0.018135	0.007439	0.014801	-0.029043	0.005501	1.32E-07	4.53E-08	0.238374	
5	TIMD4 *	rs6874202	156,964,617	T	C	0.271667	-0.02153	0.002273	5.70E-23	-0.018132	0.003855	2.59E-06	-0.023252	0.00285	3.53E-16	5.46E-20	0.285414	
5	TIMD4 *	rs62382402	156,964,807	T	C	0.153121	-0.019589	0.002809	1.00E-12	-0.016199	0.00476	0.00067	-0.021153	0.003523	1.98E-09	4.54E-11	0.402826	
5	TIMD4 *	rs4704826	156,965,071	C	A	0.271737	-0.021482	0.002273	7.30E-23	-0.018071	0.003855	2.81E-06	-0.023229	0.00285	3.79E-16	6.31E-20	0.281918	
5	TIMD4 *	rs4704827	156,965,078	T	C	0.271666	-0.021531	0.002273	5.60E-23	-0.018132	0.003855	2.59E-06	-0.023252	0.00285	3.53E-16	5.45E-20	0.285450	
5	TIMD4 *	rs12517431	156,965,237	C	T	0.271652	-0.021557	0.002273	5.10E-23	-0.01814	0.003855	2.57E-06	-0.023287	0.00285	3.21E-16	4.92E-20	0.282973	
5	TIMD4 *	rs28735189	156,967,082	C	T	0.271007	-0.021515	0.002281	8.80E-23	-0.018132	0.003868	2.81E-06	-0.023244	0.00286	4.64E-16	7.73E-20	0.287943	
5	TIMD4 *	rs9715911	156,967,430	G	A	0.270964	-0.021628	0.002282	5.90E-23	-0.018262	0.003869	2.40E-06	-0.023349	0.002861	3.49E-16	5.01E-20	0.290387	
5	TIMD4 *	rs11745603	156,967,507	C	T	0.270955	-0.021634	0.002282	5.90E-23	-0.018289	0.003869	2.32E-06	-0.023339	0.002861	3.60E-16	5.00E-20	0.293978	
5	TIMD4 *	rs12657266	156,968,992	C	T	0.270644	-0.021693	0.002286	4.70E-23	-0.018273	0.003874	2.44E-06	-0.02341	0.002867	3.37E-16	4.92E-20	0.286503	
5	TIMD4 *	rs10043150	156,969,464	A	C	0.152076	-0.019611	0.002825	1.00E-12	-0.015926	0.004784	0.000876	-0.021336	0.003545	1.81E-09	5.36E-11	0.363525	
5	TIMD4 *	rs1393207	156,970,529	T	A	0.270483	-0.021759	0.002288	3.60E-23	-0.018437	0.003877	2.02E-06	-0.023432	0.002869	3.35E-16	4.07E-20	0.300336	
5	TIMD4 *	rs6882345	156,970,662	G	A	0.270479	-0.021742	0.002288	3.90E-23	-0.018485	0.003877	1.89E-06	-0.02339	0.002869	3.78E-16	4.32E-20	0.309232	
5	TIMD4 *	rs6883317	156,971,242	A	G	0.151952	-0.019815	0.002827	6.00E-13	-0.016175	0.004787	0.000732	-0.021537	0.003547	1.31E-09	3.29E-11	0.368207	
5	TIMD4 *	rs58198139	156,972,028	C	T	0.270465	-0.021758	0.002289	3.90E-23	-0.018727	0.003879	1.40E-06	-0.023274	0.002871	5.42E-16	4.61E-20	0.345963	
5	TIMD4 *	rs1134475	156,972,939	A	G	0.270438	-0.021714	0.00229	4.90E-23	-0.018697	0.00388	1.47E-06	-0.023238	0.002872	6.14E-16	5.46E-20	0.346805	
5	TIMD4 *	rs28722027	156,973,514	T	C	0.264021	-0.021032	0.002308	3.00E-21	-0.018761	0.003911	1.64E-06	-0.022064	0.002894	2.59E-14	2.42E-18	0.497291	
5	TIMD4 *	rs6891318	156,973,733	C	A	0.264116	-0.020961	0.002308	4.20E-21	-0.018755	0.003911	1.65E-06	-0.021976	0.002894	3.27E-14	3.08E-18	0.50789	
5	TIMD4 *	rs55776147	156,973,797	A	G	0.270842	-0.02159	0.00229	9.30E-23	-0.018523	0.003882	1.86E-06	-0.023188	0.002872	7.09E-16	7.90E-20	0.334048	
5	TIMD4 *	rs7175848	156,974,467	G	C	0.151598	-0.019828	0.002832	6.10E-13	-0.016046	0.004797	0.000827	-0.021597	0.003553	1.24E-09	3.51E-11	0.352391	
5	TIMD4 *	rs7702004	156,974,719	C	T	0.262357	-0.020995	0.002316	5.70E-21	-0.018685	0.003923	1.94E-06	-0.022098	0.002905	2.93E-14	4.84E-19	0.484569	
5	TIMD4 *	rs7770200	156,975,624	C	T	0.132413	-0.019527	0.003038	7.00E-11	-0.015865	0.005154	0.002089	-0.021515	0.003809	1.66E-08	1.04E-09	0.377967	
5	TIMD4 *	rs7379358	156,976,582	T	A	0.392068	-0.013855	0.002113	2.40E-11	-0.010153	0.003578	0.004557	-0.016326	0.002651	7.53E-10	1.03E-10	0.165632	
5	TIMD4 *	rs10055656	156,977,360	C	T	0.258926	-0.020726	0.002324	2.50E-20	-0.018828	0.003942	1.82E-06	-0.021661	0.002914	1.10E-13	1.12E-17	0.563272	
5	TIMD4 *	rs28575973	156,977,576	A	C	0.258784	-0.02064	0.002325	3.70E-20	-0.018808	0.003944	1.88E-06	-0.021535	0.002915	1.56E-13	1.62E-17	0.578159	
5	TIMD4 *	rs10062571	156,977,625	T	G	0.145919	-0.019684	0.00288	2.80E-12	-0.016775	0.004876	0.000585	-0.021185	0.003614	4.68E-09	9.26E-11	0.467516	
5	TIMD4 *	rs10059560	156,978,773	C	T	0.196804	-0.01722	0.002555	3.90E-12	-0.015411	0.004334	0.000379	-0.01864	0.003202	6.00E-09	7.86E-11	0.549057	
5	TIMD4 *	rs10050384	156,978,935	T	C	0.196235	-0.017064	0.002557	6.40E-12	-0.015447	0.004337	0.000371	-0.018368	0.003205	1.03E-08	1.30E-10	0.588095	
5	TIMD4 *	rs12187385	156,979,446	C	A	0.196733	-0.017112	0.002555	5.30E-12	-0.015218	0.004334	0.000449	-0.018592	0.003202	6.58E-09	1.01E-10	0.531269	
5	TIMD4 *	rs4704728	156,979,597	G	C	0.388425	-0.014103	0.002096	5.10E-12	-0.010001	0.00355	0.004863	-0.016774	0.002629	1.82E-10	2.73E-11	0.125199	
5	TIMD4 *	rs4704830	156,979,708	G	A	0.388491	-0.014071	0.002096	5.90E-12	-0.009953	0.003551	0.005076	-0.016756	0.002629	1.91E-10	1.23E-11	0.123595	
5	TIMD4 *	rs4704831	156,979,709	C	G	0.388643	-0.014076	0.002096	6.10E-12	-0.009873	0.003551	0.00544	-0.016799	0.002629	1.71E-10	2.85E-11	0.116935	
5	TIMD4 *	rs1973491	156,982,536	T	C	0.130526	-0.021632	0.00302	2.10E-13	-0.018293	0.005122	0.000358	-0.023292	0.003786	7.86E-10	1.03E-11	0.432548	
5	TIMD4 *	rs56308765	156,984,044	A	C	0.192597	-0.017783	0.00258	9.20E-13	-0.016279	0.004382	0.000205	-0.019018	0.003231	4.06E-09	3.02E-11	0.614993	
5	TIMD4 *	rs7736899	156,984,196	A	C	0.377823	-0.01404	0.002104	9.10E-12	-0.010826	0.003565	0.002401	-0.016158	0.002639	9.51E-10	7.22E-11	0.229304	
5	TIMD4 *	rs10059263	156,984,250	C	T	0.196746	-0.016903	0.002556	8.50E-12	-0.015665	0.004337	0.000306	-0.017981	0.003204	2.04E-08	2.12E-10	0.667661	
5	TIMD4 *	rs10039097	156,984,874	C	T	0.194486	-0.017811	0.002564	7.40E-13	-0.016401	0.004353	0.000166	-0.019013	0.003213	3.37E-09	2.06E-11	0.629355	
5	TIMD4 *	rs6866930	156,985,611	C	G	0.377867	-0.014048	0.002105	8.80E-12	-0.010917	0.003567	0.002215	-0.016134	0.00264	1.01E-09	7.13E-11	0.239669	
5	TIMD4 *	rs55875237	156,988,018	T	C	0.143619	-0.020916	0.002899	1.70E-13	-0.018676	0.004908	0.000143	-0.022023	0.003638	1.46E-09	7.94E-12	0.583919	
5	TIMD4 *	rs111273781	156,989,163	T	C	0.131449	-0.021213	0.00301	5.20E-13	-0.017762	0.005107	0.000508	-0.022965	0.003772	1.18E-09	2.11E-11	0.412495	
5	TIMD4 *	rs10044267	156,989,418	A	G	0.143626	-0.020911	0.002899	1.80E-13	-0.01865	0.004908	0.000146	-0.02202	0.003638	1.47E-09	8.13E-12	0.581153	
5	TIMD4 *	rs12659077	156,989,695	G	T	0.384083	-0.014815	0.002099	4.00E-13	-0.011024	0.003557	0.001948	-0.017368	0.002632	4.29E-11	2.87E-12	0.15166	
5	HAVCR1 *	rs10075548	156,997,238	C	T	0.144719	-0.020849	0.00289	1.90E-13	-0.017803	0.004891	0.000275	-0.02234	0.003627	7.50E-10	4.65E-12	0.456203	
5	HAVCR1 *	rs66891562	156,998,368	C	T	0.408715	-0.013208	0.002068	3.90E-11	-0.00942	0.003508	0.007261	-0.015678	0.002592	1.51E-09	3.11E-10	0.151386	
5	HAVCR1 *	rs10079422	156,998,650	A	T	0.196528	-0.017841	0.002554	5.10E-13	-0.015873	0.004337	0.000254	-0.019359	0.003199	1.48E-09	1.38E-11	0.517775	
5	HAVCR1 *	rs1501906	157,000,648	G	A	0.409586	-0.013019	0.002053	5.90E-11	-0.008934	0.003485	0.010387	-0.015625	0.002573	1.29E-09	3.67E-10	0.122448	
5	HAVCR1 *	rs67899516	157,001,721	G	A	0.409428	-0.013061	0.002053	4.80E-11	-0.008986	0.003485	0.009944	-0.015696	0.002573	1.09E-09	2.99E-10	0.121436	
5	HAVCR1 *	rs7714118	157,001,727	G	T	0.402889	-0.012453	0.002058	4.90E-10	-0.009118	0.003494	0.00908	-0.014627	0.002579	1.45E-08	0.204557		
5	HAVCR1 *	rs1546288	157,003,694	G	A	0.409429	-0.013044	0.002054	5.10E-11	-0.009097	0.003487	0.0091	-0.015622	0.002574	1.33E-09	3.34E-10	0.13214	
5	HAVCR1 *	rs66512776	157,004,261	C	T	0.409962	-0.012998	0.002056	6.90E-11	-0.008857	0.003491	0.011187	-0.015702	0.002577	1.14E-09	3.46E-10	0.114625	
5	HAVCR1 *	rs6870058	157,004,262	A	G	0.403059	-0.012433	0.00206	5.40E-10	-0.009278	0.003497	0.007988	-0.014531	0.002581	1.84E-08	3.86E-09	0.226737	
5	HAVCR1 *	rs2102151	157,005,007	T	C	0.197715	-0.017726	0.002538	6.30E-13	-0.015455	0.00431	0.000338	-0.019371	0.003181	1.16E-09	1.42E-11	0.464741	
5	HAVCR1 *	rs7721033	157,005,512	T	C	0.197716	-0.017682	0.002538	7.20E-13	-0.015345	0.00431	0.000373	-0.019358	0.00318	1.19E-09	1.59E-11	0.4537	
5	HAVCR1 *	rs10036890	157,006,640	A	T	0.197746	-0.017699	0.002538	6.90E-13	-0.015338	0.00431	0.000375	-0.019393	0.00318	1.10E-09	1.49E-11	0.44899	
5	HAVCR1 *	rs10076109	157,007,151	T	C	0.197743	-0.017684	0.002538	7.20E-13	-0.015256	0.00431	0.000403	-0.019413	0.00318	1.06E-09	1.53E-11	0.437623	
5	HAVCR1 *	rs9791162	157,007,697	C	T	0.409638	-0.013083	0.002056	5.90E-11	-0.008931	0.003489	0.010494	-0.015749	0.002577	1.02E-09	2.94E-10	0.116002	
5	HAVCR1 *	rs10062923	157,008,228	A	G	0.14556	-0.020655											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
5	HAVCR1 *	rs6555801	157,018,625	A	C	0.141466	-0.020693	0.002905	3.50E-13	-0.017172	0.004915	0.000479	-0.022508	0.003646	6.90E-10	1.19E-11	0.383229	
5	HAVCR1 *	rs10462973	157,022,494	G	A	0.405924	-0.012642	0.00206	2.20E-10	-0.008361	0.003495	0.016764	-0.015474	0.002582	2.13E-09	9.11E-10	0.101647	
5	HAVCR1 *	rs7707445	157,022,737	A	G	0.194013	-0.0173	0.002551	2.20E-12	-0.014527	0.00433	0.000798	-0.019308	0.003196	1.57E-09	4.27E-11	0.374358	
5	HAVCR1 *	rs35242034	157,025,733	C	T	0.405846	-0.012654	0.002061	2.20E-10	-0.008363	0.003497	0.01681	-0.015495	0.002583	2.05E-09	8.82E-10	0.100882	
5	HAVCR1 *	rs6866758	157,028,101	T	C	0.255438	-0.020206	0.002319	1.30E-19	-0.017549	0.003936	8.36E-06	-0.021706	0.002906	8.41E-14	3.70E-17	0.395483	
5	HAVCR1	rs2134230	157,029,946	C	G	0.194086	-0.017074	0.00255	3.70E-12	-0.014529	0.004331	0.000799	-0.018972	0.003195	2.96E-09	7.92E-11	0.409087	
5	HAVCR1	rs68145045	157,031,185	G	A	0.40615	-0.012405	0.002062	5.40E-10	-0.008331	0.003498	0.01727	-0.015126	0.002584	4.93E-09	2.13E-09	0.118173	
5	HAVCR1	rs2277025	157,033,084	T	C	0.40638	-0.012418	0.002063	5.30E-10	-0.008382	0.0035	0.016654	-0.015102	0.002585	5.29E-09	2.20E-09	0.12245	
5	HAVCR1	rs6896306	157,034,265	G	T	0.193916	-0.016808	0.002555	8.70E-12	-0.014738	0.004338	0.000684	-0.018485	0.003201	7.89E-09	1.78E-10	0.487058	
5	HAVCR1	rs10213795	157,038,032	T	A	0.194773	-0.016602	0.002596	4.80E-11	-0.016696	0.004401	0.00015	-0.016473	0.003254	4.24E-07	2.05E-09	0.967473	
5	HAVCR1	rs6887832	157,038,245	A	T	0.216767	-0.018616	0.002457	8.60E-15	-0.018683	0.004164	7.35E-06	-0.018849	0.003081	9.76E-10	3.17E-13	0.974486	
5	HAVCR1	rs10059699	157,039,143	C	T	0.192715	-0.017175	0.002563	4.30E-12	-0.015083	0.00435	0.000528	-0.018832	0.003211	4.64E-09	8.34E-11	0.488077	
5	HAVCR1	rs56182597	157,040,299	C	A	0.186301	-0.018136	0.002626	1.10E-12	-0.015179	0.004457	0.000664	-0.020444	0.003291	5.38E-10	1.26E-11	0.341946	
5	HAVCR1	rs17054133	157,040,380	C	T	0.19273	-0.017125	0.002562	4.80E-12	-0.015021	0.004349	0.000556	-0.018802	0.003211	4.89E-09	9.21E-11	0.484275	
5	HAVCR1	rs6555819	157,041,528	A	G	0.193318	-0.016913	0.00256	7.40E-12	-0.015025	0.004345	0.000547	-0.018502	0.003208	8.30E-09	1.52E-10	0.519713	
5	HAVCR1	rs6874311	157,041,787	T	G	0.193323	-0.016895	0.00256	7.80E-12	-0.014979	0.004344	0.000569	-0.018497	0.003208	8.36E-09	1.59E-10	0.514797	
5	HAVCR1	rs9313418	157,042,213	T	C	0.19328	-0.016834	0.00256	9.10E-12	-0.014961	0.004346	0.000581	-0.01838	0.003208	1.03E-08	1.98E-10	0.526788	
5	HAVCR1	rs2270926	157,042,772	A	G	0.140596	-0.020628	0.002914	5.50E-13	-0.017782	0.004929	0.000311	-0.022056	0.003658	1.69E-09	1.90E-11	0.486279	
5	HAVCR1	rs10038271	157,043,390	T	C	0.140502	-0.020701	0.002914	4.30E-13	-0.017791	0.00493	0.00031	-0.02216	0.003659	1.43E-09	1.61E-11	0.476676	
5	HAVCR1	rs17054136	157,045,814	A	G	0.062742	0.021476	0.004169	4.50E-08	0.02348	0.007094	0.000938	0.018812	0.005217	0.000313	6.27E-06	0.596067	
5	HAVCR1	rs35931650	157,046,505	G	A	0.192442	-0.016567	0.002561	1.90E-11	-0.014185	0.004352	0.001123	-0.018467	0.003207	8.74E-09	3.12E-10	0.428389	
5	HAVCR1	rs62382456	157,046,893	A	G	0.19224	-0.016595	0.002562	1.80E-11	-0.014193	0.004353	0.001118	-0.018497	0.003209	8.44E-09	3.00E-10	0.426137	
5	HAVCR1	rs7706174	157,048,387	G	T	0.192262	-0.016487	0.002563	2.50E-11	-0.014071	0.004352	0.001231	-0.018398	0.00321	1.02E-08	3.95E-10	0.423617	
5	HAVCR1	rs1553318	157,052,312	G	C	0.197922	-0.017222	0.002537	1.60E-12	-0.013441	0.004314	0.001843	-0.019977	0.003175	3.23E-10	1.97E-11	0.222322	
5	HAVCR1	rs11134525	157,053,637	A	T	0.197066	-0.017026	0.00255	3.80E-12	-0.013731	0.004335	0.001544	-0.019547	0.003192	9.42E-10	4.77E-11	0.279957	
5	HAVCR1	rs2270925	157,055,088	T	C	0.187464	-0.0166	0.002633	8.70E-11	-0.014061	0.004473	0.001677	-0.01859	0.003299	1.79E-08	9.06E-10	0.415104	
5	HAVCR1	rs2270924	157,055,090	A	T	0.187464	-0.0166	0.002633	8.70E-11	-0.014061	0.004473	0.001677	-0.01859	0.003299	1.79E-08	9.06E-10	0.415104	
6	RREB1	rs9328401	7,225,441	C	A	0.203673	0.013344	0.002539	2.90E-08	0.018098	0.00432	2.83E-05	0.010171	0.003177	0.001374	9.17E-07	0.139314	
6	RREB1	rs9505085	7,226,726	T	C	0.202103	0.013724	0.002548	1.50E-08	0.018442	0.004332	2.10E-05	0.010549	0.003188	0.000941	4.87E-07	0.142245	
6	RREB1	rs9328402	7,227,278	T	C	0.202012	0.013706	0.002549	1.70E-08	0.018527	0.004334	1.94E-05	0.010428	0.003189	0.001082	5.14E-07	0.132288	
6	TRIM27	rs9368581	28,914,454	T	C	0.055077	-0.024712	0.004552	1.20E-08	-0.030396	0.007817	0.000102	-0.021763	0.005666	0.000124	0.371239	0.326E-07	
6	OR10C1 *	rs9368601	29,444,646	T	C	0.086247	-0.021414	0.003748	1.40E-08	-0.02502	0.006381	8.91E-05	-0.019682	0.004687	2.71E-05	6.80E-08	0.500245	
6	MASL1 *	rs9393967	29,501,712	T	C	0.081131	-0.024133	0.003874	6.00E-10	-0.028523	0.006606	1.59E-05	-0.022209	0.00484	4.54E-06	2.40E-09	0.440721	
6	UBD *	rs9391895	29,534,259	A	G	0.08718	-0.022954	0.003758	8.00E-10	-0.025604	0.006406	6.49E-05	-0.021762	0.004696	3.63E-06	7.37E-09	0.628594	
6	GABBR1	rs150971595	29,632,584	T	C	0.095512	-0.024841	0.003661	9.30E-12	-0.029038	0.006244	3.36E-06	-0.02243	0.004574	9.56E-07	1.20E-10	0.39319	
6	MOG *	rs9380134	29,653,999	C	G	0.112135	-0.021637	0.003398	1.40E-10	-0.025202	0.005797	1.39E-05	-0.020104	0.004244	2.21E-06	1.05E-09	0.477945	
6	HLA-F *	rs75791723	29,756,751	T	C	0.109305	-0.023348	0.003446	1.10E-11	-0.027238	0.005886	3.76E-06	-0.021473	0.004301	6.08E-07	4.29E-12	0.429124	
6	HCG4 *	rs9368611	29,772,040	C	A	0.105552	-0.024038	0.003509	3.20E-12	-0.028584	0.005994	1.88E-06	-0.021654	0.00438	7.82E-07	3.50586	0.11E-11	
6	ZNRD1ASP	rs9380151	30,052,051	C	T	0.110844	-0.023924	0.003419	2.00E-12	-0.028857	0.005855	8.43E-07	-0.021109	0.004262	7.45E-07	2.50E-11	0.284688	
6	TRIM31 *	rs9261395	30,097,521	A	C	0.226078	0.015518	0.002675	1.20E-08	0.020956	0.004546	4.10E-06	0.012469	0.003349	0.000199	2.38E-08	0.132816	
6	TRIM31	rs13132680	30,105,418	A	C	0.194676	0.015611	0.00284	4.10E-08	0.023229	0.004809	1.39E-06	0.011817	0.003561	0.00091	3.49E-08	0.056531	
6	TRIM40 *	rs9393991	30,134,864	A	G	0.112228	-0.024611	0.003402	6.80E-13	-0.03065	0.005804	1.32E-07	-0.02107	0.004249	7.21E-07	4.02E-12	0.182885	
6	TRIM15 *	rs9380156	30,173,265	G	A	0.131343	-0.012524	0.002289	3.10E-08	-0.009744	0.003897	0.012422	-0.014642	0.002863	3.20E-07	9.13E-08	0.31108	
6	TRIM15 *	rs9391677	30,178,030	C	G	0.1312402	-0.012318	0.002291	4.50E-08	-0.009886	0.003899	0.011246	-0.014247	0.002865	6.71E-07	1.71E-07	0.367482	
6	TRIM26 *	rs9366754	30,184,256	C	G	0.1312469	-0.012497	0.00229	3.00E-08	-0.01007	0.003898	0.009804	-0.014404	0.002864	5.01E-07	1.14E-07	0.370153	
6	TRIM26	rs12175655	30,187,133	T	C	0.1312444	-0.012498	0.00229	2.90E-08	-0.009869	0.003898	0.011359	-0.014499	0.002864	4.22E-07	1.10E-07	0.338442	
6	TRIM26	rs2239531	30,201,052	T	C	0.1312371	-0.012488	0.00229	3.20E-08	-0.009977	0.003898	0.010506	-0.014451	0.002864	4.61E-07	1.12E-07	0.35507	
6	TRIM26	rs2284167	30,201,796	T	C	0.131223	-0.012545	0.002291	3.00E-08	-0.010137	0.0039	0.009355	-0.014449	0.002865	4.68E-07	0.372879	0.103E-07	
6	TRIM26	rs28730510	30,202,280	G	C	0.1312466	-0.012435	0.002289	3.50E-08	-0.010047	0.003897	0.009959	-0.014318	0.002863	5.82E-07	1.34E-07	0.377092	
6	TRIM26	rs117565607	30,204,594	A	T	0.111312	-0.02512	0.003424	3.50E-13	-0.030015	0.005849	2.92E-07	-0.021964	0.004275	2.83E-07	3.53E-12	0.266393	
6	TRIM26	rs2284171	30,205,173	A	G	0.1312505	-0.012478	0.00229	3.20E-08	-0.010001	0.003897	0.010296	-0.014409	0.002863	4.95E-07	1.18E-07	0.362091	
6	TRIM26	rs9391802	30,206,355	A	G	0.131137	-0.012399	0.002289	4.50E-08	-0.009853	0.003896	0.011459	-0.014334	0.002863	5.64E-07	1.47E-07	0.354088	
6	TRIM26 *	rs9378221	30,214,057	C	T	0.1312967	-0.012382	0.002289	4.00E-08	-0.009573	0.003897	0.014047	-0.014481	0.002862	4.30E-07	1.36E-07	0.310117	
6	TRIM26 *	rs9378189	30,220,745	T	C	0.1312378	-0.012534	0.002291	3.00E-08	-0.009912	0.0039	0.011051	-0.014501	0.002865	4.23E-07	1.08E-07	0.342857	
6	TRIM26 *	rs9348838	30,221,422	T	A	0.131136	-0.012454	0.002293	3.40E-08	-0.010112	0.003903	0.009598	-0.014273	0.002867	6.56E-07	1.45E-07	0.390301	
6	HCG17 *	rs12660499	30,227,096	A	G	0.1312136	-0.012549	0.002291	2.90E-08	-0.00998	0.003901	0.010535	-0.014505	0.002865	4.22E-07	1.03E-07	0.34983	
6																		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
6	DDR1 *	rs9380200	30,883,417	C	G	0.405942	0.013001	0.002289	2.90E-08	0.01891	0.003883	1.14E-06	0.009649	0.002867	0.000768	2.46E-08	0.055065	
6	DDR1 *	rs9461638	30,883,528	G	C	0.405832	0.013037	0.002289	2.70E-08	0.018945	0.003883	1.08E-06	0.009693	0.002868	0.000728	2.23E-08	0.055271	
6	DDR1	rs9468842	30,884,970	C	T	0.405887	0.01292	0.002289	3.60E-08	0.018795	0.003883	1.32E-06	0.009606	0.002867	0.000812	3.00E-08	0.056994	
6	DDR1	rs6901464	30,886,313	G	T	0.405912	0.013003	0.002289	2.90E-08	0.018931	0.003883	1.10E-06	0.009647	0.002867	0.000771	2.40E-08	0.054435	
6	DDR1	rs4618569	30,887,474	G	A	0.40611	0.013056	0.002288	2.50E-08	0.018951	0.003883	1.08E-06	0.009716	0.002867	0.000706	2.16E-08	0.055717	
6	DDR1	rs2229933	30,889,295	G	C	0.405921	0.013016	0.002289	2.80E-08	0.018981	0.003883	1.03E-06	0.009634	0.002867	0.000784	2.29E-08	0.055207	
6	DDR1	rs6924600	30,889,765	G	A	0.406165	0.01318	0.002288	1.90E-08	0.019232	0.003882	7.39E-07	0.009755	0.002866	0.00067	1.43E-08	0.049542	M
6	DDR1	rs6457282	30,890,211	T	C	0.406213	0.0129	0.002289	3.30E-08	0.018812	0.003883	1.29E-06	0.009551	0.002868	0.000871	3.12E-08	0.05507	
6	DDR1	rs7761589	30,890,470	C	G	0.406945	0.012999	0.002289	2.20E-08	0.019497	0.003884	5.27E-07	0.009332	0.002867	0.001142	1.69E-08	0.035261	M
6	DDR1	rs7743661	30,890,477	T	C	0.406147	0.01292	0.002289	3.20E-08	0.019067	0.003884	9.30E-07	0.009466	0.002868	0.000969	2.51E-08	0.046742	M
6	DDR1	rs1049622	30,891,080	C	T	0.406149	0.012917	0.002289	3.40E-08	0.018961	0.003884	1.07E-06	0.009514	0.002868	0.000913	2.72E-08	0.050382	
6	DDR1	rs9366761	30,891,743	C	T	0.434434	0.012787	0.002264	2.80E-08	0.017703	0.003838	4.04E-06	0.009975	0.002837	0.000442	4.98E-08	0.105416	
6	DDR1	rs3213644	30,893,448	G	A	0.434445	0.012829	0.002264	2.50E-08	0.017784	0.003839	3.67E-06	0.010003	0.002837	0.000426	4.38E-08	0.103093	
6	DDR1	rs9366762	30,896,283	T	C	0.242573	-0.014391	0.002524	1.20E-08	-0.020359	0.004276	1.96E-06	-0.011243	0.003165	0.000385	2.18E-08	0.086634	
6	DDR1	rs2239517	30,897,338	G	A	0.414707	0.013072	0.002274	1.70E-08	0.018309	0.003857	2.10E-06	0.009961	0.002849	0.000474	2.83E-08	0.08166	
6	DDR1	rs2239518	30,897,948	C	T	0.434735	0.012758	0.002263	3.10E-08	0.017928	0.003837	3.03E-06	0.00981	0.002837	0.000548	4.61E-08	0.08892	
6	DDR1	rs1049628	30,899,329	C	T	0.414641	0.013062	0.002274	1.80E-08	0.018366	0.003857	1.96E-06	0.009907	0.002849	0.00051	2.83E-08	0.077721	
6	DDR1	rs8408	30,899,889	T	C	0.414638	0.013071	0.002274	1.80E-08	0.018389	0.003857	1.90E-06	0.009905	0.002849	0.000511	2.76E-08	0.076891	
6	DDR1 *	rs9468844	30,900,456	G	C	0.414583	0.013054	0.002274	1.70E-08	0.018314	0.003858	2.09E-06	0.009896	0.002849	0.000517	3.06E-08	0.079232	
6	DDR1 *	rs4713400	30,901,623	T	C	0.414423	0.013105	0.002274	1.60E-08	0.018492	0.003858	1.67E-06	0.009885	0.00285	0.000526	2.50E-08	0.072755	
6	DDR1 *	rs9468845	30,901,816	G	A	0.414868	0.013079	0.002274	1.80E-08	0.018367	0.003858	1.96E-06	0.009949	0.002849	0.000483	2.70E-08	0.079238	
6	DDR1 *	rs9378150	30,901,916	G	A	0.242549	-0.014259	0.002524	1.70E-08	-0.020375	0.004276	1.92E-06	-0.01109	0.003165	0.000462	2.53E-08	0.080948	
6	DDR1 *	rs9295931	30,901,937	C	T	0.414638	0.013051	0.002274	1.90E-08	0.018366	0.003857	1.96E-06	0.009891	0.002849	0.00052	2.88E-08	0.077193	
6	DDR1 *	rs3869085	30,902,336	G	A	0.414641	0.013062	0.002274	1.80E-08	0.01837	0.003857	1.95E-06	0.009905	0.002849	0.000511	2.82E-08	0.077537	
6	DDR1 *	rs3869086	30,902,391	G	T	0.414638	0.013071	0.002274	1.80E-08	0.018389	0.003857	1.90E-06	0.009905	0.002849	0.000511	2.76E-08	0.076891	
6	DDR1 *	rs9295932	30,902,686	A	G	0.414641	0.013082	0.002274	1.70E-08	0.01842	0.003857	1.83E-06	0.009905	0.002849	0.000511	2.65E-08	0.075806	
6	DDR1 *	rs9468846	30,902,986	T	C	0.414638	0.013071	0.002274	1.80E-08	0.018389	0.003857	1.90E-06	0.009905	0.002849	0.000511	2.76E-08	0.076891	
6	DDR1 *	rs12206075	30,903,223	T	C	0.414656	0.013104	0.002274	1.60E-08	0.018452	0.003858	1.75E-06	0.009923	0.002849	0.000499	2.50E-08	0.075312	
6	DDR1 *	rs10947111	30,903,408	G	A	0.415123	0.013048	0.002275	2.00E-08	0.018638	0.003859	1.39E-06	0.009687	0.00285	0.000682	2.67E-08	0.062071	
6	DDR1 *	rs41288539	30,903,672	G	C	0.414893	0.012926	0.002275	2.50E-08	0.018359	0.003859	2.00E-06	0.009717	0.00285	0.000655	3.65E-08	0.071643	
6	DDR1 *	rs13215246	30,903,732	C	T	0.414638	0.013071	0.002274	1.80E-08	0.018389	0.003857	1.90E-06	0.009905	0.002849	0.000511	2.76E-08	0.076891	
6	DDR1 *	rs13215409	30,903,842	C	A	0.41466	0.013078	0.002274	1.70E-08	0.018389	0.003857	1.90E-06	0.009918	0.002849	0.000502	2.71E-08	0.077327	
6	DDR1 *	rs9404935	30,904,041	G	T	0.242546	-0.014301	0.002524	1.60E-08	-0.020279	0.004276	2.14E-06	-0.011149	0.003166	0.000432	2.64E-08	0.086138	
6	DDR1 *	rs9295933	30,904,093	C	T	0.435037	0.012822	0.002266	2.60E-08	0.017823	0.003842	3.56E-06	0.009945	0.00284	0.000465	4.61E-08	0.099146	
6	DDR1 *	rs9391636	30,904,155	A	T	0.342233	-0.01368	0.002252	1.10E-09	-0.018027	0.003803	2.17E-06	-0.011745	0.002829	3.35E-05	2.39E-09	0.185027	
6	GTFF2H4 *	rs9380201	30,904,922	T	C	0.414744	0.013086	0.002274	1.70E-08	0.01844	0.003858	1.79E-06	0.009905	0.002849	0.000512	2.61E-08	0.075175	
6	GTFF2H4 *	rs9501342	30,904,955	G	A	0.414744	0.013086	0.002274	1.70E-08	0.01844	0.003858	1.79E-06	0.009905	0.002849	0.000512	2.61E-08	0.075175	
6	GTFF2H4 *	rs9378191	30,905,781	C	T	0.413773	0.013356	0.002275	8.80E-09	0.018919	0.003858	9.59E-07	0.010068	0.002851	0.000415	1.17E-08	0.065041	
6	GTFF2H4 *	rs3757339	30,906,109	T	C	0.414291	0.013416	0.002277	8.10E-09	0.018995	0.003861	8.85E-07	0.010079	0.002853	0.000414	1.08E-08	0.063298	
6	GTFF2H4 *	rs3909130	30,906,388	T	C	0.413883	0.013471	0.002275	6.50E-09	0.018884	0.003858	1.00E-06	0.010239	0.00285	0.00033	9.89E-09	0.071507	
6	GTFF2H4 *	rs9295934	30,906,736	A	G	0.415098	0.013539	0.002275	6.60E-09	0.018626	0.003858	1.41E-06	0.010471	0.002851	0.000242	1.02E-08	0.08917	
6	GTFF2H4 *	rs2284175	30,907,368	T	C	0.413822	0.013271	0.002274	1.10E-08	0.018832	0.003858	1.07E-06	0.009979	0.00285	0.000466	1.46E-08	0.064928	
6	GTFF2H4 *	rs2284176	30,907,845	T	C	0.415117	0.013312	0.002275	9.10E-09	0.019148	0.003857	7.02E-07	0.009845	0.002851	0.000557	1.15E-08	0.052438	
6	GTFF2H4 *	rs3218806	30,907,887	G	T	0.413804	0.013316	0.002274	9.60E-09	0.018856	0.003858	1.04E-06	0.010023	0.00285	0.00044	1.34E-08	0.065553	
6	GTFF2H4	rs2074510	30,908,257	G	T	0.413804	0.013302	0.002274	1.00E-08	0.01885	0.003858	1.05E-06	0.010005	0.00285	0.00045	1.38E-08	0.065169	
6	GTFF2H4	rs1052693	30,908,375	C	T	0.4138	0.013312	0.002274	9.70E-09	0.018856	0.003858	1.04E-06	0.010017	0.00285	0.000443	1.35E-08	0.065349	
6	GTFF2H4	rs2074509	30,908,461	G	A	0.413808	0.01331	0.002274	9.70E-09	0.018856	0.003858	1.04E-06	0.010018	0.00285	0.000443	1.35E-08	0.06539	
6	GTFF2H4	rs2074508	30,908,661	G	A	0.413815	0.013318	0.002274	9.60E-09	0.018876	0.003858	1.01E-06	0.010017	0.00285	0.000443	1.32E-08	0.064778	
6	GTFF2H4	rs1362123	30,909,219	G	A	0.413804	0.013327	0.002274	9.40E-09	0.018856	0.003858	1.04E-06	0.010041	0.00285	0.00043	1.31E-08	0.066078	
6	GTFF2H4	rs1362122	30,909,277	G	A	0.433583	0.013037	0.002264	1.50E-08	0.018221	0.003838	2.09E-06	0.010068	0.002838	0.000391	2.36E-08	0.067617	
6	GTFF2H4	rs916920	30,909,425	T	C	0.413585	0.013353	0.002275	9.40E-09	0.018641	0.00386	1.39E-06	0.010179	0.002851	0.000359	1.47E-08	0.077859	
6	GTFF2H4	rs1419693	30,909,983	A	C	0.413819	0.013298	0.002275	1.00E-08	0.018828	0.003858	1.08E-06	0.010003	0.00285	0.000451	1.42E-08	0.065821	
6	GTFF2H4	rs3218814	30,910,802	A	T	0.413804	0.013316	0.002274	9.60E-09	0.018856	0.003858	1.04E-06	0.010023	0.00285	0.00044	1.34E-08	0.065553	
6	GTFF2H4	rs3218815	30,910,992	C	T	0.413895	0.013246	0.002275	1.10E-08	0.018877	0.003858	1.01E-06	0.009903	0.00285	0.000515	1.52E-08	0.0614	
6	GTFF2H4	rs2074512	30,911,142	T	C	0.413778	0.013278	0.002274	1.10E-08	0.018821	0.003858	1.09E-06	0.009981	0.00285	0.000464	1.47E-08	0.065342	
6	VAR52	rs9468847	30,918,341	C	T	0.433564	0.013049	0.002264	1.50E-08	0.018202	0.003838	2.14E-06	0.010094	0.002838	0.000378	2.34E-08	0.089381	
6	VAR52	rs3869091	30,919,272	T	G	0.242497	-0.014351	0.002525										

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
6	MUC22	rs9378151	31,011,395	A	C	0.358335	-0.012395	0.002224	2.70E-08	-0.016269	0.003761	1.54E-05	-0.010601	0.002792	0.000148	6.41E-08	0.226238	
6	MUC22	rs9394025	31,011,702	T	C	0.358317	-0.012388	0.002224	2.70E-08	-0.016266	0.003762	1.55E-05	-0.01058	0.002792	0.000152	6.62E-08	0.224744	
6	MUC22	rs9366764	31,012,016	A	G	0.358335	-0.012387	0.002224	2.70E-08	-0.016182	0.003761	1.71E-05	-0.01064	0.002792	0.00014	6.71E-08	0.236698	
6	MUC22	rs9380204	31,012,156	C	T	0.358319	-0.012394	0.002224	2.70E-08	-0.016207	0.003761	1.66E-05	-0.010623	0.002792	0.000143	6.68E-08	0.232625	
6	MUC22	rs9380205	31,013,584	G	C	0.358332	-0.012326	0.002224	3.10E-08	-0.016115	0.003761	1.85E-05	-0.010563	0.002792	0.000156	8.03E-08	0.235892	
6	MUC22	rs9380206	31,013,978	T	C	0.358332	-0.012373	0.002224	2.80E-08	-0.016157	0.003761	1.76E-05	-0.010617	0.002792	0.000144	7.12E-08	0.236873	
6	MUC22	rs9380207	31,014,946	T	C	0.358332	-0.012373	0.002224	2.80E-08	-0.016157	0.003761	1.76E-05	-0.010617	0.002792	0.000144	7.12E-08	0.236873	
6	MUC22	rs9391701	31,015,486	A	G	0.35831	-0.012389	0.002224	2.70E-08	-0.01615	0.003761	1.78E-05	-0.010642	0.002792	0.000139	6.95E-08	0.239679	
6	MUC22	rs3871466	31,015,906	C	T	0.358328	-0.012389	0.002224	2.70E-08	-0.016171	0.003761	1.73E-05	-0.010626	0.002792	0.000142	6.91E-08	0.236505	
6	MUC22	rs3869096	31,016,627	G	T	0.358354	-0.012382	0.002224	2.70E-08	-0.016152	0.003761	1.77E-05	-0.010629	0.002792	0.000142	7.05E-08	0.23831	
6	MUC22	rs9348846	31,016,941	G	C	0.35832	-0.012392	0.002224	2.60E-08	-0.01618	0.003761	1.72E-05	-0.010632	0.002792	0.000141	6.80E-08	0.236189	
6	MUC22	rs9368652	31,017,226	G	A	0.357874	-0.012306	0.002225	3.20E-08	-0.016172	0.003762	1.74E-05	-0.010503	0.002793	0.000171	8.24E-08	0.226266	
6	MUC22	rs13194580	31,017,238	T	C	0.357874	-0.012306	0.002225	3.20E-08	-0.016172	0.003762	1.74E-05	-0.010503	0.002793	0.000171	8.24E-08	0.226266	
6	MUC22	rs9348848	31,017,827	T	C	0.358156	-0.012472	0.002225	2.20E-08	-0.016332	0.003763	1.44E-05	-0.010666	0.002792	0.000135	5.50E-08	0.226483	
6	MUC22	rs9348849	31,017,828	T	C	0.358156	-0.012472	0.002225	2.20E-08	-0.016332	0.003763	1.44E-05	-0.010666	0.002792	0.000135	5.50E-08	0.226483	
6	MUC22	rs9394027	31,018,108	C	G	0.358307	-0.012383	0.002224	2.70E-08	-0.016207	0.003761	1.66E-05	-0.010606	0.002792	0.000147	6.83E-08	0.231751	
6	MUC22	rs9295941	31,018,887	A	C	0.356065	-0.012563	0.002222	1.80E-08	-0.016103	0.003758	1.85E-05	-0.010842	0.002789	0.000102	5.38E-08	0.26093	
6	MUC22	rs9295942	31,019,233	T	G	0.358488	-0.012278	0.002225	3.50E-08	-0.016166	0.003762	1.75E-05	-0.010464	0.002792	0.00018	8.71E-08	0.223566	
6	MUC22	rs4713416	31,019,800	A	G	0.358285	-0.012369	0.002224	2.80E-08	-0.016224	0.003761	1.63E-05	-0.010562	0.002792	0.000156	7.12E-08	0.226727	
6	MUC22	rs13207269	31,020,129	G	C	0.358284	-0.012373	0.002224	2.80E-08	-0.016236	0.003761	1.61E-05	-0.010562	0.002792	0.000156	7.02E-08	0.225736	
6	MUC22	rs9391703	31,020,534	C	T	0.357114	-0.012273	0.002228	3.80E-08	-0.016248	0.003767	1.63E-05	-0.010443	0.002796	0.00019	8.55E-08	0.229796	
6	MUC22	rs9391704	31,020,560	T	G	0.358058	-0.012368	0.002225	2.80E-08	-0.016272	0.003763	1.55E-05	-0.010542	0.002793	0.000161	7.01E-08	0.22141	
6	MUC22	rs9501343	31,021,704	A	T	0.35816	-0.012376	0.002226	2.80E-08	-0.015969	0.003764	2.24E-05	-0.010663	0.002794	0.000136	8.47E-08	0.257654	
6	MUC22	rs9501345	31,021,883	T	C	0.358169	-0.012373	0.002226	2.80E-08	-0.015935	0.003764	2.33E-05	-0.010678	0.002794	0.000134	8.63E-08	0.262048	
6	MUC22	rs9501346	31,021,966	T	C	0.358248	-0.012337	0.002226	3.10E-08	-0.015841	0.003764	2.60E-05	-0.010673	0.002794	0.000135	9.68E-08	0.270256	
6	MUC22	rs13201420	31,022,070	C	T	0.358102	-0.01243	0.002227	2.50E-08	-0.015938	0.003765	2.33E-05	-0.01077	0.002795	0.000118	7.68E-08	0.270368	
6	MUC22	rs9394029	31,022,280	G	C	0.358242	-0.012371	0.002226	2.90E-08	-0.01595	0.003764	2.29E-05	-0.010671	0.002794	0.000135	8.61E-08	0.260142	
6	MUC22	rs28894975	31,022,442	C	T	0.357465	-0.012181	0.002229	4.40E-08	-0.015835	0.003769	2.68E-05	-0.010462	0.002797	0.000186	1.35E-07	0.252205	
6	MUC22	rs28894976	31,022,443	T	C	0.357465	-0.012181	0.002229	4.40E-08	-0.015835	0.003769	2.68E-05	-0.010462	0.002797	0.000186	1.35E-07	0.252205	
6	MUC22	rs13220447	31,023,472	G	A	0.35818	-0.012476	0.002227	2.30E-08	-0.016052	0.003766	2.05E-05	-0.010768	0.002795	0.000118	6.81E-08	0.25983	
6	MUC22	rs9394031	31,023,866	C	T	0.358182	-0.012548	0.002227	1.90E-08	-0.01626	0.003767	1.60E-05	-0.010767	0.002796	0.000119	5.41E-08	0.241627	
6	MUC22	rs4713417	31,024,957	T	G	0.357393	-0.012542	0.002233	2.00E-08	-0.015901	0.003775	2.56E-05	-0.011029	0.002803	8.43E-05	6.12E-08	0.300196	
6	MUC22	rs4713418	31,024,964	C	G	0.357393	-0.012542	0.002233	2.00E-08	-0.015892	0.003775	2.59E-05	-0.011036	0.002803	8.35E-05	6.12E-08	0.301646	
6	MUC22	rs4713419	31,025,459	G	A	0.354713	-0.012778	0.002238	1.10E-08	-0.016481	0.003784	1.34E-05	-0.011092	0.002809	7.94E-05	3.12E-08	0.252801	
6	MUC22	rs3094672	31,025,600	T	A	0.360372	-0.014443	0.002222	7.40E-11	-0.017305	0.003765	4.38E-06	-0.013184	0.002786	2.25E-06	3.78972		
6	MUC22	rs4713420	31,025,790	T	G	0.354251	-0.013347	0.002222	1.10E-09	-0.016598	0.003761	1.03E-05	-0.011958	0.002787	1.80E-05	5.93E-09	0.321481	
6	MUC22	rs6457300	31,030,965	G	T	0.326723	0.016165	0.002232	6.80E-13	0.020572	0.003789	5.78E-08	0.013819	0.002796	7.82E-07	1.96E-12	0.151526	
6	MUC22	rs6457301	31,031,102	C	T	0.326548	0.016171	0.002232	6.20E-13	0.020601	0.003789	5.53E-08	0.013825	0.002795	7.72E-07	1.86E-12	0.150082	
6	MUC22	rs6457302	31,031,288	T	C	0.475853	-0.012904	0.002213	6.60E-09	-0.017702	0.003751	2.41E-06	-0.01032	0.002773	2.00E-04	1.44E-08	0.113562	
6	MUC22	rs6457303	31,031,401	A	G	0.475861	-0.012912	0.002213	6.40E-09	-0.017701	0.003751	2.41E-06	-0.010333	0.002773	0.000196	1.41E-08	0.114209	
6	MUC22	rs4713421	31,031,850	A	C	0.475482	-0.012869	0.002213	7.30E-09	-0.017688	0.003751	2.45E-06	-0.010305	0.002774	0.000205	1.49E-08	0.113498	
6	MUC22	rs4713422	31,032,125	G	C	0.476034	-0.013039	0.002211	4.40E-09	-0.017755	0.003749	2.22E-06	-0.010481	0.002772	0.000157	1.06E-08	0.118764	
6	MUC22	rs10947121	31,032,220	T	C	0.475866	-0.012916	0.002212	6.30E-09	-0.017731	0.00375	2.30E-06	-0.010303	0.002772	0.000203	1.11E-07	0.111667	
6	MUC22	rs10807077	31,033,690	G	A	0.326859	0.016356	0.002232	3.70E-13	0.020738	0.00379	4.55E-08	0.014074	0.002796	4.88E-07	9.86E-13	0.157024	
6	MUC22	rs10947124	31,033,719	T	G	0.326782	0.01628	0.002232	4.70E-13	0.020676	0.003789	4.97E-08	0.01398	0.002795	5.80E-07	1.27E-12	0.155017	
6	MUC22	rs11969581	31,033,729	T	A	0.26314	0.013261	0.002334	1.20E-08	0.016132	0.003953	4.53E-05	0.012241	0.002926	2.91E-05	3.83E-08	0.428873	
6	MUC22	rs11964623	31,033,742	T	C	0.26314	0.013261	0.002334	1.20E-08	0.016132	0.003953	4.53E-05	0.012241	0.002926	2.91E-05	3.83E-08	0.428873	
6	MUC22	rs10947125	31,033,856	G	A	0.326796	0.016276	0.002232	4.70E-13	0.020706	0.003789	4.76E-08	0.013957	0.002795	6.06E-07	1.27E-12	0.151741	
6	MUC22	rs10947126	31,033,891	A	G	0.328172	0.016397	0.002219	2.70E-13	0.020445	0.003765	5.77E-08	0.014245	0.00278	3.06E-07	7.91E-13	0.185256	
6	MUC22	rs28360042	31,034,004	T	C	0.372728	0.014117	0.002353	1.10E-09	0.019571	0.003988	9.36E-07	0.011822	0.00295	6.19E-05	1.91E-09	0.118202	
6	MUC22 *	rs9357105	31,036,146	A	G	0.129038	-0.018166	0.003237	1.90E-08	-0.020476	0.005488	0.000192	-0.016679	0.004057	3.98E-05	2.03E-07	0.577932	
6	HCG22 *	rs9380213	31,074,619	A	G	0.125433	-0.017824	0.003285	4.10E-08	-0.020169	0.005564	0.000291	-0.01625	0.004119	8.07E-05	5.86E-07	0.571327	
6	HCG22 *	rs9263460	31,077,336	T	C	0.223706	-0.014109	0.002625	2.80E-08	-0.017169	0.004447	0.000114	-0.012368	0.003291	0.000172	4.97E-07	0.385471	
6	HCG22 *	rs9295949	31,078,024	A	C	0.225828	-0.013916	0.002614	3.30E-08	-0.017713	0.004429	6.41E-05	-0.011637	0.003278	0.000387	6.15E-07	0.270132	
6	HCG22 *	rs9295950	31,078,025	T	C	0.225828	-0.013916	0.002614	3.30E-08	-0.017713	0.004429	6.41E-05	-0.011637	0.003278	0.000387	6.15E-07	0.270132	
6	HCG22 *	rs9380215	31,081,878	A	G	0.225904	-0.013797	0.002614	4.10E-08	-0.017641	0.004428	6.84E-05	-0.011532	0.003277	0.000436	7.31E-07	0.267417	
6	HCG22 *	rs4713431	31,083,231	A	G	0.225896	-0.013797											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
6	C6orf15 *	rs4947299	31,105,995	A	G	0.226401	-0.013787	0.00261	4.50E-08	-0.018003	0.004423	4.75E-05	-0.011359	0.003273	0.000523	6.13E-07	0.227225	
6	C6orf15 *	rs4947302	31,106,351	T	G	0.226405	-0.013785	0.00261	4.50E-08	-0.018003	0.004423	4.75E-05	-0.011356	0.003273	0.000524	6.15E-07	0.227043	
6	C6orf15 *	rs4947246	31,106,371	T	G	0.226396	-0.013799	0.00261	4.50E-08	-0.017917	0.004423	5.16E-05	-0.011427	0.003273	0.000483	6.16E-07	0.238176	
6	C6orf15 *	rs9263625	31,107,384	A	G	0.393762	-0.013574	0.002318	2.60E-09	-0.013688	0.003933	0.000504	-0.01344	0.002903	3.72E-06	5.20E-08	0.959489	
6	C6orf15 *	rs9295951	31,109,869	T	C	0.393685	-0.013537	0.002318	2.90E-09	-0.01353	0.003933	0.000586	-0.013467	0.002904	3.57E-06	5.75E-08	0.989713	
6	C6orf15	rs2233978	31,111,926	G	C	0.39339	-0.013443	0.002318	3.90E-09	-0.013378	0.003932	0.000673	-0.013341	0.002904	4.42E-06	8.04E-08	0.993958	
6	C6orf15	rs2233977	31,112,117	G	A	0.393575	-0.013566	0.002318	2.90E-09	-0.013582	0.003933	0.000558	-0.013487	0.002903	3.45E-06	5.31E-08	0.984505	
6	C6orf15 *	rs2233969	31,112,655	G	A	0.388448	-0.012835	0.002324	1.80E-08	-0.014197	0.003946	0.000323	-0.011948	0.00291	4.07E-05	3.37E-07	0.646366	
6	C6orf15 *	rs1265051	31,112,927	G	T	0.28465	-0.0151	0.002423	1.20E-10	-0.01751	0.004107	2.04E-05	-0.013788	0.003036	5.69E-06	3.76E-09	0.466143	
6	C6orf15 *	rs4495304	31,112,941	C	T	0.225931	-0.013814	0.002614	4.10E-08	-0.017866	0.004432	5.60E-05	-0.011449	0.003276	0.000477	6.58E-07	0.244259	
6	C6orf15 *	rs4486065	31,112,956	G	C	0.284331	-0.01525	0.002423	8.80E-11	-0.017685	0.004108	1.69E-05	-0.01394	0.003037	4.51E-06	2.52E-09	0.463212	
6	C6orf15 *	rs2233967	31,113,051	G	C	0.283007	-0.015742	0.002429	2.10E-11	-0.017768	0.004115	1.60E-05	-0.0147	0.003045	1.41E-06	7.78E-10	0.549069	
6	C6orf15 *	rs2233965	31,113,122	G	T	0.282843	-0.01574	0.002429	2.10E-11	-0.017712	0.004116	1.70E-05	-0.014707	0.003045	1.39E-06	8.20E-10	0.557281	
6	C6orf15 *	rs2233964	31,113,142	G	A	0.284328	-0.015105	0.002423	1.30E-10	-0.01733	0.004107	2.48E-05	-0.013927	0.003037	4.59E-06	3.69E-09	0.505289	
6	C6orf15 *	rs2233962	31,113,204	C	T	0.284282	-0.015197	0.002426	1.20E-10	-0.01744	0.004113	2.26E-05	-0.014005	0.003041	4.17E-06	3.09E-09	0.501891	
6	C6orf15 *	rs1265047	31,113,687	G	A	0.398256	-0.014422	0.002301	2.30E-10	-0.013701	0.003906	0.000456	-0.014838	0.002883	2.70E-07	3.76E-09	0.814808	
6	HCG27 *	rs7742179	31,191,243	A	T	0.403957	0.01241	0.002178	2.90E-08	0.011095	0.003696	0.002691	0.013791	0.002729	4.43E-07	3.15E-08	0.557232	
6	HCG27	rs6921948	31,203,480	C	A	0.42442	0.014964	0.002261	3.30E-12	0.018642	0.003844	1.26E-06	0.013387	0.002829	2.27E-06	1.08E-10	0.270827	
6	HCG27 *	rs3887381	31,204,574	T	C	0.311367	0.015077	0.002264	5.50E-12	0.017153	0.003845	8.27E-06	0.014272	0.002835	4.89E-07	1.50E-10	0.546526	
6	HCG27 *	rs3998077	31,205,656	A	G	0.423952	0.0149	0.00226	4.20E-12	0.018625	0.003842	1.27E-06	0.013305	0.002828	2.59E-06	1.23E-10	0.264667	
6	HCG27 *	rs6930065	31,205,892	C	T	0.367996	0.014279	0.002404	2.40E-10	0.016547	0.004085	5.15E-05	0.013622	0.003009	6.09E-06	9.71E-09	0.564188	
6	HCG27 *	rs6930462	31,206,156	G	T	0.424387	0.014954	0.002261	3.40E-12	0.018662	0.003844	1.22E-06	0.013355	0.00283	2.40E-06	1.10E-10	0.26614	
6	HCG27 *	rs6930643	31,206,258	C	T	0.410499	0.014471	0.002309	2.50E-11	0.017401	0.003925	9.40E-06	0.013333	0.00289	4.00E-06	1.28E-09	0.403924	
6	HCG27 *	rs2894181	31,206,750	G	A	0.424899	0.015149	0.00226	1.80E-12	0.018793	0.003842	1.02E-06	0.013609	0.002829	1.53E-06	6.03E-11	0.2772	
6	HCG27 *	rs6936604	31,207,149	C	T	0.36784	0.014228	0.002405	2.80E-10	0.016225	0.004088	7.28E-05	0.013728	0.00301	5.18E-06	1.16E-08	0.622841	
6	HCG27 *	rs6936825	31,207,267	C	T	0.424249	0.014907	0.002262	4.10E-12	0.018472	0.003845	1.58E-06	0.013381	0.00283	2.30E-06	1.36E-10	0.286273	
6	HCG27 *	rs6914215	31,207,401	A	C	0.424247	0.014927	0.002262	3.80E-12	0.018502	0.003846	1.53E-06	0.013397	0.00283	2.24E-06	1.28E-10	0.28494	
6	HCG27 *	rs6914076	31,207,429	G	A	0.424247	0.014927	0.002262	3.80E-12	0.018502	0.003846	1.53E-06	0.013397	0.00283	2.24E-06	1.28E-10	0.28494	
6	HCG27 *	rs4249311	31,207,831	C	T	0.422904	0.014644	0.002267	9.00E-12	0.018798	0.003856	1.11E-06	0.012892	0.002836	5.57E-06	2.26E-10	0.217206	
6	HCG27 *	rs9263911	31,207,890	G	A	0.408467	0.014185	0.002297	1.40E-10	0.017406	0.003909	8.60E-06	0.012994	0.002872	6.16E-06	1.78E-09	0.363144	
6	HCG27 *	rs6919603	31,208,135	G	A	0.358504	0.014389	0.002429	4.50E-10	0.015112	0.004129	0.000254	0.014632	0.003039	1.50E-06	1.14E-08	0.925389	
6	HCG27 *	rs4410769	31,208,469	T	C	0.424672	0.014945	0.002261	3.50E-12	0.018798	0.003845	1.03E-06	0.01328	0.002829	2.73E-06	1.06E-10	0.247685	
6	HCG27 *	rs4457201	31,209,595	C	T	0.439408	0.01457	0.002243	7.60E-12	0.018473	0.003813	1.29E-06	0.012796	0.002807	5.22E-06	2.45E-10	0.230477	
6	HCG27 *	rs9263927	31,210,456	T	C	0.439023	0.014488	0.002244	9.80E-12	0.018029	0.003816	2.34E-06	0.012892	0.002808	4.49E-06	3.78E-10	0.278184	
6	HCG27 *	rs9263928	31,210,547	G	T	0.439449	0.014576	0.002243	7.40E-12	0.018458	0.003813	1.31E-06	0.012824	0.002806	4.96E-06	2.38E-10	0.234022	
6	HCG27 *	rs9263929	31,210,551	A	G	0.439445	0.014591	0.002243	7.10E-12	0.018419	0.003813	1.38E-06	0.012862	0.002806	4.65E-06	2.35E-10	0.240394	
6	HCG27 *	rs9263931	31,210,770	G	A	0.438863	0.01455	0.002245	8.50E-12	0.018281	0.003816	1.69E-06	0.012845	0.00281	4.91E-06	3.00E-10	0.251304	
6	HCG27 *	rs9263933	31,210,849	G	A	0.438358	0.014483	0.002246	1.10E-11	0.01791	0.003818	2.76E-06	0.012934	0.00281	4.24E-06	4.19E-10	0.293917	
6	HCG27 *	rs9263936	31,211,382	C	A	0.439445	0.014591	0.002243	7.10E-12	0.018419	0.003813	1.38E-06	0.012862	0.002806	4.65E-06	2.35E-10	0.240394	
6	HCG27 *	rs9263938	31,211,601	T	C	0.439534	0.014612	0.002243	6.80E-12	0.018336	0.003814	1.55E-06	0.012929	0.002807	4.18E-06	2.37E-10	0.253527	
6	HCG27 *	rs9263940	31,211,715	T	C	0.43953	0.014636	0.002243	6.40E-12	0.018408	0.003814	1.41E-06	0.012929	0.002807	4.18E-06	2.17E-10	0.247209	
6	HCG27 *	rs9263944	31,212,646	G	A	0.43952	0.014636	0.002243	6.30E-12	0.018439	0.003814	1.36E-06	0.01291	0.002807	4.32E-06	2.15E-10	0.242986	
6	HCG27 *	rs9263947	31,212,903	G	T	0.43952	0.014636	0.002243	6.30E-12	0.018439	0.003814	1.36E-06	0.01291	0.002807	4.32E-06	2.15E-10	0.242986	
6	HCG27 *	rs9263953	31,213,931	C	T	0.43952	0.014635	0.002243	6.30E-12	0.018439	0.003814	1.36E-06	0.012909	0.002807	4.33E-06	2.16E-10	0.242953	
6	HCG27 *	rs9263956	31,215,194	T	C	0.439515	0.014646	0.002243	6.10E-12	0.018468	0.003814	1.31E-06	0.012913	0.002807	4.30E-06	2.07E-10	0.24085	
6	HCG27 *	rs3869109	31,216,419	G	A	0.43992	0.014548	0.002243	8.30E-12	0.018781	0.003814	8.61E-07	0.012603	0.002807	7.21E-06	2.27E-10	0.191963	
6	HCG27 *	rs9263960	31,217,100	C	T	0.43935	0.014533	0.002243	8.90E-12	0.01831	0.003813	1.60E-06	0.01282	0.002807	5.01E-06	2.91E-10	0.246263	
6	HCG27 *	rs9263964	31,218,262	T	C	0.422316	0.013254	0.002283	1.10E-09	0.017605	0.003879	5.75E-06	0.011206	0.002858	8.89E-05	1.54E-08	0.184123	
6	HCG27 *	rs9263967	31,218,468	G	A	0.439693	0.014566	0.002243	7.90E-12	0.018538	0.003813	1.18E-06	0.012758	0.002806	5.54E-06	2.39E-10	0.222117	
6	HCG27 *	rs9263968	31,218,591	A	G	0.439568	0.01455	0.002243	8.30E-12	0.018482	0.003814	1.28E-06	0.012764	0.002807	5.51E-06	2.27E-10	0.227226	
6	HCG27 *	rs9263978	31,219,791	G	A	0.439654	0.014618	0.002243	6.80E-12	0.018597	0.003813	1.10E-06	0.012808	0.002806	5.10E-06	2.05E-10	0.221439	
6	HCG27 *	rs9263980	31,220,620	G	A	0.440403	0.014491	0.002242	9.00E-12	0.018474	0.003812	1.28E-06	0.012672	0.002807	6.43E-06	2.97E-10	0.220233	
6	HCG27 *	rs6928399	31,227,441	T	C	0.288533	0.013285	0.002322	4.70E-09	0.014241	0.003943	0.000306	0.013043	0.002908	7.38E-06	6.28E-08	0.806902	
6	HCG27 *	rs6934133	31,228,026	A	G	0.305266	0.01484	0.002281	2.10E-11	0.015547	0.003877	6.13E-05	0.014747	0.002855	2.45E-07	5.19E-10	0.868119	
6	HCG27 *	rs6933818	31,228,027	T	C	0.305266	0.01484	0.002281	2.10E-11	0.015547	0.003877	6.13E-05	0.014747	0.002855	2.45E-07	5.19E-10	0.868119	
6	HCG27 *	rs10807083	31,228,164	A	G	0.30588	0.014591	0.002279	4.00E-11	0.015246	0.003873	8.35E-05	0.014528	0.002853	3.62E-07	1.01E-09	0.881351	
6	HCG27 *	rs7769211	31,228,241	C	T	0.355444	-0.011963	0.00223										

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
6	HCG27 *	rs9264086	31,233,907	A	G	0.43282	0.014836	0.002246	4.90E-12	0.017801	0.003819	3.20E-06	0.013627	0.002811	1.27E-06	1.51E-10	0.378742	
6	HLA-C *	rs28397298	31,239,909	G	A	0.292375	0.013321	0.002316	3.10E-09	0.015549	0.003935	7.84E-05	0.012502	0.002899	1.64E-05	3.73E-08	0.533131	
6	HLA-C *	rs113075583	31,254,848	T	C	0.064025	0.021709	0.004199	3.10E-08	0.022679	0.007171	0.001571	0.020561	0.005242	8.86E-05	3.07E-06	0.811526	
6	HLA-C *	rs181793732	31,257,904	C	T	0.064111	0.021533	0.004197	3.80E-08	0.022203	0.00717	0.001964	0.020541	0.005238	8.89E-05	3.79E-06	0.851493	
6	HLA-C *	rs112253861	31,258,519	T	C	0.063582	0.022504	0.004207	1.30E-08	0.023459	0.007186	0.001103	0.021369	0.005253	4.78E-05	1.24E-06	0.814395	
6	HLA-C *	rs183076319	31,258,889	T	C	0.063542	0.022631	0.004209	1.00E-08	0.023497	0.00719	0.001089	0.021536	0.005254	4.20E-05	1.08E-06	0.825654	
6	HLA-C *	rs17191797	31,260,763	G	T	0.063566	0.022026	0.004207	2.60E-08	0.022295	0.007187	0.001929	0.021258	0.005252	5.23E-05	2.25E-06	0.907163	
6	HLA-C *	rs17191904	31,261,222	A	G	0.063569	0.022017	0.004207	2.60E-08	0.022295	0.007187	0.001929	0.021231	0.005252	5.34E-05	2.30E-06	0.904821	
6	HLA-C *	rs72854960	31,261,346	T	A	0.063569	0.022017	0.004207	2.60E-08	0.022295	0.007187	0.001929	0.021231	0.005252	5.34E-05	2.30E-06	0.904821	
6	HLA-C *	rs116556510	31,261,644	T	G	0.06357	0.022019	0.004207	2.60E-08	0.022295	0.007187	0.001929	0.021236	0.005252	5.32E-05	2.29E-06	0.905222	
6	HLA-C *	rs113700423	31,261,720	T	C	0.06525	0.021137	0.004156	3.90E-08	0.020421	0.007101	0.004044	0.020917	0.005187	5.57E-05	4.71E-06	0.955012	
6	HLA-C *	rs17192134	31,262,216	T	G	0.062362	0.023327	0.004219	5.20E-09	0.021003	0.007219	0.003635	0.023411	0.005262	8.74E-06	7.30E-07	0.787564	
6	HLA-C *	rs112445341	31,264,169	T	C	0.062367	0.023375	0.004219	4.80E-09	0.020971	0.007219	0.003686	0.023489	0.005261	8.13E-06	6.90E-07	0.778028	
6	HLA-C *	rs2853961	31,264,212	A	G	0.133035	0.017279	0.003277	1.10E-08	0.013122	0.005588	0.018887	0.018873	0.004095	4.11E-06	1.55E-06	0.406474	
6	HLA-C *	rs66509442	31,264,498	T	A	0.062365	0.023528	0.004219	3.80E-09	0.020922	0.007219	0.003766	0.023774	0.005262	6.34E-06	5.55E-07	0.749565	
6	HLA-C *	rs67524139	31,266,505	C	T	0.062374	0.023535	0.004219	3.90E-09	0.020677	0.007219	0.004196	0.023905	0.005262	5.63E-06	5.46E-07	0.717842	
6	HLA-C *	rs2524103	31,266,825	C	T	0.392947	-0.013179	0.002228	9.50E-11	-0.011323	0.003879	0.003525	-0.013518	0.002851	2.16E-06	1.86E-07	0.648445	
6	HLA-C *	rs113509869	31,267,416	A	T	0.064632	0.021688	0.004159	4.50E-08	0.018651	0.007119	0.008818	0.022249	0.005186	1.81E-05	3.26E-06	0.682918	
6	HLA-C *	rs112126458	31,267,423	T	C	0.063429	0.021617	0.004199	4.60E-08	0.01854	0.007178	0.009815	0.022236	0.00524	2.23E-05	4.38E-06	0.677514	
6	HLA-C *	rs2524101	31,267,821	C	G	0.339037	-0.013131	0.002228	9.50E-11	-0.011195	0.003881	0.003933	-0.013512	0.002852	2.20E-06	2.09E-07	0.630521	
6	HLA-C *	rs9264579	31,267,969	A	G	0.361707	-0.01438	0.002276	6.90E-12	-0.011212	0.00387	0.003774	-0.015152	0.002849	1.06E-07	1.08E-08	0.41224	
6	HLA-C *	rs113792081	31,267,998	C	T	0.071858	0.022826	0.003946	1.40E-09	0.020417	0.006754	0.002512	0.023051	0.004921	2.86E-06	1.78E-07	0.752613	
6	HLA-C *	rs2524096	31,268,690	T	G	0.433967	-0.01361	0.002223	1.60E-11	-0.013612	0.00378	0.000319	-0.012981	0.002782	3.13E-06	2.87E-08	0.893114	
6	HLA-C	rs41553018	31,271,965	C	G	0.061821	0.023666	0.00424	4.70E-09	0.02154	0.007258	0.00301	0.023613	0.005287	8.07E-06	5.70E-07	0.817455	
6	HLA-C	rs2074493	31,271,999	C	A	0.339191	0.016861	0.002459	9.10E-14	0.017535	0.004179	2.75E-05	0.0167	0.003077	5.85E-08	6.03E-11	0.872108	
6	HLA-C *	rs2074489	31,272,351	T	C	0.329071	0.01634	0.002506	1.40E-12	0.017778	0.004259	3.02E-05	0.015964	0.003136	3.64E-07	3.88E-10	0.731616	
6	HLA-C *	rs5010528	31,273,255	G	A	0.062436	0.022834	0.004227	1.30E-08	0.021232	0.007234	0.003344	0.022532	0.005272	1.94E-05	1.45E-06	0.884563	
6	HLA-C *	rs58019823	31,273,438	G	A	0.063489	0.023606	0.004186	2.60E-09	0.022426	0.007162	0.001749	0.022934	0.00522	1.13E-05	4.79E-07	0.954294	
6	HLA-C *	rs67058142	31,274,016	A	G	0.062162	0.023227	0.004229	6.60E-09	0.020692	0.007265	0.004408	0.0234	0.005263	8.86E-06	8.82E-07	0.762717	
6	HLA-C *	rs3132482	31,275,643	A	G	0.480805	0.013084	0.002293	3.30E-09	0.019599	0.003902	5.20E-07	0.009898	0.002867	0.000561	8.62E-09	0.045155	M
6	HLA-C *	rs9378228	31,278,594	T	G	0.127078	-0.017523	0.003269	4.70E-08	-0.021361	0.005537	0.000116	-0.015081	0.004099	0.000236	6.75E-07	0.362019	
6	HLA-C *	rs9468914	31,282,829	C	A	0.363015	0.013552	0.002393	7.40E-10	0.014618	0.00407	0.000331	0.012885	0.002994	1.70E-05	1.50E-07	0.731603	
6	HLA-C *	rs9468915	31,283,024	C	A	0.30323	0.013059	0.002581	1.50E-08	0.010385	0.004392	0.018082	0.014165	0.003228	1.16E-05	4.04E-06	0.488146	
6	HLA-C *	rs9468916	31,283,032	C	T	0.303316	0.012955	0.002581	1.90E-08	0.010386	0.004392	0.018066	0.013975	0.003228	1.51E-05	5.19E-06	0.510227	
6	HLA-C *	rs9468917	31,283,141	T	C	0.303305	0.012958	0.002581	1.90E-08	0.010398	0.004392	0.017933	0.013973	0.003228	1.52E-05	5.17E-06	0.511918	
6	HLA-C *	rs28367587	31,283,201	A	G	0.303325	0.012973	0.00258	1.80E-08	0.010327	0.004392	0.018723	0.014029	0.003227	1.40E-05	4.97E-06	0.496971	
6	HLA-C *	rs28367588	31,283,226	A	G	0.303325	0.012973	0.00258	1.80E-08	0.010327	0.004392	0.018723	0.014029	0.003227	1.40E-05	4.97E-06	0.496971	
6	HLA-C *	rs28367589	31,283,255	A	C	0.363035	0.01355	0.002393	7.50E-10	0.014527	0.00407	0.000361	0.012925	0.002993	1.59E-05	1.53E-07	0.751129	
6	HLA-C *	rs9461681	31,283,263	A	G	0.303325	0.012973	0.00258	1.80E-08	0.010327	0.004392	0.018723	0.014029	0.003227	1.40E-05	4.97E-06	0.496971	
6	HLA-C *	rs3873374	31,283,534	C	T	0.303324	0.012959	0.00258	1.80E-08	0.010365	0.004392	0.018299	0.01399	0.003227	1.48E-05	5.13E-06	0.505912	
6	HLA-C *	rs3873375	31,283,583	T	C	0.304205	0.012846	0.00257	2.00E-08	0.010075	0.004371	0.021195	0.013955	0.003216	1.44E-05	5.70E-06	0.474512	
6	HLA-C *	rs2394963	31,283,685	T	C	0.303141	0.01288	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013963	0.00323	1.56E-05	5.98E-06	0.488333	
6	HLA-C *	rs2394964	31,283,765	T	C	0.303152	0.012886	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013967	0.003229	1.54E-05	5.94E-06	0.487869	
6	HLA-C *	rs2894206	31,283,781	T	A	0.303152	0.012886	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013967	0.003229	1.54E-05	5.94E-06	0.487869	
6	HLA-C *	rs2394965	31,283,804	T	G	0.303152	0.012886	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013967	0.003229	1.54E-05	5.94E-06	0.487869	
6	HLA-C *	rs6910962	31,285,332	T	C	0.303147	0.012898	0.002583	2.10E-08	0.010182	0.004397	0.020598	0.013986	0.003229	1.50E-05	5.79E-06	0.485653	
6	HLA-C *	rs7754443	31,286,486	A	G	0.303159	0.012884	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013962	0.003229	1.56E-05	5.98E-06	0.488466	
6	HLA-C *	rs9468920	31,287,159	A	G	0.303322	0.012937	0.002583	1.90E-08	0.010107	0.004398	0.021574	0.014099	0.00323	1.29E-05	5.21E-06	0.464414	
6	HLA-C *	rs9468921	31,287,304	G	A	0.303152	0.012886	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013967	0.003229	1.54E-05	5.94E-06	0.487869	
6	HLA-C *	rs9468922	31,287,509	A	G	0.304348	0.012966	0.002581	1.70E-08	0.010896	0.004393	0.013149	0.013747	0.003227	2.07E-05	5.30E-06	0.600884	
6	HLA-C *	rs9468923	31,287,745	C	T	0.303152	0.012886	0.002583	2.20E-08	0.010182	0.004397	0.020598	0.013967	0.003229	1.54E-05	5.94E-06	0.487869	
6	HLA-C *	rs4628144	31,289,327	C	T	0.303668	0.013216	0.002576	9.40E-09	0.010501	0.004382	0.016578	0.014398	0.003223	8.02E-06	2.62E-06	0.473747	
6	HLA-C *	rs9468925	31,291,060	A	G	0.357132	0.013097	0.002409	3.40E-09	0.014048	0.004096	0.000608	0.012627	0.003015	2.85E-05	4.34E-07	0.779883	
6	HLA-C *	rs3906269	31,291,191	A	G	0.303158	0.012873	0.002583	2.20E-08	0.010158	0.004397	0.020904	0.013956	0.003229	1.57E-05	6.11E-06	0.486377	
6	HLA-C *	rs28367595	31,291,610	A	G	0.304409	0.012903	0.00258	2.00E-08	0.010781	0.004392	0.014134	0.013709	0.003227	2.18E-05	5.93E-06	0.5911	
6	HLA-C *	rs9468926	31,292,441	T	C	0.304498	0.012985	0.002579	1.60E-08	0.011159	0.00439	0.011044	0.013709	0.003225	2.16E-05	4.72E-06	0.639775	
6	HLA-C *	rs3906276	31,293,307	A	T	0.303147	0.012886	0.002583	2.20E-08	0.0								

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
6	HLA-B *	rs9265552	31,330,519	G	C	0.262631	0.014463	0.002741	3.30E-09	0.015712	0.004665	0.000761	0.013163	0.003429	0.000125	2.17E-06	0.659819	
6	HLA-B *	rs9265554	31,330,535	G	A	0.263536	0.014254	0.002743	4.30E-09	0.015966	0.004665	0.000624	0.012867	0.003433	0.000179	2.54E-06	0.592608	
6	HLA-B *	rs9265559	31,330,589	G	C	0.264538	0.013922	0.002737	7.90E-09	0.014954	0.004653	0.001316	0.012877	0.003425	0.000171	4.87E-06	0.719192	
6	HLA-B *	rs9265560	31,330,617	G	C	0.264643	0.013655	0.002736	1.30E-08	0.014674	0.004653	0.00162	0.01268	0.003423	0.000214	7.27E-06	0.730074	
6	HLA-B *	rs9265561	31,330,649	G	A	0.263369	0.014045	0.002744	5.80E-09	0.01532	0.004667	0.001033	0.012983	0.003433	0.000157	3.59E-06	0.686685	
6	HLA-B *	rs9265562	31,330,662	A	G	0.264791	0.013784	0.002735	9.90E-09	0.014838	0.004651	0.001429	0.012774	0.003422	0.000191	5.82E-06	0.720818	
6	HLA-B *	rs9265566	31,330,743	T	A	0.264789	0.01379	0.002735	9.80E-09	0.01485	0.004651	0.001415	0.012774	0.003422	0.000191	5.77E-06	0.719159	
6	HLA-B *	rs9265568	31,330,790	T	C	0.265065	0.013814	0.002733	9.80E-09	0.015238	0.004648	0.00105	0.012615	0.00342	0.000227	5.14E-06	0.649509	
6	HLA-B *	rs9265569	31,330,813	A	G	0.265061	0.013797	0.002733	1.00E-08	0.015238	0.004648	0.00105	0.012594	0.00342	0.000232	5.26E-06	0.646792	
6	HLA-B *	rs6938680	31,331,524	A	G	0.264185	0.013866	0.002739	9.80E-09	0.015174	0.004658	0.001128	0.012743	0.003428	0.000203	4.95E-06	0.674158	
6	HLA-B *	rs6938855	31,331,573	C	A	0.264318	0.01367	0.002739	1.40E-08	0.014882	0.004657	0.001402	0.012589	0.003428	0.000242	7.13E-06	0.69181	
6	HLA-B *	rs9265614	31,331,831	A	T	0.264778	0.013728	0.002736	1.00E-08	0.014888	0.004654	0.001387	0.012719	0.003423	0.000204	6.03E-06	0.70738	
6	HLA-B *	rs9265618	31,331,893	T	C	0.264696	0.013723	0.002737	1.00E-08	0.014759	0.004655	0.001531	0.012749	0.003424	0.000198	6.41E-06	0.728046	
6	HLA-B *	rs9265620	31,331,908	C	T	0.27136	0.014268	0.002699	1.60E-09	0.016357	0.004591	0.000369	0.012619	0.003377	0.000188	1.62E-06	0.511946	
6	HLA-B *	rs9265624	31,332,007	A	C	0.263738	0.013912	0.002742	8.10E-09	0.014988	0.004667	0.001326	0.012893	0.00343	0.000172	4.92E-06	0.717581	
6	HLA-B *	rs9265627	31,332,082	C	T	0.264258	0.013999	0.002739	6.30E-09	0.015296	0.004659	0.001033	0.012923	0.003426	0.000164	3.72E-06	0.681552	
6	HLA-B *	rs9265644	31,332,404	C	T	0.264552	0.013653	0.002739	1.50E-08	0.015232	0.004657	0.001077	0.012461	0.003427	0.000279	6.39E-06	0.631706	
6	HLA-B *	rs6902116	31,332,509	G	A	0.258888	0.014213	0.002769	7.70E-09	0.014818	0.004706	0.001647	0.013616	0.003467	8.66E-05	3.14E-06	0.837148	
6	HLA-B *	rs142459005	31,361,146	T	A	0.138736	-0.017455	0.00316	1.10E-08	-0.020503	0.005358	0.000131	-0.015368	0.00396	0.000105	3.54E-07	0.440834	
6	MICA *	rs117884751	31,434,029	A	T	0.132161	-0.017126	0.003215	4.20E-08	-0.020122	0.005455	0.000227	-0.015282	0.004029	0.00015	8.34E-07	0.475462	
6	GRM4 *	rs141604279	34,186,105	A	G	0.080089	-0.020502	0.003832	2.20E-08	-0.030129	0.006468	3.24E-06	-0.016066	0.004815	0.000852	7.41E-08	0.081136	
6	GRM4 *	rs117658820	34,186,528	T	A	0.080118	-0.020549	0.003832	2.10E-08	-0.029998	0.006466	3.55E-06	-0.016219	0.004815	0.00076	7.29E-08	0.08744	
6	GRM4 *	rs148061387	34,189,310	A	G	0.080464	-0.020422	0.003828	2.70E-08	-0.030441	0.006463	2.52E-06	-0.015817	0.004808	0.001008	6.81E-08	0.069474	
6	GRM4 *	rs79658451	34,195,307	C	G	0.092884	-0.020017	0.003517	1.70E-09	-0.028624	0.005966	1.63E-06	-0.016673	0.004408	0.000157	7.84E-09	0.107124	
6	HMG1A *	rs111643014	34,197,531	A	G	0.08288	-0.020483	0.003694	3.60E-09	-0.026931	0.006254	1.68E-05	-0.018171	0.004634	8.89E-05	4.31E-08	0.260385	
6	HMG1A *	rs141574601	34,199,567	G	T	0.082238	-0.021048	0.003712	1.80E-09	-0.027866	0.006286	9.43E-06	-0.01854	0.004655	6.88E-05	1.94E-08	0.233131	
6	HMG1A *	rs1817718	34,201,243	A	T	0.107237	-0.018381	0.003298	7.70E-09	-0.024784	0.005601	9.78E-06	-0.016025	0.004129	0.000105	3.00E-08	0.208114	
6	HMG1A *	rs1817715	34,204,278	C	A	0.110968	-0.017812	0.003257	1.70E-08	-0.024413	0.005531	1.03E-05	-0.015293	0.004078	0.000178	5.19E-08	0.184409	
6	HMG1A *	rs10807136	34,210,781	T	C	0.096344	-0.018844	0.003457	1.10E-08	-0.024417	0.005867	3.20E-05	-0.01691	0.004331	9.52E-05	8.49E-08	0.303267	
6	HMG1A *	rs138997002	34,210,816	T	C	0.082573	-0.021079	0.003704	1.60E-09	-0.027524	0.006271	1.15E-05	-0.018752	0.004645	5.48E-05	1.90E-08	0.260978	
6	HMG1A *	rs6913361	34,211,613	A	G	0.096279	-0.018675	0.003461	1.50E-08	-0.024662	0.005874	2.72E-05	-0.016494	0.004335	0.000143	1.07E-07	0.263174	
6	HMG1A *	rs7751671	34,211,979	A	G	0.080921	-0.020739	0.00377	1.10E-08	-0.026901	0.006398	2.65E-05	-0.01788	0.004724	0.000155	1.12E-07	0.256653	
6	HMG1A *	rs139173280	34,212,499	T	C	0.08251	-0.020845	0.003706	2.30E-09	-0.027488	0.006275	1.20E-05	-0.018404	0.004648	7.59E-05	2.69E-08	0.244724	
6	HMG1A *	rs9357174	34,214,218	C	T	0.112922	-0.017063	0.003222	3.90E-08	-0.023994	0.005473	1.18E-05	-0.014132	0.004035	0.000464	1.45E-07	0.146937	
6	HMG1A *	rs10807137	34,215,249	C	T	0.112788	-0.017051	0.003224	4.50E-08	-0.023745	0.005477	1.48E-05	-0.014317	0.004037	0.000393	1.54E-07	0.165843	
6	HMG1A *	rs1592269	34,215,280	G	A	0.094792	-0.018947	0.003483	8.30E-09	-0.025029	0.0059	2.24E-05	-0.016766	0.004368	0.000125	7.81E-08	0.260305	
6	HMG1A *	rs1776901	34,215,317	A	G	0.092733	-0.019356	0.003514	4.80E-09	-0.025597	0.005949	1.71E-05	-0.017211	0.004408	9.53E-05	4.67E-08	0.257361	
6	HMG1A *	rs6911780	34,216,690	T	C	0.08589	-0.020385	0.003638	3.00E-09	-0.027297	0.006165	9.67E-06	-0.017678	0.00456	0.000107	3.02E-08	0.209752	
6	HMG1A *	rs10807138	34,217,161	G	A	0.116752	-0.017166	0.003177	3.10E-08	-0.023906	0.005398	9.62E-06	-0.01438	0.003977	0.000302	7.99E-08	0.155394	
6	HMG1A *	rs10807139	34,217,235	T	C	0.093012	-0.020187	0.003505	1.60E-09	-0.027017	0.005942	5.53E-06	-0.017412	0.004394	7.48E-05	1.26E-08	0.193691	
6	HMG1A *	rs151044302	34,217,884	T	C	0.085791	-0.02064	0.003638	2.10E-09	-0.027281	0.006167	9.81E-06	-0.018105	0.004561	7.27E-05	2.13E-08	0.231493	
6	HMG1A *	rs2797963	34,217,972	C	T	0.104788	-0.019657	0.003333	9.30E-10	-0.027552	0.005658	1.14E-06	-0.01626	0.004174	9.89E-05	3.60E-09	0.10829	
6	HMG1A *	rs2797964	34,217,978	C	T	0.109912	-0.018179	0.003264	9.90E-09	-0.026352	0.005545	2.05E-06	-0.014551	0.004086	0.000372	2.20E-08	0.086681	
6	HMG1A *	rs147929923	34,217,995	C	T	0.083869	-0.02071	0.003682	4.20E-09	-0.027973	0.006241	7.50E-06	-0.017843	0.004616	0.000112	2.47E-08	0.19187	
6	HMG1A *	rs9469745	34,220,690	G	A	0.110032	-0.018163	0.003252	8.60E-09	-0.025567	0.005523	3.72E-06	-0.014873	0.004073	0.000263	2.82E-08	0.119145	
6	HMG1A *	rs12214804	34,221,089	C	T	0.10865	-0.018976	0.003288	2.30E-09	-0.026154	0.005582	2.83E-06	-0.01589	0.004118	0.000115	1.00E-08	0.138937	
6	HMG1A *	rs10947487	34,221,835	A	G	0.093389	-0.020102	0.003495	1.60E-09	-0.026586	0.005923	7.26E-06	-0.01749	0.004381	6.61E-05	1.46E-08	0.216932	
6	HMG1A *	rs77510989	34,223,158	G	A	0.088795	-0.019584	0.003581	9.20E-09	-0.025451	0.00607	2.79E-05	-0.017318	0.00449	0.000116	8.94E-08	0.28138	
6	HMG1A *	rs7753429	34,224,101	C	G	0.093322	-0.020095	0.003497	1.60E-09	-0.026334	0.005924	8.91E-06	-0.01761	0.004384	5.97E-05	1.61E-08	0.236542	
6	HMG1A *	rs117525671	34,224,197	T	C	0.086107	-0.020444	0.003629	2.60E-09	-0.026726	0.006148	1.40E-05	-0.018059	0.00445	7.28E-05	2.99E-08	0.257122	
6	HMG1A *	rs1776899	34,225,453	G	A	0.093322	-0.020095	0.003497	1.60E-09	-0.026334	0.005924	8.91E-06	-0.01761	0.004384	5.97E-05	1.61E-08	0.236542	
6	HMG1A *	rs1776898	34,226,315	C	T	0.110002	-0.018014	0.003253	1.20E-08	-0.025445	0.005523	4.14E-06	-0.014684	0.004073	0.000315	3.70E-08	0.116823	
6	HMG1A *	rs1759645	34,227,089	C	T	0.113722	-0.017747	0.003204	2.40E-08	-0.024622	0.005449	6.32E-06	-0.014209	0.004009	0.000396	6.90E-08	0.123728	
6	HMG1A *	rs1776897	34,227,234	G	T	0.111197	-0.017679	0.003234	1.60E-08	-0.024573	0.005494	7.83E-06	-0.014604	0.004049	0.000312	6.77E-08	0.144058	
6	HMG1A *	rs1759646	34,227,670	C	T	0.110399	-0.01794	0.003247	1.30E-08	-0.025047	0.005517	5.72E-06	-0.014853	0.004065	0.00026	4.22E-08	0.136844	
6	HMG1A *	rs148811065	34,228,788	T	C	0.086122	-0.020393	0.003628	2.90E-09	-0.02656	0.006149	1.58E-05	-0.018069	0.004549	7.19E-05	3.32E-08	0.266894	
6	HMG1A *	rs1759627	34,229,328	C	T	0.113091												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
6	C6orf1 *	rs147736074	34,254,817	C	G	0.092965	-0.018988	0.003506	2.40E-09	-0.025772	0.00594	1.45E-05	-0.017753	0.004396	5.45E-05	2.35E-08	0.277867	
6	C6orf1 *	rs9366846	34,255,162	A	G	0.111989	-0.018051	0.003231	1.30E-08	-0.024805	0.005493	6.40E-06	-0.015076	0.004044	0.000194	3.58E-08	0.153727	
6	C6orf1 *	rs9348936	34,255,453	T	C	0.095255	-0.019213	0.00347	7.70E-09	-0.024856	0.00588	2.40E-05	-0.017118	0.00435	8.40E-05	5.72E-08	0.29008	
6	C6orf1 *	rs9394202	34,256,234	A	G	0.093546	-0.020173	0.003503	1.40E-09	-0.025469	0.00593	1.77E-05	-0.018301	0.004393	3.14E-05	1.69E-08	0.331396	
6	C6orf1 *	rs9469750	34,256,257	T	C	0.092931	-0.020053	0.003507	1.90E-09	-0.025791	0.005942	1.44E-05	-0.017949	0.004398	4.52E-05	1.96E-08	0.288801	
6	C6orf1 *	rs9461968	34,256,389	T	G	0.092849	-0.020231	0.00351	1.50E-09	-0.025511	0.005946	1.80E-05	-0.018403	0.004401	2.93E-05	1.61E-08	0.336581	
6	C6orf1 *	rs9461969	34,256,491	A	C	0.093138	-0.020005	0.003504	1.80E-09	-0.025543	0.005936	1.71E-05	-0.018092	0.004394	3.87E-05	1.98E-08	0.313035	
6	C6orf1 *	rs9368804	34,256,532	C	A	0.112413	-0.018303	0.003232	7.60E-09	-0.024615	0.005493	7.53E-06	-0.015559	0.004045	0.000121	2.67E-08	0.184304	
6	C6orf1 *	rs2780216	34,256,769	G	A	0.09322	-0.020018	0.003505	1.90E-09	-0.025465	0.005938	1.82E-05	-0.018049	0.004395	4.06E-05	2.21E-08	0.315504	
6	C6orf1 *	rs2797967	34,257,060	T	C	0.112211	-0.01807	0.003229	1.20E-08	-0.024555	0.005488	7.78E-06	-0.015257	0.004041	0.000161	3.61E-08	0.1725	
6	C6orf1 *	rs9368805	34,257,298	G	C	0.094853	-0.02076	0.00349	4.70E-10	-0.025632	0.005908	1.45E-05	-0.019253	0.004378	1.11E-05	5.38E-09	0.385705	
6	C6orf1 *	rs9394204	34,257,492	C	T	0.112207	-0.018048	0.003229	1.20E-08	-0.024538	0.005488	7.89E-06	-0.015227	0.004041	0.000166	3.77E-08	0.171891	
6	C6orf1 *	rs13201774	34,257,707	G	C	0.093165	-0.020072	0.003504	1.80E-09	-0.025486	0.005936	1.78E-05	-0.018158	0.004395	3.64E-05	1.95E-08	0.321046	
6	C6orf1 *	rs13217823	34,257,826	T	A	0.10749	-0.018162	0.0033	8.60E-09	-0.024924	0.005595	8.51E-06	-0.015312	0.004136	0.000215	5.17E-08	0.167098	
6	C6orf1 *	rs10947491	34,257,829	T	A	0.093349	-0.019875	0.003504	2.30E-09	-0.025407	0.005936	1.89E-05	-0.017873	0.004393	4.79E-05	2.68E-08	0.307582	
6	C6orf1 *	rs2483211	34,258,154	T	C	0.112194	-0.018033	0.003229	1.30E-08	-0.024531	0.005488	7.94E-06	-0.015205	0.004042	0.00017	3.88E-08	0.171192	
6	C6orf1 *	rs7761883	34,259,149	T	C	0.093131	-0.020119	0.003504	1.60E-09	-0.025699	0.005938	1.52E-05	-0.018118	0.004394	3.77E-05	1.74E-08	0.304723	
6	C6orf1 *	rs73419191	34,259,832	C	T	0.093132	-0.020124	0.003504	1.60E-09	-0.025699	0.005938	1.52E-05	-0.018125	0.004394	3.74E-05	1.73E-08	0.305202	
6	C6orf1 *	rs3997803	34,260,907	G	A	0.096325	-0.02007	0.003454	1.70E-09	-0.026179	0.005862	8.09E-06	-0.017743	0.004327	4.18E-05	1.04E-08	0.246923	
6	C6orf1 *	rs7768482	34,260,983	T	A	0.096325	-0.02007	0.003454	1.70E-09	-0.026179	0.005862	8.09E-06	-0.017743	0.004327	4.18E-05	1.04E-08	0.246923	
6	C6orf1 *	rs9394205	34,262,254	C	G	0.096748	-0.020377	0.003451	9.10E-10	-0.026748	0.005858	5.04E-06	-0.017935	0.004323	3.38E-05	5.44E-09	0.226053	
6	C6orf1 *	rs7470907	34,262,666	C	G	0.09303	-0.020266	0.003506	1.20E-09	-0.025845	0.005939	1.37E-05	-0.018245	0.004396	3.36E-05	1.41E-08	0.303679	
6	C6orf1 *	rs6457769	34,263,793	C	T	0.096312	-0.019993	0.003455	2.00E-09	-0.026173	0.005863	8.14E-06	-0.017598	0.004328	4.82E-05	1.20E-08	0.239265	
6	C6orf1 *	rs4713762	34,263,884	A	G	0.093022	-0.020133	0.003506	1.60E-09	-0.025761	0.00594	1.46E-05	-0.018058	0.004396	4.04E-05	1.78E-08	0.297171	
6	C6orf1 *	rs4713763	34,263,887	A	G	0.096312	-0.019993	0.003455	2.00E-09	-0.026173	0.005863	8.14E-06	-0.017598	0.004328	4.82E-05	1.20E-08	0.239265	
6	C6orf1 *	rs4713764	34,264,114	C	T	0.096312	-0.019993	0.003455	2.00E-09	-0.026173	0.005863	8.14E-06	-0.017598	0.004328	4.82E-05	1.20E-08	0.239265	
6	C6orf1 *	rs4713765	34,264,346	T	C	0.096317	-0.019986	0.003455	2.00E-09	-0.026171	0.005863	8.15E-06	-0.017586	0.004328	4.88E-05	1.22E-08	0.238683	
6	C6orf1 *	rs148899910	34,264,482	C	G	0.093027	-0.020133	0.003506	1.60E-09	-0.025759	0.00594	1.47E-05	-0.018053	0.004396	4.06E-05	1.80E-08	0.297025	
6	C6orf1 *	rs12530053	34,264,564	C	T	0.096323	-0.019983	0.003455	2.00E-09	-0.026168	0.005863	8.18E-06	-0.01758	0.004328	4.91E-05	1.23E-08	0.238538	
6	C6orf1 *	rs7765484	34,265,150	T	A	0.093988	-0.019747	0.003502	3.90E-09	-0.025886	0.005944	1.35E-05	-0.017201	0.004387	8.90E-05	3.49E-08	0.239724	
6	C6orf1 *	rs1573905	34,265,675	G	A	0.093133	-0.020042	0.003505	1.90E-09	-0.025683	0.005938	1.55E-05	-0.017961	0.004394	4.41E-05	2.04E-08	0.295872	
6	C6orf1 *	rs9469758	34,265,986	C	A	0.093131	-0.020049	0.003505	1.90E-09	-0.025683	0.005938	1.55E-05	-0.017966	0.004394	4.39E-05	2.04E-08	0.296195	
6	C6orf1 *	rs73420913	34,266,243	A	C	0.09313	-0.020048	0.003505	1.90E-09	-0.025677	0.005938	1.55E-05	-0.017966	0.004394	4.39E-05	2.04E-08	0.296551	
6	C6orf1 *	rs6090030	34,267,462	T	C	0.096573	-0.020068	0.00345	1.70E-09	-0.026032	0.005856	8.91E-06	-0.017702	0.004322	4.25E-05	1.17E-08	0.252434	
6	C6orf1 *	rs6899897	34,267,480	C	A	0.096573	-0.020068	0.00345	1.70E-09	-0.026032	0.005856	8.91E-06	-0.017702	0.004322	4.25E-05	1.17E-08	0.252434	
6	C6orf1 *	rs6922851	34,267,515	C	T	0.096573	-0.02007	0.00345	1.70E-09	-0.026032	0.005856	8.91E-06	-0.017705	0.004322	4.24E-05	1.16E-08	0.252582	
6	C6orf1 *	rs6900387	34,267,630	T	C	0.096366	-0.020033	0.003455	2.00E-09	-0.026301	0.005865	7.41E-06	-0.017553	0.004327	5.02E-05	1.15E-08	0.229976	
6	NUDT3 *	rs9469761	34,268,652	A	G	0.096566	-0.020089	0.003451	1.70E-09	-0.026165	0.005857	8.03E-06	-0.017666	0.004322	4.41E-05	1.09E-08	0.242921	
6	NUDT3 *	rs9469762	34,268,653	A	G	0.084796	-0.020902	0.003664	1.90E-09	-0.026776	0.006215	1.67E-05	-0.01883	0.004591	4.15E-05	2.07E-08	0.303757	
6	NUDT3 *	rs9461975	34,268,682	T	C	0.096566	-0.020089	0.003451	1.70E-09	-0.026165	0.005857	8.03E-06	-0.017666	0.004322	4.41E-05	1.09E-08	0.242921	
6	NUDT3 *	rs2780215	34,269,196	G	A	0.082726	-0.020993	0.003719	2.60E-09	-0.026824	0.006311	2.16E-05	-0.019175	0.004659	3.90E-05	2.51E-08	0.32951	
6	NUDT3 *	rs186766320	34,269,213	A	G	0.082162	-0.020422	0.003722	6.60E-09	-0.026448	0.006318	2.87E-05	-0.018505	0.004662	7.27E-05	5.92E-08	0.311668	
6	NUDT3 *	rs1759637	34,269,353	C	T	0.111166	-0.01999	0.003248	2.50E-10	-0.024583	0.005525	8.74E-06	-0.018136	0.004063	8.15E-06	2.37E-09	0.347184	
6	NUDT3 *	rs1690799	34,269,619	T	C	0.097896	-0.020209	0.003428	1.10E-09	-0.02539	0.005826	1.33E-05	-0.018153	0.004291	2.36E-05	9.77E-09	0.31778	
6	NUDT3 *	rs1776891	34,269,844	A	G	0.085155	-0.020732	0.003651	2.20E-09	-0.026539	0.006186	1.81E-05	-0.018752	0.004577	4.23E-05	2.28E-08	0.311571	
6	NUDT3 *	rs1776890	34,269,970	G	A	0.097923	-0.020273	0.003428	9.40E-10	-0.025477	0.005826	1.24E-05	-0.018202	0.00429	2.23E-05	8.68E-09	0.314661	
6	NUDT3 *	rs2797961	34,270,020	G	A	0.115341	-0.0192	0.00319	9.30E-10	-0.023949	0.005427	1.03E-05	-0.017195	0.00399	1.66E-05	5.47E-09	0.316006	
6	NUDT3 *	rs6918981	34,270,737	G	A	0.118243	-0.018288	0.003151	4.20E-09	-0.022408	0.005365	2.99E-05	-0.016492	0.00394	2.87E-05	0.374065	0.340563	
6	NUDT3 *	rs13207853	34,271,169	C	T	0.110449	-0.018694	0.003251	6.00E-09	-0.023191	0.005535	2.83E-05	-0.01671	0.004066	4.00E-05	3.32E-08	0.345342	
6	NUDT3 *	rs60952447	34,271,383	A	G	0.085741	-0.020104	0.003638	7.00E-09	-0.024789	0.006165	5.86E-05	-0.01856	0.004561	4.76E-05	7.82E-08	0.416663	
6	NUDT3 *	rs1187130	34,271,696	G	A	0.104948	-0.018413	0.003329	1.90E-08	-0.0234	0.005654	3.53E-05	-0.016458	0.004168	7.93E-05	7.84E-08	0.322993	
6	NUDT3 *	rs1187129	34,272,212	A	G	0.084322	-0.019415	0.003681	2.90E-08	-0.024254	0.006237	0.000102	-0.01807	0.004616	9.13E-05	2.45E-07	0.4255	
6	NUDT3 *	rs1307274	34,272,799	T	G	0.101464	-0.018236	0.003396	3.10E-08	-0.023204	0.00576	5.67E-05	-0.016608	0.004256	9.63E-05	1.48E-07	0.357002	
6	NUDT3 *	rs1307273	34,273,109	G	A	0.119212	-0.017937	0.003171	1.00E-08	-0.022293	0.00539	3.57E-05	-0.016407	0.003968	3.60E-05	3.74E-08	0.379136	
6	VEGFA *	rs79469752	43,770,044	T	C	0.059193	-0.024285	0.004368	2.30E-08	-0.031672	0.007347	1.65E-05	-0.019662	0.005	0.000352	1.55E-07	0.190661	
6	VEGFA *	rs4711750	43,789,345	T	A	0.437178	-0.019321	0.002032	1.30E-22	-0.019069	0.003446	3.21E-08	-0.01975	0.002546	9.15E-15	1.93E-20	0.873772	
6	VEGFA *	rs998584	43,790,159	C	A	0.443724	-0.019214	0.002										

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
6	GSTA2	rs2749012	52,762,252	C	G	0.110378	0.017774	0.003221	3.20E-08	0.00818	0.005465	0.134432	0.021724	0.004037	7.54E-08	1.68E-07	0.046219	F
6	GSTA2	rs2749013	52,762,367	A	G	0.110378	0.017774	0.003221	3.20E-08	0.00818	0.005465	0.134432	0.021724	0.004037	7.54E-08	1.68E-07	0.046219	F
6	GSTA2	rs2749014	52,762,524	G	A	0.110378	0.017774	0.003221	3.20E-08	0.00818	0.005465	0.134432	0.021724	0.004037	7.54E-08	1.68E-07	0.046219	F
6	GSTA2	rs2070774	52,763,237	C	T	0.110378	0.017774	0.003221	3.20E-08	0.00818	0.005465	0.134432	0.021724	0.004037	7.54E-08	1.68E-07	0.046219	F
6	GSTA2 *	rs2749019	52,763,753	A	G	0.110385	0.017793	0.003221	3.10E-08	0.008206	0.005464	0.13314	0.021724	0.004037	7.54E-08	1.66E-07	0.046613	F
6	GSTA2 *	rs4715316	52,764,200	C	T	0.11063	0.017845	0.003221	2.80E-08	0.008229	0.005462	0.131908	0.021852	0.004037	6.36E-08	1.40E-07	0.044903	F
6	GSTA2 *	rs4715317	52,764,212	T	G	0.110385	0.017793	0.003221	3.10E-08	0.008206	0.005464	0.13314	0.021724	0.004037	7.54E-08	1.66E-07	0.046613	F
6	GSTA2 *	rs6458868	52,765,355	C	T	0.110392	0.017838	0.003221	2.80E-08	0.00824	0.005464	0.131516	0.021782	0.004036	6.96E-08	1.52E-07	0.046221	F
6	GSTA2 *	rs6458869	52,765,471	C	A	0.110392	0.017838	0.003221	2.80E-08	0.00824	0.005464	0.131516	0.021782	0.004036	6.96E-08	1.52E-07	0.046221	F
6	GSTA2 *	rs2749024	52,765,789	T	A	0.110395	0.01784	0.003221	2.80E-08	0.008248	0.005464	0.131121	0.021782	0.004036	6.96E-08	1.52E-07	0.046349	F
6	GSTA2 *	rs2749026	52,765,837	A	G	0.110395	0.01784	0.003221	2.80E-08	0.008248	0.005464	0.131121	0.021782	0.004036	6.96E-08	1.52E-07	0.046349	F
6	GSTA2 *	rs2749029	52,766,390	A	G	0.110403	0.017828	0.003221	2.90E-08	0.008248	0.005464	0.131121	0.021761	0.004036	7.15E-08	1.56E-07	0.046682	F
6	GSTA2 *	rs2608639	52,767,415	C	T	0.110469	0.017915	0.003221	2.50E-08	0.008168	0.005464	0.134905	0.021956	0.004037	5.49E-08	1.23E-07	0.042418	F
6	GSTA2 *	rs2749035	52,769,135	G	A	0.110363	0.017835	0.003221	2.90E-08	0.008262	0.005466	0.130643	0.021739	0.004036	7.37E-08	1.60E-07	0.047349	F
6	GSTA2 *	rs4715318	52,770,533	T	C	0.110377	0.017774	0.003221	3.20E-08	0.008133	0.005466	0.136761	0.021709	0.004035	7.63E-08	1.72E-07	0.045725	F
6	GSTA2 *	rs9395816	52,772,796	A	G	0.110415	0.017832	0.003221	3.00E-08	0.008177	0.005467	0.134708	0.021739	0.004036	7.34E-08	1.63E-07	0.04597	F
6	GSTA2 *	rs2608644	52,775,315	A	C	0.110484	0.01774	0.003219	3.30E-08	0.008314	0.005463	0.128029	0.021511	0.004033	9.83E-08	2.09E-07	0.05197	
6	GSTA2 *	rs9357746	52,776,573	T	C	0.1104	0.017911	0.003221	2.50E-08	0.008076	0.005467	0.139593	0.021947	0.004035	5.48E-08	1.27E-07	0.041212	F
6	GSTA2 *	rs9395817	52,777,044	C	T	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs2608652	52,777,970	C	T	0.110408	0.017817	0.003221	3.00E-08	0.008204	0.005466	0.133368	0.021724	0.004034	7.42E-08	1.64E-07	0.046582	F
6	GSTA1 *	rs9395819	52,779,189	G	C	0.109828	0.017845	0.00323	3.00E-08	0.008739	0.005483	0.110963	0.021493	0.004046	1.11E-07	2.09E-07	0.061235	
6	GSTA1 *	rs2608653	52,779,558	A	T	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs9382138	52,781,312	A	T	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs9382139	52,782,746	G	A	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs2608659	52,782,862	T	G	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs9367495	52,783,308	G	A	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs9474321	52,783,479	C	T	0.110375	0.017774	0.003221	3.20E-08	0.008137	0.005466	0.136594	0.021707	0.004035	7.65E-08	1.72E-07	0.045809	F
6	GSTA1 *	rs1072340	52,783,930	C	T	0.11001	0.017561	0.003227	4.90E-08	0.007708	0.005479	0.159423	0.021567	0.004043	9.77E-08	2.45E-07	0.041829	F
6	GSTA1 *	rs1075181	52,784,046	A	G	0.110036	0.017555	0.003228	4.90E-08	0.007667	0.005479	0.161692	0.021596	0.004043	9.43E-08	2.40E-07	0.040831	F
6	GSTA1 *	rs1072341	52,784,108	T	A	0.109982	0.017564	0.003228	4.90E-08	0.007638	0.00548	0.163388	0.021608	0.004043	9.26E-08	2.37E-07	0.040238	F
6	GSTA1 *	rs2608664	52,784,186	C	A	0.109982	0.017564	0.003228	4.90E-08	0.007638	0.00548	0.163388	0.021608	0.004043	9.26E-08	2.37E-07	0.040238	F
6	GSTA1 *	rs9395820	52,784,209	A	T	0.109982	0.017564	0.003228	4.90E-08	0.007638	0.00548	0.163388	0.021608	0.004043	9.26E-08	2.37E-07	0.040238	F
6	GSTA1 *	rs4715322	52,784,411	C	G	0.109979	0.017584	0.003228	4.70E-08	0.007638	0.00548	0.163388	0.021635	0.004043	8.93E-08	2.29E-07	0.039855	F
6	GSTA1 *	rs4715325	52,785,466	A	T	0.109973	0.017583	0.003228	4.70E-08	0.007638	0.00548	0.163388	0.021637	0.004043	8.92E-08	2.29E-07	0.039841	F
6	GSTA1 *	rs2608668	52,785,724	A	G	0.109973	0.017583	0.003228	4.70E-08	0.007638	0.00548	0.163388	0.021637	0.004043	8.92E-08	2.29E-07	0.039841	F
6	GSTA1 *	rs62407587	52,787,305	T	C	0.109966	0.017574	0.003228	4.80E-08	0.007625	0.005481	0.164178	0.021639	0.004043	8.89E-08	2.29E-07	0.03964	F
6	GSTA1 *	rs6458870	52,787,363	T	A	0.109966	0.017574	0.003228	4.80E-08	0.007625	0.005481	0.164178	0.021639	0.004043	8.89E-08	2.29E-07	0.03964	F
6	GSTA1 *	rs1986661	52,787,542	C	T	0.109966	0.017574	0.003228	4.80E-08	0.007625	0.005481	0.164178	0.021639	0.004043	8.89E-08	2.29E-07	0.03964	F
6	GSTA1 *	rs2397104	52,787,795	A	C	0.109966	0.017574	0.003228	4.80E-08	0.007625	0.005481	0.164178	0.021639	0.004043	8.89E-08	2.29E-07	0.03964	F
6	GSTA1 *	rs2397105	52,788,526	G	A	0.109963	0.017558	0.003228	4.90E-08	0.007625	0.005481	0.164178	0.021614	0.004043	9.21E-08	2.37E-07	0.040003	F
6	GSTA1 *	rs4715332	52,804,387	C	A	0.110275	0.01752	0.003222	4.30E-08	0.008159	0.005474	0.136035	0.021196	0.004035	1.52E-07	3.35E-07	0.055228	
6	RG517	rs3910736	153,091,341	C	T	0.324224	-0.011123	0.002151	2.80E-08	-0.004436	0.00365	0.224194	-0.014677	0.002695	5.30E-08	1.74E-07	0.024027	F
6	RG517	rs3910737	153,091,342	A	G	0.323318	-0.011217	0.002152	2.10E-08	-0.004508	0.00365	0.216889	-0.014779	0.002696	4.33E-08	1.40E-07	0.023643	F
6	RG517	rs9371672	153,101,005	C	G	0.320653	-0.011355	0.002162	1.50E-08	-0.005402	0.003668	0.140859	-0.014568	0.002708	7.66E-08	1.76E-07	0.044436	F
6	RG517	rs6557271	153,116,600	T	C	0.311552	-0.010989	0.00217	4.60E-08	-0.004917	0.00368	0.181419	-0.014336	0.002719	1.37E-07	3.76E-07	0.039551	F
7	MIR148A *	rs12672425	25,900,103	G	T	0.423497	-0.011937	0.002075	8.90E-09	-0.016752	0.003531	2.12E-06	-0.008496	0.002597	0.001077	6.15E-08	0.05965	
7	MIR148A *	rs4722555	25,973,632	C	T	0.442848	0.01118	0.002031	3.10E-08	0.00631	0.00346	0.068196	0.01396	0.002541	4.02E-08	5.28E-08	0.074716	
7	MIR148A *	rs6970673	25,975,022	T	C	0.440496	0.011157	0.002032	2.70E-08	0.006397	0.00346	0.064457	0.013927	0.002543	4.42E-08	5.53E-08	0.079474	
7	MIR148A *	rs28537499	25,975,772	C	A	0.440959	0.011193	0.002032	2.40E-08	0.00651	0.003459	0.05984	0.013919	0.002542	4.49E-08	5.28E-08	0.084393	
7	MIR148A *	rs2893237	25,998,964	G	A	0.462307	0.011439	0.002035	2.40E-08	0.007101	0.003455	0.039839	0.013688	0.00255	8.13E-08	6.68E-08	0.125016	
7	MIR148A *	rs4722562	25,999,068	T	C	0.462308	0.011439	0.002035	2.40E-08	0.0071	0.003455	0.039875	0.013688	0.00255	8.13E-08	6.68E-08	0.124941	
7	MIR148A *	rs6461905	26,000,782	T	C	0.461985	0.011471	0.002033	2.00E-08	0.007029	0.003453	0.041804	0.013792	0.002548	6.31E-08	5.44E-08	0.114985	
7	MIR148A *	rs58292232	26,001,109	G	T	0.462016	0.011455	0.002033	2.10E-08	0.006965	0.003453	0.043685	0.01381	0.002548	6.07E-08	5.44E-08	0.110651	
7	MIR148A *	rs12112544	26,002,259	G	A	0.462952	0.011383	0.002032	2.70E-08	0.007112	0.00345	0.039296	0.013597	0.002547	9.54E-08	7.71E-08	0.130455	
7	MIR148A *	rs12112549	26,002,308	G	A	0.462952	0.011383	0.002032	2.70E-08	0.007112	0.00345	0.039302	0.013597	0.002547	9.53E-08	7.71E-08	0.130429	
7	MIR148A *	rs6979761	26,002,804	C	T	0.464711	0.011529	0.002032	1.80E-08	0.007144	0.003448	0.038278	0.013806	0.002546	6.03E-08	4.83E-08	0.12011	
7	MIR148A *	rs6959733	26,002,919	T	C	0.												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
7	NFE2L3 *	rs9639528	26,080,958	T	C	0.496588	0.012755	0.002033	5.50E-10	0.009525	0.003448	0.005758	0.013681	0.00255	8.23E-08	1.23E-08	0.332476	
7	NFE2L3 *	rs7805293	26,081,178	C	A	0.496227	0.012626	0.002034	7.20E-10	0.009345	0.00345	0.006765	0.013648	0.00255	8.90E-08	1.54E-08	0.315896	
7	NFE2L3 *	rs2391223	26,082,321	A	G	0.495666	0.012473	0.002031	1.10E-09	0.008834	0.003445	0.010358	0.01364	0.002547	8.70E-08	2.20E-08	0.261868	
7	POLD2	rs2075070	44,115,653	G	A	0.261616	-0.013482	0.002348	4.70E-09	-0.014286	0.003981	0.000335	-0.013657	0.002944	3.56E-06		0.9899	
7	POLD2	rs3087367	44,116,547	A	G	0.261401	-0.013233	0.002348	1.00E-08	-0.014068	0.003979	0.00041	-0.013424	0.002945	5.22E-06		0.986357	
7	POLD2	rs3217964	44,118,226	C	T	0.238828	-0.014765	0.002406	3.70E-10	-0.01415	0.004079	0.000526	-0.015775	0.003016	1.73E-07		0.748881	
7	POLD2	rs3217962	44,118,379	G	A	0.262303	-0.013306	0.00234	6.70E-09	-0.013913	0.003968	0.000457	-0.013538	0.002933	3.99E-06		0.939385	
7	POLD2	rs3087370	44,122,210	G	A	0.234617	-0.014681	0.002409	4.70E-10	-0.014242	0.004091	0.000502	-0.015566	0.003019	2.57E-07		0.794487	
7	POLD2 *	rs3217944	44,124,463	A	C	0.234787	-0.014842	0.002405	2.90E-10	-0.014052	0.004087	0.000589	-0.015802	0.003012	1.59E-07		0.730388	
7	POLD2 *	rs3217943	44,124,492	C	T	0.235238	-0.01483	0.002403	2.80E-10	-0.014072	0.004083	0.000572	-0.015817	0.003011	1.52E-07		0.730847	
7	POLD2 *	rs113784062	44,126,070	T	C	0.235192	-0.014899	0.002403	2.40E-10	-0.014251	0.004083	0.000485	-0.015784	0.003009	1.60E-07		0.762574	
7	POLD2 *	rs12538223	44,127,298	G	A	0.23542	-0.014406	0.002399	7.10E-10	-0.013806	0.004077	0.000714	-0.015311	0.003004	3.52E-07		0.766357	
7	POLD2 *	rs12535289	44,129,230	G	A	0.235909	-0.014259	0.002392	8.60E-10	-0.013883	0.004067	0.000645	-0.015038	0.002995	5.25E-07		0.819135	
7	POLD2 *	rs55907525	44,129,790	C	G	0.232452	-0.014697	0.002407	3.50E-10	-0.015048	0.004094	0.000239	-0.015212	0.003013	4.55E-07		0.974173	
7	POLD2 *	rs1776956	44,129,973	C	A	0.23598	-0.014388	0.002391	6.20E-10	-0.013985	0.004066	0.000586	-0.015175	0.002994	4.08E-07		0.81381	
7	POLD2 *	rs56902462	44,130,156	A	G	0.235366	-0.01434	0.002393	8.10E-10	-0.013651	0.004069	0.000799	-0.015257	0.002996	3.62E-07		0.750529	
7	POLD2 *	rs12531534	44,130,798	T	C	0.236125	-0.014315	0.00239	7.60E-10	-0.013811	0.004063	0.00068	-0.015144	0.002992	4.23E-07		0.791609	
7	MYL7 *	rs17831589	44,133,526	A	G	0.236098	-0.014001	0.002388	1.50E-09	-0.013708	0.004061	0.000741	-0.014692	0.002989	9.02E-07		0.845622	
7	MYL7 *	rs62460070	44,134,541	T	C	0.236447	-0.014312	0.002384	5.90E-10	-0.013733	0.004055	0.000712	-0.015102	0.002984	4.25E-07		0.785728	
7	MYL7 *	rs4397301	44,135,828	G	C	0.237991	-0.014177	0.002376	6.60E-10	-0.013531	0.004043	0.000823	-0.014977	0.002973	4.82E-07		0.773315	
7	MYL7 *	rs9791709	44,136,188	T	C	0.238322	-0.014476	0.002374	2.60E-10	-0.013839	0.00404	0.000618	-0.01526	0.00297	2.83E-07		0.776837	
7	MYL7 *	rs17136076	44,137,592	G	A	0.240101	-0.014509	0.002369	2.50E-10	-0.013897	0.004037	0.000581	-0.015191	0.002962	2.99E-07		0.796154	
7	MYL7 *	rs17769733	44,137,813	T	C	0.239837	-0.014586	0.00237	2.10E-10	-0.013885	0.004039	0.00059	-0.01533	0.002964	2.36E-07		0.772984	
7	MYL7 *	rs882021	44,138,273	C	T	0.242142	-0.014278	0.002364	4.30E-10	-0.013423	0.004027	0.000862	-0.015112	0.002957	3.27E-07		0.73529	
7	MYL7	rs1008384	44,139,027	G	A	0.257063	-0.01334	0.002343	3.30E-09	-0.010804	0.003987	0.006742	-0.015117	0.002933	2.59E-07		0.835514	
7	MYL7	rs741033	44,140,166	G	C	0.25483	-0.014795	0.002375	1.50E-10	-0.014816	0.004035	0.000242	-0.015458	0.002976	2.10E-07		0.89812	
7	GCK	rs270971	44,157,984	T	G	0.256031	0.014952	0.002362	3.70E-10	0.011392	0.00401	0.004513	0.01715	0.00296	7.09E-09		0.248042	
7	GCK	rs1799831	44,159,543	T	C	0.256496	0.014705	0.002358	6.60E-10	0.011203	0.004001	0.005131	0.01686	0.002956	1.20E-08		0.255438	
7	GCK	rs62460075	44,161,550	T	C	0.211907	-0.018048	0.002526	2.20E-13	-0.017829	0.004298	3.38E-05	-0.018658	0.003161	3.70E-09		0.876619	
7	GCK	rs12540369	44,165,915	A	A	0.23361	-0.018507	0.002387	1.10E-15	-0.017255	0.004054	2.10E-05	-0.019883	0.002991	3.09E-11		0.601965	
7	GCK	rs12535229	44,166,006	A	G	0.233614	-0.018499	0.002387	1.20E-15	-0.017227	0.004054	2.17E-05	-0.019883	0.002991	3.09E-11		0.598069	
7	GCK	rs2971672	44,166,307	C	A	0.458761	0.014597	0.002025	6.30E-13	0.010393	0.003444	0.002555	0.017649	0.002535	3.47E-12		0.08969	
7	GCK	rs62460076	44,166,795	A	T	0.233496	-0.018402	0.002389	1.60E-15	-0.016925	0.004056	3.04E-05	-0.019871	0.002993	3.26E-11		0.559015	
7	GCK	rs62460077	44,167,083	T	C	0.233621	-0.018491	0.002387	1.20E-15	-0.017213	0.004054	2.20E-05	-0.019873	0.002991	3.17E-11		0.597557	
7	GCK	rs73112269	44,168,408	A	G	0.233789	-0.01848	0.002386	1.20E-15	-0.017042	0.004052	2.63E-05	-0.019936	0.00299	2.68E-11		0.565499	
7	GCK	rs16881016	44,171,808	C	T	0.235174	-0.018444	0.00238	1.50E-15	-0.016718	0.004041	3.55E-05	-0.02	0.002982	2.06E-11		0.513484	
7	GCK	rs112745774	44,172,019	T	C	0.234796	-0.018418	0.002382	1.80E-15	-0.016886	0.004044	3.00E-05	-0.019863	0.002985	2.94E-11		0.553672	
7	GCK	rs60275913	44,172,686	T	G	0.234998	-0.018329	0.002381	2.40E-15	-0.016595	0.004042	4.08E-05	-0.019875	0.002983	2.80E-11		0.513759	
7	GCK	rs59419319	44,174,275	T	C	0.235942	-0.018834	0.002378	4.80E-16	-0.017271	0.004036	1.90E-05	-0.020266	0.002981	1.10E-11		0.550684	
7	GCK	rs3779606	44,175,415	C	T	0.236071	-0.018868	0.002377	4.10E-16	-0.017343	0.004034	1.74E-05	-0.02027	0.00298	1.07E-11		0.55957	
7	GCK	rs62460080	44,176,272	A	G	0.236077	-0.018876	0.002377	3.90E-16	-0.01736	0.004034	1.70E-05	-0.020271	0.00298	1.06E-11		0.561673	
7	GCK	rs17172566	44,176,513	A	G	0.236078	-0.018875	0.002377	3.90E-16	-0.017356	0.004034	1.71E-05	-0.020271	0.00298	1.06E-11		0.561039	
7	GCK	rs2908290	44,176,538	A	G	0.458149	0.015161	0.002024	6.90E-14	0.01069	0.003441	0.001902	0.018368	0.002533	4.32E-13		0.072389	
7	GCK	rs62459064	44,176,698	T	C	0.236066	-0.018902	0.002377	3.60E-16	-0.017413	0.004034	1.61E-05	-0.020282	0.00298	1.03E-11		0.56731	
7	GCK	rs2284777	44,176,999	C	T	0.235786	-0.018767	0.002379	5.40E-16	-0.01723	0.004036	1.99E-05	-0.020165	0.002982	1.41E-11		0.558761	
7	GCK	rs2284775	44,177,762	G	A	0.2362	-0.018887	0.002377	4.00E-16	-0.017039	0.004035	2.44E-05	-0.020437	0.002979	7.17E-12		0.498102	
7	GCK	rs2284774	44,178,742	A	G	0.236171	-0.018843	0.002377	4.70E-16	-0.01699	0.004035	2.58E-05	-0.020395	0.00298	7.97E-12		0.497321	
7	GCK	rs2300587	44,179,195	C	T	0.236176	-0.018836	0.002377	4.80E-16	-0.016985	0.004035	2.59E-05	-0.02039	0.00298	8.05E-12		0.497236	
7	GCK	rs12534104	44,180,143	A	C	0.226616	-0.019493	0.002448	2.50E-16	-0.018085	0.004415	1.33E-05	-0.021064	0.003071	7.19E-12		0.563987	
7	GCK	rs1990458	44,183,203	T	C	0.320284	-0.013247	0.002201	2.50E-09	-0.009546	0.003734	0.010582	-0.015259	0.002759	3.25E-08		0.64E-09	
7	GCK	rs34780996	44,183,696	A	G	0.094142	-0.023126	0.003456	3.50E-11	-0.028452	0.005856	1.20E-06	-0.019992	0.004336	4.06E-06		0.2456	
7	GCK	rs59727929	44,183,959	T	C	0.094067	-0.023359	0.003458	2.20E-11	-0.028621	0.005857	1.04E-06	-0.020207	0.004338	3.25E-06		0.248288	
7	GCK	rs730497	44,184,122	A	G	0.196928	0.02181	0.002538	1.20E-17	0.022191	0.004319	2.84E-07	0.020298	0.003177	1.72E-10		0.724035	
7	GCK	rs2908289	44,184,343	A	G	0.196908	0.021777	0.002539	1.40E-17	0.022083	0.00432	3.26E-07	0.020323	0.003178	1.66E-10		0.742807	
7	GCK	rs3808319	44,185,252	A	G	0.3588	-0.013749	0.002108	4.00E-11	-0.008771	0.003578	0.014262	-0.01634	0.002642	6.42E-10		0.088838	
7	GCK	rs34859037	44,185,887	C	G	0.094206	-0.023375	0.003456	2.30E-11	-0.028844	0.005854	8.51E-07	-0.020117	0.004336	3.55E-06		0.230962	
7	GCK	rs34807880	44,186,230	G	A	0.094209	-0.023375	0.003456	2.30E-11	-0.028824	0.005854	8.64E-07	-0.020117	0.004336	3.55E-06		0.232005	
7	GCK	rs2268570	44,186,491	G	C	0.370187	-0.013555	0.002093	5.10E-11	-0.009113	0.003548	0.010226	-0.015918	0.002625	1.36E-09		0.123074	
7	GCK	rs2971670	44,186,502	T	C	0.19451	0.0021891	0.002557	1.70E-17	0.022147	0.004353	3.70E-07	0.020451	0.003199	1.67E-10		0.753577	
7	GCK																	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
7	GCK *	rs62459077	44,192,990	T	C	0.093477	-0.023206	0.003466	3.40E-11	-0.027948	0.005868	1.94E-06	-0.020303	0.004349	3.09E-06	2.20E-10	0.295218	
7	GCK *	rs7789273	44,193,006	T	C	0.370625	-0.013515	0.002093	4.40E-11	-0.008901	0.003549	0.01217	-0.015959	0.002625	1.23E-09	4.04E-10	0.109808	
7	GCK *	rs58053084	44,193,014	G	T	0.093513	-0.023144	0.003465	3.80E-11	-0.028176	0.005867	1.59E-06	-0.020139	0.004349	3.70E-06	2.16E-10	0.271062	
7	GCK *	rs741037	44,193,234	A	G	0.198166	-0.021923	0.002538	1.10E-17	0.02258	0.004319	1.75E-07	0.020247	0.003175	1.87E-10	1.73E-15	0.663449	
7	GCK *	rs62459079	44,193,279	T	C	0.093477	-0.023206	0.003466	3.40E-11	-0.027948	0.005868	1.94E-06	-0.020303	0.004349	3.09E-06	2.20E-10	0.295218	
7	GCK *	rs62459080	44,193,319	A	G	0.093477	-0.023206	0.003466	3.40E-11	-0.027948	0.005868	1.94E-06	-0.020303	0.004349	3.09E-06	2.20E-10	0.295218	
7	GCK *	rs735670	44,193,746	T	A	0.093477	-0.023206	0.003466	3.40E-11	-0.027948	0.005868	1.94E-06	-0.020303	0.004349	3.09E-06	2.20E-10	0.295218	
7	GCK *	rs35902302	44,194,829	A	C	0.093363	-0.023106	0.003468	3.90E-11	-0.027776	0.005871	2.27E-06	-0.020268	0.004354	3.29E-06	2.71E-10	0.304257	
7	GCK *	rs741036	44,195,114	A	G	0.09336	-0.023092	0.003469	4.00E-11	-0.027776	0.005871	2.27E-06	-0.020243	0.004354	3.38E-06	2.78E-10	0.302686	
7	GCK *	rs2908286	44,195,138	C	C	0.197834	0.021881	0.002537	1.00E-17	0.022103	0.004318	3.13E-07	0.020408	0.003175	1.33E-10	1.71E-15	0.751816	
7	YKT6 *	rs741034	44,195,261	T	C	0.09336	-0.023092	0.003469	4.00E-11	-0.027776	0.005871	2.27E-06	-0.020243	0.004354	3.38E-06	2.78E-10	0.302686	
7	YKT6 *	rs71533226	44,195,594	T	A	0.092416	-0.023333	0.003487	2.80E-11	-0.028126	0.005902	1.92E-06	-0.020288	0.004378	3.64E-06	2.54E-10	0.28617	
7	YKT6 *	rs4607517	44,196,069	A	G	0.197949	0.021786	0.002533	1.10E-17	0.021823	0.00431	4.21E-07	0.020512	0.00317	1.01E-10	2.21E-15	0.806589	
7	YKT6 *	rs55794846	44,196,764	G	C	0.093345	-0.023078	0.003469	4.10E-11	-0.027701	0.005872	2.43E-06	-0.020263	0.004354	3.31E-06	2.92E-10	0.308884	
7	YKT6 *	rs150486663	44,200,116	A	G	0.093329	-0.023142	0.00347	3.80E-11	-0.027734	0.005874	2.38E-06	-0.020354	0.004355	3.00E-06	2.60E-10	0.312864	
7	YKT6 *	rs1985469	44,200,725	T	A	0.19171	0.021294	0.002589	2.30E-16	0.021491	0.004403	1.07E-06	0.020212	0.003242	4.70E-10	2.44E-14	0.815027	
7	YKT6 *	rs1004558	44,200,808	T	C	0.197721	0.021729	0.002538	1.60E-17	0.021812	0.004322	4.57E-07	0.020317	0.003175	1.62E-10	3.80E-15	0.780363	
7	YKT6 *	rs35832856	44,200,964	T	C	0.093172	-0.023038	0.003472	4.80E-11	-0.027249	0.005878	3.60E-06	-0.020402	0.004359	2.90E-06	3.76E-10	0.349363	
7	YKT6	rs11540050	44,201,065	T	G	0.092432	-0.022761	0.003488	8.00E-11	-0.027772	0.005902	2.57E-06	-0.019678	0.004378	7.07E-06	6.38E-10	0.270668	
7	YKT6	rs61324019	44,201,373	A	G	0.093331	-0.023144	0.00347	3.80E-11	-0.027738	0.005874	2.38E-06	-0.020355	0.004355	3.00E-06	2.60E-10	0.31263	
7	YKT6	rs34110131	44,202,297	C	T	0.093341	-0.023087	0.00347	4.20E-11	-0.027707	0.005874	2.44E-06	-0.020287	0.004354	3.23E-06	2.86E-10	0.310179	
7	YKT6	rs2971668	44,203,839	C	G	0.20676	0.020951	0.002495	9.30E-17	0.020712	0.004248	1.11E-06	0.019737	0.003121	2.62E-10	1.42E-14	0.853257	
7	YKT6	rs2072440	44,204,895	C	G	0.093319	-0.023128	0.00347	3.80E-11	-0.027672	0.005874	2.51E-06	-0.020377	0.004355	2.93E-06	2.68E-10	0.318474	
7	YKT6	rs2971667	44,205,461	C	T	0.198013	0.021737	0.002535	1.50E-17	0.021808	0.004314	4.38E-07	0.020394	0.003172	1.33E-10	2.99E-15	0.791718	
7	YKT6	rs10278336	44,205,764	G	A	0.368917	-0.013458	0.002093	6.30E-11	-0.008934	0.003549	0.011843	-0.015742	0.002624	2.05E-09	6.46E-10	0.122982	
7	YKT6	rs917793	44,206,254	T	A	0.198039	0.021751	0.002534	1.50E-17	0.021801	0.004314	4.41E-07	0.020431	0.003172	1.22E-10	2.77E-15	0.798131	
7	YKT6	rs2075068	44,206,935	G	A	0.093414	-0.022906	0.003468	5.90E-11	-0.027354	0.005872	3.24E-06	-0.02021	0.004352	3.47E-06	4.03E-10	0.328356	
7	YKT6	rs41279621	44,207,134	C	A	0.093414	-0.022906	0.003468	5.90E-11	-0.027354	0.005872	3.24E-06	-0.02021	0.004352	3.47E-06	4.03E-10	0.328356	
7	YKT6	rs3824065	44,207,659	T	C	0.369402	-0.013614	0.002088	3.30E-11	-0.009217	0.003541	0.00925	-0.015872	0.002618	1.39E-09	3.54E-10	0.130748	
7	YKT6	rs34256495	44,209,029	T	C	0.093393	-0.022929	0.003468	5.50E-11	-0.027328	0.005873	3.32E-06	-0.020244	0.004352	3.35E-06	3.99E-10	0.332529	
7	YKT6	rs57597270	44,209,121	C	T	0.093394	-0.022929	0.003468	5.50E-11	-0.027328	0.005873	3.32E-06	-0.020243	0.004352	3.36E-06	4.00E-10	0.332427	
7	YKT6	rs2908282	44,209,229	A	G	0.197895	0.021733	0.002536	1.60E-17	0.021762	0.004316	4.70E-07	0.020452	0.003174	1.21E-10	2.93E-15	0.806814	
7	YKT6	rs12675084	44,212,419	G	C	0.093296	-0.022723	0.003472	8.20E-11	-0.027037	0.00588	4.33E-06	-0.020056	0.004357	4.23E-06	6.43E-10	0.340132	
7	YKT6	rs11540051	44,213,422	T	G	0.09326	-0.022747	0.003472	7.80E-11	-0.027092	0.00588	4.14E-06	-0.02008	0.004357	4.11E-06	5.99E-10	0.337941	
7	YKT6	rs1045776	44,213,786	C	T	0.093257	-0.02278	0.003472	7.40E-11	-0.02719	0.005881	3.83E-06	-0.02008	0.004357	4.11E-06	5.56E-10	0.331272	
7	YKT6 *	rs62459085	44,215,304	G	C	0.093339	-0.022801	0.003471	7.00E-11	-0.027659	0.00588	2.59E-06	-0.01985	0.004356	5.26E-06	4.84E-10	0.285905	
7	YKT6 *	rs62459086	44,215,515	C	T	0.093336	-0.022828	0.003472	6.60E-11	-0.027663	0.00588	2.58E-06	-0.019894	0.004356	5.02E-06	4.62E-10	0.288357	
7	YKT6 *	rs62459087	44,215,516	T	G	0.093336	-0.022828	0.003472	6.60E-11	-0.027663	0.00588	2.58E-06	-0.019894	0.004356	5.02E-06	4.62E-10	0.288357	
7	CAMK2B *	rs35197372	44,215,937	G	A	0.093303	-0.022895	0.003473	5.60E-11	-0.027644	0.00588	2.63E-06	-0.020013	0.004358	4.45E-06	4.18E-10	0.297151	
7	CAMK2B *	rs878521	44,216,044	A	G	0.354908	0.019189	0.002107	2.20E-19	0.021696	0.003587	1.50E-09	0.017845	0.002637	1.36E-11	1.29E-18	0.386969	
7	CAMK2B	rs78359497	44,217,896	A	G	0.172006	0.020722	0.002709	1.70E-14	0.019954	0.004595	1.43E-05	0.020155	0.003397	3.04E-09	1.82E-12	0.971927	
7	CAMK2B	rs758982	44,218,344	T	C	0.173119	0.020217	0.002704	5.00E-14	0.019143	0.004587	3.04E-05	0.019791	0.00339	5.45E-09	6.60E-12	0.909529	
7	CAMK2B	rs35148004	44,219,975	T	C	0.09292	-0.022901	0.003483	6.20E-11	-0.027428	0.005902	3.42E-06	-0.02011	0.004369	4.23E-06	5.12E-10	0.31901	
7	CAMK2B	rs1065359	44,220,107	A	G	0.355896	-0.013791	0.002115	2.30E-11	-0.008057	0.003588	0.024754	-0.016656	0.002652	3.50E-10	2.20E-10	0.053989	
7	CAMK2B	rs1127065	44,220,272	T	C	0.370488	-0.013611	0.002094	3.70E-11	-0.006527	0.003552	0.066163	-0.017152	0.002625	6.58E-11	9.85E-11	0.016164	F
7	CAMK2B	rs34775092	44,221,182	A	G	0.097772	-0.021856	0.003406	2.30E-10	-0.025389	0.005778	1.13E-05	-0.019983	0.00427	2.92E-06	1.13E-09	0.451823	
7	CAMK2B	rs59877240	44,221,670	A	G	0.098037	-0.021554	0.003403	3.60E-10	-0.024853	0.005773	1.69E-05	-0.019822	0.004266	3.43E-06	1.94E-09	0.483397	
7	CAMK2B	rs56958012	44,221,683	T	C	0.097665	-0.021768	0.003408	2.80E-10	-0.025397	0.005782	1.14E-05	-0.019822	0.004272	3.54E-06	1.37E-09	0.43808	
7	CAMK2B	rs62459090	44,222,066	A	G	0.097678	-0.02189	0.00341	2.20E-10	-0.025249	0.005785	1.29E-05	-0.020105	0.004274	2.60E-06	1.15E-09	0.474592	
7	CAMK2B	rs62459091	44,222,249	A	G	0.097591	-0.021832	0.00341	2.40E-10	-0.025324	0.005785	1.22E-05	-0.019965	0.004274	3.05E-06	1.26E-09	0.456276	
7	CAMK2B	rs732360	44,222,379	A	G	0.197583	0.02032	0.002568	3.90E-15	0.020729	0.004378	2.22E-06	0.018566	0.00321	7.50E-09	7.36E-13	0.690358	
7	CAMK2B	rs2003563	44,222,454	G	T	0.095715	-0.021615	0.003446	5.20E-10	-0.025918	0.005846	9.39E-06	-0.019389	0.004319	7.26E-06	2.27E-09	0.369001	
7	CAMK2B	rs75929284	44,222,646	G	A	0.097124	-0.022035	0.003421	1.90E-10	-0.02549	0.005803	1.14E-05	-0.02027	0.004288	2.32E-06	9.09E-10	0.469382	
7	CAMK2B	rs62459093	44,224,074	A	G	0.094683	-0.022287	0.003479	2.30E-10	-0.02618	0.005901	9.25E-06	-0.020362	0.004361	3.07E-06	9.80E-10	0.427756	
7	CAMK2B	rs2877285	44,226,036	A	G	0.094853	-0.022254	0.003492	3.90E-10	-0.023871	0.005928	5.72E-05	-0.02132	0.004376	1.12E-06	1.21E-09	0.729164	
7	CAMK2B	rs917792	44,226,380	T	C	0.096655	-0.021374	0.00347	1.40E-09	-0.022337	0.005895	0.000153	-0.020804	0.004346	1.72E-06	8.07E-09	0.834216	
7	CAMK2B	rs117998298	44,229,771	T	C	0.082031	-											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
7	FKBP6 *	rs200456061	73,371,588	T	C	0.015965	-0.064047	0.008084	1.60E-17	-0.057018	0.013892	4.10E-05	-0.06769	0.010065	1.81E-11	3.31E-14	0.533894	
7	FKBP6 *	rs186391487	73,384,030	A	G	0.015912	-0.06482	0.008101	9.20E-18	-0.058953	0.013919	2.31E-05	-0.067917	0.010085	1.71E-11	1.81E-14	0.602063	
7	FZD9 *	rs42123	73,425,622	G	T	0.109503	-0.050235	0.003273	7.00E-58	-0.043027	0.005594	1.53E-14	-0.054642	0.004087	9.80E-41	2.14E-52	0.093611	
7	FZD9 *	rs42122	73,427,493	A	G	0.092473	-0.058285	0.003497	8.10E-67	-0.050903	0.00597	1.60E-17	-0.062501	0.004368	2.14E-46	5.72E-61	0.116949	
7	FZD9 *	rs868953856	73,432,413	T	A	0.074758	-0.06172	0.003886	4.70E-60	-0.052065	0.006613	3.63E-15	-0.066692	0.004863	9.30E-43	5.05E-55	0.074783	
7	FZD9 *	rs782289776	73,432,414	T	C	0.074758	-0.06172	0.003886	4.70E-60	-0.052065	0.006613	3.63E-15	-0.066692	0.004863	9.30E-43	5.05E-55	0.074783	
7	FZD9	rs138414411	73,434,563	T	C	0.020952	-0.055613	0.007068	1.70E-15	-0.034161	0.012164	0.004994	-0.066019	0.008792	6.23E-14	1.11E-14	0.033811	F
7	FZD9	rs1178947	73,435,848	C	T	0.090607	-0.059405	0.00352	5.80E-69	-0.050915	0.006004	2.36E-17	-0.064439	0.004401	1.65E-48	6.61E-63	0.069246	
7	BAZ1B	rs2240466	73,441,939	A	G	0.091864	-0.059653	0.003492	1.70E-70	-0.049996	0.005955	4.86E-17	-0.065146	0.004365	2.56E-50	0.040195	F	
7	BAZ1B	rs1178979	73,442,100	C	T	0.091315	-0.059725	0.003502	2.40E-70	-0.05019	0.005977	4.80E-17	-0.065119	0.004376	4.89E-50	4.01E-64	0.043894	F
7	BAZ1B	rs1178977	73,442,719	G	A	0.091258	-0.059711	0.003503	2.70E-70	-0.049975	0.005979	6.69E-17	-0.065193	0.004377	3.98E-50	4.53E-64	0.040032	F
7	BAZ1B	rs113452856	73,444,805	A	G	0.021269	-0.053147	0.007018	1.80E-14	-0.031727	0.012085	0.008675	-0.063423	0.008728	3.85E-13	1.09E-13	0.033507	F
7	BAZ1B	rs146626977	73,448,166	C	T	0.01193	-0.080484	0.009309	7.30E-20	-0.077962	0.015962	1.06E-06	-0.084608	0.011603	3.18E-13	1.88E-17	0.73626	
7	BAZ1B	rs13231516	73,448,919	G	T	0.096065	-0.057974	0.003422	1.30E-69	-0.049161	0.005837	3.87E-17	-0.062846	0.004278	8.22E-49	5.39E-63	0.058625	
7	BAZ1B	rs2074756	73,449,425	C	T	0.011937	-0.080118	0.009306	9.50E-20	-0.076822	0.015948	1.48E-06	-0.084608	0.011603	3.18E-13	2.60E-17	0.692994	
7	BAZ1B	rs714052	73,450,539	G	A	0.096449	-0.057571	0.003418	5.80E-69	-0.048706	0.005826	6.59E-17	-0.06247	0.004274	2.40E-48	2.64E-62	0.056796	
7	BAZ1B	rs34763247	73,452,286	T	A	0.095995	-0.058097	0.003424	8.20E-70	-0.04913	0.005837	4.06E-17	-0.063052	0.00428	4.48E-49	3.09E-63	0.054433	
7	BAZ1B	rs1306476	73,454,192	G	A	0.095997	-0.05805	0.003424	1.10E-69	-0.049004	0.005837	4.90E-17	-0.063038	0.00428	4.78E-49	3.96E-63	0.052538	
7	BAZ1B	rs35330527	73,455,877	G	A	0.097482	-0.056962	0.003406	7.50E-68	-0.047371	0.005809	3.67E-16	-0.062207	0.004257	2.58E-48	1.55E-61	0.039407	F
7	BAZ1B	rs60982449	73,459,090	G	A	0.090003	-0.060183	0.003528	3.10E-70	-0.050137	0.006014	8.04E-17	-0.065812	0.004411	2.78E-50	3.80E-64	0.035605	F
7	BAZ1B	rs2074755	73,462,836	C	T	0.095254	-0.058385	0.003436	6.00E-70	-0.049084	0.005852	5.23E-17	-0.063521	0.004298	2.22E-49	1.97E-63	0.046789	F
7	BAZ1B	rs35797675	73,463,714	G	T	0.097445	-0.057476	0.003406	2.90E-69	-0.048213	0.005805	1.05E-16	-0.062714	0.004258	4.68E-49	8.22E-63	0.043997	F
7	BAZ1B	rs12056034	73,464,315	G	A	0.096607	-0.057463	0.003416	1.30E-68	-0.048941	0.005827	4.76E-17	-0.062177	0.004269	5.35E-48	4.27E-62	0.066931	
7	BAZ1B	rs71556715	73,467,477	T	C	0.095238	-0.058516	0.003436	3.00E-70	-0.049329	0.005852	3.68E-17	-0.063586	0.004298	1.80E-49	1.13E-63	0.049621	F
7	BAZ1B	rs62465144	73,468,776	C	T	0.095893	-0.058168	0.003426	7.20E-70	-0.049114	0.005839	4.29E-17	-0.063179	0.004284	3.52E-49	2.56E-63	0.052152	
7	BAZ1B	rs6976930	73,471,480	A	G	0.090629	-0.060326	0.003515	3.80E-71	-0.050267	0.005992	5.20E-17	-0.065981	0.004395	6.74E-51	6.02E-65	0.03446	F
7	BAZ1B	rs141027825	73,471,893	C	G	0.013927	-0.073732	0.008662	3.50E-19	-0.070667	0.014812	1.86E-06	-0.077046	0.010812	1.08E-12	1.08E-16	0.727995	
7	BAZ1B	rs139267697	73,475,356	A	G	0.011941	-0.080174	0.009305	9.10E-20	-0.076825	0.015948	1.48E-06	-0.084623	0.0116	3.11E-13	2.54E-17	0.692521	
7	BAZ1B	rs35695283	73,479,073	G	A	0.091146	-0.059969	0.003505	9.50E-71	-0.050231	0.00598	4.69E-17	-0.065484	0.004381	1.83E-50	1.48E-64	0.039651	F
7	BAZ1B	rs75229905	73,481,616	C	T	0.095889	-0.058078	0.003426	1.10E-69	-0.049185	0.005839	3.86E-17	-0.063013	0.004283	6.03E-49	3.95E-63	0.056222	
7	BAZ1B	rs7797566	73,482,065	C	A	0.095889	-0.058078	0.003426	1.10E-69	-0.049185	0.005839	3.86E-17	-0.063013	0.004283	6.03E-49	3.95E-63	0.056222	
7	BAZ1B	rs17145713	73,490,480	T	C	0.095283	-0.05841	0.003436	4.90E-70	-0.049235	0.005852	4.20E-17	-0.06346	0.004297	2.65E-49	1.89E-63	0.050099	
7	BAZ1B	rs111837003	73,493,129	T	C	0.090481	-0.06061	0.003518	1.20E-71	-0.050803	0.005996	2.53E-17	-0.066142	0.004398	4.64E-51	2.04E-65	0.039154	F
7	BAZ1B	rs118023175	73,494,447	G	C	0.011974	-0.079982	0.009292	9.40E-20	-0.076133	0.015928	1.78E-06	-0.084753	0.011584	2.66E-13	2.61E-17	0.661657	
7	BAZ1B	rs117830225	73,494,457	C	G	0.011941	-0.080177	0.009305	9.10E-20	-0.076825	0.015948	1.48E-06	-0.084627	0.0116	3.11E-13	2.54E-17	0.69239	
7	BAZ1B	rs13244268	73,497,513	C	T	0.095925	-0.058887	0.003433	4.00E-71	-0.049626	0.005846	2.21E-17	-0.064056	0.004294	2.83E-50	1.08E-64	0.046693	F
7	BAZ1B	rs34482346	73,501,191	C	G	0.095232	-0.058609	0.003436	1.90E-70	-0.049512	0.005853	2.85E-17	-0.063624	0.004298	1.58E-49	7.69E-64	0.051998	
7	BAZ1B	rs79862839	73,507,279	C	T	0.095235	-0.058621	0.003436	1.80E-70	-0.049538	0.005853	2.74E-17	-0.063629	0.004298	1.55E-49	7.29E-64	0.052345	
7	BAZ1B	rs13221253	73,507,903	G	A	0.095124	-0.058524	0.003439	2.90E-70	-0.049363	0.005856	3.65E-17	-0.063581	0.004301	2.15E-49	1.34E-63	0.050385	
7	BAZ1B	rs34437827	73,509,008	G	A	0.095225	-0.058608	0.003437	1.90E-70	-0.049512	0.005853	2.85E-17	-0.063638	0.004299	1.54E-49	7.49E-64	0.051773	
7	BAZ1B	rs7811265	73,520,180	G	A	0.086719	-0.059516	0.003599	3.90E-66	-0.04778	0.006143	7.73E-15	-0.066346	0.004497	3.22E-49	3.94E-61	0.014762	F
7	BAZ1B *	rs62466264	73,524,388	C	T	0.095469	-0.058627	0.003434	1.60E-70	-0.049262	0.005849	3.88E-17	-0.063766	0.004296	8.78E-50	5.81E-64	0.045666	F
7	BAZ1B *	rs11983997	73,524,914	C	G	0.09512	-0.058485	0.003439	4.30E-70	-0.049329	0.005856	3.83E-17	-0.063547	0.004301	2.42E-49	1.58E-63	0.050385	
7	BAZ1B *	rs80189144	73,525,609	C	T	0.09512	-0.058485	0.003439	4.30E-70	-0.049329	0.005856	3.83E-17	-0.063547	0.004301	2.42E-49	1.58E-63	0.050385	
7	BCL7B *	rs66579735	73,530,040	T	C	0.382466	0.01073	0.002103	4.20E-08	0.005025	0.003567	0.158819	0.013526	0.002636	2.95E-07	7.13E-07	0.05351	
7	BCL7B *	rs143934761	73,533,607	G	A	0.020926	-0.054445	0.007066	3.90E-15	-0.035088	0.012186	0.003997	-0.063578	0.008781	4.66E-13	6.55E-14	0.057874	
7	BCL7B *	rs4717094	73,535,752	T	C	0.436521	0.011307	0.002047	3.90E-08	0.015548	0.003482	8.09E-06	0.009295	0.002563	0.00029	6.52E-08	0.148034	
7	BCL7B	rs142030730	73,542,085	T	C	0.012995	-0.054383	0.008921	2.70E-11	-0.049816	0.015231	0.001078	-0.05645	0.011145	4.16E-07	1.28E-08	0.72522	
7	BCL7B	rs17145732	73,555,938	G	T	0.099289	-0.06143	0.003376	2.90E-79	-0.054619	0.005741	1.96E-21	-0.065191	0.004226	1.22E-53	4.69E-72	0.138029	
7	BCL7B	rs13233571	73,556,901	T	C	0.09525	-0.064374	0.003435	1.20E-83	-0.058345	0.005833	1.59E-23	-0.0678	0.004304	7.39E-56	2.46E-76	0.192139	
7	BCL7B	rs7793710	73,557,201	G	C	0.095197	-0.064425	0.003437	1.10E-83	-0.058133	0.005836	2.43E-23	-0.067984	0.004306	4.13E-56	2.10E-76	0.174377	
7	BCL7B	rs13234157	73,557,398	A	C	0.094234	-0.063773	0.003463	4.70E-81	-0.05792	0.005881	7.45E-23	-0.067239	0.004339	4.13E-54	6.28E-74	0.202273	
7	BCL7B *	rs13244614	73,559,524	A	C	0.095179	-0.064458	0.003437	9.00E-84	-0.058111	0.005836	2.52E-23	-0.068048	0.004307	3.52E-56	1.86E-76	0.1707	
7	BCL7B *	rs140173690	73,560,328	A	C	0.01714	-0.062896	0.007777	7.70E-18	-0.058772	0.01328	9.75E-06	-0.065202	0.009715	1.99E-11	9.24E-15	0.695972	
7	BCL7B *	rs11269058	73,561,372	T	C	0.095187	-0.064471	0.003437	8.60E-84	-0.058116	0.005836	2.50E-23	-0.068064	0.004307	3.32E-56	1.74E-76	0.170206	
7	BCL7B *	rs13225333	73,561,688	T	C	0.09516	-0.064491	0.003438	8.10E-84	-0.058187	0.005837	2.23E-23	-0.068069	0.004307	3.33E-56	1.56E-76	0.173136	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
7	TBL2 *	rs67644909	73,581,624	T	C	0.093823	-0.0644	0.003465	2.50E-82	-0.057515	0.005877	1.38E-22	-0.068193	0.004343	1.68E-55	4.77E-75	0.143985	
7	TBL2 *	rs9638180	73,584,622	G	A	0.095265	-0.064719	0.003438	2.80E-84	-0.058609	0.005836	1.06E-23	-0.068192	0.004307	2.12E-56	4.74E-77	0.186411	
7	TBL2 *	rs9638181	73,584,713	G	A	0.095265	-0.064719	0.003438	2.80E-84	-0.058609	0.005836	1.06E-23	-0.068192	0.004307	2.12E-56	4.74E-77	0.186411	
7	TBL2 *	rs9638182	73,584,775	G	T	0.095265	-0.064719	0.003438	2.80E-84	-0.058609	0.005836	1.06E-23	-0.068192	0.004307	2.12E-56	4.74E-77	0.186411	
7	MLXIPL *	rs35173225	73,586,691	T	C	0.095301	-0.064709	0.003438	3.40E-84	-0.058593	0.005835	1.06E-23	-0.068172	0.004309	2.55E-56	5.74E-77	0.18659	
7	MLXIPL *	rs187404224	73,588,697	G	A	0.095201	-0.064733	0.003438	2.70E-84	-0.058513	0.005836	1.24E-23	-0.06827	0.004308	1.66E-56	4.38E-77	0.178573	
7	MLXIPL *	rs185081604	73,588,973	C	A	0.095201	-0.064733	0.003438	2.70E-84	-0.058513	0.005836	1.24E-23	-0.06827	0.004308	1.66E-56	4.38E-77	0.178573	
7	MLXIPL *	rs145099458	73,589,985	T	C	0.090722	-0.063483	0.003529	4.10E-77	-0.058289	0.005982	2.10E-22	-0.066427	0.004427	7.44E-51	3.06E-70	0.274127	
7	MLXIPL *	rs35866503	73,591,446	T	C	0.0952	-0.064736	0.003438	2.70E-84	-0.058522	0.005836	1.22E-23	-0.06827	0.004308	1.66E-56	4.31E-77	0.178969	
7	MLXIPL *	rs13225660	73,592,058	T	C	0.0952	-0.064736	0.003438	2.70E-84	-0.058522	0.005836	1.22E-23	-0.06827	0.004308	1.66E-56	4.31E-77	0.178969	
7	MLXIPL	rs1051921	73,593,613	A	G	0.0952	-0.064732	0.003438	2.70E-84	-0.058522	0.005836	1.22E-23	-0.068266	0.004308	1.69E-56	4.38E-77	0.179161	
7	MLXIPL	rs13247874	73,596,112	T	C	0.097106	-0.066142	0.00341	7.70E-89	-0.060836	0.005783	7.57E-26	-0.069358	0.004275	3.92E-59	6.68E-82	0.23599	
7	MLXIPL	rs35332062	73,597,712	A	G	0.097901	-0.066035	0.003395	2.30E-89	-0.060373	0.005759	1.10E-25	-0.069416	0.004257	9.91E-60	2.47E-82	0.206657	
7	MLXIPL	rs79624003	73,598,455	G	A	0.097818	-0.066411	0.003398	3.30E-90	-0.060642	0.005764	7.50E-26	-0.069858	0.004259	2.12E-60	3.62E-83	0.198478	
7	MLXIPL	rs35732917	73,598,939	C	A	0.097717	-0.066648	0.0034	1.10E-90	-0.060729	0.005767	6.70E-26	-0.070171	0.004263	7.79E-61	1.19E-83	0.187905	
7	MLXIPL	rs13235543	73,599,571	T	C	0.097652	-0.066735	0.003401	7.90E-91	-0.06074	0.005767	6.55E-26	-0.070301	0.004264	5.05E-61	7.58E-84	0.182469	
7	MLXIPL	rs13240065	73,601,039	A	G	0.096609	-0.066667	0.003423	1.70E-89	-0.0616	0.005803	2.74E-26	-0.069803	0.004292	2.06E-59	1.29E-82	0.255722	
7	MLXIPL	rs34346326	73,601,851	C	T	0.09747	-0.06657	0.003405	2.90E-90	-0.060694	0.005775	8.37E-26	-0.070123	0.004269	1.36E-60	2.60E-83	0.189162	
7	MLXIPL	rs13240994	73,602,532	C	T	0.08821	-0.071826	0.003577	3.50E-95	-0.065721	0.006061	2.30E-27	-0.075577	0.004487	1.34E-63	7.37E-88	0.191187	
7	MLXIPL	rs13226650	73,602,675	G	A	0.0976	-0.066567	0.003405	2.80E-90	-0.060691	0.005775	8.38E-26	-0.070162	0.004269	1.18E-60	2.24E-83	0.187198	
7	MLXIPL	rs35368205	73,603,327	T	C	0.088513	-0.071256	0.003553	5.60E-95	-0.065103	0.006024	3.43E-27	-0.074722	0.004455	4.22E-63	3.44E-87	0.199151	
7	MLXIPL	rs34166762	73,604,194	C	T	0.088981	-0.074196	0.003552	2.30E-102	-0.06665	0.006028	2.20E-28	-0.078614	0.004451	9.57E-70	5.35E-95	0.110349	
7	MLXIPL	rs61010704	73,605,645	G	A	0.086336	-0.075735	0.003591	2.80E-104	-0.068513	0.006093	2.67E-29	-0.079886	0.004502	2.17E-70	1.50E-96	0.133304	
7	MLXIPL	rs3812316	73,606,007	G	C	0.086346	-0.075923	0.003591	8.50E-105	-0.068901	0.006091	1.24E-29	-0.07993	0.004501	1.74E-70	5.61E-97	0.1453	
7	MLXIPL	rs6968170	73,606,346	A	G	0.086384	-0.075757	0.00359	2.10E-104	-0.068509	0.00609	2.50E-29	-0.079921	0.0045	1.66E-70	1.08E-96	0.131772	
7	MLXIPL	rs77048596	73,607,881	A	G	0.086376	-0.07578	0.00359	2.00E-104	-0.068694	0.00609	1.80E-29	-0.079867	0.004501	2.16E-70	1.01E-96	0.140196	
7	MLXIPL	rs13246993	73,608,416	A	G	0.086377	-0.075773	0.00359	2.10E-104	-0.068721	0.00609	1.71E-29	-0.079843	0.004501	2.39E-70	1.06E-96	0.141924	
7	MLXIPL	rs12531645	73,609,551	A	G	0.086298	-0.075734	0.003592	3.20E-104	-0.068871	0.006093	1.35E-29	-0.079689	0.004503	5.09E-70	1.79E-96	0.153286	
7	MLXIPL	rs13234131	73,611,645	G	A	0.099476	-0.069383	0.003363	1.60E-98	-0.059216	0.0057	3.01E-25	-0.074857	0.004219	2.15E-70	1.57E-92	0.027445	F
7	MLXIPL	rs13234378	73,611,821	T	A	0.09994	-0.069188	0.00336	2.40E-98	-0.059064	0.005695	3.57E-25	-0.074618	0.004214	4.11E-70	3.53E-92	0.028134	F
7	MLXIPL	rs17145750	73,612,048	T	C	0.09985	-0.069474	0.003358	4.20E-99	-0.059521	0.00569	1.42E-25	-0.074786	0.004212	1.75E-70	6.05E-93	0.031084	F
7	MLXIPL	rs7808877	73,613,120	G	C	0.09968	-0.069216	0.003361	3.30E-98	-0.05903	0.005695	3.85E-25	-0.074686	0.004216	3.65E-70	3.38E-92	0.027172	F
7	MLXIPL	rs139002804	73,613,553	A	G	0.011682	-0.083105	0.00942	1.00E-20	-0.072176	0.016115	7.61E-06	-0.091614	0.011755	6.82E-15	2.85E-18	0.027995	
7	MLXIPL	rs33951980	73,615,107	T	C	0.099681	-0.069213	0.003361	3.30E-98	-0.059032	0.005695	3.83E-25	-0.074678	0.004216	3.77E-70	3.47E-92	0.027264	F
7	MLXIPL	rs2074768	73,615,773	C	A	0.099674	-0.069149	0.003361	4.40E-98	-0.059032	0.005695	3.83E-25	-0.074572	0.004216	6.08E-70	5.60E-92	0.028331	F
7	MLXIPL	rs13229619	73,615,845	A	G	0.099674	-0.069149	0.003361	4.40E-98	-0.059032	0.005695	3.83E-25	-0.074572	0.004216	6.08E-70	5.60E-92	0.028331	F
7	MLXIPL	rs7798357	73,617,935	C	G	0.09962	-0.069041	0.003363	1.00E-97	-0.05921	0.005698	2.90E-25	-0.07431	0.004218	2.06E-69	1.43E-91	0.033187	F
7	MLXIPL	rs7785479	73,618,505	C	T	0.099619	-0.069057	0.003363	9.30E-98	-0.059218	0.005698	2.85E-25	-0.07433	0.004218	1.90E-69	1.30E-91	0.033053	F
7	MLXIPL	rs34062580	73,619,229	A	G	0.099619	-0.06905	0.003363	9.60E-98	-0.059194	0.005698	3.00E-25	-0.074329	0.004218	1.92E-69	1.38E-91	0.032792	F
7	MLXIPL	rs6975495	73,619,700	G	A	0.099619	-0.069107	0.003363	9.90E-98	-0.059283	0.005698	2.56E-25	-0.074359	0.004218	1.70E-69	1.04E-91	0.033486	F
7	MLXIPL	rs71556736	73,620,599	T	C	0.099688	-0.069059	0.003362	9.20E-98	-0.059585	0.005696	1.41E-25	-0.074121	0.004217	4.11E-69	1.40E-91	0.040276	F
7	MLXIPL	rs7800944	73,621,527	C	T	0.100045	-0.068135	0.003358	2.20E-95	-0.058187	0.005692	1.69E-24	-0.073354	0.004211	6.73E-68	2.67E-89	0.032215	F
7	MLXIPL	rs1207541622	73,621,799	C	T	0.012049	-0.090142	0.009363	3.60E-23	-0.056629	0.016153	0.000458	-0.110154	0.011632	2.98E-21	7.20E-23	0.007184	F
7	MLXIPL	rs2736909	73,621,803	G	C	0.012049	-0.090142	0.009363	3.60E-23	-0.056629	0.016153	0.000458	-0.110154	0.011632	2.98E-21	7.20E-23	0.007184	F
7	MLXIPL	rs55747707	73,623,036	A	G	0.099585	-0.069141	0.003365	5.80E-98	-0.059574	0.005701	1.57E-25	-0.074227	0.004221	3.54E-69	1.34E-91	0.038861	F
7	MLXIPL	rs34060476	73,623,626	G	A	0.099558	-0.069122	0.003365	6.00E-98	-0.059646	0.005701	1.39E-25	-0.074178	0.004222	4.63E-69	1.55E-91	0.040545	F
7	MLXIPL *	rs34593868	73,625,076	G	C	0.099564	-0.069173	0.003365	4.10E-98	-0.059703	0.005701	1.26E-25	-0.074198	0.004222	4.38E-69	1.33E-91	0.04106	F
7	MLXIPL *	rs34121855	73,626,484	G	T	0.097506	-0.06929	0.003403	1.10E-96	-0.059935	0.005769	2.99E-25	-0.074222	0.004268	1.09E-67	7.72E-90	0.046507	F
7	MLXIPL *	rs62466318	73,627,755	T	C	0.107917	-0.063248	0.003248	2.70E-88	-0.054752	0.005503	2.73E-23	-0.067635	0.004074	7.53E-62	4.50E-82	0.059908	
7	MLXIPL *	rs117739002	73,628,073	T	C	0.017739	-0.066662	0.007642	4.70E-18	-0.045542	0.013042	0.000483	-0.076434	0.009549	1.26E-15	2.74E-17	0.056004	
7	MLXIPL *	rs6460047	73,628,113	C	T	0.109403	-0.062212	0.003232	5.00E-86	-0.054004	0.005477	6.58E-23	-0.06648	0.004055	2.30E-60	3.25E-80	0.067115	
7	MLXIPL *	rs7805504	73,628,255	C	T	0.109294	-0.062331	0.003233	2.90E-86	-0.053699	0.005477	1.16E-22	-0.066844	0.004057	5.94E-61	1.48E-80	0.053799	
7	MLXIPL *	rs7786376	73,628,284	G	A	0.110626	-0.061877	0.003218	8.00E-86	-0.052357	0.005451	8.19E-22	-0.066948	0.004037	1.03E-61	1.79E-80	0.031498	F
7	MLXIPL *	rs35340690	73,628,738	C	G	0.152235	-0.042298	0.002836	3.20E-53	-0.039437	0.00482	2.95E-16	-0.043941	0.003552	4.04E-35	1.69E-48	0.451919	
7	MLXIPL *	rs34958196	73,628,771	A	G	0.139737	-0.049131	0.002931	2.30E-66	-0.045651	0.004978	4.96E-20	-0.051086	0.003673	6.06E-44	5.23E-61	0.379597	
7	MLXIPL *	rs34430945	73,629,335	C	T	0.139253	-0.048829	0.002934	1.90E-65	-0.044872	0.00498	2.19E-19	-0.051038	0.003677	9.14E-44	3.41E-60	0.319219	
7	MLXIPL *	rs34321592	73,															

CHR	GENE	SNP	Pos (hg38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
7	CLDN3	rs6460054	73,770,204	T	C	0.475026	0.010679	0.002026	3.00E-08	0.009483	0.003456	0.006084	0.011215	0.002532	9.62E-06	1.28E-06	0.686041	
7	CLDN3 *	rs28408072	73,771,842	G	A	0.475441	0.010687	0.002026	2.80E-08	0.009321	0.003455	0.006993	0.011356	0.002532	7.39E-06	1.13E-06	0.634845	
7	CLDN3 *	rs4484568	73,773,321	A	G	0.475345	0.010711	0.002025	2.60E-08	0.009365	0.003455	0.006731	0.011385	0.002532	6.98E-06	1.03E-06	0.637127	
7	CLDN3 *	rs4131376	73,773,988	T	C	0.474784	0.010729	0.002025	2.60E-08	0.009509	0.003455	0.005931	0.011295	0.002531	8.22E-06	1.07E-06	0.676708	
7	WBSCR28 *	rs6964950	73,894,020	A	C	0.031951	-0.032865	0.005765	9.90E-10	-0.028468	0.00986	0.003897	-0.03624	0.007195	4.82E-07	4.79E-08	0.524312	
7	WBSCR28 *	rs13241670	73,903,956	C	T	0.032313	-0.031934	0.005731	2.40E-09	-0.027963	0.009796	0.004323	-0.035123	0.007155	9.33E-07	9.96E-08	0.555053	
7	WBSCR28 *	rs73144858	73,922,565	G	C	0.019937	-0.049304	0.007247	2.70E-13	-0.040534	0.012311	0.000999	-0.053271	0.009079	4.54E-09	1.48E-10	0.405026	
7	ELN *	rs188072556	73,999,294	T	C	0.016791	-0.05856	0.007864	1.30E-15	-0.054595	0.013421	4.80E-05	-0.060292	0.009826	8.71E-10	1.70E-12	0.73199	
7	RFC2	rs148741166	74,252,973	A	C	0.012912	-0.051692	0.008983	1.20E-10	-0.045883	0.015285	0.002694	-0.053881	0.011243	1.68E-06	1.73E-07	0.673373	
7	CLIP2	rs151126504	74,392,493	T	C	0.020739	-0.0495	0.007133	1.00E-13	-0.049783	0.012182	4.43E-05	-0.049431	0.00891	2.97E-08	4.91E-11	0.981352	
7	GTF2IRD1 *	rs145049525	74,440,602	G	C	0.015991	-0.042391	0.008123	9.00E-09	-0.043655	0.013806	0.001573	-0.042178	0.010172	3.42E-05	1.25E-06	0.931329	
7	GNAT3 *	rs142895840	80,521,969	T	C	0.020002	-0.042658	0.007229	7.90E-10	-0.060256	0.012447	1.31E-06	-0.035448	0.008991	8.14E-05	3.43E-09	0.106144	
7	GNAT3 *	rs145638771	80,550,968	G	A	0.020689	-0.04346	0.007097	2.40E-10	-0.061021	0.012249	6.42E-07	-0.036482	0.008816	3.54E-05	7.80E-10	0.103946	
7	CD36 *	rs182480663	80,567,623	G	A	0.020685	-0.043413	0.007098	2.50E-10	-0.060813	0.012252	7.05E-07	-0.036496	0.008816	3.51E-05	1.07E-10	0.107166	
7	CD36 *	rs531971155	80,601,582	T	G	0.020132	-0.05429	0.007194	9.70E-11	-0.061617	0.012411	7.01E-07	-0.039498	0.008938	1.01E-05	2.55E-10	0.148103	
7	CD36	rs577611417	80,651,863	A	C	0.019981	-0.044908	0.007226	1.10E-10	-0.059084	0.012438	2.07E-06	-0.039768	0.008988	9.79E-06	7.06E-10	0.208123	
7	SEMA3C *	rs186972232	80,740,942	G	C	0.03422	-0.031444	0.005615	1.40E-08	-0.036571	0.00967	0.000157	-0.029139	0.006983	3.05E-05	1.30E-07	0.533212	
7	CDK6	rs2282987	92,683,489	C	G	0.353802	0.01171	0.002122	4.70E-08	0.015253	0.003607	2.37E-05	0.010007	0.002658	0.000168	1.09E-07	0.241546	
7	KLF14 *	rs6973807	130,739,211	G	A	0.308867	-0.015572	0.002223	2.10E-12	-0.005724	0.003766	0.128514	-0.020537	0.002789	1.86E-13	5.26E-13	0.00158	F
7	KLF14 *	rs6974400	130,739,314	A	G	0.308854	-0.015558	0.002222	2.10E-12	-0.005681	0.003765	0.131312	-0.020553	0.002788	1.74E-13	5.02E-13	0.001508	F
7	KLF14 *	rs6974288	130,739,451	G	A	0.308986	-0.015572	0.002221	1.80E-12	-0.005742	0.003763	0.126948	-0.020558	0.002786	1.66E-13	4.66E-13	0.00156	F
7	KLF14 *	rs11762784	130,739,885	A	G	0.309065	-0.015415	0.002218	3.00E-12	-0.00578	0.003759	0.124177	-0.020297	0.002782	3.07E-13	8.41E-13	0.001916	F
7	KLF14 *	rs3996350	130,742,296	C	G	0.310062	-0.015738	0.002204	8.40E-13	-0.006638	0.003739	0.075812	-0.020358	0.002763	1.81E-13	3.38E-13	0.003177	F
7	KLF14 *	rs13234269	130,744,427	A	T	0.311045	-0.016054	0.002194	2.00E-13	-0.006758	0.003721	0.069315	-0.020701	0.00275	5.41E-14	9.55E-14	0.002591	F
7	KLF14 *	rs4731701	130,746,171	T	C	0.309862	-0.01557	0.002203	1.40E-12	-0.005768	0.003734	0.12242	-0.020486	0.002763	1.27E-13	3.49E-13	0.001539	F
7	KLF14 *	rs10260148	130,746,210	T	C	0.399232	0.014631	0.002096	1.60E-12	0.003255	0.00356	0.360586	0.020533	0.002626	5.63E-15	3.52E-14	9.50E-05	F
7	KLF14 *	rs340727254	130,747,710	A	G	0.311787	-0.01582	0.002182	3.40E-13	-0.006086	0.003703	0.100283	-0.020676	0.002734	4.12E-14	9.84E-14	0.001533	F
7	KLF14 *	rs6971365	130,747,722	C	T	0.401573	0.014493	0.002088	2.90E-12	0.002835	0.003547	0.424016	0.020044	0.002616	5.87E-15	4.05E-14	6.55E-05	F
7	KLF14 *	rs13241165	130,747,779	T	A	0.311839	-0.015806	0.002182	3.50E-13	-0.006076	0.003703	0.100822	-0.02067	0.002734	4.18E-14	1.00E-13	0.001528	F
7	KLF14 *	rs4731702	130,748,625	T	C	0.311632	-0.015959	0.00218	2.10E-13	-0.006387	0.003701	0.084426	-0.020729	0.002731	3.35E-14	6.99E-14	0.001828	F
7	KLF14 *	rs11976955	130,748,835	G	C	0.403049	0.013946	0.002089	1.70E-11	0.002032	0.003548	0.566769	0.020039	0.002617	2.00E-14	1.58E-13	4.47E-05	F
7	KLF14 *	rs6961342	130,749,185	A	C	0.403034	0.013998	0.002088	1.50E-11	0.002197	0.003546	0.535545	0.020035	0.002616	1.98E-14	1.53E-13	5.22E-05	F
7	KLF14 *	rs35722851	130,749,741	C	T	0.310709	-0.015981	0.002189	2.40E-13	-0.006169	0.003717	0.096967	-0.020866	0.002743	2.96E-14	6.91E-14	0.001472	F
7	KLF14 *	rs35057928	130,749,767	C	T	0.310329	-0.016055	0.00219	1.90E-13	-0.006231	0.003718	0.093749	-0.020939	0.002744	2.46E-14	5.62E-14	0.001466	F
7	KLF14 *	rs34282904	130,749,770	A	G	0.310576	-0.015982	0.00219	2.40E-13	-0.006153	0.003717	0.097809	-0.020868	0.002744	2.96E-14	6.98E-14	0.001454	F
7	KLF14 *	rs287621	130,750,422	T	C	0.401548	0.014286	0.002087	6.20E-12	0.002577	0.003545	0.467317	0.020259	0.002615	9.85E-15	7.12E-14	6.03E-05	F
7	KLF14 *	rs11979110	130,751,700	T	C	0.312163	-0.016013	0.002183	1.80E-13	-0.006377	0.003707	0.085356	-0.020858	0.002735	2.55E-14	5.39E-14	0.001677	F
7	KLF14 *	rs13230111	130,752,365	G	A	0.311492	-0.016111	0.002183	1.20E-13	-0.006241	0.003707	0.092278	-0.021027	0.002736	1.59E-14	3.61E-14	0.001338	F
7	KLF14 *	rs7810507	130,752,717	A	G	0.402124	0.01433	0.002085	4.70E-12	0.002542	0.003542	0.472953	0.020315	0.002612	7.78E-15	5.68E-14	5.44E-05	F
7	KLF14 *	rs13233731	130,752,930	A	G	0.311443	-0.016025	0.002183	1.60E-13	-0.00614	0.003706	0.097619	-0.020945	0.002736	2.00E-14	4.74E-14	0.001316	F
7	KLF14 *	rs13234407	130,753,455	A	G	0.311451	-0.016016	0.002183	1.60E-13	-0.006154	0.003707	0.096854	-0.02092	0.002736	2.14E-14	5.03E-14	0.001356	F
7	KLF14 *	rs7783857	130,754,299	G	C	0.42154	0.014942	0.002053	2.20E-13	0.002618	0.003494	0.453648	0.02131	0.002569	1.16E-16	8.77E-16	1.66E-05	F
7	KLF14 *	rs13241538	130,755,103	C	G	0.312222	-0.016225	0.002179	6.90E-14	-0.006448	0.003701	0.081468	-0.021081	0.002731	1.21E-14	2.50E-14	0.001472	F
7	KLF14 *	rs13228906	130,757,125	A	G	0.311881	-0.016045	0.002183	1.30E-13	-0.006097	0.003707	0.100003	-0.020966	0.002734	1.83E-14	4.43E-14	0.001252	F
7	KLF14 *	rs6467314	130,757,382	G	C	0.420416	0.015079	0.002051	1.20E-13	0.002851	0.003493	0.414354	0.021369	0.002566	8.63E-17	6.21E-16	1.96E-05	F
7	KLF14 *	rs17185445	130,757,868	T	C	0.312185	-0.016096	0.002184	1.20E-13	-0.00606	0.003709	0.10226	-0.021033	0.002736	1.58E-14	3.89E-14	0.001165	F
7	KLF14 *	rs3996352	130,760,175	G	A	0.309873	-0.015983	0.002191	1.70E-13	-0.00571	0.003721	0.124923	-0.021072	0.002745	1.72E-14	4.96E-14	0.000898	F
7	KLF14 *	rs13240528	130,760,369	A	C	0.309778	-0.016078	0.002192	1.30E-13	-0.00574	0.003722	0.122979	-0.021201	0.002746	1.22E-14	3.48E-14	0.000834	F
7	KLF14 *	rs17789506	130,760,815	A	G	0.310208	-0.015933	0.002192	2.00E-13	-0.00563	0.003721	0.13024	-0.021056	0.002746	1.83E-14	5.45E-14	0.000856	F
7	KLF14 *	rs11765979	130,761,118	C	A	0.310186	-0.015934	0.002192	2.00E-13	-0.005569	0.003722	0.134514	-0.021075	0.002747	1.77E-14	5.41E-14	0.000807	F
7	KLF14 *	rs1364422	130,761,222	T	C	0.422063	0.014936	0.002043	1.30E-13	0.002564	0.003479	0.461115	0.021255	0.002556	9.55E-17	7.30E-16	1.51E-05	F
7	KLF14 *	rs59326756	130,762,371	G	A	0.423991	0.014553	0.002046	7.50E-13	0.002471	0.003484	0.478145	0.02072	0.00256	6.08E-16	4.63E-15	2.46E-05	F
7	KLF14 *	rs12667251	130,764,699	G	A	0.344348	-0.013236	0.002153	3.70E-10	-0.004311	0.003655	0.238193	-0.018048	0.002698	2.31E-11	9.54E-11	0.002507	F
7	KLF14 *	rs185963	130,765,392	C	T	0.342509	-0.01276	0.002155	1.50E-09	-0.00345	0.003658	0.345581	-0.017777	0.0027	4.75E-11	2.48E-10	0.001634	F
7	KLF14 *	rs288484	130,765,438	A	G	0.342437	-0.012739	0.002155	1.60E-09	-0.003525	0.003658	0.335213	-0.017707	0.0027	5.66E-11	2.89E-10	0.001824	F
7	KLF14 *	rs172306	130,765,628	G	A	0.344364	-0.013121	0.002152	5.30E-10	-0.004021	0.003654	0.271108	-0.018033	0.002697	2.38E-11	1.07		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
7	KLF14 *	rs6467317	130,779,901	A	G	0.343708	-0.012239	0.002141	6.30E-09	-0.003537	0.003633	0.330254	-0.016926	0.002684	2.93E-10	1.43E-09	0.003044	F
7	KLF14 *	rs9641894	130,780,295	T	G	0.342997	-0.012184	0.002139	6.60E-09	-0.0033	0.00363	0.363347	-0.017002	0.002682	2.37E-10	1.24E-09	0.002405	F
7	KLF14 *	rs1447059	130,780,895	A	G	0.343252	-0.012092	0.002138	8.40E-09	-0.003071	0.003628	0.397305	-0.017038	0.00268	2.12E-10	1.17E-09	0.001964	F
7	KLF14 *	rs1447060	130,781,332	A	G	0.340905	-0.012185	0.002139	7.80E-09	-0.003496	0.003628	0.335327	-0.016978	0.002681	2.48E-10	1.23E-09	0.002813	F
7	KLF14 *	rs972283	130,782,095	A	G	0.314356	-0.012428	0.002173	1.00E-08	-0.003817	0.003688	0.300593	-0.016917	0.002724	5.42E-10	2.45E-09	0.004286	F
7	KLF14 *	rs972284	130,782,207	C	T	0.342061	-0.012257	0.002134	5.00E-09	-0.003113	0.003621	0.390023	-0.017298	0.002674	1.02E-10	5.64E-10	0.001632	F
8	NAT2 *	rs35548819	18,371,107	C	T	0.472483	0.017945	0.002035	2.60E-19	0.01746	0.003459	4.57E-07	0.017797	0.002551	3.12E-12	7.88E-17	0.937354	
8	NAT2 *	rs2172426	18,371,511	C	T	0.441761	-0.018506	0.002036	3.60E-21	-0.017172	0.003464	7.26E-07	-0.019081	0.00255	7.62E-14	3.20E-18	0.657273	
8	NAT2 *	rs28504072	18,372,368	T	A	0.29352	-0.013192	0.002247	3.50E-10	-0.012673	0.003814	0.000895	-0.012974	0.002817	4.18E-06	0.949413		
8	NAT2 *	rs1845376	18,372,655	T	C	0.439113	-0.018166	0.002035	1.80E-20	-0.016829	0.003462	1.19E-06	-0.018609	0.002549	2.97E-13	1.96E-17	0.678905	
8	NAT2 *	rs12156288	18,373,470	T	A	0.295668	-0.012854	0.002239	7.10E-10	-0.012177	0.003802	0.001367	-0.012778	0.002808	5.42E-06	0.888707		
8	NAT2 *	rs28556847	18,374,233	G	A	0.299489	-0.012694	0.002228	8.40E-10	-0.011794	0.003783	0.001834	-0.012857	0.002794	4.26E-06	1.96E-07	0.821058	
8	NAT2 *	rs13267304	18,374,424	T	C	0.490549	-0.018024	0.002013	5.10E-20	0.017542	0.003421	2.99E-07	0.018092	0.002524	7.85E-13	1.35E-17	0.897112	
8	NAT2 *	rs7818089	18,375,037	C	T	0.300165	-0.012617	0.002226	1.00E-09	-0.011644	0.003781	0.002082	-0.012859	0.002779	4.12E-06	0.795982		
8	NAT2 *	rs7835476	18,375,604	A	C	0.490641	-0.017909	0.002013	8.10E-20	0.017133	0.003421	4.13E-07	0.018036	0.002523	9.15E-13	2.14E-17	0.867914	
8	NAT2 *	rs10090387	18,375,924	C	T	0.299584	-0.012932	0.002226	4.50E-10	-0.011752	0.003782	0.001896	-0.01321	0.00279	2.23E-06	1.09E-35	0.76393	
8	NAT2 *	rs7006687	18,376,073	C	T	0.463162	-0.018518	0.002018	2.40E-21	-0.01822	0.003436	1.17E-07	-0.01854	0.002527	2.29E-13	1.61E-18	0.940175	
8	NAT2 *	rs4481648	18,378,050	G	T	0.461898	-0.018321	0.002031	1.40E-20	-0.018152	0.003456	1.54E-07	-0.018187	0.002542	8.82E-13	7.94E-18	0.993469	
8	NAT2 *	rs2047252	18,380,477	T	C	0.486994	0.017978	0.002049	1.80E-19	0.016075	0.003481	3.93E-06	0.018379	0.002568	8.67E-13	1.78E-16	0.594299	
8	NAT2 *	rs7010068	18,381,888	C	G	0.226966	-0.014109	0.002436	1.20E-08	-0.012096	0.004146	0.003536	-0.015109	0.003051	7.49E-07	6.71E-08	0.558351	
8	NAT2 *	rs10448136	18,382,184	A	C	0.174534	-0.016374	0.002671	9.70E-10	-0.014318	0.004554	0.001674	-0.017577	0.003341	1.46E-07	6.97E-09	0.564041	
8	NAT2 *	rs13266992	18,382,187	C	T	0.476963	-0.018042	0.002048	1.60E-19	0.017447	0.003479	5.39E-07	0.017611	0.002567	7.11E-12	2.07E-16	0.969615	
8	NAT2 *	rs62492994	18,382,666	T	A	0.266063	-0.012903	0.0023	2.00E-09	-0.011943	0.003909	0.002259	-0.012888	0.002882	7.84E-06	4.26E-07	0.845726	
8	NAT2 *	rs28417619	18,383,255	A	G	0.272963	-0.011866	0.002282	3.20E-08	-0.011524	0.003881	0.002995	-0.011341	0.00286	7.39E-05	4.68E-06	0.969755	
8	NAT2 *	rs28638278	18,383,265	A	G	0.222047	-0.013569	0.002447	3.80E-08	-0.01139	0.004162	0.00622	-0.014851	0.003065	1.28E-06	1.88E-07	0.503027	
8	NAT2 *	rs59416053	18,383,290	C	G	0.474683	0.017512	0.002038	1.10E-18	0.01704	0.00346	8.58E-07	0.0171	0.002555	2.27E-11	1.01E-15	0.988789	
8	NAT2 *	rs28679048	18,383,662	T	A	0.276594	-0.011473	0.002258	4.80E-08	-0.010461	0.00384	0.006466	-0.011168	0.002829	7.95E-05	1.01E-05	0.882097	
8	NAT2 *	rs35354956	18,383,809	C	T	0.476815	0.017943	0.002031	1.20E-19	0.017635	0.003448	3.22E-07	0.017342	0.002547	1.02E-11	1.80E-16	0.945492	
8	NAT2 *	rs13277738	18,383,997	T	C	0.473967	0.017663	0.002033	4.20E-19	0.017531	0.00345	3.81E-07	0.017007	0.002549	2.63E-11	5.34E-16	0.902806	
8	NAT2 *	rs73666635	18,384,071	C	T	0.277444	-0.01155	0.002255	3.90E-08	-0.010809	0.003831	0.004799	-0.011151	0.002826	8.01E-05	0.942593		
8	NAT2 *	rs17642674	18,384,245	C	T	0.178353	-0.015485	0.002644	3.70E-09	-0.013561	0.004502	0.002604	-0.01659	0.00331	5.50E-07	3.77E-08	0.587917	
8	NAT2 *	rs4921906	18,385,268	A	T	0.218563	-0.013867	0.002448	2.30E-08	-0.012148	0.00416	0.003509	-0.014786	0.003068	1.46E-06	1.27E-07	0.609825	
8	NAT2 *	rs13262341	18,385,587	G	A	0.478329	0.017957	0.002029	1.30E-19	0.017199	0.003442	5.94E-07	0.01758	0.002546	5.18E-12	1.67E-16	0.929176	
8	NAT2 *	rs7016785	18,385,603	C	T	0.278041	-0.011536	0.002255	4.00E-08	-0.010778	0.003825	0.004852	-0.011089	0.002828	8.92E-05	6.88E-06	0.947893	
8	NAT2 *	rs6992093	18,385,683	A	G	0.277317	-0.011613	0.002256	3.60E-08	-0.010495	0.003828	0.006133	-0.011329	0.002829	6.27E-05	7.68E-06	0.860983	
8	NAT2 *	rs10109286	18,386,093	C	T	0.475586	0.018	0.002029	7.80E-20	0.01734	0.00344	4.74E-07	0.017607	0.002546	4.87E-12	1.26E-16	0.950241	
8	NAT2 *	rs10095072	18,387,152	T	G	0.499421	0.018117	0.002025	3.30E-20	0.016576	0.003437	1.44E-06	0.018262	0.00254	6.72E-13	5.25E-17	0.693102	
8	NAT2 *	rs10095159	18,387,174	G	A	0.50032	-0.018082	0.002029	4.80E-20	-0.016718	0.003444	1.23E-06	-0.018137	0.002544	1.05E-12	1.740372		
8	NAT2 *	rs75501607	18,387,243	T	C	0.499077	0.017945	0.002024	5.00E-20	0.016447	0.003434	1.71E-06	0.018038	0.002538	1.22E-12	1.12E-16	0.709515	
8	NAT2 *	rs11783019	18,387,343	T	G	0.174877	-0.015361	0.002661	6.40E-09	-0.014091	0.004529	0.001871	-0.016072	0.003332	1.43E-06	7.01E-08	0.724656	
8	NAT2 *	rs13282367	18,387,476	G	T	0.480134	0.017814	0.002028	2.30E-19	0.017652	0.003441	2.97E-07	0.017122	0.002544	1.75E-11	2.81E-16	0.901323	
8	NAT2 *	rs10085931	18,387,939	A	G	0.500318	-0.018568	0.002032	3.10E-21	-0.016968	0.00345	8.87E-07	-0.018777	0.002549	1.82E-13	9.12E-18	0.673232	
8	NAT2 *	rs11780884	18,388,543	A	G	0.491481	0.018031	0.002031	3.80E-20	0.017238	0.003447	5.82E-07	0.017859	0.002548	2.50E-12	7.99E-17	0.884755	
8	NAT2 *	rs11992530	18,388,623	C	A	0.29172	-0.011514	0.002223	2.10E-08	-0.011601	0.003769	0.00209	-0.010804	0.002791	0.000109	4.87E-06	0.865093	
8	NAT2 *	rs4646241	18,389,186	C	T	0.272518	-0.012447	0.002262	3.20E-09	-0.012232	0.003835	0.001431	-0.011734	0.002839	3.62E-05	0.916968		
8	NAT2 *	rs4646242	18,389,939	G	A	0.272494	-0.012588	0.002262	2.20E-09	-0.012599	0.003834	0.001021	-0.011743	0.002838	3.55E-05	8.66E-07	0.857586	
8	NAT2 *	rs4646243	18,390,099	C	T	0.475573	0.018394	0.002018	6.60E-21	0.018674	0.003424	5.04E-08	0.017378	0.002531	6.87E-12	2.02E-17	0.760761	
8	NAT2 *	rs4646244	18,390,208	A	T	0.272931	-0.012517	0.002259	2.40E-09	-0.012412	0.003831	0.001202	-0.011723	0.002835	3.58E-05	1.02E-06	0.885002	
8	NAT2 *	rs4646267	18,390,403	G	A	0.475561	0.018354	0.002018	7.20E-21	0.018666	0.003424	5.10E-08	0.017335	0.002531	7.69E-12	2.28E-17	0.754718	
8	NAT2 *	rs4345600	18,390,698	G	A	0.175505	-0.015554	0.002651	3.40E-09	-0.014436	0.004512	0.001384	-0.016283	0.003319	9.47E-07	3.56E-08	0.741657	
8	NAT2 *	rs4345601	18,390,703	T	A	0.174262	-0.015231	0.002665	7.80E-09	-0.014176	0.004533	0.001773	-0.015937	0.003338	1.83E-06	8.43E-08	0.754521	
8	NAT2 *	rs4271002	18,390,758	C	G	0.176505	-0.014737	0.002641	1.70E-08	-0.013845	0.004498	0.002095	-0.015333	0.003305	3.55E-06	1.86E-07	0.789815	
8	NAT2 *	rs4646246	18,391,151	G	A	0.473439	0.018272	0.00202	1.20E-20	0.018508	0.003426	6.74E-08	0.017295	0.002534	9.14E-12	3.54E-17	0.775995	
8	NAT2	rs6984200	18,392,807	T	A	0.272838	-0.011856	0.002265	1.30E-08	-0.011914	0.003837	0.001912	-0.011078	0.002843	9.82E-05	4.06E-06	0.861001	
8	NAT2	rs55686478	18,392,865	A	G	0.472149	0.018115	0.002024	2.30E-20	0.018427	0.003431	7.99E-08	0.017046	0.00254	2.01E-11	9.03E-17	0.746266	
8	NAT2	rs2087852	18,394,416	G	A	0.273064	-0.011819	0.002264	1.40E-08	-0.012069	0.003837	0.001666	-0.010926	0.002842	0.000122	4.39E-06	0.810863	
8	NAT2	rs79533018	18,395,972	A	G	0.172733	-0.015713	0.002669	4.00E-09	-0.014124	0.004546	0.001897	-0.016586					

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
8	NAT2 *	rs115942586	18,404,518	C	T	0.166209	-0.016573	0.002707	7.30E-10	-0.013452	0.004605	0.003502	-0.018611	0.003391	4.15E-08	4.04E-09	0.367006	
8	NAT2 *	rs4646254	18,404,549	G	A	0.480615	0.01797	0.002021	5.00E-20	0.017453	0.003426	3.56E-07	0.017416	0.002536	6.85E-12	1.34E-16	0.993051	
8	NAT2 *	rs4921909	18,404,610	C	T	0.306209	-0.011674	0.002184	2.00E-08	-0.012091	0.003706	0.001109	-0.010372	0.002739	0.000154	3.76E-06	0.709303	
8	NAT2 *	rs4646256	18,404,921	C	T	0.306343	-0.011613	0.002184	2.40E-08	-0.011909	0.003707	0.001321	-0.010374	0.00274	0.000154	4.42E-06	0.739071	
8	NAT2 *	rs4244446	18,405,008	T	C	0.30633	-0.011581	0.002185	2.60E-08	-0.011865	0.003707	0.001377	-0.010352	0.00274	0.000159	4.74E-06	0.742637	
8	NAT2 *	rs4646257	18,405,036	T	C	0.479892	0.018081	0.00202	3.20E-20	0.017386	0.003423	3.86E-07	0.017621	0.002536	3.84E-12	9.95601		
8	NAT2 *	rs1495745	18,405,213	G	T	0.306322	-0.011575	0.002185	2.60E-08	-0.011869	0.003707	0.001373	-0.010336	0.00274	0.000163	4.83E-06	0.739576	
8	NAT2 *	rs1495746	18,405,332	T	C	0.305402	-0.011678	0.002187	2.10E-08	-0.011505	0.003711	0.001943	-0.010619	0.002743	0.000109	4.54E-06	0.847862	
8	NAT2 *	rs1495747	18,405,351	C	T	0.306305	-0.011576	0.002185	2.70E-08	-0.011878	0.003707	0.00136	-0.010329	0.00274	0.000165	4.84E-06	0.736816	
8	NAT2 *	rs12674710	18,406,153	C	A	0.484046	0.01807	0.002021	3.40E-20	0.017498	0.003425	3.31E-07	0.017527	0.002537	5.06E-12	9.28E-17	0.994456	
8	NAT2 *	rs2088200	18,407,894	G	C	0.169183	-0.015839	0.002691	2.60E-09	-0.012373	0.004577	0.006879	-0.018054	0.003371	1.53E-08	0.317621		
8	NAT2 *	rs74303991	18,408,156	A	G	0.161652	-0.017417	0.002739	1.90E-10	-0.014666	0.004657	0.001644	-0.019049	0.003433	2.94E-08	1.44E-09	0.448687	
8	NAT2 *	rs12676857	18,409,062	C	T	0.473057	0.017975	0.002027	6.80E-20	0.017757	0.003434	2.37E-07	0.017155	0.002546	1.65E-11	2.15E-16	0.888031	
8	NAT2 *	rs2898475	18,409,186	C	T	0.428934	-0.014303	0.002046	3.60E-13	-0.01473	0.00347	2.21E-05	-0.013388	0.002568	1.88E-07	1.53E-10	0.755981	
8	NAT2 *	rs2410561	18,409,264	A	G	0.473011	0.018028	0.002027	5.10E-20	0.017779	0.003433	2.28E-07	0.017221	0.002546	1.38E-11	1.74E-16	0.896033	
8	NAT2 *	rs2410562	18,409,322	C	T	0.428932	-0.014302	0.002046	3.60E-13	-0.014725	0.00347	2.23E-05	-0.01339	0.002568	1.88E-07	1.53E-10	0.757126	
8	NAT2 *	rs7837608	18,409,337	A	G	0.428932	-0.014302	0.002046	3.60E-13	-0.014725	0.00347	2.23E-05	-0.01339	0.002568	1.88E-07	1.53E-10	0.757126	
8	NAT2 *	rs2898476	18,409,414	A	G	0.472484	0.018085	0.002028	4.10E-20	0.017937	0.003434	1.80E-07	0.017244	0.002547	1.33E-11	1.32E-16	0.871261	
8	NAT2 *	rs7460653	18,409,473	C	G	0.474253	0.017895	0.002029	9.80E-20	0.017847	0.003436	2.10E-07	0.017063	0.002547	2.17E-11	2.50E-16	0.854494	
8	NAT2 *	rs10103029	18,409,828	G	A	0.474848	0.017869	0.002027	1.10E-19	0.017753	0.003434	2.38E-07	0.017048	0.002545	2.20E-11	2.85E-16	0.868898	
8	NAT2 *	rs10103148	18,409,919	C	A	0.476236	0.017733	0.002028	2.10E-19	0.017925	0.003434	1.82E-07	0.016772	0.002546	4.62E-11	4.55E-16	0.787305	
8	NAT2 *	rs10087857	18,409,951	C	G	0.47482	0.017828	0.002027	1.30E-19	0.017723	0.003434	2.50E-07	0.016999	0.002546	2.51E-11	3.40E-16	0.865537	
8	NAT2 *	rs10103281	18,410,032	A	G	0.426664	-0.014228	0.002047	5.20E-13	-0.01507	0.003473	1.45E-05	-0.013145	0.002569	3.17E-07	1.68E-10	0.655852	
8	NAT2 *	rs10088333	18,410,368	A	G	0.474804	0.01781	0.002027	1.50E-19	0.017725	0.003434	2.50E-07	0.016963	0.002546	2.77E-11	3.73E-16	0.858606	
8	NAT2 *	rs1603290	18,411,760	G	A	0.424523	-0.0145	0.002049	2.20E-13	-0.014745	0.003475	2.23E-05	-0.013697	0.00257	1.01E-07	8.37E-11	0.808464	
8	NAT2 *	rs10089958	18,411,833	G	A	0.477333	0.017988	0.002027	7.10E-20	0.017645	0.003434	2.84E-07	0.017261	0.002545	1.22E-11	1.90E-16	0.928528	
8	NAT2 *	rs57180587	18,412,071	T	A	0.476879	0.018096	0.002028	4.40E-20	0.017858	0.003435	2.04E-07	0.017335	0.002545	1.01E-11	1.14E-16	0.902539	
8	NAT2 *	rs1845735	18,413,520	T	C	0.427204	-0.014023	0.002049	1.20E-12	-0.014301	0.003475	3.91E-05	-0.013229	0.002571	2.72E-07	3.74E-10	0.804206	
8	NAT2 *	rs12543818	18,414,402	G	T	0.433968	-0.013687	0.002042	5.20E-12	-0.012438	0.003463	0.00033	-0.013736	0.002562	8.43E-08	9.03E-10	0.763222	
8	NAT2 *	rs12545528	18,414,438	T	G	0.433639	-0.013779	0.002041	3.90E-12	-0.012889	0.003461	0.000198	-0.013611	0.00256	1.08E-07	7.11E-10	0.86689	
8	NAT2 *	rs4921911	18,414,597	T	C	0.387914	-0.015108	0.002067	5.10E-14	-0.01285	0.003508	0.000251	-0.015807	0.002592	1.10E-09	1.02E-11	0.497923	
8	NAT2 *	rs4921912	18,414,623	G	A	0.388244	-0.015206	0.002065	3.20E-14	-0.013187	0.003506	0.00017	-0.015772	0.00259	1.17E-09	7.54E-12	0.553095	
8	NAT2 *	rs4921913	18,414,867	T	C	0.480682	-0.017988	0.002012	4.70E-20	-0.015187	0.003413	8.72E-06	-0.018839	0.002525	8.89E-14	4.06E-17	0.389608	
8	NAT2 *	rs4921914	18,414,928	T	C	0.484704	-0.01797	0.002018	7.30E-20	-0.01545	0.003422	6.43E-06	-0.018623	0.002533	2.04E-13	6.86E-17	0.456189	
8	NAT2 *	rs4921915	18,414,956	A	G	0.481874	-0.018365	0.002012	1.20E-20	-0.015669	0.003412	4.46E-06	-0.019092	0.002525	4.20E-14	1.02E-17	0.42012	
8	NAT2 *	rs35246381	18,415,025	T	C	0.48473	-0.018049	0.002012	4.20E-20	-0.015379	0.003411	6.62E-06	-0.018759	0.002525	1.15E-13	4.01E-17	0.425835	
8	NAT2 *	rs35570672	18,415,125	C	T	0.484407	-0.018117	0.002013	3.30E-20	-0.015586	0.003411	4.98E-06	-0.018733	0.002526	1.26E-13	3.34E-17	0.458478	
8	NAT2 *	rs1495741	18,415,371	A	G	0.483585	-0.018065	0.002012	3.90E-20	-0.015141	0.003411	9.16E-06	-0.018913	0.002525	7.17E-14	3.45E-17	0.374106	
8	NAT2 *	rs1495742	18,415,391	T	C	0.267596	-0.016006	0.002278	2.50E-12	-0.011423	0.003869	0.003162	-0.018495	0.002856	9.81E-11	1.01E-11	0.141396	
8	NAT2 *	rs13254811	18,415,508	G	A	0.468668	0.017078	0.002027	5.50E-18	0.015218	0.003435	9.54E-06	0.017119	0.002543	1.75E-11	7.94E-15	0.656436	
8	NAT2 *	rs1495743	18,415,790	C	G	0.484327	-0.017961	0.002015	6.90E-20	-0.014947	0.003416	1.23E-05	-0.018835	0.002528	9.72E-14	6.16E-17	0.360255	
8	NAT2 *	rs6998188	18,416,466	T	C	0.314036	-0.013473	0.002183	7.90E-10	-0.011236	0.003705	0.002436	-0.01453	0.002738	1.14E-07	7.73E-09	0.4747	
8	NAT2 *	rs6998197	18,416,486	T	C	0.313825	-0.013437	0.002184	9.50E-10	-0.010652	0.003707	0.004071	-0.014681	0.00274	8.59E-08	9.38E-09	0.382093	
8	NAT2 *	rs7815666	18,416,695	T	C	0.313549	-0.013536	0.002185	7.30E-10	-0.011076	0.003709	0.002836	-0.014705	0.00274	8.22E-08	6.47E-09	0.431381	
8	NAT2 *	rs7828813	18,416,714	C	G	0.313966	-0.013498	0.002183	7.80E-10	-0.011069	0.003706	0.002831	-0.014644	0.002738	9.08E-08	7.11E-09	0.43787	
8	NAT2 *	rs7815686	18,416,734	T	C	0.313928	-0.013471	0.002184	8.50E-10	-0.011005	0.003706	0.002998	-0.014641	0.002738	9.16E-08	7.55E-09	0.430055	
8	NAT2 *	rs7815698	18,416,746	T	A	0.31409	-0.013512	0.002184	7.40E-10	-0.010992	0.003707	0.003033	-0.014719	0.002739	7.87E-08	6.59E-09	0.418701	
8	NAT2 *	rs35942058	18,416,888	A	G	0.469139	0.017134	0.002028	7.10E-18	0.0153	0.003436	8.61E-06	0.017224	0.002547	1.39E-11	5.77E-15	0.652757	
8	NAT2 *	rs34987019	18,416,933	C	T	0.469159	0.017122	0.002028	7.40E-18	0.015285	0.003436	8.79E-06	0.017224	0.002547	1.40E-11	5.90E-15	0.650325	
8	NAT2 *	rs7812546	18,417,104	A	T	0.468453	0.017014	0.002032	1.70E-17	0.015161	0.003443	1.08E-05	0.017092	0.002552	2.18E-11	1.11E-14	0.652294	
8	NAT2 *	rs34537991	18,417,174	C	G	0.470283	0.017219	0.002031	6.50E-18	0.015519	0.003442	6.61E-06	0.017265	0.002549	1.31E-11	4.23E-15	0.683541	
8	NAT2 *	rs7828489	18,417,249	G	T	0.478724	0.01734	0.002032	3.00E-18	0.015147	0.003445	1.11E-05	0.017827	0.002551	2.87E-12	1.56E-15	0.531774	
8	NAT2 *	rs12545875	18,417,281	C	T	0.170673	-0.015926	0.00269	3.70E-09	-0.011276	0.00458	0.013826	-0.018766	0.003367	2.56E-08	8.69E-09	0.1876	
8	NAT2 *	rs7816847	18,417,679	C	A	0.470713	0.017186	0.002028	4.60E-18	0.015216	0.003437	9.70E-06	0.017342	0.002545	9.86E-12	4.60E-15	0.619177	
8	NAT2 *	rs8180964	18,417,979	T	C	0.151523	-0.017259	0.00283	2.90E-09	-0.012891	0.004814	0.007426	-0.019595	0.003545	3.33E-08	6.45E-09	0.262068	
8	NAT2 *	rs4560828	18,418,784	T	A	0.47073	0.017253	0.002034	6.40E-18	0.015571	0.003449	6.43E-06	0.017282	0.002553	1.33E-11	4.16E-15	0.69005	
8	NAT2 *	rs13255048	18,419,130	A	G	0.468679	0.017582	0.002032	1.10E-18	0.015767	0.003446	4.81E-06	0.01					

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
8	INTS10 *	rs10503666	19,887,085	C	G	0.086965	-0.03738	0.003581	6.50E-27	-0.034421	0.006109	1.80E-08	-0.038989	0.004479	3.37E-18	4.49E-24	0.546458	
8	INTS10 *	rs17482310	19,889,365	T	G	0.096787	-0.032614	0.003418	1.50E-22	-0.032038	0.005832	4.04E-08	-0.032863	0.004275	1.56E-14	4.09E-20	0.909152	
8	INTS10 *	rs79396901	19,890,937	C	T	0.087314	-0.037227	0.003571	8.30E-27	-0.033905	0.006094	2.71E-08	-0.039087	0.004466	2.22E-18	4.44E-24	0.492826	
8	INTS10 *	rs7822518	19,891,345	C	T	0.49014	0.011188	0.002023	2.10E-08	0.010977	0.003454	0.001487	0.011152	0.002253	1.06E-05	3.86E-07	0.967379	
8	INTS10 *	rs138094414	19,892,729	C	G	0.083911	-0.037516	0.003633	1.50E-26	-0.03595	0.006189	6.46E-09	-0.037968	0.004548	7.27E-17	3.45E-23	0.792797	
8	INTS10 *	rs112861901	19,893,440	C	T	0.087139	-0.037379	0.003573	3.50E-27	-0.034447	0.006093	1.61E-08	-0.039087	0.00447	2.38E-18	2.87E-24	0.539243	
8	INTS10 *	rs12550077	19,893,888	A	G	0.082608	-0.03763	0.003659	1.80E-26	-0.036346	0.00624	5.88E-09	-0.038099	0.004577	8.97E-17	3.88E-23	0.820771	
8	INTS10 *	rs1441776	19,894,049	G	C	0.48122	0.01156	0.002039	9.80E-09	0.011075	0.003479	0.001461	0.011583	0.002551	5.68E-06	2.09E-07	0.960308	
8	LPL *	rs17482386	19,896,010	G	A	0.098585	-0.034367	0.003393	2.60E-25	-0.032173	0.005786	2.75E-08	-0.035811	0.004244	3.41E-17	6.68E-23	0.61216	
8	LPL *	rs1919482	19,897,207	T	A	0.099864	-0.032798	0.003375	3.20E-24	-0.03179	0.005746	3.23E-08	-0.033605	0.004226	1.92E-15	4.18E-21	0.799108	
8	LPL *	rs76085257	19,897,616	A	C	0.082679	-0.037545	0.003654	1.70E-26	-0.03671	0.006239	4.11E-09	-0.03781	0.004568	1.32E-16	4.01E-23	0.886925	
8	LPL *	rs73597688	19,897,664	A	C	0.096895	-0.035311	0.00342	7.70E-27	-0.034786	0.00582	2.34E-09	-0.035765	0.004282	7.07E-17	1.25E-23	0.892185	
8	LPL *	rs73597690	19,898,115	A	C	0.088664	-0.03654	0.003554	7.40E-27	-0.036318	0.006063	2.16E-09	-0.036526	0.004446	2.22E-16	3.56E-23	0.977834	
8	LPL *	rs12543154	19,898,466	T	G	0.087688	-0.03706	0.003569	3.20E-27	-0.036531	0.006084	1.98E-09	-0.03726	0.004466	7.59E-17	1.13E-23	0.923017	
8	LPL *	rs10091649	19,898,910	G	T	0.092088	-0.037768	0.003508	1.50E-29	-0.0365	0.005959	9.31E-10	-0.038427	0.004398	2.52E-18	1.88E-25	0.794723	
8	LPL *	rs73597699	19,899,081	T	C	0.078715	-0.037295	0.00377	8.80E-25	-0.035819	0.006425	2.53E-08	-0.037754	0.004717	1.27E-15	2.20E-21	0.80819	
8	LPL *	rs10102717	19,899,302	T	C	0.089707	-0.037803	0.003548	4.30E-29	-0.037808	0.006031	3.76E-10	-0.037756	0.004445	2.12E-17	6.35E-25	0.994502	
8	LPL *	rs1441771	19,899,789	T	C	0.08944	-0.038629	0.003555	3.50E-30	-0.038332	0.006038	2.24E-10	-0.038669	0.004458	4.38E-18	8.07E-26	0.964254	
8	LPL *	rs1441770	19,899,808	A	G	0.089602	-0.038425	0.003552	6.30E-30	-0.038423	0.006037	2.02E-10	-0.038383	0.004451	6.86E-18	1.14E-25	0.995774	
8	LPL *	rs183801835	19,904,479	C	T	0.020348	-0.066302	0.007152	8.30E-23	-0.082591	0.012324	2.13E-11	-0.056788	0.008898	1.80E-10	2.53E-19	0.0896	
8	LPL *	rs77032723	19,906,481	T	C	0.128694	-0.039951	0.003044	2.30E-42	-0.040681	0.005179	4.17E-15	-0.038552	0.003813	5.24E-24	2.49E-36	0.740656	
8	LPL *	rs192423215	19,907,403	C	G	0.019474	-0.06891	0.007302	1.30E-23	-0.083335	0.012599	3.86E-11	-0.060269	0.009078	3.26E-11	8.47E-20	0.137432	
8	LPL *	rs60526148	19,909,692	T	C	0.153415	-0.043566	0.002814	1.20E-57	-0.04634	0.004797	4.79E-22	-0.041514	0.003521	4.84E-32	3.64E-51	0.417328	
8	LPL *	rs3988301	19,912,868	G	T	0.157988	-0.043955	0.002784	5.10E-60	-0.047451	0.00475	1.80E-23	-0.041929	0.003481	2.27E-33	6.73E-54	0.348409	
8	LPL *	rs28834434	19,917,379	A	C	0.151077	-0.04471	0.00281	4.50E-61	-0.048557	0.004787	3.78E-24	-0.041972	0.003517	8.41E-33	5.27E-54	0.267519	
8	LPL *	rs4466415	19,919,470	C	A	0.162359	-0.043754	0.002743	7.70E-61	-0.047806	0.00468	1.83E-24	-0.041178	0.00343	3.57E-33	1.09E-54	0.25326	
8	LPL *	rs77899453	19,922,799	A	G	0.150649	-0.045029	0.002818	2.00E-61	-0.049081	0.004804	1.80E-24	-0.042106	0.003526	7.79E-33	2.34E-54	0.241779	
8	LPL *	rs12179692	19,922,946	C	G	0.151708	-0.044463	0.002811	2.30E-60	-0.048907	0.004795	2.13E-24	-0.041314	0.003516	7.58E-32	2.66E-53	0.201602	
8	LPL *	rs3866470	19,927,611	A	G	0.016467	-0.072601	0.007919	1.80E-22	-0.088966	0.01365	7.40E-11	-0.06322	0.00985	1.42E-10	6.78E-19	0.126138	
8	LPL *	rs7816032	19,929,380	T	C	0.156964	-0.043776	0.002765	3.60E-60	-0.047732	0.004718	5.03E-24	-0.040755	0.003457	4.90E-32	4.04E-53	0.23296	
8	LPL *	rs139001474	19,931,094	A	T	0.160841	-0.043765	0.002747	8.00E-61	-0.047408	0.004691	5.61E-24	-0.041257	0.003434	3.26E-33	3.29E-54	0.290027	
8	LPL *	rs149764042	19,931,164	C	G	0.068047	-0.070477	0.004029	3.60E-73	-0.078561	0.006907	6.04E-30	-0.066186	0.005025	1.43E-39	1.73E-66	0.14739	
8	LPL *	rs4592053	19,931,255	G	A	0.161242	-0.043754	0.002745	6.20E-61	-0.047553	0.004688	3.81E-24	-0.041124	0.003432	4.70E-33	2.99E-54	0.26847	
8	LPL *	rs150331294	19,932,487	A	T	0.15639	-0.043754	0.002773	5.80E-60	-0.047951	0.004734	4.42E-24	-0.040728	0.003468	8.11E-32	5.86E-53	0.218328	
8	LPL *	rs182893294	19,933,207	C	T	0.013494	-0.067966	0.008755	9.10E-16	-0.069406	0.014911	3.30E-06	-0.066775	0.010959	1.14E-09	8.86E-36	0.886936	
8	LPL *	rs9694336	19,933,560	T	C	0.149634	-0.044919	0.002831	4.80E-61	-0.048028	0.004823	2.49E-23	-0.042441	0.003543	4.94E-33	2.02E-53	0.350465	
8	LPL *	rs145353248	19,933,835	T	C	0.149554	-0.045056	0.002831	2.20E-61	-0.048248	0.004823	1.58E-23	-0.042578	0.003543	3.11E-33	8.13E-54	0.343465	
8	LPL *	rs3779787	19,940,405	T	G	0.157065	-0.042562	0.002778	4.10E-57	-0.046035	0.004739	2.79E-22	-0.039884	0.003474	1.80E-30	7.76E-50	0.2952	
8	LPL *	rs1534649	19,942,130	T	G	0.157083	-0.043796	0.002775	1.90E-60	-0.046495	0.00473	8.92E-23	-0.041615	0.003473	4.75E-33	6.86E-53	0.405622	
8	LPL *	rs112127208	19,944,019	G	T	0.155681	-0.044189	0.002782	5.50E-61	-0.047242	0.004742	2.37E-23	-0.041756	0.003481	4.06E-33	1.57E-53	0.350924	
8	LPL *	rs10104051	19,944,891	T	C	0.155869	-0.044167	0.002781	5.70E-61	-0.047187	0.004742	2.70E-23	-0.041751	0.003479	3.85E-33	1.71E-53	0.355353	
8	LPL *	rs3779788	19,945,582	T	C	0.154965	-0.044371	0.002787	4.90E-61	-0.047874	0.004751	7.54E-24	-0.041713	0.003488	6.25E-33	7.79E-54	0.29588	
8	LPL *	rs56321069	19,946,485	A	T	0.154313	-0.044989	0.002799	3.00E-62	-0.047485	0.004772	2.69E-23	-0.04292	0.003503	1.74E-34	7.80E-55	0.440612	
8	LPL *	rs8716337	19,949,160	G	C	0.15368	-0.046001	0.002818	5.80E-64	-0.048309	0.004803	8.97E-24	-0.044036	0.003526	9.54E-36	1.47E-56	0.473203	
8	LPL *	rs74304285	19,950,519	A	G	0.152242	-0.046685	0.002849	8.10E-65	-0.048784	0.00485	9.08E-24	-0.044691	0.003567	5.68E-36	8.87E-57	0.496595	
8	LPL *	rs113023641	19,950,620	A	G	0.152173	-0.046745	0.00285	6.10E-65	-0.048884	0.004853	7.79E-24	-0.044727	0.003569	5.40E-36	7.24E-57	0.490109	
8	LPL *	rs73667472	19,952,184	C	T	0.059887	-0.07493	0.004285	1.30E-73	-0.083455	0.00735	7.66E-30	-0.070686	0.005343	6.48E-40	9.98E-67	0.159928	
8	LPL *	rs343	19,953,276	A	C	0.150343	-0.019359	0.00287	2.40E-12	-0.019217	0.004859	7.74E-05	-0.019254	0.003605	9.46E-08	2.57E-10	0.995105	
8	LPL *	rs249	19,953,495	C	T	0.060341	-0.078746	0.004264	3.40E-81	-0.08973	0.007326	1.86E-34	-0.073411	0.005313	2.19E-43	9.10E-75	0.071335	
8	LPL *	rs254	19,954,386	G	C	0.218289	-0.041038	0.002469	1.00E-66	-0.043659	0.004198	2.66E-25	-0.039509	0.003094	2.64E-37	1.26E-59	0.426075	
8	LPL *	rs255	19,954,390	C	T	0.218293	-0.041066	0.002469	8.30E-67	-0.043633	0.004198	2.86E-25	-0.039567	0.003094	2.08E-37	1.07E-59	0.435648	
8	LPL *	rs256	19,954,456	T	C	0.218869	-0.04148	0.002464	2.50E-68	-0.044217	0.004192	5.61E-26	-0.039865	0.003086	3.84E-38	3.97E-61	0.403143	
8	LPL *	rs263	19,955,301	T	C	0.220321	-0.041762	0.002439	2.40E-70	-0.043826	0.004154	5.46E-26	-0.040329	0.003053	8.71E-40	8.95E-63	0.497597	
8	LPL *	rs264	19,955,669	A	G	0.210153	-0.037944	0.002474	2.40E-56	-0.039267	0.004212	1.21E-20	-0.036816	0.003097	1.52E-32	2.81E-50	0.63921	
8	LPL *	rs269	19,956,156	G	T	0.219606	-0.042822	0.002455	1.30E-72	-0.043519	0.004177	2.20E-25	-0.042165	0.003075	9.73E-43	4.10E-65	0.794081	
8	LPL *	rs271	19,956,191	A	G	0.218975	-0.042747	0.002457	3.00E-72	-0.043116	0.00418	6.51E-25	-0.042208	0.003078	9.39E-43	1.16E-64	0.861161	
8	LPL *	rs285	19,957,678	T	C	0.352508	-0.037142	0.002153	8.90E-72	-0.042075	0.003652	1.13E-30	-0.03441	0.002702	4.10E-37	9.12		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
8	LPL	rs12679834	19,962,922	C	T	0.103326	-0.08412	0.003306	2.20E-153	-0.088739	0.005676	4.70E-55	-0.082329	0.004122	1.03E-88	1.87E-140	0.36077	
8	LPL	rs117199990	19,963,405	T	C	0.101117	-0.084522	0.003344	2.70E-151	-0.089461	0.005738	9.37E-55	-0.082591	0.004169	2.85E-87	1.02E-138	0.332704	
8	LPL	rs145391587	19,963,422	C	A	0.100168	-0.0851	0.003359	3.70E-152	-0.089758	0.005763	1.20E-54	-0.08327	0.004189	7.30E-88	3.38E-139	0.362504	
8	LPL	rs75278536	19,963,914	G	T	0.103029	-0.084222	0.003311	2.00E-153	-0.089209	0.00568	1.57E-55	-0.082281	0.004128	2.37E-88	1.45E-140	0.323786	
8	LPL	rs77069344	19,964,271	G	T	0.103029	-0.084221	0.003311	2.00E-153	-0.089205	0.00568	1.59E-55	-0.082281	0.004128	2.37E-88	1.46E-140	0.324085	
8	LPL	rs11570891	19,965,299	T	C	0.103244	-0.084058	0.003308	5.10E-153	-0.088771	0.005678	4.70E-55	-0.082217	0.004123	2.05E-88	3.72E-140	0.350272	
8	LPL	rs3208305	19,966,137	T	A	0.196939	-0.057392	0.002536	1.70E-119	-0.060235	0.004321	4.00E-44	-0.055692	0.003174	7.35E-69	9.12E-110	0.396838	
8	LPL	rs1803924	19,966,163	T	C	0.103246	-0.084065	0.003308	4.90E-153	-0.088777	0.005678	4.62E-55	-0.082227	0.004123	1.93E-88	3.44E-140	0.350613	
8	LPL	rs3735964	19,966,534	A	C	0.103293	-0.084048	0.003306	3.70E-153	-0.089008	0.005676	2.30E-55	-0.082107	0.004121	2.96E-88	0.325173		
8	LPL	rs13702	19,966,981	C	T	0.200863	-0.057504	0.002511	3.40E-122	-0.060909	0.004278	5.92E-46	-0.055595	0.003143	5.55E-70	1.05E-112	0.316713	
8	LPL	rs1059611	19,967,052	C	T	0.103324	-0.08398	0.003306	5.80E-153	-0.089045	0.005676	2.01E-55	-0.082008	0.004121	4.53E-88	3.51E-140	0.315718	
8	LPL	rs15285	19,967,156	T	C	0.20038	-0.057608	0.002512	2.90E-122	-0.060601	0.004281	1.89E-45	-0.055968	0.003144	7.82E-71	4.70E-113	0.383054	
8	LPL *	rs3916027	19,967,357	A	G	0.200329	-0.057606	0.002513	3.80E-122	-0.060633	0.004282	1.76E-45	-0.05596	0.003145	9.08E-71	5.11E-113	0.379023	
8	LPL *	rs77150190	19,968,791	C	G	0.094687	-0.082536	0.003439	2.50E-136	-0.086461	0.00591	2.04E-48	-0.08123	0.004284	3.97E-80	2.81E-125	0.473607	
8	LPL *	rs77729186	19,968,807	G	A	0.094687	-0.082536	0.003439	2.50E-136	-0.086461	0.00591	2.04E-48	-0.08123	0.004284	3.97E-80	2.81E-125	0.473607	
8	LPL *	rs2197089	19,968,862	A	G	0.346001	-0.036331	0.002116	7.90E-70	-0.041338	0.003596	1.50E-30	-0.033862	0.002652	2.72E-37	8.05E-65	0.094301	
8	LPL *	rs79108221	19,969,190	T	C	0.094642	-0.0825	0.003439	3.60E-136	-0.086541	0.00591	1.68E-48	-0.081128	0.004285	6.71E-80	3.93E-125	0.45842	
8	LPL *	rs10105606	19,970,337	A	C	0.200062	-0.057706	0.002514	1.70E-122	-0.061138	0.004285	3.82E-46	-0.055836	0.003146	1.92E-70	2.34E-113	0.318519	
8	LPL *	rs1962909	19,972,659	G	T	0.021651	-0.077068	0.006919	4.70E-30	-0.078653	0.011866	3.52E-11	-0.076894	0.008629	5.37E-19	1.65E-27	0.904547	
8	LPL *	rs1011685	19,973,258	T	C	0.102385	-0.083903	0.003319	2.90E-151	-0.088871	0.005694	7.04E-55	-0.081885	0.00414	4.95E-87	1.33E-138	0.320991	
8	LPL *	rs10096633	19,973,410	T	C	0.102498	-0.083785	0.003318	4.70E-151	-0.088463	0.005692	1.99E-54	-0.08191	0.004137	3.61E-87	2.75E-138	0.351662	
8	LPL *	rs17482753	19,975,135	T	G	0.101912	-0.083894	0.003326	1.50E-150	-0.088823	0.005705	1.29E-54	-0.081902	0.004148	1.06E-86	5.19E-138	0.326444	
8	LPL *	rs78963197	19,979,135	C	T	0.098808	-0.081979	0.003386	4.30E-139	-0.088807	0.005799	6.88E-53	-0.078939	0.004225	7.59E-78	1.87E-127	0.169023	
8	LPL *	rs74855321	19,979,473	T	C	0.100972	-0.083421	0.003342	3.90E-148	-0.088245	0.005733	2.08E-53	-0.081432	0.004168	5.77E-85	4.48E-135	0.336472	
8	LPL *	rs4464984	19,980,958	T	C	0.196084	-0.057358	0.002541	8.20E-119	-0.060547	0.004327	1.91E-44	-0.055512	0.003182	4.12E-68	2.44E-109	0.348493	
8	LPL *	rs58946909	19,982,830	A	G	0.101778	-0.083522	0.003331	1.00E-148	-0.088542	0.005712	3.77E-54	-0.081409	0.004155	1.97E-85	2.81E-136	0.312512	
8	LPL *	rs75551077	19,982,897	C	G	0.101823	-0.083509	0.00333	9.80E-149	-0.088621	0.005711	2.99E-54	-0.081336	0.004154	2.50E-85	2.83E-136	0.302253	
8	LPL *	rs17091891	19,985,660	C	T	0.092029	-0.083944	0.003507	2.10E-135	-0.08903	0.00601	1.30E-49	-0.081788	0.004376	6.80E-78	3.08E-124	0.329899	
8	LPL *	rs17410914	19,985,951	A	C	0.099091	-0.084654	0.003371	1.50E-149	-0.089209	0.005784	1.27E-53	-0.082744	0.004203	3.22E-86	1.55E-136	0.365904	
8	LPL *	rs117227752	19,986,350	A	G	0.101941	-0.084115	0.003326	1.60E-151	-0.088674	0.005706	2.04E-54	-0.082309	0.004148	1.43E-87	1.12E-138	0.366963	
8	LPL *	rs59147390	19,986,368	C	T	0.101938	-0.084118	0.003326	1.50E-151	-0.088678	0.005706	2.01E-54	-0.08231	0.004148	1.42E-87	1.10E-138	0.366675	
8	LPL *	rs184371102	19,986,419	T	G	0.078423	-0.081439	0.003749	5.60E-113	-0.089039	0.006431	1.48E-43	-0.0778	0.004675	3.94E-62	1.72E-102	0.15748	
8	LPL *	rs12678919	19,986,711	G	A	0.10222	-0.083665	0.003322	2.00E-150	-0.08821	0.005699	5.43E-54	-0.081891	0.004142	5.97E-87	1.23E-137	0.369768	
8	LPL *	rs7819706	19,986,904	G	A	0.101764	-0.084043	0.00333	5.30E-151	-0.088289	0.005711	7.15E-54	-0.082381	0.004153	1.64E-87	4.47E-138	0.402769	
8	LPL *	rs115129770	19,986,928	G	C	0.101764	-0.084043	0.00333	5.30E-151	-0.088289	0.005711	7.15E-54	-0.082381	0.004153	1.64E-87	4.47E-138	0.402769	
8	LPL *	rs7841189	19,987,865	T	C	0.102238	-0.083845	0.003325	2.10E-150	-0.088152	0.005699	6.45E-54	-0.082276	0.004147	1.55E-87	3.80E-138	0.404458	
8	LPL *	rs78458743	19,988,803	G	T	0.101872	-0.084123	0.003328	2.40E-151	-0.088772	0.005708	1.72E-54	-0.082276	0.004151	2.22E-87	1.46E-138	0.357382	
8	LPL *	rs14566157	19,988,978	G	C	0.101872	-0.084123	0.003328	2.40E-151	-0.088772	0.005708	1.72E-54	-0.082276	0.004151	2.22E-87	1.46E-138	0.357382	
8	LPL *	rs139894713	19,989,069	A	C	0.021639	-0.07764	0.00692	2.00E-30	-0.078726	0.011866	3.37E-11	-0.077769	0.008631	2.18E-19	6.51E-28	0.947985	
8	LPL *	rs12682115	19,989,549	A	G	0.101872	-0.084123	0.003328	2.40E-151	-0.088772	0.005708	1.72E-54	-0.082276	0.004151	2.22E-87	1.46E-138	0.357382	
8	LPL *	rs78013771	19,989,712	C	T	0.101871	-0.084121	0.003328	2.40E-151	-0.088764	0.005708	1.76E-54	-0.082276	0.004151	2.22E-87	1.49E-138	0.357936	
8	LPL *	rs76496571	19,989,930	A	C	0.101914	-0.084155	0.003327	1.60E-151	-0.08849	0.005707	3.51E-54	-0.082476	0.00415	7.63E-88	1.02E-138	0.394072	
8	LPL *	rs15003669	19,990,179	A	C	0.102015	-0.084005	0.003322	2.20E-151	-0.088179	0.005696	5.10E-54	-0.082408	0.004145	6.50E-88	1.27E-138	0.412551	
8	LPL *	rs17410962	19,990,569	A	G	0.101938	-0.084175	0.003327	1.20E-151	-0.088557	0.005705	2.67E-54	-0.082445	0.004149	8.43E-88	8.62E-139	0.386226	
8	LPL *	rs117604010	19,990,885	A	G	0.078798	-0.081575	0.00374	7.40E-114	-0.088728	0.006414	1.78E-43	-0.078211	0.004664	4.53E-63	2.38E-103	0.184793	
8	LPL *	rs17489185	19,990,988	C	G	0.101939	-0.084178	0.003327	1.20E-151	-0.088557	0.005705	2.67E-54	-0.082449	0.004149	8.26E-88	8.45E-139	0.386561	
8	LPL *	rs17410983	19,991,182	T	C	0.10194	-0.084175	0.003327	1.30E-151	-0.088557	0.005705	2.67E-54	-0.082443	0.004149	8.50E-88	8.69E-139	0.386102	
8	LPL *	rs17489226	19,991,367	T	A	0.10194	-0.084173	0.003327	1.30E-151	-0.088557	0.005705	2.67E-54	-0.082441	0.004149	8.59E-88	8.78E-139	0.385939	
8	LPL *	rs17410996	19,991,761	G	T	0.101863	-0.084116	0.003328	2.90E-151	-0.088629	0.005706	2.32E-54	-0.082343	0.004151	1.61E-87	1.43E-138	0.372946	
8	LPL *	rs75801420	19,992,159	G	T	0.101937	-0.084001	0.003328	7.00E-151	-0.088472	0.005707	3.73E-54	-0.082267	0.004151	2.40E-87	3.41E-138	0.379205	
8	LPL *	rs17091905	19,992,246	A	G	0.10196	-0.084192	0.003326	1.20E-151	-0.088615	0.005702	2.05E-54	-0.08248	0.004149	7.30E-88	5.72E-139	0.384329	
8	LPL *	rs114964604	19,992,478	G	A	0.101105	-0.083955	0.003343	9.30E-150	-0.088895	0.00573	3.14E-54	-0.08199	0.00417	4.99E-86	5.94E-137	0.329894	
8	LPL *	rs73600084	19,992,481	C	T	0.101105	-0.083955	0.003343	9.30E-150	-0.088895	0.00573	3.14E-54	-0.08199	0.00417	4.99E-86	5.94E-137	0.329894	
8	LPL *	rs76975037	19,993,997	A	C	0.101899	-0.084274	0.003328	7.10E-152	-0.089255	0.005706	4.17E-55	-0.082218	0.004151	2.97E-87	4.76E-139	0.318629	
8	LPL *	rs17489268	19,994,534	A	T	0.19991	-0.057275	0.00252	2.00E-120	-0.060305	0.004291	8.10E-45	-0.055487	0.003154	3.23E-69	8.20E-111	0.36564	
8	LPL *	rs17411024	19,994,623	A	G	0.101719	-0.084165	0.003331	2.10E-151	-0.089036	0.005711	9.61E-55	-0.082163	0.004154	5.19E-87	1.91E-138	0.33043	
8	LPL *	rs17091909	19,994,645	T	G	0.101876												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
8	LPL *	rs17411113	19,997,495	G	C	0.10195	-0.084131	0.003329	2.50E-151	-0.089272	0.005705	3.89E-55	-0.081964	0.004152	1.13E-86	1.68E-138		0.300353
8	LPL *	rs79734126	19,997,519	T	C	0.078227	-0.08138	0.003754	1.20E-112	-0.088521	0.006443	6.52E-43	-0.077898	0.004679	3.49E-62	6.65E-102		0.182139
8	LPL *	rs34564316	19,997,710	T	C	0.200026	-0.057275	0.002521	1.80E-120	-0.060302	0.004293	9.11E-45	-0.055446	0.003156	5.09E-69	1.45E-110		0.362103
8	LPL *	rs17411126	19,997,761	C	T	0.199964	-0.057404	0.002519	5.10E-121	-0.060429	0.00429	5.06E-45	-0.055584	0.003153	1.75E-69	2.79E-111		0.362821
8	LPL *	rs17411133	19,997,820	A	T	0.199992	-0.057362	0.002519	7.20E-121	-0.060492	0.004289	4.02E-45	-0.055488	0.003153	2.91E-69	3.67E-111		0.347215
8	LPL *	rs17489373	19,997,833	A	G	0.199998	-0.057364	0.002519	7.40E-121	-0.060492	0.004289	4.02E-45	-0.055494	0.003153	2.81E-69	3.55E-111		0.347725
8	LPL *	rs17411168	19,998,089	C	T	0.200228	-0.057238	0.002516	1.00E-120	-0.060336	0.004285	5.48E-45	-0.055329	0.00315	5.03E-69	8.64E-111		0.346424
8	LPL *	rs34932218	19,998,150	G	A	0.200286	-0.057222	0.002516	9.80E-121	-0.060304	0.004283	5.66E-45	-0.055332	0.003149	4.77E-69	8.47E-111		0.349607
8	LPL *	rs2165558	19,998,749	G	T	0.220103	-0.052009	0.002467	1.50E-103	-0.054394	0.004199	2.49E-38	-0.050388	0.003088	8.44E-60	0.442223		0.347218
8	LPL *	rs4523270	19,999,028	C	T	0.200332	-0.057152	0.002515	1.40E-120	-0.060253	0.004282	6.43E-45	-0.055257	0.003148	6.48E-69	1.30E-110		0.347218
8	LPL *	rs2103325	20,000,832	T	C	0.200023	-0.057311	0.002516	3.10E-121	-0.060606	0.004285	2.22E-45	-0.055335	0.003149	4.54E-69	3.17E-111		0.321513
8	LPL *	rs1581675	20,000,988	A	T	0.20003	-0.05732	0.002516	2.90E-121	-0.060591	0.004285	2.33E-45	-0.055358	0.003149	3.96E-69	2.90E-111		0.325101
8	LPL *	rs4490856	20,001,609	C	T	0.353766	-0.03975	0.00212	3.40E-83	-0.044783	0.003598	1.58E-35	-0.037061	0.002658	3.89E-44	1.41E-76		0.084294
8	LPL *	rs2119690	20,002,028	A	G	0.200114	-0.057306	0.002515	2.90E-121	-0.060487	0.004284	3.13E-45	-0.055395	0.003148	2.99E-69	2.95E-111		0.338076
8	LPL *	rs2165556	20,002,116	T	C	0.200113	-0.057303	0.002515	3.10E-121	-0.060443	0.004284	3.68E-45	-0.055415	0.003148	2.66E-69	3.08E-111		0.344252
8	LPL *	rs12541912	20,002,280	C	G	0.200491	-0.057107	0.002513	1.30E-120	-0.060082	0.00428	1.03E-44	-0.055288	0.003146	4.36E-69	1.41E-110		0.366847
8	LPL *	rs74869266	20,002,686	C	A	0.021754	-0.078593	0.006901	2.60E-31	-0.080284	0.011829	1.18E-11	-0.078391	0.008609	9.12E-20	9.85E-29		0.897027
8	LPL *	rs79236614	20,002,949	G	C	0.101753	-0.084054	0.00333	4.10E-151	-0.089391	0.005709	3.30E-55	-0.081854	0.004153	1.99E-86	2.52E-138		0.285651
8	LPL *	rs34818360	20,003,236	A	G	0.199846	-0.057146	0.002516	2.00E-120	-0.060222	0.004285	8.11E-45	-0.055293	0.00315	6.35E-69	1.61E-110		0.354014
8	LPL *	rs4083261	20,003,715	C	T	0.2005	-0.057233	0.002513	4.00E-121	-0.060211	0.00428	6.60E-45	-0.055415	0.003146	2.16E-69	4.47E-111		0.36658
8	LPL *	rs3844510	20,003,850	C	A	0.20018	-0.057476	0.002515	6.70E-122	-0.060672	0.004283	1.63E-45	-0.055558	0.003148	1.16E-69	5.96E-112		0.335973
8	LPL *	rs2410625	20,004,709	T	C	0.20016	-0.057474	0.002515	6.40E-122	-0.060655	0.004283	1.72E-45	-0.05557	0.003148	1.09E-69	5.95E-112		0.338786
8	LPL *	rs4644277	20,005,059	C	T	0.20016	-0.057474	0.002515	6.40E-122	-0.060655	0.004283	1.72E-45	-0.05557	0.003148	1.09E-69	5.95E-112		0.338786
8	LPL *	rs4389957	20,005,235	A	G	0.354414	-0.038669	0.002116	2.50E-79	-0.043891	0.003592	2.73E-34	-0.035847	0.002654	1.61E-41	9.60E-73		0.071711
8	LPL *	rs1441766	20,005,277	T	A	0.201923	-0.05715	0.002512	4.60E-121	-0.059992	0.004277	1.20E-44	-0.055403	0.003145	2.06E-69	7.75E-111		0.387418
8	LPL *	rs1441764	20,005,513	T	C	0.200506	-0.05724	0.002513	3.70E-121	-0.060238	0.00428	5.94E-45	-0.055415	0.003146	2.16E-69	4.03E-111		0.363891
8	LPL *	rs6586884	20,005,847	C	T	0.101882	-0.084554	0.003328	6.90E-153	-0.08941	0.005706	2.72E-55	-0.08256	0.004151	5.75E-88	6.04E-140		0.33165
8	LPL *	rs6999813	20,005,960	A	T	0.101882	-0.084554	0.003328	6.90E-153	-0.08941	0.005706	2.72E-55	-0.08256	0.004151	5.75E-88	6.04E-140		0.33165
8	LPL *	rs2119689	20,005,996	T	C	0.20016	-0.057474	0.002515	6.40E-122	-0.060655	0.004283	1.72E-45	-0.05557	0.003148	1.09E-69	5.95E-112		0.338786
8	LPL *	rs1441763	20,007,045	C	T	0.200166	-0.057474	0.002515	6.00E-122	-0.060653	0.004282	1.70E-45	-0.05557	0.003148	1.09E-69	5.89E-112		0.338931
8	LPL *	rs1441762	20,007,176	A	G	0.200327	-0.057544	0.002516	4.10E-122	-0.060789	0.004284	1.17E-45	-0.055607	0.003149	9.96E-70	3.71E-112		0.329716
8	LPL *	rs1441761	20,007,237	C	G	0.199509	-0.05734	0.002519	6.30E-121	-0.060269	0.004288	7.87E-45	-0.055528	0.003153	2.40E-69	5.94E-111		0.373062
8	LPL *	rs1441760	20,007,238	T	C	0.199509	-0.05734	0.002519	6.30E-121	-0.060269	0.004288	7.87E-45	-0.055528	0.003153	2.40E-69	5.94E-111		0.373062
8	LPL *	rs2083637	20,007,664	G	A	0.200128	-0.057434	0.002514	7.50E-122	-0.060551	0.004281	2.23E-45	-0.055577	0.003148	1.07E-69	7.55E-112		0.349254
8	LPL *	rs2083636	20,007,752	G	T	0.200595	-0.057292	0.002512	2.00E-121	-0.060277	0.004277	4.68E-45	-0.055461	0.003146	1.60E-69	2.37E-111		0.364357
8	LPL *	rs77237194	20,007,944	T	A	0.101922	-0.084523	0.003327	7.70E-153	-0.089373	0.005704	2.80E-55	-0.082534	0.00415	6.06E-88	6.55E-140		0.3323
8	LPL *	rs35495249	20,007,998	A	C	0.199024	-0.057829	0.002522	1.30E-122	-0.061316	0.004295	3.38E-46	-0.055785	0.003158	8.61E-70	9.29E-113		0.299452
8	LPL *	rs894211	20,008,236	T	C	0.199095	-0.057838	0.002522	1.10E-122	-0.061343	0.004294	3.02E-46	-0.055774	0.003157	8.49E-70	9.18E-113		0.296066
8	LPL *	rs894210	20,008,332	A	G	0.355683	-0.039194	0.002113	1.40E-81	-0.044539	0.003586	2.22E-35	-0.036297	0.002651	1.25E-42	6.20E-75		0.064582
8	LPL *	rs765547	20,008,763	A	G	0.200236	-0.057506	0.002514	4.50E-122	-0.060716	0.00428	1.25E-45	-0.055589	0.003148	9.45E-70	3.76E-112		0.334544
8	LPL *	rs765548	20,009,083	T	C	0.200225	-0.057511	0.002514	4.20E-122	-0.060713	0.00428	1.27E-45	-0.055599	0.003148	8.96E-70	3.63E-112		0.335692
8	LPL *	rs765549	20,009,120	G	A	0.200535	-0.057262	0.002513	3.00E-121	-0.060304	0.004278	4.33E-45	-0.055421	0.003146	2.18E-69	2.98E-111		0.357834
8	LPL *	rs1441758	20,009,367	T	A	0.200225	-0.057511	0.002514	4.20E-122	-0.060713	0.00428	1.27E-45	-0.055599	0.003148	8.96E-70	3.63E-112		0.335692
8	LPL *	rs9644637	20,009,709	C	T	0.200225	-0.057511	0.002514	4.20E-122	-0.060713	0.00428	1.27E-45	-0.055599	0.003148	8.96E-70	3.63E-112		0.335692
8	LPL *	rs9644638	20,009,889	T	C	0.199804	-0.057398	0.002517	2.40E-121	-0.060384	0.004285	4.63E-45	-0.055572	0.003152	1.57E-69	2.30E-111		0.365619
8	LPL *	rs11986942	20,009,934	G	C	0.200535	-0.057262	0.002513	3.00E-121	-0.060304	0.004278	4.33E-45	-0.055421	0.003146	2.18E-69	2.98E-111		0.357834
8	LPL *	rs34327087	20,009,983	T	G	0.200157	-0.057449	0.002514	7.40E-122	-0.060599	0.004281	1.93E-45	-0.055563	0.003148	1.16E-69	7.08E-112		0.343299
8	LPL *	rs34345068	20,010,025	T	G	0.200158	-0.057408	0.002514	1.10E-121	-0.060519	0.004282	2.62E-45	-0.055557	0.003148	1.16E-69	9.58E-112		0.350473
8	LPL *	rs2009493	20,010,342	A	G	0.200227	-0.057504	0.002514	4.70E-122	-0.060705	0.00428	1.31E-45	-0.055596	0.003148	9.14E-70	3.81E-112		0.336247
8	LPL *	rs1837843	20,010,591	T	C	0.19635	-0.056604	0.002534	8.30E-117	-0.059468	0.004315	3.56E-43	-0.054832	0.003173	7.32E-67	7.90E-107		0.386712
8	LPL *	rs1837842	20,010,779	C	T	0.200227	-0.057504	0.002514	4.70E-122	-0.060705	0.00428	1.31E-45	-0.055596	0.003148	9.14E-70	3.81E-112		0.336247
8	LPL *	rs1441757	20,010,866	C	G	0.200227	-0.057504	0.002514	4.70E-122	-0.060705	0.00428	1.31E-45	-0.055596	0.003148	9.14E-70	3.81E-112		0.336247
8	LPL *	rs1441755	20,011,377	C	T	0.200227	-0.057504	0.002514	4.70E-122	-0.060705	0.00428	1.31E-45	-0.055596	0.003148	9.14E-70	3.81E-112		0.336247
8	LPL *	rs1441754	20,011,428	A	G	0.199451	-0.057769	0.00252	1.50E-122	-0.060673	0.004289	2.15E-45	-0.055971	0.003155	2.33E-70	1.59E-112		0.377122
8	LPL *	rs4064609	20,011,460	C	T	0.199259	-0.057116	0.002523	1.20E-119	-0.061024	0.004296	9.27E-46	-0.054797	0.003159	2.39E-67	6.94E-110		0.242844
8	LPL *	rs1441753	20,011,553	A	G	0.200227	-0.057504	0.002514	4.70E-122	-0.060705	0.00428	1.31E-45	-0.055596	0.003148	9.14E-70	3.81E-112		0.336247
8	LPL *	rs4126104	20,011,855	T	G	0.200227	-0.057504	0.002514	4									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
8	LPL *	rs2898495	20,014,381	G	A	0.185626	-0.053139	0.002596	1.50E-98	-0.054277	0.004409	8.59E-35	-0.052037	0.003254	1.63E-57	3.58E-89	0.682707	
8	LPL *	rs4593558	20,014,497	G	A	0.185638	-0.053133	0.002596	1.50E-98	-0.054296	0.004409	8.13E-35	-0.052023	0.003254	1.72E-57	3.58E-89	0.678352	
8	LPL *	rs6986010	20,015,269	C	T	0.185627	-0.05314	0.002596	1.50E-98	-0.05426	0.004409	9.00E-35	-0.05205	0.003254	1.53E-57	3.52E-89	0.686687	
8	LPL *	rs35465966	20,016,045	A	C	0.185276	-0.053171	0.002598	1.40E-98	-0.054018	0.004413	2.02E-34	-0.052201	0.003257	9.27E-58	4.78E-89	0.740467	
8	LPL *	rs34693282	20,016,055	G	A	0.18554	-0.053112	0.002596	2.00E-98	-0.054206	0.00441	1.08E-34	-0.052025	0.003255	1.86E-57	5.13E-89	0.690799	
8	LPL *	rs17489539	20,016,071	A	T	0.185364	-0.053112	0.002598	2.90E-98	-0.054089	0.004412	1.64E-34	-0.052065	0.003257	1.77E-57	7.38E-89	0.712177	
8	LPL *	rs4922118	20,016,634	T	C	0.18533	-0.053328	0.002602	9.70E-99	-0.054043	0.004417	2.22E-34	-0.052447	0.003262	4.21E-58	2.39E-89	0.771236	
8	LPL *	rs4922119	20,016,642	T	C	0.18533	-0.053328	0.002602	9.70E-99	-0.054043	0.004417	2.22E-34	-0.052447	0.003262	4.21E-58	2.39E-89	0.771236	
8	LPL *	rs4375019	20,016,987	A	T	0.181686	-0.052174	0.002619	6.60E-94	-0.052779	0.00445	2.04E-32	-0.051233	0.003283	4.76E-55	2.35E-84	0.792251	
8	LPL *	rs4333617	20,017,493	G	A	0.182267	-0.051806	0.002616	5.80E-93	-0.052464	0.004444	3.95E-32	-0.050918	0.003279	2.44E-54	2.32E-83	0.779589	
8	LPL *	rs2410630	20,017,589	T	C	0.182328	-0.051693	0.002616	1.40E-92	-0.05226	0.004443	6.66E-32	-0.05084	0.003279	3.52E-54	5.60E-83	0.797084	
8	LPL *	rs6586886	20,017,897	A	G	0.18244	-0.051804	0.002614	5.50E-93	-0.052666	0.004439	2.00E-32	-0.050817	0.003276	3.28E-54	1.59E-83	0.737658	
8	LPL *	rs73208815	20,018,604	C	G	0.182249	-0.052023	0.002614	1.30E-93	-0.05315	0.004442	5.85E-33	-0.050897	0.003277	2.33E-54	3.32E-84	0.683126	
8	LPL *	rs28675909	20,018,723	T	A	0.084719	-0.081396	0.003621	4.10E-121	-0.081938	0.006172	3.48E-40	-0.081331	0.00453	5.11E-72	5.40E-109	0.936712	
8	LPL *	rs79198716	20,018,753	T	C	0.08492	-0.081332	0.003616	2.00E-121	-0.082334	0.006163	1.15E-40	-0.080983	0.004525	1.39E-71	4.86E-109	0.85979	
8	LPL *	rs78300069	20,019,013	T	C	0.085300	-0.081144	0.003606	1.80E-121	-0.081924	0.006149	1.89E-40	-0.080957	0.004511	5.71E-72	3.28E-109	0.89904	
8	LPL *	rs76737188	20,019,083	C	G	0.089079	-0.081468	0.003534	9.30E-127	-0.082825	0.006031	7.08E-43	-0.081018	0.004419	5.12E-75	1.16E-114	0.809023	
8	LPL *	rs7016880	20,019,235	C	G	0.08914	-0.081226	0.003533	3.10E-126	-0.082648	0.00603	1.03E-42	-0.080759	0.004417	1.25E-74	4.10E-114	0.800512	
8	LPL *	rs7007609	20,019,286	C	T	0.089079	-0.081468	0.003534	9.30E-127	-0.082825	0.006031	7.08E-43	-0.081018	0.004419	5.12E-75	1.16E-114	0.809023	
8	LPL *	rs7007797	20,019,459	G	T	0.08908	-0.081467	0.003534	9.40E-127	-0.082822	0.006031	7.13E-43	-0.081018	0.004419	5.12E-75	1.17E-114	0.809324	
8	LPL *	rs7004149	20,019,697	G	A	0.08908	-0.081467	0.003534	9.40E-127	-0.082822	0.006031	7.13E-43	-0.081018	0.004419	5.12E-75	1.17E-114	0.809324	
8	LPL *	rs7004158	20,019,722	C	A	0.08908	-0.081467	0.003534	9.40E-127	-0.082822	0.006031	7.13E-43	-0.081018	0.004419	5.12E-75	1.17E-114	0.809324	
8	LPL *	rs6983430	20,019,742	C	G	0.08908	-0.081467	0.003534	9.40E-127	-0.082822	0.006031	7.13E-43	-0.081018	0.004419	5.12E-75	1.17E-114	0.809324	
8	LPL *	rs77219697	20,019,950	C	T	0.089084	-0.08145	0.003535	1.10E-126	-0.082832	0.006031	7.06E-43	-0.08099	0.00442	5.99E-75	1.35E-114	0.805435	
8	LPL *	rs12678603	20,020,221	T	C	0.085396	-0.081194	0.003607	1.10E-121	-0.081874	0.00615	2.17E-40	-0.081076	0.004512	3.96E-72	2.61E-109	0.91662	
8	LPL *	rs12678604	20,020,262	G	C	0.085367	-0.081258	0.003607	8.30E-122	-0.081989	0.00615	1.67E-40	-0.081104	0.004512	3.52E-72	1.79E-109	0.907593	
8	LPL *	rs1534650	20,020,643	C	T	0.350198	-0.036845	0.002127	2.00E-72	-0.03942	0.003598	6.59E-28	-0.035353	0.002672	6.49E-40	8.33E-65	0.364144	
8	LPL *	rs7013777	20,020,845	C	T	0.186824	-0.05275	0.00259	1.00E-97	-0.054132	0.0044	9.47E-35	-0.051569	0.003247	9.39E-57	2.26E-88	0.639296	
8	LPL *	rs4922120	20,021,087	G	A	0.349569	-0.036479	0.002126	3.70E-71	-0.039233	0.003597	1.16E-27	-0.034846	0.00267	6.99E-39	1.55E-63	0.327449	
8	LPL *	rs112994260	20,021,193	A	T	0.089037	-0.081558	0.003536	6.30E-127	-0.082876	0.006033	6.66E-43	-0.081161	0.004422	3.47E-75	7.37E-115	0.818599	
8	LPL *	rs142117848	20,021,359	A	C	0.08904	-0.081568	0.003536	5.90E-127	-0.082901	0.006033	6.30E-43	-0.081162	0.004422	3.45E-75	6.94E-115	0.81617	
8	LPL *	rs4335137	20,021,363	T	A	0.187819	-0.052447	0.002585	5.00E-97	-0.053622	0.004391	2.91E-34	-0.051378	0.00324	1.39E-56	1.02E-87	0.680996	
8	LPL *	rs1819092	20,021,566	C	T	0.186809	-0.052845	0.00259	4.50E-98	-0.054229	0.0044	7.33E-35	-0.051675	0.003247	5.63E-57	1.05E-88	0.640513	
8	LPL *	rs1819094	20,021,804	G	C	0.183423	-0.051609	0.00261	1.10E-92	-0.052232	0.004434	5.40E-32	-0.050779	0.003272	2.83E-54	3.65E-83	0.792095	
8	LPL *	rs75082673	20,022,298	A	G	0.08531	-0.081285	0.003608	7.60E-122	-0.08197	0.006153	1.87E-40	-0.081147	0.004514	3.27E-72	1.87E-109	0.914049	
8	LPL *	rs11989309	20,022,819	T	C	0.088986	-0.081542	0.003537	6.40E-127	-0.082888	0.006034	6.75E-43	-0.081121	0.004423	4.47E-75	9.63E-115	0.813264	
8	LPL *	rs75675136	20,023,215	T	C	0.08897	-0.081571	0.003537	5.30E-127	-0.08291	0.006035	6.58E-43	-0.081137	0.004424	4.32E-75	9.06E-115	0.812623	
8	LPL *	rs74511807	20,023,529	A	G	0.085285	-0.081214	0.003609	1.20E-121	-0.082011	0.006152	1.70E-40	-0.081021	0.004515	5.85E-72	3.04E-109	0.896852	
8	LPL *	rs78404258	20,023,547	G	A	0.089037	-0.081414	0.003536	1.50E-126	-0.082833	0.006032	7.25E-43	-0.080938	0.004423	9.24E-75	2.13E-114	0.799986	
8	LPL *	rs74615535	20,023,725	A	G	0.088961	-0.081574	0.003537	5.30E-127	-0.083086	0.006034	4.29E-43	-0.081048	0.004424	6.48E-75	8.87E-115	0.795347	
8	LPL *	rs60223219	20,024,290	G	A	0.089004	-0.081535	0.003537	7.30E-127	-0.083041	0.006033	4.64E-43	-0.081021	0.004423	6.85E-75	1.01E-114	0.787126	
8	LPL *	rs7816447	20,025,439	C	T	0.087661	-0.081641	0.003567	2.80E-125	-0.083942	0.006084	2.93E-43	-0.080808	0.004461	2.86E-73	2.65E-113	0.677798	
8	LPL *	rs1919487	20,026,019	A	T	0.182834	-0.051958	0.002612	1.10E-93	-0.052916	0.004438	9.66E-33	-0.050955	0.003274	1.42E-54	3.34E-84	0.722156	
8	LPL *	rs73208819	20,026,413	C	T	0.223915	0.016449	0.002421	4.30E-13	0.020562	0.004122	6.22E-07	0.014968	0.00303	7.98E-07	2.00E-11	0.274243	
8	LPL *	rs114650503	20,026,746	A	G	0.085261	-0.081194	0.003609	1.20E-121	-0.08218	0.006153	1.20E-40	-0.080893	0.004516	1.04E-71	3.81E-109	0.86599	
8	LPL *	rs9644639	20,027,436	G	C	0.08523	-0.08129	0.003611	8.60E-122	-0.082263	0.006155	1.08E-40	-0.081007	0.004517	7.50E-72	2.46E-109	0.869392	
8	LPL *	rs2410631	20,028,057	T	A	0.184202	-0.051679	0.002604	4.20E-93	-0.053687	0.004424	7.50E-34	-0.050062	0.003263	4.54E-53	8.29E-84	0.509672	
8	LPL *	rs2410632	20,028,146	A	G	0.184074	-0.051693	0.002605	4.30E-93	-0.05383	0.004426	5.42E-34	-0.050031	0.003265	5.76E-53	7.60E-84	0.489764	
8	LPL *	rs11984636	20,028,215	C	T	0.085806	-0.081203	0.003602	9.20E-122	-0.083228	0.006144	9.07E-42	-0.080214	0.004506	7.82E-71	2.18E-109	0.692452	
8	LPL *	rs11984698	20,028,423	C	T	0.085773	-0.081194	0.003604	1.10E-121	-0.0833	0.006144	7.83E-42	-0.080196	0.004508	9.85E-71	2.36E-109	0.683785	
8	LPL *	rs11995475	20,029,177	T	C	0.085746	-0.081244	0.003604	9.00E-122	-0.083362	0.006145	7.03E-42	-0.080238	0.004508	8.31E-71	1.79E-109	0.681937	
8	LPL *	rs75469215	20,029,651	T	A	0.085201	-0.080746	0.003622	3.80E-119	-0.084703	0.006177	9.32E-43	-0.078945	0.00453	5.89E-68	1.67E-107	0.452218	
8	LPL *	rs4543558	20,030,818	G	C	0.184108	-0.051745	0.002607	1.90E-93	-0.05335	0.004429	2.20E-33	-0.050406	0.003268	1.22E-53	6.50E-84	0.592725	
8	LPL *	rs2178296	20,031,614	T	G	0.167223	-0.05224	0.002699	6.60E-89	-0.053054	0.004594	8.06E-31	-0.051547	0.003381	1.88E-52	3.52E-80	0.791551	
8	LPL *	rs78358410	20,031,888	G	T	0.099437	-0.078933	0.003395	6.50E-129	-0.082617	0.005794	4.38E-46	-0.077341	0.004245	4.17E-74	5.99E-117	0.462665	
8	LPL *	rs10103634	20,033,101	A	G	0.249959	-0.035419	0.002334	5.50E-57	-0.03769	0.00397	2.39E-21	-0.034568	0.002923	3.14E-32	1.16E-50	0.526658	
8	LPL *	rs139315015	20,035,786	G	A	0.113525	-0.062781	0.003184	4.80E-95	-0.066876	0.00543							

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
8	SLC18A1 *	rs6999158	20,070,502	A	T	0.264676	-0.038006	0.002316	4.30E-66	-0.040458	0.003932	8.49E-25	-0.036819	0.002905	8.95E-37	1.35E-58	0.456727	
8	SLC18A1 *	rs10106652	20,070,649	A	G	0.263216	-0.038215	0.002321	1.10E-66	-0.040928	0.003939	2.98E-25	-0.036939	0.00291	7.19E-37	3.83E-59	0.415405	
8	SLC18A1 *	rs9644568	20,071,071	A	G	0.112729	-0.060751	0.003184	2.80E-90	-0.063288	0.005432	2.49E-31	-0.060497	0.003981	4.18E-52	2.42E-80	0.678512	
8	SLC18A1 *	rs76722925	20,073,987	G	A	0.045851	-0.028333	0.004845	6.90E-11	-0.034432	0.008202	2.73E-05	-0.026589	0.006084	1.26E-05	1.06E-08	0.442506	
8	SLC18A1 *	rs80026582	20,075,352	T	C	0.042844	-0.027368	0.005023	1.80E-09	-0.03598	0.008518	2.43E-05	-0.023843	0.006302	0.000156	1.04E-07	0.252021	
8	SLC18A1 *	rs79445051	20,075,578	G	C	0.042592	-0.026601	0.005039	4.60E-09	-0.035577	0.008537	3.12E-05	-0.022841	0.006325	0.000307	2.50E-07	0.230647	
8	SLC18A1 *	rs80302977	20,076,828	C	T	0.041479	-0.02724	0.005117	5.10E-09	-0.03609	0.008689	3.31E-05	-0.023353	0.006415	0.000274	2.38E-07	0.238253	
8	SLC18A1 *	rs13281248	20,077,573	A	G	0.055447	-0.077829	0.004463	1.00E-74	-0.079891	0.007585	6.53E-26	-0.076861	0.005593	6.17E-43	7.83E-66	0.747884	
8	SLC18A1 *	rs13257289	20,077,715	C	T	0.056893	-0.075915	0.004427	3.80E-72	-0.077411	0.007509	6.88E-25	-0.07507	0.005555	1.41E-41	1.82E-63	0.802083	
8	SLC18A1 *	rs28597716	20,079,176	G	A	0.120839	-0.018639	0.003161	4.50E-10	-0.023062	0.005378	1.83E-05	-0.015696	0.003959	7.42E-05	3.93E-08	0.270032	
8	SLC18A1 *	rs7001307	20,081,435	C	T	0.116693	-0.020788	0.003155	6.20E-12	-0.025068	0.005378	3.19E-06	-0.0182	0.003947	4.07E-06	4.63E-10	0.30322	
8	SLC18A1 *	rs12542766	20,082,161	G	A	0.215528	-0.015573	0.00245	1.40E-10	-0.018685	0.004153	6.92E-06	-0.013069	0.003075	2.16E-05	4.81E-09	0.277144	
8	SLC18A1 *	rs11204085	20,083,285	C	T	0.120561	-0.020125	0.003093	1.10E-11	-0.023903	0.005262	5.63E-06	-0.017764	0.003874	4.58E-06	8.94E-10	0.347461	
8	SLC18A1 *	rs11204086	20,083,434	G	T	0.120561	-0.020125	0.003093	1.10E-11	-0.023903	0.005262	5.63E-06	-0.017764	0.003874	4.58E-06	8.94E-10	0.347461	
8	SLC18A1 *	rs11204087	20,083,516	T	C	0.120679	-0.02005	0.003091	1.20E-11	-0.023851	0.005258	5.82E-06	-0.017676	0.003871	5.04E-06	1.01E-09	0.344296	
8	SLC18A1 *	rs6586892	20,083,634	A	C	0.212093	-0.015806	0.00246	8.60E-11	-0.018634	0.004171	8.00E-06	-0.013331	0.003088	1.60E-05	4.14E-09	0.306768	
8	SLC18A1 *	rs12544702	20,083,748	C	T	0.120477	-0.020243	0.003094	8.80E-12	-0.024258	0.005265	4.13E-06	-0.017755	0.003875	4.67E-06	6.77E-10	0.319758	
8	SLC18A1 *	rs6989064	20,083,937	T	C	0.204205	-0.016346	0.002497	4.10E-11	-0.020453	0.004231	1.36E-06	-0.013441	0.003134	1.82E-05	8.53E-10	0.182872	
8	SLC18A1 *	rs4543559	20,084,343	G	A	0.216195	-0.015589	0.002443	1.20E-10	-0.018232	0.004414	1.08E-05	-0.01326	0.003066	1.55E-05	5.36E-09	0.33455	
8	SLC18A1 *	rs13263508	20,084,670	T	G	0.200635	-0.016124	0.002516	9.90E-11	-0.020051	0.004263	2.60E-06	-0.013131	0.003159	3.26E-05	2.77E-09	0.192111	
8	SLC18A1 *	rs34758843	20,085,184	T	C	0.120437	-0.020252	0.003095	9.20E-12	-0.024182	0.005266	4.46E-06	-0.017805	0.003875	4.40E-06	6.89E-10	0.329444	
8	SLC18A1 *	rs35005862	20,085,189	C	T	0.120437	-0.020252	0.003095	9.20E-12	-0.024182	0.005266	4.46E-06	-0.017805	0.003875	4.40E-06	6.89E-10	0.329444	
8	SLC18A1 *	rs73210856	20,085,295	G	A	0.120283	-0.020362	0.003097	7.50E-12	-0.024312	0.00527	4.03E-06	-0.017917	0.003879	3.91E-06	5.57E-10	0.328465	
8	SLC18A1 *	rs73210858	20,085,296	A	T	0.120283	-0.020362	0.003097	7.50E-12	-0.024312	0.00527	4.03E-06	-0.017917	0.003879	3.91E-06	5.57E-10	0.328465	
8	SLC18A1 *	rs11986461	20,085,397	A	C	0.210195	-0.016187	0.002473	3.10E-11	-0.018221	0.004193	1.41E-05	-0.014124	0.003104	5.43E-06	2.53E-09	0.432284	
8	SLC18A1 *	rs28475019	20,085,440	A	T	0.12033	-0.020145	0.003097	1.20E-11	-0.02422	0.005271	4.40E-06	-0.017629	0.003878	5.55E-06	4.88E-10	0.31379	
8	SLC18A1 *	rs13265866	20,085,516	A	G	0.120171	-0.020043	0.003099	1.50E-11	-0.024183	0.005276	4.64E-06	-0.01749	0.003881	6.67E-06	1.06E-09	0.306873	
8	SLC18A1 *	rs28450859	20,085,556	C	G	0.120004	-0.020124	0.003102	1.30E-11	-0.024213	0.00528	4.59E-06	-0.017603	0.003884	5.92E-06	9.40E-10	0.31324	
8	SLC18A1 *	rs13273470	20,085,675	C	G	0.118761	-0.019912	0.003122	3.30E-11	-0.023152	0.005308	1.31E-05	-0.017868	0.003911	4.97E-06	2.17E-09	0.422955	
8	SLC18A1 *	rs13275622	20,085,708	A	C	0.118255	-0.019976	0.003131	3.30E-11	-0.023475	0.005321	1.04E-05	-0.017733	0.003924	6.30E-06	2.19E-09	0.385161	
8	SLC18A1 *	rs13276972	20,085,797	G	A	0.139059	-0.017724	0.002951	4.40E-10	-0.019734	0.005011	8.30E-05	-0.015986	0.0037	1.58E-05	5.47418	0.504718	
8	SLC18A1 *	rs12676079	20,085,853	T	C	0.115912	-0.019486	0.003172	1.30E-10	-0.022392	0.005384	3.23E-05	-0.017708	0.003977	8.62E-06	8.70E-09	0.484102	
8	KCNJ1 *	rs56687477	36,974,792	A	G	0.320123	0.012683	0.002181	7.50E-09	0.011189	0.003704	0.002527	0.013224	0.002735	1.35E-06	8.74E-08	0.658475	
8	KCNJ1 *	rs7816345	36,988,591	T	C	0.335909	0.011849	0.002134	3.00E-08	0.011053	0.003626	0.00231	0.011938	0.002674	8.15E-06	4.51E-07	0.844224	
8	KCNJ1 *	rs75772194	36,988,917	G	A	0.335792	0.011832	0.002134	3.10E-08	0.010935	0.003626	0.002573	0.011971	0.002674	7.70E-06	4.72E-07	0.818173	
8	KCNJ1 *	rs10086016	36,990,191	C	T	0.335776	0.011835	0.002134	3.00E-08	0.010948	0.003626	0.002543	0.011969	0.002674	7.72E-06	4.68E-07	0.820592	
8	KCNJ1 *	rs28735403	36,990,520	C	T	0.335775	0.011838	0.002134	3.00E-08	0.010948	0.003626	0.002543	0.011975	0.002674	7.65E-06	4.64E-07	0.819643	
8	KCNJ1 *	rs16885613	36,990,839	C	T	0.335778	0.011836	0.002134	3.00E-08	0.010948	0.003626	0.002543	0.01197	0.002674	7.71E-06	4.68E-07	0.820437	
8	KCNJ1 *	rs4286946	36,992,428	G	C	0.335768	0.01189	0.002134	2.60E-08	0.011038	0.003625	0.002338	0.011995	0.002674	7.37E-06	4.15E-07	0.831826	
8	KCNJ1 *	rs10955009	36,994,383	A	C	0.335775	0.011826	0.002134	3.10E-08	0.011023	0.003626	0.002372	0.011908	0.002674	8.57E-06	4.85E-07	0.844232	
8	KCNJ1 *	rs10096213	36,995,695	T	C	0.335385	0.011965	0.002135	2.00E-08	0.010976	0.003627	0.002488	0.012168	0.002677	5.55E-06	3.34E-07	0.791407	
8	KCNJ1 *	rs10095380	36,995,699	C	G	0.335385	0.011965	0.002135	2.00E-08	0.010976	0.003627	0.002488	0.012168	0.002677	5.55E-06	3.34E-07	0.791407	
8	KCNJ1 *	rs10092900	36,997,193	G	T	0.335441	0.011953	0.002135	2.20E-08	0.010934	0.003628	0.002591	0.012139	0.002676	5.80E-06	3.62E-07	0.78938	
8	KCNJ1 *	rs10087804	37,000,622	G	C	0.335333	0.011938	0.002135	2.30E-08	0.010876	0.003629	0.002735	0.012144	0.002675	5.72E-06	3.75E-07	0.778626	
8	KCNJ1 *	rs13365225	37,000,965	G	A	0.335345	0.011945	0.002135	2.30E-08	0.010838	0.003629	0.00283	0.01217	0.002675	5.45E-06	3.70E-07	0.767605	
8	CYP7A1	rs28483956	58,492,900	A	G	0.257562	-0.012357	0.002326	7.60E-09	-0.014211	0.003958	0.000333	-0.010814	0.002912	0.000206	1.61E-06	0.489462	
8	CYP7A1	rs6997473	58,493,664	G	A	0.256527	-0.012191	0.002327	1.20E-08	-0.014086	0.003958	0.000376	-0.010666	0.002914	0.000254	2.20E-06	0.486556	
8	CYP7A1	rs112784971	58,493,931	T	C	0.230694	-0.013876	0.002404	6.90E-10	-0.015298	0.004091	0.000186	-0.012714	0.00301	2.43E-05	1.23E-07	0.610941	
8	CYP7A1 *	rs16923530	58,506,936	T	C	0.214288	-0.014183	0.002458	5.20E-09	-0.016056	0.004171	0.00012	-0.013533	0.003082	1.14E-05	3.95E-08	0.626784	
8	CYP7A1 *	rs200378757	58,506,959	G	A	0.210967	-0.013578	0.002479	3.50E-08	-0.015792	0.004211	0.000178	-0.012656	0.003107	4.69E-05	2.20E-07	0.549086	
8	CYP7A1 *	rs202181871	58,506,961	A	G	0.213888	-0.014242	0.00246	4.90E-09	-0.016405	0.004176	8.64E-05	-0.013387	0.003085	1.45E-05	3.63E-08	0.561122	
8	CYP7A1 *	rs76133469	58,508,253	A	T	0.215707	-0.013947	0.002451	9.00E-09	-0.015647	0.004158	0.000169	-0.013366	0.003074	1.39E-05	6.61E-08	0.65922	
8	CYP7A1 *	rs58021454	58,509,233	A	C	0.215705	-0.013958	0.002451	8.70E-09	-0.015647	0.004158	0.000169	-0.013386	0.003074	1.35E-05	6.42E-08	0.662049	
8	CYP7A1 *	rs57586133	58,510,150	G	C	0.21594	-0.013893	0.002451	1.00E-08	-0.015676	0.00416	0.000166	-0.013282	0.003074	1.58E-05	7.30E-08	0.643572	
8	CYP7A1 *	rs79242462	58,513,517	T	C	0.215655	-0.013946	0.002451	8.50E-09	-0.015659	0.004158	0.000168	-0.013352	0.003074	1.42E-05	6.67E-08	0.655663	
8	CYP7A1 *	rs4738689	58,518,054	C	A	0.215733	-0.013893	0.002451	1.00E-08	-0.015651	0.004159	0.000169						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
8	SDCBP *	rs60163136	58,542,629	G	A	0.214275	-0.01378	0.002457	1.00E-08	-0.015075	0.00417	0.000302	-0.013451	0.003082	1.29E-05	1.06E-07	0.754224	
8	SDCBP *	rs78897568	58,550,819	G	C	0.214091	-0.013755	0.00246	1.10E-08	-0.014882	0.004173	0.000365	-0.013514	0.003085	1.20E-05	1.18E-07	0.792097	
8	SDCBP *	rs74407357	58,550,842	C	A	0.213839	-0.013776	0.002461	1.10E-08	-0.015172	0.004177	0.000283	-0.013378	0.003087	1.49E-05	1.14E-07	0.729725	
8	SDCBP	rs7121175	58,554,876	G	T	0.227648	-0.013813	0.002401	6.60E-09	-0.014095	0.004072	0.00054	-0.013829	0.003013	4.50E-06	6.66E-08	0.958119	
8	SDCBP	rs58586560	58,555,472	G	A	0.227644	-0.013828	0.002401	6.30E-09	-0.014095	0.004072	0.00054	-0.01385	0.003013	4.36E-06	6.45E-08	0.961408	
8	SDCBP	rs58276148	58,557,610	G	T	0.227648	-0.01381	0.002401	6.60E-09	-0.01408	0.004072	0.000548	-0.013833	0.003013	4.48E-06	6.71E-08	0.961015	
8	SDCBP	rs75120937	58,561,531	A	C	0.22765	-0.013812	0.002401	6.60E-09	-0.01408	0.004072	0.000548	-0.013837	0.003013	4.45E-06	6.67E-08	0.961613	
8	SDCBP	rs77422315	58,565,102	T	C	0.227541	-0.013866	0.002402	5.90E-09	-0.014044	0.004074	0.00057	-0.013927	0.003014	3.88E-06	6.07E-08	0.981508	
8	SDCBP	rs79273134	58,571,506	A	G	0.227653	-0.013748	0.002401	7.90E-09	-0.014082	0.004072	0.000547	-0.013742	0.003013	5.17E-06	7.69E-08	0.946622	
8	SDCBP	rs15137362	58,573,770	G	A	0.227651	-0.013746	0.002401	7.90E-09	-0.014079	0.004072	0.000548	-0.013742	0.003013	5.17E-06	7.71E-08	0.947094	
8	SDCBP	rs16923573	58,573,961	T	C	0.227651	-0.013746	0.002401	7.90E-09	-0.014079	0.004072	0.000548	-0.013742	0.003013	5.17E-06	7.71E-08	0.947094	
8	SDCBP	rs77342596	58,574,294	A	C	0.226781	-0.013946	0.002407	5.00E-09	-0.014563	0.004083	0.000365	-0.013741	0.00302	5.43E-06	5.52E-08	0.871496	
8	SDCBP	rs80072390	58,574,300	T	A	0.226781	-0.013946	0.002407	5.00E-09	-0.014563	0.004083	0.000365	-0.013741	0.00302	5.43E-06	5.52E-08	0.871496	
8	SDCBP	rs7833413	58,575,730	G	A	0.227722	-0.013687	0.002401	9.00E-09	-0.013998	0.004072	0.00059	-0.013686	0.003013	5.65E-06	8.98E-08	0.950818	
8	SDCBP	rs60600243	58,580,172	T	A	0.22757	-0.013815	0.002402	6.50E-09	-0.0142	0.004072	0.000492	-0.013806	0.003014	4.69E-06	6.35E-08	0.938133	
8	SDCBP	rs3739326	58,582,153	A	T	0.2275	-0.013737	0.002402	8.10E-09	-0.013941	0.004075	0.000627	-0.013781	0.003014	4.90E-06	8.30E-08	0.974741	
8	NSMAF	rs59644857	58,584,375	T	C	0.227453	-0.01343	0.002403	1.70E-08	-0.013876	0.004075	0.000665	-0.013352	0.003015	9.65E-06	1.68E-07	0.917698	
8	NSMAF	rs76354168	58,585,855	T	A	0.226851	-0.0136	0.00241	1.50E-08	-0.014394	0.004085	0.000429	-0.01334	0.003025	1.05E-05	1.21E-07	0.835804	
8	TRPS1	rs727582	115,638,241	G	A	0.346398	-0.011191	0.002126	4.60E-08	-0.009451	0.003605	0.008771	-0.011578	0.002667	1.44E-05	2.61E-06	0.635329	
8	TRPS1	rs727581	115,638,264	C	T	0.346457	-0.011187	0.002126	4.50E-08	-0.009447	0.003605	0.008808	-0.011568	0.002668	1.47E-05	2.67E-06	0.636226	
8	TRPS1	rs2178950	115,640,791	C	G	0.345141	-0.011294	0.002127	3.70E-08	-0.009829	0.003606	0.006438	-0.011567	0.002669	1.48E-05	2.03E-06	0.698445	
8	TRPS1	rs2721956	115,641,429	A	C	0.344153	-0.011341	0.002128	3.30E-08	-0.009807	0.003609	0.006591	-0.011665	0.00267	1.27E-05	1.79E-06	0.679087	
8	TRPS1	rs1983541	115,642,330	T	C	0.343532	-0.011214	0.002131	4.50E-08	-0.009627	0.003613	0.00772	-0.011585	0.002673	1.49E-05	2.40E-06	0.663039	
8	TRPS1	rs2721959	115,643,980	G	T	0.344967	-0.011334	0.002125	3.00E-08	-0.009746	0.003603	0.006854	-0.011596	0.002666	1.38E-05	2.01E-06	0.679833	
8	TRPS1	rs2721960	115,644,502	A	G	0.344432	-0.011356	0.002124	3.00E-08	-0.009749	0.003604	0.006845	-0.011688	0.002665	1.17E-05	1.71E-06	0.665283	
8	TRPS1	rs2737239	115,644,722	G	A	0.34443	-0.011356	0.002124	3.00E-08	-0.009749	0.003604	0.006845	-0.011687	0.002665	1.17E-05	1.72E-06	0.665509	
8	TRPS1	rs2737241	115,645,229	A	G	0.344414	-0.011366	0.002124	2.90E-08	-0.009725	0.003604	0.006897	-0.011711	0.002665	1.12E-05	1.68E-06	0.657597	
8	TRPS1	rs2737242	115,645,500	C	T	0.344396	-0.011378	0.002124	2.80E-08	-0.009747	0.003604	0.00686	-0.011716	0.002665	1.11E-05	1.64E-06	0.660453	
8	TRPS1	rs2737243	115,645,654	C	G	0.344465	-0.011467	0.002127	2.30E-08	-0.009726	0.003607	0.007023	-0.011814	0.00267	9.79E-06	1.48E-06	0.641743	
8	TRPS1	rs2737244	115,646,004	A	A	0.34407	-0.011571	0.002128	1.70E-08	-0.009882	0.003608	0.006179	-0.011957	0.002671	7.68E-06	1.04E-06	0.643865	
8	TRPS1	rs3808478	115,666,050	C	T	0.36584	-0.011237	0.002097	4.30E-08	-0.008261	0.003561	0.020373	-0.01238	0.002628	2.51E-06	1.03E-06	0.352044	
8	TRPS1 *	rs179456	115,682,885	A	G	0.353251	-0.0119	0.002127	1.50E-08	-0.008956	0.003608	0.013068	-0.013295	0.002669	6.46E-07	1.89E-07	0.333593	
8	TRPS1 *	rs17729317	115,683,666	A	G	0.353154	-0.011849	0.002128	1.70E-08	-0.008909	0.003608	0.013553	-0.013247	0.00267	7.11E-07	2.14E-07	0.333785	
8	TRPS1 *	rs10505262	115,685,625	T	A	0.354241	-0.011549	0.002129	4.20E-08	-0.0086	0.00361	0.017211	-0.012952	0.002672	1.28E-06	4.63E-07	0.332498	
8	TRPS1 *	rs4876612	115,686,812	T	C	0.352905	-0.011855	0.002129	1.70E-08	-0.00888	0.00361	0.013908	-0.013281	0.002671	6.74E-07	2.07E-07	0.327007	
8	TRPS1 *	rs12682033	115,688,903	T	C	0.355269	-0.011703	0.002124	2.20E-08	-0.008918	0.003602	0.0133	-0.013092	0.002665	9.18E-07	2.69E-07	0.351526	
8	TRPS1 *	rs751078958	115,690,717	A	C	0.35345	-0.011951	0.002128	1.20E-08	-0.009243	0.003608	0.010426	-0.013279	0.00267	6.70E-07	1.60E-07	0.36854	
8	TRPS1 *	rs9297543	115,692,754	C	T	0.419607	-0.011453	0.002066	6.50E-09	-0.009046	0.003504	0.009842	-0.012608	0.002591	1.16E-06	2.58E-07	0.413705	
8	TRPS1 *	rs800562	115,696,794	C	T	0.355683	-0.011651	0.002124	2.60E-08	-0.00892	0.003601	0.013255	-0.013037	0.002665	1.01E-06	2.95E-07	0.358063	
8	TRPS1 *	rs800566	115,697,608	A	G	0.353198	-0.011967	0.002128	1.20E-08	-0.008952	0.003608	0.013111	-0.013408	0.00267	5.21E-07	1.54E-07	0.32079	
8	TRPS1 *	rs800575	115,703,162	C	T	0.353964	-0.011773	0.002126	2.00E-08	-0.009117	0.003604	0.011446	-0.012986	0.002668	1.15E-06	2.94E-07	0.388306	
8	TRPS1 *	rs800574	115,705,224	A	C	0.343102	-0.012188	0.002138	6.60E-09	-0.010914	0.003625	0.002616	-0.012739	0.002683	2.09E-06	1.37E-07	0.685661	
8	TRPS1 *	rs800572	115,706,211	A	G	0.344979	-0.011871	0.002134	1.40E-08	-0.010792	0.003619	0.002871	-0.01237	0.002678	3.92E-06	7.72E-07	0.725902	
8	TRPS1 *	rs2960151	115,706,393	C	A	0.343085	-0.012166	0.002138	7.00E-09	-0.010922	0.003625	0.002595	-0.012707	0.002683	2.22E-06	1.44E-07	0.692414	
8	TRPS1 *	rs800534	115,707,671	C	T	0.40223	-0.011293	0.002073	1.30E-08	-0.01086	0.003515	0.002016	-0.011468	0.002601	1.05E-05	5.08E-07	0.889296	
8	TRPS1 *	rs800535	115,708,163	T	G	0.401699	-0.01131	0.002073	1.20E-08	-0.010778	0.003516	0.002183	-0.011493	0.002601	1.01E-05	5.26E-07	0.870181	
8	TRPS1 *	rs800536	115,708,179	A	T	0.401725	-0.011301	0.002073	1.30E-08	-0.010783	0.003516	0.002173	-0.011477	0.002601	1.04E-05	5.38E-07	0.873817	
8	TRPS1 *	rs800537	115,709,757	C	T	0.357338	-0.011503	0.002117	3.20E-08	-0.01049	0.003588	0.003467	-0.01191	0.002656	7.45E-06	6.00E-07	0.750487	
8	TRPS1 *	rs800538	115,710,763	A	G	0.32646	-0.012776	0.002162	2.10E-09	-0.011709	0.003665	0.001406	-0.01298	0.002714	1.76E-06	6.56E-08	0.780488	
8	TRPS1 *	rs2736231	115,711,170	C	T	0.404254	-0.011122	0.002076	2.30E-08	-0.009955	0.00352	0.004693	-0.01162	0.002604	8.23E-06	8.70E-07	0.703761	
8	TRPS1 *	rs2694027	115,711,171	T	G	0.404294	-0.011297	0.002074	1.40E-08	-0.010289	0.003517	0.003448	-0.011751	0.002602	6.40E-06	5.17E-07	0.73836	
8	TRPS1 *	rs800539	115,712,972	G	A	0.325695	-0.012924	0.002166	1.40E-09	-0.011937	0.00367	0.001148	-0.013086	0.002719	1.51E-06	4.69E-08	0.801216	
8	TRPS1 *	rs800541	115,717,911	G	T	0.328517	-0.01234	0.002159	6.60E-09	-0.011577	0.00366	0.001568	-0.01246	0.00271	4.35E-06	1.73E-07	0.846338	
8	TRPS1 *	rs800542	115,719,218	C	T	0.326741	-0.012728	0.002162	2.50E-09	-0.011858	0.003663	0.001215	-0.012858	0.002713	2.18E-06	7.05E-08	0.826344	
8	TRPS1 *	rs800571	115,720,681	T	C	0.326468	-0.012687	0.002162	2.80E-09	-0.011799	0.003664	0.001288	-0.012831	0.002713	2.29E-06	7.80E-08	0.82098	
8	TRPS1 *	rs2694034	115,728,597	A	G	0.404072	-0.01119	0.002064	1.50E-08	-0.011577	0.003504	0.000958	-0.01087	0.002589	2.72E-05	6.34E-07	0.871138	
8	TRPS1 *	rs7834801	115,731,575	T	C	0.332101	-0.011											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
8	TRPS1 *	rs2975510	115,742,985	T	C	0.332062	-0.011777	0.002135	2.10E-08	-0.012291	0.003623	0.000697	-0.011284	0.002678	2.54E-05	4.42E-07	0.823165	
8	TRPS1 *	rs2960146	115,743,211	A	G	0.331387	-0.011751	0.002135	2.30E-08	-0.012426	0.003622	0.000607	-0.011115	0.002677	3.15E-05	4.77E-07	0.776994	
8	TRPS1 *	rs2223058	115,744,962	G	A	0.33298	-0.011558	0.002132	3.60E-08	-0.012255	0.003618	0.000711	-0.010999	0.002674	3.94E-05	6.83E-07	0.780062	
8	TRPS1 *	rs800505	115,750,077	G	C	0.331079	-0.011544	0.002147	4.30E-08	-0.012687	0.003645	0.000503	-0.010735	0.002693	6.78E-05	0.666697		
8	TRPS1 *	rs800540	115,779,523	A	C	0.36283	-0.011483	0.002096	4.60E-08	-0.012453	0.003563	0.000476	-0.010672	0.002627	4.91E-05	5.79E-07	0.687424	
8	TRPS1 *	rs2736202	115,780,200	C	T	0.417381	-0.011255	0.002038	9.00E-09	-0.011027	0.003463	0.001458	-0.011464	0.002554	7.24E-06	2.64E-07	0.919121	
8	TRPS1 *	rs2736203	115,781,341	T	C	0.386246	-0.011623	0.002064	6.90E-09	-0.011812	0.003507	0.000762	-0.011429	0.002586	1.00E-05	1.97E-07	0.929886	
8	TRPS1 *	rs2694037	115,782,005	G	A	0.38617	-0.011641	0.002064	6.80E-09	-0.011874	0.003509	0.00072	-0.011396	0.002587	1.07E-05	2.00E-07	0.91275	
8	TRPS1 *	rs2694036	115,782,050	G	T	0.386246	-0.011623	0.002064	6.90E-09	-0.011812	0.003507	0.000762	-0.011429	0.002586	1.00E-05	1.97E-07	0.929886	
8	TRPS1 *	rs2694035	115,782,367	T	C	0.436509	-0.010968	0.002027	1.40E-08	-0.010232	0.003444	0.002977	-0.011366	0.002541	7.80E-06	5.46E-07	0.79111	
8	TRPS1 *	rs2960157	115,783,315	G	G	0.436679	-0.011045	0.002027	1.20E-08	-0.010268	0.003444	0.002879	-0.011457	0.002541	6.61E-06	4.52E-07	0.781234	
8	TRPS1 *	rs2960156	115,783,651	A	G	0.386362	-0.011539	0.002066	9.30E-09	-0.01185	0.003512	0.000745	-0.011315	0.00259	1.26E-05	2.41E-07	0.902471	
8	TRPS1 *	rs800507	115,784,313	G	T	0.3868	-0.011748	0.002067	4.80E-09	-0.0121	0.003515	0.000579	-0.011517	0.002591	8.88E-06	1.36E-07	0.893723	
8	TRPS1 *	rs800508	115,784,686	C	A	0.417292	-0.011262	0.002037	9.10E-09	-0.010971	0.003463	0.00154	-0.011511	0.002553	6.63E-06	2.55E-07	0.900021	
8	TRPS1 *	rs800509	115,785,304	A	C	0.417292	-0.011262	0.002037	9.10E-09	-0.010971	0.003463	0.00154	-0.011511	0.002553	6.63E-06	2.55E-07	0.900021	
8	TRPS1 *	rs800510	115,786,001	G	A	0.417293	-0.011263	0.002037	9.10E-09	-0.010972	0.003463	0.001538	-0.011511	0.002553	6.63E-06	2.55E-07	0.900205	
8	TRPS1 *	rs813889	115,786,626	C	T	0.436511	-0.010962	0.002027	1.50E-08	-0.010214	0.003444	0.003028	-0.011366	0.002541	7.80E-06	5.46E-07	0.787759	
8	TRPS1 *	rs800511	115,786,942	C	A	0.38624	-0.01162	0.002064	7.10E-09	-0.011814	0.003507	0.00076	-0.011425	0.002586	1.01E-05	1.98E-07	0.928828	
8	TRPS1 *	rs800512	115,787,367	C	T	0.38624	-0.01162	0.002064	7.10E-09	-0.011814	0.003507	0.00076	-0.011425	0.002586	1.01E-05	1.98E-07	0.928828	
8	TRPS1 *	rs808982	115,788,025	T	G	0.417261	-0.011266	0.002038	9.10E-09	-0.010965	0.003463	0.001551	-0.011516	0.002553	6.57E-06	2.54E-07	0.898093	
8	TRPS1 *	rs800514	115,788,658	T	A	0.386558	-0.011736	0.002065	5.30E-09	-0.012007	0.003509	0.000627	-0.011527	0.002588	8.51E-06	1.41E-07	0.912319	
8	TRPS1 *	rs800516	115,789,141	A	G	0.386321	-0.011696	0.002063	5.30E-09	-0.01198	0.003506	0.000638	-0.011458	0.002585	9.45E-06	1.58E-07	0.904635	
8	TRPS1 *	rs800517	115,789,263	G	A	0.417306	-0.011404	0.002037	5.60E-09	-0.011147	0.003462	0.001287	-0.011628	0.002553	5.30E-06	1.75E-07	0.910986	
8	TRPS1 *	rs800518	115,789,554	C	T	0.416921	-0.011276	0.002038	8.30E-09	-0.011069	0.003464	0.001403	-0.011454	0.002554	7.42E-06	2.61E-07	0.928625	
8	TRPS1 *	rs1065806	115,790,856	A	G	0.387382	-0.011941	0.002065	3.00E-09	-0.011574	0.003509	0.000979	-0.011996	0.002587	3.60E-06	9.34E-08	0.922781	
8	TRPS1 *	rs1065805	115,790,904	C	T	0.417319	-0.011459	0.002037	4.90E-09	-0.011095	0.003462	0.001359	-0.011731	0.002553	4.40E-06	1.53E-07	0.882369	
8	TRPS1 *	rs1089116	115,792,232	C	A	0.386899	-0.011698	0.002062	5.20E-09	-0.012027	0.003506	0.000607	-0.01139	0.002584	1.06E-05	1.69E-07	0.883693	
8	TRPS1 *	rs1089117	115,793,066	T	C	0.417323	-0.011455	0.002037	5.00E-09	-0.011095	0.003462	0.001359	-0.011724	0.002553	4.46E-06	1.55E-07	0.883726	
8	TRPS1 *	rs800519	115,793,803	A	G	0.436966	-0.011183	0.002027	7.60E-09	-0.010236	0.003443	0.002962	-0.011636	0.00254	4.71E-06	3.35E-07	0.74357	
8	TRPS1 *	rs702775	115,794,278	G	A	0.386308	-0.011752	0.002063	4.60E-09	-0.011864	0.003507	0.000721	-0.01158	0.002586	7.61E-06	1.44E-07	0.947992	
8	TRPS1 *	rs702774	115,794,425	G	A	0.387067	-0.011672	0.002065	5.60E-09	-0.011717	0.003511	0.00085	-0.011555	0.002588	8.12E-06	1.79E-07	0.970394	
8	TRPS1 *	rs702773	115,794,432	C	A	0.437388	-0.011151	0.002029	8.10E-09	-0.010255	0.003447	0.002943	-0.011624	0.002543	4.92E-06	3.47E-07	0.749398	
8	TRPS1 *	rs702772	115,794,691	G	A	0.386891	-0.011685	0.002062	5.40E-09	-0.012017	0.003506	0.000614	-0.011373	0.002584	1.09E-05	1.76E-07	0.882427	
8	TRPS1 *	rs2736207	115,797,429	C	T	0.436378	-0.011101	0.002027	1.00E-08	-0.010264	0.003443	0.002882	-0.011547	0.00254	5.56E-06	3.83E-07	0.764415	
8	TRPS1 *	rs2694033	115,797,806	G	A	0.437137	-0.011079	0.002026	9.80E-09	-0.010527	0.003443	0.002243	-0.011334	0.002539	8.17E-06	4.41E-07	0.850332	
8	TRPS1 *	rs800591	115,799,160	T	C	0.410273	-0.010831	0.002043	3.20E-08	-0.010659	0.003474	0.002159	-0.01103	0.00256	1.66E-05	8.38E-07	0.931571	
8	TRPS1 *	rs800590	115,800,352	C	T	0.412674	-0.010755	0.002049	4.80E-08	-0.010468	0.003484	0.00267	-0.010967	0.002568	1.97E-05	1.20E-06	0.908268	
8	TRPS1 *	rs800589	115,800,477	T	C	0.379433	-0.011129	0.002071	3.20E-08	-0.011363	0.003521	0.001256	-0.010906	0.002595	2.67E-05	8.00E-07	0.916784	
8	TRPS1 *	rs800588	115,800,917	T	G	0.410579	-0.010704	0.002041	4.80E-08	-0.010402	0.00347	0.002728	-0.010905	0.002557	2.03E-05	1.26E-06	0.906966	
8	TRPS1 *	rs800587	115,801,052	T	G	0.379433	-0.011129	0.002071	3.20E-08	-0.011363	0.003521	0.001256	-0.010906	0.002595	2.67E-05	8.00E-07	0.916784	
8	TRPS1 *	rs800586	115,801,679	G	A	0.439023	-0.010704	0.002025	3.00E-08	-0.010142	0.003439	0.0032	-0.011047	0.002539	1.37E-05	1.00E-06	0.832387	
8	TRPS1 *	rs800585	115,801,697	T	A	0.379432	-0.011126	0.002071	3.20E-08	-0.011335	0.003521	0.001292	-0.010922	0.002595	2.60E-05	8.00E-07	0.924916	
8	TRPS1 *	rs800553	115,804,366	T	C	0.379205	-0.011333	0.002077	1.90E-08	-0.011417	0.003529	0.001222	-0.011231	0.002604	1.63E-05	4.88E-07	0.966158	
8	TRPS1 *	rs800552	115,804,530	G	T	0.379805	-0.011253	0.002077	2.40E-08	-0.011536	0.003529	0.001084	-0.011016	0.002603	2.34E-05	6.15E-07	0.905719	
8	TRPS1 *	rs800551	115,807,041	C	G	0.408204	-0.011044	0.002054	2.20E-08	-0.010875	0.003488	0.001828	-0.010986	0.002575	2.01E-05	8.61E-07	0.979507	
8	TRPS1 *	rs702771	115,807,640	C	T	0.380075	-0.011176	0.00208	3.30E-08	-0.011513	0.003535	0.001131	-0.01087	0.002608	3.11E-05	8.39E-07	0.883688	
8	TRPS1 *	rs800547	115,807,948	T	G	0.379687	-0.011292	0.002078	2.20E-08	-0.011634	0.00353	0.000989	-0.011021	0.002605	2.35E-05	5.68E-07	0.888913	
8	TRPS1 *	rs800546	115,808,960	C	A	0.408194	-0.011127	0.002055	1.80E-08	-0.010885	0.003489	0.001818	-0.011123	0.002576	1.59E-05	6.88E-07	0.95609	
8	TRPS1 *	rs800545	115,810,420	A	G	0.40757	-0.011155	0.002055	1.60E-08	-0.01075	0.003489	0.002074	-0.011264	0.002578	1.26E-05	6.20E-07	0.905609	
8	TRPS1 *	rs800544	115,811,384	A	G	0.37916	-0.011452	0.002079	1.40E-08	-0.011706	0.003532	0.000923	-0.011254	0.002607	1.60E-05	3.69E-07	0.918	
8	TRPS1 *	rs2694045	115,811,975	G	A	0.378661	-0.011704	0.002086	7.60E-09	-0.011531	0.003544	0.001145	-0.011769	0.002614	6.82E-06	1.99E-07	0.957027	
8	TRPS1 *	rs2254401	115,812,474	C	T	0.365667	-0.011733	0.002101	8.40E-09	-0.014539	0.003569	4.69E-05	-0.010389	0.002634	8.08E-05	1.04E-07	0.349518	
8	TRPS1 *	rs1040333	115,813,123	T	C	0.415853	-0.010982	0.002048	1.80E-08	-0.013092	0.003477	0.000168	-0.010163	0.002568	7.66E-05	3.32E-07	0.497976	
8	TRPS1 *	rs1474517	115,813,316	C	T	0.365129	-0.011545	0.002091	1.50E-08	-0.014259	0.003549	5.95E-05	-0.010283	0.002622	8.88E-05	1.43E-07	0.367565	
8	TRPS1 *	rs1474518	115,813,464	C	T	0.365352	-0.011577	0.002091	1.40E-08	-0.014102	0.00355	7.18E-05	-0.010402	0.002622	7.35E-05	1.43E-07	0.401881	
8	TRPS1 *	rs2736208	115,814,018	T	C	0.396761	-0.010892	0.002064	3.70E-08	-0.012803	0.003504	0.00026	-0.010268	0.002588	7.35E-05	4.82E-07	0.560599	
8	TRPS1 *	rs2694043	115,814,036	A	G	0.365536	-0.011582											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
8	TRPS1 *	rs2975507	115,820,984	T	C	0.415535	-0.0114	0.002045	6.30E-09	-0.013265	0.003468	0.000132	-0.010689	0.002565	3.12E-05	1.13E-07	0.550437	
8	TRPS1 *	rs800555	115,822,721	G	C	0.415644	-0.0114	0.002044	6.50E-09	-0.0132	0.003468	0.000142	-0.010745	0.002565	2.82E-05	1.10E-07	0.569154	
8	TRPS1 *	rs800556	115,823,198	A	G	0.415645	-0.011392	0.002044	6.60E-09	-0.013204	0.003468	0.000142	-0.010729	0.002565	2.91E-05	1.13E-07	0.566076	
8	TRPS1 *	rs800557	115,823,633	G	T	0.395849	-0.011129	0.00206	2.40E-08	-0.012959	0.003497	0.000212	-0.010476	0.002583	5.04E-05	2.79E-07	0.567838	
8	TRPS1 *	rs800558	115,824,362	C	T	0.36863	-0.011634	0.00209	1.10E-08	-0.014462	0.003548	4.64E-05	-0.010313	0.00262	8.35E-05	1.07E-07	0.346858	
8	TRPS1 *	rs800559	115,824,846	A	C	0.416077	-0.011306	0.002044	8.30E-09	-0.013311	0.003469	0.000125	-0.010535	0.002564	4.02E-05	1.37E-07	0.519941	
8	TRPS1 *	rs800560	115,825,661	C	G	0.368492	-0.011844	0.00209	6.00E-09	-0.014386	0.003548	5.07E-05	-0.010707	0.002621	4.44E-05	6.38E-08	0.404235	
8	TRPS1 *	rs1014180	115,827,487	A	T	0.395876	-0.011048	0.00206	3.00E-08	-0.012784	0.003497	0.000259	-0.010445	0.002582	5.30E-05	3.52E-07	0.590525	
8	TRPS1 *	rs2358065	115,827,713	T	C	0.415647	-0.011296	0.002044	8.70E-09	-0.01304	0.003468	0.000171	-0.010675	0.002564	3.18E-05	1.47E-07	0.583455	
8	TRPS1 *	rs2960152	115,828,444	C	T	0.395881	-0.011119	0.00206	2.60E-08	-0.012848	0.003497	0.000241	-0.010534	0.002583	4.58E-05	2.87E-07	0.594602	
8	TRPS1 *	rs2975508	115,828,544	A	G	0.365612	-0.011561	0.002093	1.50E-08	-0.013644	0.003555	0.000125	-0.010661	0.002625	4.93E-05	0.499555		
8	TRPS1 *	rs800533	115,828,760	C	T	0.415595	-0.01134	0.002045	8.00E-09	-0.013163	0.003469	0.000149	-0.010663	0.002565	3.27E-05	1.32E-07	0.562222	
8	TRPS1 *	rs800532	115,829,884	A	G	0.429937	-0.011646	0.002042	2.30E-09	-0.012615	0.003462	0.000271	-0.011405	0.002562	8.66E-06	6.53E-08	0.778786	
8	TRPS1 *	rs800531	115,831,047	T	C	0.359803	-0.011282	0.002128	3.00E-08	-0.012428	0.00361	0.000579	-0.011113	0.00267	3.20E-05	0.769603		
8	TRPS1 *	rs800530	115,831,666	C	T	0.389662	-0.010927	0.002103	4.00E-08	-0.012271	0.003569	0.000589	-0.010528	0.002639	6.68E-05	9.47E-07	0.694568	
8	SLC30A8	rs11558471	117,173,494	G	A	0.467177	-0.010948	0.002014	3.70E-08	-0.01071	0.003439	0.001852	-0.010896	0.002517	1.52E-05	0.965173		
8	SLC30A8 *	rs11774700	117,208,031	C	T	0.47086	-0.010836	0.002018	4.30E-08	-0.011424	0.003443	0.000912	-0.010205	0.002524	5.33E-05	1.15E-06	0.775192	
8	TRIB1 *	rs2003370	125,456,589	C	A	0.125647	0.0178	0.003094	3.70E-09	0.0181	0.005245	0.000562	0.017268	0.003884	8.86E-06	1.32E-07	0.898441	
8	TRIB1 *	rs12678799	125,458,589	T	C	0.127608	0.01841	0.003065	9.40E-10	0.019462	0.005196	0.000181	0.017669	0.003846	4.41E-06	2.34E-08	0.781481	
8	TRIB1 *	rs68089270	125,460,482	G	A	0.128827	0.018673	0.003048	4.30E-10	0.019741	0.005164	0.000133	0.017997	0.003827	2.60E-06	1.06E-08	0.786086	
8	TRIB1 *	rs6983834	125,460,570	A	G	0.12886	0.018713	0.003047	3.90E-10	0.020011	0.005163	0.000107	0.017894	0.003825	2.94E-06	9.68E-09	0.741836	
8	TRIB1 *	rs10956249	125,461,257	T	C	0.129184	0.018465	0.003038	5.80E-10	0.019106	0.005145	0.000206	0.018027	0.003815	2.33E-06	1.43E-08	0.866254	
8	TRIB1 *	rs12679189	125,461,323	C	T	0.129442	0.01825	0.003034	9.10E-10	0.01905	0.00514	0.000212	0.01772	0.003809	3.33E-06	2.08E-08	0.835251	
8	TRIB1 *	rs6999569	125,463,528	G	A	0.144804	-0.023183	0.002888	2.40E-16	-0.023279	0.004915	2.21E-06	-0.023068	0.003616	1.83E-10	1.96E-14	0.972376	
8	TRIB1 *	rs2980856	125,464,137	G	C	0.144535	-0.023017	0.002887	4.10E-16	-0.023174	0.004914	2.45E-06	-0.022863	0.003615	2.63E-10	3.07E-14	0.959328	
8	TRIB1 *	rs2954017	125,464,631	T	C	0.434925	0.031515	0.00203	2.80E-56	0.04017	0.003446	2.31E-31	0.026405	0.002546	3.64E-25	1.39E-53	0.001322	M
8	TRIB1 *	rs2954018	125,464,911	C	T	0.297002	0.026942	0.002203	1.50E-35	0.036979	0.003725	3.42E-23	0.020868	0.002769	5.04E-14	1.86E-34	0.000522	M
8	TRIB1 *	rs2980855	125,465,234	C	T	0.14454	-0.023043	0.002887	3.80E-16	-0.023183	0.004914	2.43E-06	-0.022887	0.003615	2.51E-10	2.90E-14	0.961195	
8	TRIB1 *	rs2980854	125,465,255	T	C	0.144546	-0.023053	0.002887	3.70E-16	-0.023237	0.004914	2.30E-06	-0.022887	0.003615	2.51E-10	2.75E-14	0.954255	
8	TRIB1 *	rs2954019	125,465,517	A	G	0.144398	-0.023104	0.002889	3.40E-16	-0.023182	0.004916	2.45E-06	-0.022984	0.003617	2.16E-10	2.54E-14	0.974148	
8	TRIB1 *	rs2001945	125,465,736	G	C	0.434991	0.031533	0.00203	2.40E-56	0.040224	0.003446	1.89E-31	0.026395	0.002546	3.77E-25	1.18E-53	0.001254	M
8	TRIB1 *	rs2980853	125,466,108	A	C	0.441586	0.031022	0.002028	1.40E-54	0.039459	0.003441	2.06E-30	0.026126	0.002543	9.94E-25	3.31E-52	0.001839	M
8	TRIB1 *	rs2001846	125,466,208	T	C	0.435015	0.031526	0.002031	2.50E-56	0.040214	0.003446	2.00E-31	0.026393	0.002547	3.87E-25	1.28E-53	0.001265	M
8	TRIB1 *	rs2001845	125,466,402	A	G	0.297036	0.026942	0.002204	1.50E-35	0.037108	0.003726	2.43E-23	0.020789	0.002769	6.34E-14	1.66E-34	0.000442	M
8	TRIB1 *	rs2001844	125,466,503	A	G	0.441656	0.031078	0.002028	9.40E-55	0.039683	0.003441	9.88E-31	0.026059	0.002544	1.34E-24	2.14E-52	0.001461	M
8	TRIB1 *	rs7015677	125,466,516	G	A	0.137529	0.017831	0.002927	4.70E-10	0.017597	0.004973	0.000405	0.018098	0.003668	8.22E-07	9.91E-09	0.93525	
8	TRIB1 *	rs6982636	125,467,073	G	A	0.441773	0.031067	0.002028	9.50E-55	0.039687	0.00344	9.42E-31	0.026308	0.002543	1.43E-24	2.18E-52	0.001428	M
8	TRIB1 *	rs6982502	125,467,120	C	T	0.435024	0.031481	0.00203	3.30E-56	0.040178	0.003445	2.13E-31	0.026301	0.002546	5.55E-25	1.95E-53	0.001204	M
8	TRIB1 *	rs2980886	125,467,846	G	A	0.441827	0.031032	0.002027	1.20E-54	0.039629	0.00344	1.11E-30	0.026305	0.002543	1.44E-24	2.59E-52	0.001489	M
8	TRIB1 *	rs4871603	125,468,125	C	T	0.303941	0.026084	0.002188	8.50E-34	0.036048	0.003697	1.95E-22	0.020157	0.002751	2.44E-13	4.95E-33	0.000567	M
8	TRIB1 *	rs2980882	125,468,458	A	G	0.441857	0.031026	0.002028	1.30E-54	0.039617	0.00344	1.18E-30	0.026045	0.002543	1.40E-24	2.68E-52	0.001519	M
8	TRIB1 *	rs2980880	125,468,730	G	A	0.297232	0.026899	0.002202	1.70E-35	0.037102	0.003722	2.26E-23	0.020701	0.002767	7.74E-14	1.88E-34	0.000409	M
8	TRIB1 *	rs2980879	125,469,233	A	T	0.297038	0.026619	0.0022	7.10E-35	0.036686	0.00372	6.47E-23	0.020461	0.002766	1.45E-13	9.88E-34	0.000468	M
8	TRIB1 *	rs2980876	125,469,452	C	T	0.29731	0.026848	0.002202	2.30E-35	0.037121	0.003722	2.14E-23	0.020619	0.002767	9.61E-14	2.21E-34	0.000376	M
8	TRIB1 *	rs2980875	125,469,505	A	G	0.448751	0.03126	0.002027	1.30E-55	0.039665	0.003439	9.60E-31	0.026345	0.002542	3.97E-25	6.24E-53	0.001849	M
8	TRIB1 *	rs2954020	125,469,710	A	G	0.297396	0.026964	0.002201	1.30E-35	0.036988	0.00372	2.92E-23	0.02084	0.002767	5.27E-14	1.67E-34	5.00E-04	M
8	TRIB1 *	rs2954021	125,469,835	A	G	0.440838	0.031964	0.002028	4.40E-58	0.040753	0.003441	2.57E-32	0.026746	0.002544	7.96E-26	3.48E-55	0.00107	M
8	TRIB1 *	rs2954022	125,470,379	C	A	0.447474	0.031482	0.002025	1.80E-56	0.040071	0.003436	2.14E-31	0.026486	0.002541	2.06E-25	7.34E-54	0.001484	M
8	TRIB1 *	rs28495284	125,470,681	G	A	0.310176	0.025035	0.002218	1.30E-30	0.034322	0.003752	6.23E-20	0.019222	0.002786	5.40E-12	3.13E-29	0.00124	M
8	TRIB1 *	rs2954024	125,470,688	A	G	0.297434	0.026893	0.002202	1.90E-35	0.037062	0.003724	2.60E-23	0.020713	0.002767	7.48E-14	2.10E-34	0.000428	M
8	TRIB1 *	rs17406109	125,470,898	T	C	0.143327	0.018635	0.002875	3.20E-11	0.018452	0.004884	0.000159	0.018868	0.003604	1.69E-07	8.91E-10	0.945353	
8	TRIB1 *	rs12544593	125,471,585	A	G	0.142902	0.018582	0.002879	3.80E-11	0.018462	0.004892	0.000162	0.018818	0.003609	1.89E-07	1.01E-09	0.953246	
8	TRIB1 *	rs2980870	125,471,598	A	G	0.311505	0.025835	0.002202	5.10E-33	0.035788	0.003721	7.25E-22	0.020023	0.002768	4.88E-13	3.58E-32	0.00068	M
8	TRIB1 *	rs4336630	125,472,034	T	C	0.304586	0.025752	0.002186	3.70E-33	0.035995	0.003695	2.13E-22	0.01966	0.002748	8.74E-13	1.89E-32	0.000391	M
8	TRIB1 *	rs2954025	125,472,221	C	T	0.304593	0.025763	0.002186	3.50E-33	0.035983	0.003695	2.20E-22	0.019683	0.002748	8.20E-13	1.83E-32	0.000403	M
8	TRIB1 *	rs2954026	125,472,284	T	G	0.297802	0.026577	0.0022	8.20E-35	0.036964	0.003721	3.13E-23	0.020271	0.002765	2.39E-13	7.89E-34	0.000319	M
8	TRIB1 *	rs2980862	125,472,396	G	C	0.297787	0.026619											

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
8	TRIB1 *	rs34417638	125,476,332	C	T	0.143307	0.018679	0.002876	3.10E-11	0.0186	0.004885	0.000142	0.018859	0.003605	1.71E-07	8.09E-10	0.965877	
8	TRIB1 *	rs2980871	125,476,688	G	A	0.126351	-0.024881	0.003044	1.50E-16	-0.024369	0.005176	2.55E-06	-0.025118	0.003814	4.68E-11	5.88E-15	0.907306	
8	TRIB1 *	rs2954029	125,478,730	A	T	0.447994	0.031576	0.002024	7.20E-57	0.040318	0.003435	8.74E-32	0.026401	0.002539	2.75E-25	4.02E-54	0.001127	M
8	TRIB1 *	rs2954030	125,479,062	T	C	0.318156	0.023818	0.002163	6.00E-29	0.033564	0.003661	5.07E-20	0.018032	0.002718	3.37E-11	1.53E-28	0.000661	M
8	TRIB1 *	rs2954031	125,479,491	G	T	0.461806	0.030228	0.002021	3.20E-52	0.038989	0.003428	6.09E-30	0.025104	0.002535	4.26E-23	4.04E-50	0.001132	M
8	TRIB1 *	rs13258507	125,480,355	G	T	0.143071	0.018811	0.002877	2.40E-11	0.019251	0.004889	8.32E-05	0.018661	0.003606	2.32E-07	6.58E-10	0.922667	
8	TRIB1 *	rs12679547	125,480,843	A	G	0.142902	0.018815	0.00288	2.30E-11	0.0193	0.004894	8.11E-05	0.018641	0.00361	2.47E-07	6.81E-10	0.913738	
8	TRIB1 *	rs2954032	125,481,150	A	G	0.297539	0.026821	0.002203	1.60E-35	0.037444	0.003727	1.03E-23	0.02041	0.002768	1.75E-13	1.93E-34	0.000246	M
8	TRIB1 *	rs2954033	125,481,504	A	G	0.298259	0.026801	0.0022	1.80E-35	0.037359	0.003721	1.09E-23	0.020396	0.002764	1.66E-13	1.93E-34	0.000255	M
8	TRIB1 *	rs4457349	125,482,075	G	A	0.418962	-0.02018	0.002041	7.30E-24	-0.029552	0.003472	1.80E-17	-0.014819	0.002556	6.91E-09	9.30E-24	0.000636	M
8	TRIB1 *	rs12680798	125,483,251	G	C	0.097882	-0.027728	0.003425	5.20E-16	-0.028239	0.005819	1.24E-06	-0.026514	0.004292	6.73E-10	4.00E-14	0.811449	
8	TRIB1 *	rs10808546	125,483,576	T	C	0.125904	-0.024735	0.003036	1.40E-16	-0.024293	0.005161	2.55E-06	-0.024733	0.003804	8.24E-11	1.03E-14	0.945294	
8	TRIB1 *	rs6470358	125,483,683	G	A	0.436916	0.010953	0.002034	4.50E-08	0.020308	0.003456	4.33E-09	0.00555	0.002549	0.029454	2.98E-09	0.000593	M
8	TRIB1 *	rs35309034	125,486,023	A	C	0.152451	0.019618	0.002803	7.50E-13	0.020209	0.004768	2.28E-05	0.019326	0.003511	3.80E-08	3.32E-11	0.88148	
8	TRIB1 *	rs4870941	125,486,586	C	G	0.160584	0.016816	0.002751	2.50E-10	0.018183	0.004674	0.000101	0.016237	0.003448	2.54E-06	7.93E-09	0.737539	
8	TRIB1 *	rs4870942	125,486,661	C	T	0.440193	0.011169	0.002041	2.30E-08	0.01998	0.003468	8.57E-09	0.006037	0.002558	0.018316	3.83E-09	0.00122	M
8	TRIB1 *	rs2980859	125,487,187	C	G	0.283268	0.029053	0.002239	5.60E-40	0.039833	0.00379	8.26E-26	0.022188	0.002813	3.23E-15	3.16E-38	0.000187	M
8	TRIB1 *	rs4351435	125,487,636	G	A	0.283267	0.029043	0.002239	5.90E-40	0.039851	0.00379	7.85E-26	0.022162	0.002813	3.49E-15	3.24E-38	0.00018	M
8	TRIB1 *	rs28601761	125,487,789	G	C	0.150973	-0.02459	0.002821	3.00E-19	-0.025046	0.0048	1.85E-07	-0.02355	0.003533	2.72E-11	2.75E-16	0.80176	
8	TRIB1 *	rs8180991	125,488,108	G	C	0.154942	0.019201	0.002779	1.50E-12	0.02024	0.004726	1.87E-05	0.018626	0.003482	9.00E-08	6.34E-11	0.783266	
8	TRIB1 *	rs2980858	125,488,935	T	C	0.283746	0.028911	0.002238	1.20E-39	0.03981	0.003788	8.31E-26	0.02197	0.002811	5.79E-15	5.65E-38	0.00017	M
8	TRIB1 *	rs12677676	125,490,284	G	A	0.154696	0.019125	0.002782	1.90E-12	0.020043	0.004731	2.30E-05	0.01862	0.003486	9.44E-08	8.09E-11	0.808646	
8	TRIB1 *	rs55921265	125,491,673	A	G	0.154698	0.019123	0.002782	2.00E-12	0.020041	0.004731	2.30E-05	0.01861	0.003486	9.59E-08	8.22E-11	0.807618	
8	TRIB1 *	rs13252684	125,492,119	A	G	0.140935	0.020676	0.002927	6.40E-13	0.021235	0.00497	1.96E-05	0.020549	0.003671	2.22E-08	1.70E-11	0.911576	
8	TRIB1 *	rs13252187	125,492,126	T	C	0.137388	0.02143	0.002969	2.90E-13	0.021437	0.00504	2.14E-05	0.021618	0.003724	6.61E-09	5.69E-12	0.976871	
8	TRIB1 *	rs13252202	125,492,129	T	C	0.137388	0.02143	0.002969	2.90E-13	0.021437	0.00504	2.14E-05	0.021618	0.003724	6.61E-09	5.69E-12	0.976871	
8	TRIB1 *	rs6987702	125,492,484	T	C	0.434318	0.011243	0.002035	2.20E-08	0.019663	0.00346	1.36E-08	0.006401	0.00225	0.012088	4.16E-09	0.00204	M
8	TRIB1 *	rs34087092	125,492,520	A	G	0.154689	0.019058	0.002782	2.40E-12	0.019827	0.004731	2.81E-05	0.018614	0.003486	9.52E-08	9.88E-11	0.83654	
8	TRIB1 *	rs7598532	125,493,463	C	T	0.403623	-0.021042	0.002057	1.60E-25	-0.031343	0.003499	3.52E-19	-0.015307	0.002576	2.89E-09	8.10E-26	0.000225	M
8	TRIB1 *	rs13271368	125,493,898	T	C	0.160337	0.017966	0.002749	2.10E-11	0.020289	0.004676	1.45E-05	0.016918	0.003444	9.15E-07	4.69E-10	0.561594	
8	TRIB1 *	rs112875651	125,494,452	A	G	0.130443	-0.02442	0.002998	2.20E-16	-0.025081	0.005089	8.44E-07	-0.023084	0.003761	8.58E-10	3.50E-14	0.75227	
8	TRIB1 *	rs2980888	125,495,066	T	C	0.281184	0.029603	0.002241	1.40E-41	0.03984	0.003797	1.01E-25	0.023105	0.002813	2.25E-16	2.78E-39	0.000401	M
8	TRIB1 *	rs2954038	125,495,147	C	A	0.281354	0.029721	0.00224	6.60E-42	0.039782	0.003796	1.14E-25	0.023294	0.002812	1.24E-16	1.74E-39	0.000485	M
8	TRIB1 *	rs6987904	125,495,783	T	C	0.402681	-0.020764	0.00207	1.40E-24	-0.031395	0.003521	5.06E-19	-0.014914	0.002593	9.11E-09	3.56E-25	0.000165	M
8	TRIB1 *	rs6989280	125,496,504	G	A	0.439109	0.011321	0.002063	2.10E-08	0.020105	0.003498	9.32E-09	0.006223	0.002589	0.016266	3.75E-09	0.001432	M
9	DMRT2 *	rs10958983	1,035,081	C	T	0.371824	0.012174	0.002098	1.50E-08	0.009927	0.003569	0.005428	0.012842	0.002624	1.01E-06	1.32E-07	0.510677	
9	DMRT2 *	rs4741016	1,036,132	C	T	0.371603	0.012236	0.002097	1.30E-08	0.00971	0.003568	0.006516	0.013084	0.002624	6.27E-07	9.84E-08	0.446152	
9	DMRT2 *	rs12001314	1,038,063	C	A	0.37398	0.012277	0.002093	1.00E-08	0.009822	0.003562	0.00584	0.013025	0.002618	6.64E-07	9.42E-08	0.468661	
9	DMRT2 *	rs10959032	1,038,666	T	C	0.372216	0.012376	0.002097	8.40E-09	0.009847	0.003572	0.005851	0.013155	0.002622	5.35E-07	7.65E-08	0.455283	
9	ABCA1	rs2740488	104,899,461	C	A	0.230758	-0.016678	0.002395	6.30E-13	-0.014018	0.004066	0.000569	-0.01837	0.002999	9.37E-10	1.88E-11	0.388992	
9	ABCA1	rs1883025	104,902,020	T	C	0.23343	-0.017287	0.002379	1.10E-13	-0.015165	0.004037	0.000174	-0.01865	0.002981	4.06E-10	2.72E-12	0.487375	
9	ABCA1	rs2575876	104,903,458	A	G	0.231243	-0.017501	0.002387	5.40E-14	-0.015303	0.004052	0.00016	-0.018985	0.002989	2.19E-10	1.38E-12	0.46455	
9	ABCA1	rs1800978	104,903,697	G	C	0.165987	-0.014393	0.002712	3.40E-08	-0.012526	0.0046	0.006487	-0.016002	0.003399	2.54E-06	3.77E-07	0.543431	
9	ABCA1	rs2524708	104,904,866	C	T	0.16403	-0.015091	0.002737	1.00E-08	-0.013495	0.004646	0.003686	-0.016528	0.003429	1.46E-06	1.33E-07	0.599411	
9	PTPN3	rs149557654	109,434,560	A	G	0.201425	-0.01761	0.002534	8.70E-13	-0.01718	0.004293	6.35E-05	-0.017585	0.003177	3.19E-08	7.41E-11	0.939489	
9	PTPN3	rs61543659	109,434,691	G	A	0.266156	-0.014337	0.002302	7.70E-11	-0.010993	0.003902	0.004862	-0.015509	0.002886	7.88E-08	1.01E-08	0.352195	
9	PTPN3	rs17201500	109,434,773	A	G	0.201584	-0.017755	0.002532	5.30E-13	-0.017333	0.00429	5.39E-05	-0.017743	0.003175	2.34E-08	4.70E-11	0.9387	
9	PTPN3	rs75992442	109,434,977	G	A	0.2016	-0.017795	0.002532	4.70E-13	-0.017462	0.00429	4.74E-05	-0.017741	0.003175	2.35E-08	4.18E-11	0.958424	
9	PTPN3	rs16914135	109,435,232	C	A	0.266318	-0.014449	0.002301	5.60E-11	-0.011222	0.003901	0.004033	-0.015546	0.002885	7.23E-08	7.87E-09	0.372713	
9	PTPN3	rs75714696	109,435,291	C	G	0.201696	-0.017711	0.002532	6.00E-13	-0.017359	0.004289	5.24E-05	-0.017668	0.003174	2.67E-08	5.20E-11	0.953834	
9	PTPN3	rs7044766	109,435,739	T	C	0.266392	-0.01442	0.002301	5.80E-11	-0.011209	0.003901	0.00407	-0.015508	0.002885	7.80E-08	8.55E-09	0.375525	
9	PTPN3	rs56208012	109,436,498	T	A	0.266397	-0.014408	0.002301	6.00E-11	-0.01118	0.003901	0.004167	-0.015503	0.002885	7.89E-08	8.83E-09	0.372941	
9	PTPN3	rs112194983	109,437,194	T	C	0.201976	-0.017672	0.00253	6.10E-13	-0.017511	0.004286	4.44E-05	-0.017478	0.003172	3.69E-08	6.08E-11	0.994999	
9	PTPN3	rs17793718	109,437,226	A	G	0.201904	-0.017661	0.002531	6.40E-13	-0.01741	0.004287	4.94E-05	-0.017525	0.003173	3.41E-08	6.24E-11	0.982745	
9	PTPN3	rs17201542	109,437,914	C	T	0.202121	-0.017635	0.00253	6.30E-13	-0.017244	0.004287	5.81E-05	-0.017507	0.003172	3.48E-08	7.42E-11	0.960647	
9	PTPN3	rs17793748	109,441,345	T	C	0.283027	-0.013058	0.002241	1.90E-09	-0.011139	0.003801	0.003392	-0.013939	0.002808	7.02E-07	6.07E-08	0.55352	
9	PTPN3	rs3793527	109,443,174	A	C													

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
9	PTPN3	rs3808877	109,463,552	G	C	0.353711	-0.011869	0.002123	1.10E-08	-0.007998	0.0036	0.026337	-0.013506	0.002661	3.95E-07	2.17E-07	0.218563	
9	PTPN3	rs74479508	109,464,472	C	G	0.309846	-0.013675	0.002195	2.40E-10	-0.011213	0.00372	0.002585	-0.014611	0.002751	1.11E-07	7.96E-09	0.462786	
9	PTPN3	rs111960097	109,468,618	A	G	0.314349	-0.013892	0.00219	1.50E-10	-0.011266	0.003719	0.002457	-0.014843	0.002743	6.43E-08	4.47E-09	0.438948	
9	PTPN3	rs57707037	109,473,833	C	T	0.24473	-0.018071	0.002383	1.60E-15	-0.017843	0.004035	9.91E-06	-0.018077	0.002989	1.52E-09	6.49E-13	0.962706	
9	PTPN3	rs60227798	109,473,873	T	C	0.24478	-0.018133	0.002382	1.20E-15	-0.017881	0.004033	9.40E-06	-0.018148	0.002988	1.30E-09	5.30E-13	0.957611	
9	PTPN3	rs76298084	109,474,452	T	G	0.243929	-0.018162	0.002388	1.30E-15	-0.017958	0.004041	8.96E-06	-0.018133	0.002995	1.45E-09	5.65E-13	0.972217	
9	PTPN3	rs7046039	109,474,599	C	T	0.295024	-0.014564	0.002248	8.70E-12	-0.013168	0.00381	0.000551	-0.015162	0.002819	7.65E-08	1.33E-09	0.673807	
9	PTPN3	rs58272963	109,474,628	A	G	0.244719	-0.018293	0.002383	7.00E-16	-0.018207	0.004035	6.50E-06	-0.018227	0.002989	1.10E-09	3.17E-13	0.996836	
9	PTPN3	rs59668107	109,474,718	A	G	0.244715	-0.018292	0.002383	7.00E-16	-0.018225	0.004035	6.36E-06	-0.018218	0.002989	1.12E-09	3.16E-13	0.99876	
9	PTPN3	rs78579422	109,475,873	T	C	0.243884	-0.018485	0.002389	5.20E-16	-0.018399	0.004043	5.43E-06	-0.018428	0.002996	7.95E-10	1.94E-13	0.995463	
9	PTPN3	rs75862441	109,477,363	T	C	0.229238	-0.018757	0.002444	4.70E-16	-0.019262	0.004141	3.35E-06	-0.018293	0.003064	2.43E-09	3.65E-13	0.850679	
9	PTPN3	rs41529151	109,478,114	G	C	0.229196	-0.019588	0.002442	3.00E-17	-0.020601	0.004137	6.48E-07	-0.018748	0.003063	9.54E-10	3.00E-14	0.718891	
9	PTPN3	rs56279802	109,478,850	T	C	0.254937	-0.016869	0.002354	2.10E-14	-0.015737	0.003994	8.21E-05	-0.017348	0.002949	4.15E-09	1.30E-11	0.745498	
9	PTPN3	rs77824033	109,478,856	C	T	0.229591	-0.019518	0.002439	3.20E-17	-0.020676	0.004133	5.75E-07	-0.018625	0.002458	1.16E-09	3.23E-14	0.689948	
9	PTPN3	rs55727942	109,479,011	G	T	0.254677	-0.016649	0.002363	5.60E-14	-0.015323	0.00401	0.000134	-0.017221	0.00296	6.15E-09	3.03E-11	0.703321	
9	PTPN3	rs55824262	109,479,013	C	T	0.254791	-0.016603	0.002362	6.40E-14	-0.015394	0.004009	0.000124	-0.017098	0.002959	7.79E-09	3.55E-11	0.732375	
9	PTPN3	rs12376215	109,479,090	A	T	0.254658	-0.016984	0.002355	1.50E-14	-0.015731	0.003996	8.34E-05	-0.017532	0.00295	2.89E-09	9.27E-12	0.716792	
9	PTPN3	rs117969049	109,480,282	T	C	0.229773	-0.019235	0.002436	8.40E-17	-0.020447	0.004129	7.46E-07	-0.01829	0.003055	2.19E-09	7.73E-14	0.674507	
9	PTPN3	rs17793873	109,482,041	T	C	0.230194	-0.018838	0.002434	3.10E-16	-0.019981	0.004123	1.28E-06	-0.018025	0.003051	3.58E-09	2.10E-13	0.702908	
9	PTPN3	rs10816818	109,482,093	G	A	0.382466	-0.012767	0.002116	4.60E-10	-0.014601	0.003593	4.88E-05	-0.011419	0.002649	1.65E-05	2.39E-08	0.476009	
9	PTPN3	rs74928072	109,482,095	A	G	0.230208	-0.018862	0.002433	3.00E-16	-0.019962	0.004122	1.30E-06	-0.018078	0.003051	3.21E-09	1.93E-13	0.713348	
9	PTPN3	rs75024825	109,482,136	T	C	0.229982	-0.018857	0.002432	3.30E-16	-0.019854	0.004121	1.48E-06	-0.018123	0.00305	2.89E-09	1.96E-13	0.735699	
9	PTPN3	rs10816819	109,482,961	T	C	0.38259	-0.012917	0.002112	2.70E-10	-0.015081	0.003587	2.65E-05	-0.011419	0.002644	1.58E-05	1.29E-08	0.411203	
9	PTPN3	rs75113691	109,483,493	C	G	0.231021	-0.018683	0.002426	4.60E-16	-0.01987	0.004111	1.36E-06	-0.017889	0.003042	4.20E-09	2.61E-13	0.698448	
9	PTPN3	rs78919659	109,483,714	T	C	0.230746	-0.018634	0.002427	6.00E-16	-0.019587	0.004112	1.94E-06	-0.017946	0.003042	3.76E-09	3.30E-13	0.74842	
9	PTPN3	rs10816820	109,485,747	G	A	0.383991	-0.01241	0.002108	1.20E-09	-0.014503	0.003581	5.17E-05	-0.010907	0.00264	3.64E-05	5.38E-08	0.418808	
9	PTPN3	rs78424787	109,485,849	A	C	0.232217	-0.017849	0.002419	6.00E-15	-0.019074	0.0041	3.34E-06	-0.017029	0.003032	2.00E-08	2.83E-12	0.688452	
9	PTPN3	rs1541088	109,486,171	C	A	0.383276	-0.012584	0.002106	7.50E-10	-0.014479	0.003578	5.25E-05	-0.011124	0.002636	2.51E-05	3.83E-08	0.448583	
9	PTPN3	rs944359	109,487,352	C	T	0.388661	-0.011704	0.002073	6.90E-09	-0.012936	0.003526	0.000245	-0.010437	0.002594	5.81E-05	3.65E-07	0.568166	
9	PTPN3	rs944358	109,487,414	A	G	0.388674	-0.011705	0.002073	6.80E-09	-0.01291	0.003526	0.000252	-0.010452	0.002594	5.67E-05	3.67E-07	0.574381	
9	PTPN3	rs7860448	109,487,631	G	T	0.388673	-0.011715	0.002073	6.50E-09	-0.012888	0.003526	0.000259	-0.010481	0.002594	5.40E-05	3.58E-07	0.582326	
9	PTPN3	rs59380239	109,488,319	T	C	0.249815	-0.016919	0.002332	2.60E-14	-0.017715	0.003958	7.74E-06	-0.016052	0.00292	3.95E-08	1.23E-11	0.735288	
9	PTPN3	rs12002395	109,488,846	T	A	0.388478	-0.011757	0.002073	6.00E-09	-0.012752	0.003526	0.000301	-0.010619	0.002594	4.30E-05	3.62E-07	0.626167	
9	PTPN3	rs4978392	109,489,512	C	A	0.388533	-0.011793	0.002073	5.40E-09	-0.012793	0.003525	0.000287	-0.010659	0.002594	4.02E-05	2.98E-07	0.625887	
9	PTPN3	rs75577555	109,495,675	T	C	0.250075	-0.017236	0.002329	8.40E-15	-0.01771	0.003954	7.59E-06	-0.016576	0.002917	1.36E-08	4.26E-12	0.817427	
9	PTPN3	rs184172568	109,497,966	T	C	0.249803	-0.016897	0.002335	2.40E-14	-0.01745	0.003965	1.09E-05	-0.016171	0.002924	3.26E-08	1.41E-11	0.795141	
9	PTPN3	rs117533884	109,499,788	G	C	0.250091	-0.017184	0.002328	9.20E-15	-0.017618	0.003952	8.38E-06	-0.016547	0.002916	1.42E-08	4.90E-12	0.827345	
9	PTPN3	rs10979893	109,499,895	C	A	0.387798	-0.011968	0.00207	2.80E-09	-0.012653	0.00352	0.000327	-0.011039	0.002591	2.06E-05	7.11E-07	0.711915	
9	PTPN3	rs12685453	109,500,599	G	C	0.391866	-0.01231	0.00208	1.00E-09	-0.013207	0.003534	0.000188	-0.011232	0.002604	1.63E-05	8.50E-08	0.652849	
9	PTPN3	rs78042633	109,502,844	T	C	0.250048	-0.017142	0.002328	9.80E-15	-0.017819	0.003953	6.63E-06	-0.016391	0.002916	1.94E-08	5.31E-12	0.771249	
9	PTPN3	rs17793891	109,502,949	G	A	0.250437	-0.017075	0.002326	1.40E-14	-0.017467	0.003949	9.87E-06	-0.016434	0.002913	1.74E-08	6.96E-12	0.833192	
9	PTPN3	rs7847913	109,505,698	T	G	0.38777	-0.011916	0.00207	3.40E-09	-0.01256	0.00352	0.000361	-0.011002	0.002591	2.19E-05	2.08E-07	0.721508	
9	PTPN3	rs10123707	109,508,041	C	G	0.275322	-0.015167	0.002258	9.80E-13	-0.013208	0.003834	0.000574	-0.015967	0.002829	1.69E-08	3.18E-10	0.562515	
9	PTPN3	rs4978816	109,509,115	C	T	0.387556	-0.01169	0.002071	6.60E-09	-0.012436	0.00352	0.000414	-0.010691	0.002591	3.73E-05	3.92E-07	0.689775	
9	PTPN3	rs61358126	109,511,453	G	A	0.249963	-0.017111	0.002329	1.30E-14	-0.017717	0.003954	7.56E-06	-0.016358	0.002918	2.11E-08	6.53E-12	0.782191	
9	PTPN3	rs2150260	109,511,914	G	A	0.28179	-0.014739	0.00224	5.40E-12	-0.013165	0.003804	0.000541	-0.015305	0.002806	5.01E-08	8.65E-10	0.650822	
9	PTPN3	rs79437785	109,512,085	C	T	0.249929	-0.017065	0.00233	1.40E-14	-0.017651	0.003955	8.18E-06	-0.016317	0.002918	2.30E-08	7.65E-12	0.786134	
9	PTPN3	rs6477708	109,513,462	G	A	0.281643	-0.014703	0.002242	6.40E-12	-0.013118	0.003807	0.000574	-0.015265	0.002807	5.54E-08	1.01E-09	0.649894	
9	PTPN3	rs7341726	109,513,495	G	C	0.281632	-0.014723	0.002242	6.00E-12	-0.013145	0.003807	0.000559	-0.015274	0.002807	5.44E-08	9.65E-10	0.652644	
9	PTPN3	rs1411682	109,514,077	T	C	0.281634	-0.014731	0.002242	5.80E-12	-0.013144	0.003808	0.00056	-0.015285	0.002808	5.32E-08	9.45E-10	0.650862	
9	PTPN3	rs10124300	109,515,460	C	A	0.281569	-0.014586	0.002241	8.80E-12	-0.013117	0.003807	0.000573	-0.015066	0.002807	8.13E-08	1.46E-09	0.680292	
9	PTPN3	rs10759346	109,516,959	A	C	0.368186	-0.011364	0.002102	1.60E-08	-0.011641	0.003575	0.001134	-0.010543	0.00263	6.16E-05	1.61E-06	0.804567	
9	PTPN3	rs77218860	109,517,046	A	G	0.246912	-0.016741	0.002342	6.50E-14	-0.017058	0.003974	1.79E-05	-0.016056	0.002935	4.59E-08	3.16E-11	0.839196	
9	PTPN3	rs76636909	109,518,424	T	C	0.249241	-0.016614	0.002331	7.60E-14	-0.017325	0.003956	1.21E-05	-0.015781	0.002919	6.59E-08	3.09E-11	0.75359	
9	PTPN3	rs139346903	109,520,059	A	T	0.249244	-0.01661	0.002331	7.80E-14	-0.017323	0.003956	1.21E-05	-0.015779	0.002919	6.61E-08	3.10E-11	0.753555	
9	PTPN3	rs80070092	109,521,917	T	C	0.249244	-0.01661	0.002331	7.80E-14	-0.017323	0.003956	1.21E-05	-0.015779	0.002919	6.61E-08	3.10E-11	0.7535	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
9	PTPN3 *	rs117103218	109,574,154	A	G	0.188947	-0.01745	0.002596	9.20E-13	-0.015131	0.004422	0.000627	-0.018308	0.003246	1.74E-08	3.55E-10	0.562506	
9	PALM2 *	rs200745414	109,577,539	C	A	0.192492	-0.017358	0.002573	7.40E-13	-0.014894	0.004376	0.000669	-0.018331	0.00322	1.28E-08	2.80E-10	0.527026	
9	PALM2 *	rs76508340	109,580,420	T	C	0.178599	-0.016581	0.002661	1.30E-11	-0.014271	0.00452	0.001599	-0.017448	0.003331	1.65E-07	7.53E-09	0.571512	
9	PALM2 *	rs78815286	109,582,984	T	G	0.19295	-0.017004	0.002567	1.90E-12	-0.014597	0.004365	0.000831	-0.017913	0.003212	2.50E-08	6.56E-10	0.540581	
9	PALM2 *	rs78864591	109,583,284	T	C	0.192951	-0.017002	0.002567	1.90E-12	-0.014581	0.004365	0.000842	-0.017916	0.003212	2.49E-08	6.61E-10	0.538296	
9	PALM2 *	rs1330845	109,587,240	T	A	0.308857	-0.011675	0.002183	3.80E-08	-0.010629	0.00372	0.004284	-0.011811	0.002729	1.53E-05	1.45E-06	0.79769	
9	PALM2 *	rs10979952	109,587,348	C	A	0.221012	-0.014477	0.002439	3.00E-10	-0.01024	0.00415	0.013633	-0.016568	0.00305	5.72E-08	1.87E-08	0.219236	
9	PALM2 *	rs10979955	109,587,981	C	T	0.306245	-0.011768	0.002186	2.90E-08	-0.010896	0.003725	0.003457	-0.011784	0.002733	1.64E-05	1.27E-06	0.847536	
9	PALM2 *	rs17202062	109,591,436	C	G	0.191045	-0.017614	0.002577	3.60E-13	-0.01514	0.004381	0.000552	-0.018635	0.003225	7.76E-09	1.44E-10	0.520504	
9	PALM2 *	rs17794184	109,592,937	T	A	0.190847	-0.017754	0.002576	2.50E-13	-0.01543	0.004381	0.000431	-0.018667	0.003224	7.24E-09	1.06E-10	0.551766	
9	PALM2 *	rs10125565	109,593,113	T	G	0.218055	-0.015041	0.002449	7.60E-11	-0.010799	0.004168	0.009592	-0.017141	0.003463	2.26E-08	5.55E-09	0.220173	
9	PALM2 *	rs58105812	109,593,130	A	T	0.190845	-0.017763	0.002577	2.40E-13	-0.01543	0.004381	0.000431	-0.01868	0.003224	7.08E-09	1.04E-10	0.550195	
9	PALM2 *	rs78927344	109,593,586	G	A	0.19086	-0.017774	0.002577	2.40E-13	-0.015495	0.00438	0.000407	-0.018658	0.003224	7.38E-09	1.03E-10	0.560988	
9	PALM2 *	rs10979958	109,595,732	A	G	0.19458	-0.017269	0.002565	1.10E-12	-0.015734	0.004359	0.000309	-0.01755	0.00321	4.70E-08	4.82E-10	0.737325	
9	PALM2 *	rs75253286	109,596,281	T	C	0.19578	-0.017456	0.002555	4.90E-13	-0.015795	0.004342	0.000277	-0.017681	0.003198	3.30E-08	3.08E-10	0.726585	
9	PALM2 *	rs10979959	109,597,137	T	G	0.306261	-0.017177	0.002184	3.10E-08	-0.010588	0.003721	0.00445	-0.011893	0.00273	1.34E-05	1.32E-06	0.777305	
9	PALM2 *	rs12238594	109,598,183	C	T	0.306087	-0.011824	0.002186	2.40E-08	-0.010719	0.003725	0.004015	-0.011981	0.002732	1.17E-05	1.06E-06	0.784757	
9	PALM2 *	rs137989413	109,598,306	A	C	0.195548	-0.017348	0.002556	6.50E-13	-0.015555	0.004346	0.000347	-0.017727	0.003199	3.09E-08	3.56E-10	0.687375	
9	PALM2 *	rs1169625	109,600,193	A	G	0.305504	-0.011873	0.002189	2.10E-08	-0.010525	0.00373	0.004788	-0.012142	0.002736	9.18E-06	9.84E-07	0.72661	
10	AKR1C4	rs74827952	5,203,233	A	G	0.089524	-0.021258	0.003568	1.10E-09	-0.013923	0.00601	0.020533	-0.026727	0.004488	2.67E-09	1.36E-09	0.087824	
10	AKR1C4	rs76669111	5,203,817	T	G	0.100877	-0.019242	0.003354	3.60E-09	-0.014359	0.005658	0.011176	-0.023487	0.004214	2.56E-08	7.18E-09	0.195728	
10	AKR1C4	rs17134531	5,204,122	A	G	0.100984	-0.019277	0.00335	3.00E-09	-0.014453	0.005653	0.010587	-0.023514	0.004209	2.37E-08	6.36E-09	0.198562	
10	AKR1C4	rs77697233	5,204,162	T	C	0.100983	-0.019277	0.00335	3.00E-09	-0.014451	0.005653	0.010599	-0.023516	0.004209	2.36E-08	6.34E-09	0.198338	
10	AKR1C4	rs17134533	5,205,135	A	G	0.101026	-0.019365	0.003349	2.50E-09	-0.014458	0.005651	0.010534	-0.023673	0.004207	1.88E-08	5.06E-09	0.190852	
10	AKR1C4	rs6601924	5,205,339	T	C	0.101036	-0.019306	0.003348	2.70E-09	-0.014418	0.005651	0.010746	-0.02362	0.004207	2.02E-08	5.50E-09	0.19144	
10	AKR1C4	rs3750572	5,205,413	C	T	0.101036	-0.019306	0.003348	2.70E-09	-0.014418	0.005651	0.010746	-0.02362	0.004207	2.02E-08	5.50E-09	0.19144	
10	AKR1C4	rs3750571	5,205,471	A	C	0.101036	-0.019306	0.003348	2.70E-09	-0.014418	0.005651	0.010746	-0.02362	0.004207	2.02E-08	5.50E-09	0.19144	
10	AKR1C4	rs3750569	5,205,567	G	A	0.101036	-0.019306	0.003348	2.70E-09	-0.014418	0.005651	0.010746	-0.02362	0.004207	2.02E-08	5.50E-09	0.19144	
10	AKR1C4	rs3750568	5,205,668	A	G	0.101036	-0.019306	0.003348	2.70E-09	-0.014418	0.005651	0.010746	-0.02362	0.004207	2.02E-08	5.50E-09	0.19144	
10	AKR1C4	rs3750567	5,205,671	A	G	0.101036	-0.019306	0.003348	2.70E-09	-0.014418	0.005651	0.010746	-0.02362	0.004207	2.02E-08	5.50E-09	0.19144	
10	AKR1C4	rs7921838	5,205,738	A	G	0.101043	-0.019305	0.003348	2.70E-09	-0.014388	0.005651	0.010908	-0.023628	0.004207	1.99E-08	5.52E-09	0.189629	
10	AKR1C4	rs3829125	5,205,821	G	C	0.101176	-0.019341	0.003346	2.40E-09	-0.014134	0.005646	0.012327	-0.023824	0.004203	1.48E-08	4.61E-09	0.168627	
10	AKR1C4	rs1931679	5,208,490	T	C	0.099698	-0.018858	0.00337	6.50E-09	-0.013673	0.005686	0.016197	-0.02321	0.004235	4.33E-08	1.66E-08	0.178533	
10	AKR1C4	rs7908297	5,209,739	A	G	0.101078	-0.019229	0.003348	3.00E-09	-0.014119	0.00565	0.01248	-0.023638	0.004206	1.96E-08	6.11E-09	0.176534	
10	AKR1C4	rs7909379	5,209,851	A	C	0.101033	-0.019376	0.003349	2.20E-09	-0.014384	0.005652	0.010956	-0.02369	0.004207	1.83E-08	5.10E-09	0.186565	
10	AKR1C4	rs7909380	5,209,852	T	C	0.101033	-0.019376	0.003349	2.20E-09	-0.014384	0.005652	0.010956	-0.02369	0.004207	1.83E-08	5.10E-09	0.186565	
10	AKR1C4	rs117310669	5,210,050	G	C	0.101015	-0.019297	0.003349	2.80E-09	-0.014438	0.005652	0.010653	-0.023583	0.004207	2.13E-08	5.76E-09	0.194297	
10	AKR1C4	rs4424574	5,210,114	T	G	0.101018	-0.019291	0.003349	2.90E-09	-0.014423	0.005652	0.010731	-0.023583	0.004207	2.13E-08	5.80E-09	0.193561	
10	AKR1C4	rs7477230	5,210,768	T	C	0.10116	-0.019498	0.003348	1.90E-09	-0.014859	0.00565	0.008554	-0.023698	0.004206	1.80E-08	4.03E-09	0.209531	
10	AKR1C4	rs7477114	5,210,875	T	G	0.101018	-0.019291	0.003349	2.90E-09	-0.014423	0.005652	0.010731	-0.023583	0.004207	2.13E-08	5.80E-09	0.193561	
10	AKR1C4	rs7475279	5,210,903	C	A	0.10108	-0.019222	0.003348	3.00E-09	-0.014104	0.00565	0.01257	-0.023638	0.004206	1.96E-08	6.15E-09	0.175847	
10	AKR1C4	rs7475281	5,210,939	C	A	0.10108	-0.019222	0.003348	3.00E-09	-0.014104	0.00565	0.01257	-0.023638	0.004206	1.96E-08	6.15E-09	0.175847	
10	AKR1C4	rs117071142	5,211,396	G	T	0.100912	-0.019347	0.00335	2.40E-09	-0.014336	0.005654	0.011244	-0.023654	0.004209	1.96E-08	5.57E-09	0.18617	
10	AKR1C4	rs7078211	5,211,675	G	A	0.101086	-0.019205	0.003348	3.10E-09	-0.014087	0.00565	0.012673	-0.023618	0.004206	2.01E-08	6.36E-09	0.175985	
10	AKR1C4	rs6601927	5,212,183	G	A	0.101103	-0.019208	0.003347	3.20E-09	-0.01415	0.005649	0.012274	-0.023577	0.004206	2.12E-08	6.51E-09	0.180738	
10	AKR1C4	rs7897431	5,212,225	A	G	0.101103	-0.019208	0.003347	3.20E-09	-0.01415	0.005649	0.012274	-0.023577	0.004206	2.12E-08	6.51E-09	0.180738	
10	AKR1C4	rs4908025	5,212,857	C	A	0.100665	-0.01931	0.003355	2.80E-09	-0.014505	0.005663	0.010442	-0.02356	0.004216	2.34E-08	6.20E-09	0.199581	
10	AKR1C4	rs1831977	5,212,858	G	C	0.100665	-0.01931	0.003355	2.80E-09	-0.014505	0.005663	0.010442	-0.02356	0.004216	2.34E-08	6.20E-09	0.199581	
10	AKR1C4	rs1832007	5,212,884	G	A	0.101085	-0.018979	0.003348	4.70E-09	-0.014258	0.00565	0.011634	-0.023164	0.004206	3.73E-08	1.07E-08	0.206082	
10	AKR1C4	rs17134585	5,214,309	C	T	0.102362	-0.019287	0.003334	2.80E-09	-0.01441	0.00563	0.010499	-0.023499	0.004188	2.05E-08	5.48E-09	0.195153	
10	AKR1C4	rs56068105	5,214,375	T	A	0.109158	-0.017308	0.003293	4.20E-08	-0.011681	0.005562	0.035728	-0.022123	0.004136	9.01E-08	6.73E-08	0.131866	
10	AKR1C4	rs17134588	5,214,534	A	G	0.101274	-0.019315	0.003348	2.60E-09	-0.014349	0.005652	0.01114	-0.023641	0.004206	1.95E-08	5.49E-09	0.187136	
10	AKR1C4	rs77503049	5,214,795	T	C	0.101291	-0.019321	0.003347	2.50E-09	-0.014384	0.005648	0.010899	-0.023633	0.004206	1.96E-08	5.43E-09	0.188998	
10	AKR1C4	rs76551580	5,214,871	C	T	0.101103	-0.019181	0.003348	3.30E-09	-0.014192	0.00565	0.012038	-0.023508	0.004206	2.33E-08	7.02E-09	0.185943	
10	AKR1C4	rs78585347	5,215,134	T	G	0.101038	-0.019229	0.003349	3.20E-09	-0.014457	0.005652	0.010558	-0.023453	0.004207	2.54E-08	6.78E-09	0.201689	
10	AKR1C4	rs75406471	5,215,684	A	G	0.101041	-0.019271	0.003349	3.00E-09	-0.014457	0.005652	0.010558	-0.023512	0.004207	2.34E-08	6.27E-09	0.19	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
10	AKR1C4 *	rs79849481	5,220,133	A	G	0.101028	-0.019219	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023426	0.004208	2.65E-08	6.89E-09	0.205758	
10	AKR1C4 *	rs77355283	5,220,173	T	C	0.101028	-0.019219	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023426	0.004208	2.65E-08	6.89E-09	0.205758	
10	AKR1C4 *	rs79717793	5,220,304	A	G	0.101029	-0.019221	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023429	0.004208	2.64E-08	6.86E-09	0.205585	
10	AKR1C4 *	rs78231592	5,220,527	C	G	0.101029	-0.019221	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023429	0.004208	2.64E-08	6.86E-09	0.205585	
10	AKR1C4 *	rs75529951	5,220,549	A	G	0.101029	-0.019221	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023429	0.004208	2.64E-08	6.86E-09	0.205585	
10	AKR1C4 *	rs140168704	5,220,815	T	C	0.101029	-0.019225	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023436	0.004208	2.61E-08	6.80E-09	0.205235	
10	AKR1C4 *	rs151163925	5,220,847	T	C	0.101051	-0.0192	0.003349	3.50E-09	-0.014518	0.005653	0.010236	-0.023399	0.004207	2.73E-08	7.08E-09	0.207495	
10	AKR1C4 *	rs143690051	5,220,859	T	C	0.101051	-0.0192	0.003349	3.50E-09	-0.014518	0.005653	0.010236	-0.023399	0.004207	2.73E-08	7.08E-09	0.207495	
10	AKR1C4 *	rs112455458	5,220,920	C	G	0.101029	-0.019225	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023436	0.004208	2.61E-08	6.80E-09	0.205235	
10	AKR1C4 *	rs111932715	5,220,978	C	G	0.101029	-0.019225	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023436	0.004208	2.61E-08	6.80E-09	0.205235	
10	AKR1C4 *	rs2151901	5,221,002	C	A	0.101029	-0.019225	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023436	0.004208	2.61E-08	6.80E-09	0.205235	
10	AKR1C4 *	rs17134610	5,221,060	T	G	0.10103	-0.019218	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023426	0.004208	2.65E-08	6.89E-09	0.205738	
10	AKR1C4 *	rs142122182	5,221,378	G	A	0.097567	-0.020097	0.00341	1.30E-09	-0.015226	0.005762	0.008246	-0.024387	0.004282	1.27E-08	2.76E-09	0.201907	
10	AKR1C4 *	rs17134616	5,221,498	T	A	0.09982	-0.018676	0.003371	1.20E-08	-0.014317	0.005693	0.011931	-0.022264	0.004233	9.09E-08	2.61E-08	0.240741	
10	AKR1C4 *	rs75413156	5,221,531	A	C	0.100316	-0.019475	0.003364	2.70E-09	-0.014937	0.00568	0.008561	-0.023576	0.004225	2.46E-08	5.44E-09	0.222286	
10	AKR1C4 *	rs80011059	5,221,553	T	A	0.10103	-0.019218	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023426	0.004208	2.65E-08	6.89E-09	0.205738	
10	AKR1C4 *	rs17134617	5,221,739	A	C	0.10103	-0.019218	0.003349	3.40E-09	-0.01451	0.005653	0.010277	-0.023426	0.004208	2.65E-08	6.89E-09	0.205738	
10	AKR1C4 *	rs149977283	5,223,568	A	C	0.100564	-0.019207	0.003362	3.40E-09	-0.014671	0.005672	0.009708	-0.023198	0.004224	4.07E-08	9.95E-09	0.22787	
10	AKR1C4 *	rs138695384	5,223,859	G	A	0.101258	-0.019101	0.003348	4.10E-09	-0.014455	0.005651	0.010552	-0.02327	0.004205	3.21E-08	8.49E-09	0.210768	
10	AKR1C4 *	rs150754448	5,224,911	A	G	0.101026	-0.01919	0.003349	3.70E-09	-0.014521	0.005653	0.010219	-0.023373	0.004208	2.85E-08	7.36E-09	0.209024	
10	AKR1C4 *	rs140107293	5,225,228	G	A	0.101052	-0.019263	0.00335	3.20E-09	-0.014472	0.005656	0.010526	-0.023477	0.004208	2.48E-08	6.60E-09	0.20145	
10	AKR1C4 *	rs143431627	5,228,338	T	C	0.101117	-0.01922	0.003351	3.50E-09	-0.014466	0.005657	0.01057	-0.023418	0.004209	2.70E-08	7.20E-09	0.204216	
10	AKR1C4 *	rs7897822	5,242,594	A	G	0.10073	-0.019048	0.003364	6.40E-09	-0.013906	0.00568	0.014378	-0.023582	0.004226	2.45E-08	8.62E-09	0.171709	
10	AKR1C4 *	rs151227875	5,255,358	G	C	0.095813	-0.018529	0.003443	1.80E-08	-0.014926	0.005795	0.010022	-0.02223	0.004331	2.92E-07	6.91E-08	0.312709	
10	AKR1C4 *	rs143119289	5,255,430	G	T	0.093519	-0.018522	0.003487	2.60E-08	-0.014833	0.00586	0.011382	-0.022112	0.004391	4.85E-07	1.26E-07	0.32018	
10	AKR1C4 *	rs80079690	5,258,474	T	C	0.094464	-0.01849	0.003463	2.10E-08	-0.014295	0.00583	0.01423	-0.022336	0.004358	3.02E-07	9.76E-08	0.269237	
10	AKR1C4 *	rs12415198	5,262,828	T	C	0.092387	-0.018604	0.003506	2.70E-08	-0.014214	0.005892	0.015878	-0.022406	0.004415	3.96E-07	1.40E-07	0.265868	
10	AKR1C4 *	rs77714023	5,263,928	A	G	0.094021	-0.018717	0.003474	1.60E-08	-0.014829	0.005852	0.011297	-0.022398	0.004369	3.01E-07	7.92E-08	0.299985	
10	AKR1C4 *	rs117600605	5,263,996	T	C	0.09451	-0.01836	0.003465	2.50E-08	-0.01441	0.005833	0.013516	-0.022071	0.004359	4.19E-07	1.28E-07	0.292732	
10	AKR1C4 *	rs4339945	5,264,435	G	A	0.094551	-0.018401	0.003465	2.30E-08	-0.01441	0.005833	0.013522	-0.022128	0.004359	3.93E-07	1.20E-07	0.289211	
10	AKR1C4 *	rs117292237	5,265,566	C	T	0.094583	-0.018275	0.003465	2.80E-08	-0.014149	0.005833	0.015301	-0.022076	0.00436	4.19E-07	1.43E-07	0.276343	
10	AKR1C4 *	rs77364195	5,266,772	A	T	0.094821	-0.018392	0.003461	2.20E-08	-0.014217	0.005826	0.014693	-0.022182	0.004354	3.57E-07	1.18E-07	0.273443	
10	AKR1C4 *	rs1574227	5,270,304	A	G	0.096361	-0.018213	0.003439	2.80E-08	-0.014853	0.005792	0.010349	-0.02169	0.004325	5.41E-07	1.29E-07	0.344262	
10	AKR1C4 *	rs1574228	5,270,347	G	A	0.096373	-0.01822	0.003438	2.80E-08	-0.014916	0.005791	0.010025	-0.02165	0.004325	5.66E-07	1.31E-07	0.351519	
10	AKR1C4 *	rs1574351	5,270,402	A	G	0.096375	-0.018251	0.003438	2.60E-08	-0.014934	0.005791	0.009934	-0.021692	0.004325	5.37E-07	1.24E-07	0.349717	
10	AKR1C4 *	rs1574352	5,270,475	C	T	0.096378	-0.018233	0.003438	2.70E-08	-0.014921	0.005791	0.009998	-0.021671	0.004324	5.51E-07	1.27E-07	0.350342	
10	AKR1C4 *	rs869009	5,271,066	C	T	0.096418	-0.018266	0.003437	2.60E-08	-0.014999	0.00579	0.009604	-0.021696	0.004324	5.32E-07	1.19E-07	0.35405	
10	AKR1C4 *	rs12763722	5,271,530	C	T	0.096468	-0.018321	0.003437	2.30E-08	-0.015012	0.005789	0.009532	-0.021666	0.004323	4.89E-07	1.09E-07	0.349911	
10	AKR1C4 *	rs1889460	5,272,032	T	C	0.096496	-0.018402	0.003437	2.00E-08	-0.015027	0.005789	0.009452	-0.021878	0.004323	4.25E-07	9.43E-08	0.34292	
10	AKR1C4 *	rs1889459	5,272,080	C	G	0.095287	-0.018475	0.003454	1.90E-08	-0.014252	0.005817	0.0143	-0.022272	0.004345	3.01E-07	9.76E-08	0.269237	
10	AKR1C4 *	rs11815997	5,272,373	T	G	0.096496	-0.018402	0.003437	2.00E-08	-0.015027	0.005789	0.009452	-0.021878	0.004323	4.25E-07	9.43E-08	0.34292	
10	AKR1C4 *	rs17307911	5,272,389	C	T	0.096496	-0.018402	0.003437	2.00E-08	-0.015027	0.005789	0.009452	-0.021878	0.004323	4.25E-07	9.43E-08	0.34292	
10	AKR1C4 *	rs17399127	5,272,661	C	A	0.0965	-0.018384	0.003437	2.10E-08	-0.015026	0.005789	0.009456	-0.021854	0.004323	4.37E-07	9.70E-08	0.344568	
10	AKR1C4 *	rs12413267	5,273,161	G	A	0.096601	-0.018521	0.003436	1.50E-08	-0.015163	0.005789	0.008826	-0.021965	0.004322	3.80E-07	7.96E-08	0.346409	
10	AKR1C4 *	rs17399232	5,273,898	G	C	0.09656	-0.018538	0.003437	1.60E-08	-0.015343	0.005789	0.008062	-0.02192	0.004323	4.04E-07	7.79E-08	0.362651	
10	AKR1C4 *	rs79504871	5,273,912	T	A	0.096516	-0.018414	0.003437	2.00E-08	-0.0151	0.005789	0.009115	-0.021862	0.004322	4.32E-07	9.28E-08	0.349226	
10	AKR1C4 *	rs7082291	5,275,907	C	A	0.096937	-0.018493	0.003427	1.80E-08	-0.015329	0.005771	0.007925	-0.021833	0.004311	4.16E-07	7.90E-08	0.366549	
10	AKR1C4 *	rs17134724	5,276,549	A	G	0.095747	-0.018553	0.003444	1.70E-08	-0.014615	0.005798	0.011736	-0.022177	0.004332	3.13E-07	8.51E-08	0.296136	
10	AKR1C4 *	rs75857264	5,283,345	T	C	0.095629	-0.018806	0.003445	1.00E-08	-0.015067	0.005802	0.009427	-0.022308	0.004333	2.68E-07	6.03E-08	0.317359	
10	AKR1C4 *	rs17134733	5,283,400	A	G	0.0931	-0.018595	0.003494	2.20E-08	-0.015398	0.005874	0.00878	-0.021678	0.004	8.50E-07	1.72E-07	0.392212	
10	NRBF2 *	rs10822118	63,068,681	T	C	0.288667	0.012698	0.002264	5.60E-09	0.014637	0.003831	0.000134	0.011978	0.002841	2.52E-05	9.33E-08	0.57712	
10	NRBF2 *	rs10995445	63,114,994	A	A	0.317362	-0.013932	0.002184	3.60E-11	-0.012313	0.003707	0.000901	-0.014426	0.002736	1.38E-07	3.70E-09	0.64643	
10	NRBF2 *	rs7903602	63,115,551	T	G	0.38464	0.021174	0.002098	5.50E-26	0.018337	0.003576	2.98E-07	0.022308	0.002622	1.87E-17	3.73E-22	0.370411	
10	NRBF2 *	rs4414112	63,115,786	A	G	0.384229	0.021424	0.002091	8.50E-27	0.017985	0.003564	4.59E-07	0.022751	0.002614	3.35E-18	1.04E-22	0.280823	
10	NRBF2 *	rs4545434	63,115,985	C	T	0.375188	0.020949	0.002099	1.00E-25	0.017224	0.003578	1.51E-06	0.02249	0.002623	1.05E-17	1.01E-21	0.235237	
10	NRBF2 *	rs7084569	63,116,794	A	G	0.316356	-0.013957	0.002184	3.10E-11	-0.011789	0.003708	0.001483	-0.014697	0.002735				

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	NRBF2 *	rs10995448	63,127,299	G	A	0.336064	-0.012888	0.002141	5.50E-10	-0.009914	0.003648	0.006586	-0.013801	0.002676	2.57E-07	4.19E-08	0.39017	
10	NRBF2 *	rs12771984	63,127,434	A	T	0.336212	-0.012934	0.002142	5.00E-10	-0.009939	0.003649	0.006466	-0.013869	0.002677	2.26E-07	3.64E-08	0.385229	
10	NRBF2 *	rs10995449	63,127,712	A	G	0.336529	-0.012989	0.002143	4.30E-10	-0.009895	0.003652	0.006755	-0.013944	0.002679	1.99E-07	3.34E-08	0.371306	
10	NRBF2 *	rs10822143	63,128,096	T	C	0.318046	-0.014108	0.002176	2.20E-11	-0.012201	0.003697	0.000972	-0.014628	0.002724	8.08E-08	2.597E-09	0.597149	
10	NRBF2 *	rs10761718	63,128,127	T	C	0.335789	-0.012627	0.002146	1.50E-09	-0.009679	0.003656	0.008138	-0.013455	0.002683	5.41E-07	1.04E-07	0.40497	
10	NRBF2 *	rs7082200	63,128,561	G	C	0.335903	-0.012724	0.002143	1.00E-09	-0.009603	0.003651	0.008548	-0.013697	0.002679	3.22E-07	6.60E-08	0.365808	
10	NRBF2 *	rs10995450	63,129,151	C	T	0.336059	-0.012881	0.002141	5.60E-10	-0.009877	0.003648	0.006788	-0.013807	0.002676	2.54E-07	4.25E-08	0.385012	
10	NRBF2 *	rs10740105	63,129,957	T	C	0.336054	-0.01288	0.002141	5.50E-10	-0.00988	0.003648	0.006775	-0.013799	0.002677	2.58E-07	4.32E-08	0.386379	
10	NRBF2 *	rs10761719	63,130,337	G	A	0.335457	-0.012685	0.002143	1.00E-09	-0.009648	0.003651	0.008243	-0.013618	0.002679	3.78E-07	7.45E-08	0.380574	
10	NRBF2 *	rs7923014	63,130,405	T	C	0.336065	-0.012862	0.002141	5.80E-10	-0.00988	0.003648	0.006772	-0.013771	0.002676	2.72E-07	4.55E-08	0.389805	
10	NRBF2 *	rs7908890	63,130,890	A	T	0.33607	-0.012852	0.002141	5.90E-10	-0.009934	0.003648	0.006478	-0.01373	0.002676	2.95E-07	4.73E-08	0.401509	
10	NRBF2 *	rs4746974	63,132,292	T	G	0.378453	0.020699	0.002083	1.90E-25	0.016479	0.003549	3.49E-06	0.022508	0.002604	5.77E-18	1.25E-21	0.170812	
10	NRBF2 *	rs1533068	63,132,407	C	A	0.336119	-0.012811	0.00214	6.60E-10	-0.009803	0.003647	0.007202	-0.013736	0.002675	2.89E-07	5.09E-08	0.384527	
10	NRBF2 *	rs1533069	63,132,408	A	C	0.336119	-0.012811	0.00214	6.60E-10	-0.009803	0.003647	0.007202	-0.013736	0.002675	2.89E-07	5.09E-08	0.384527	
10	NRBF2	rs871690	63,134,299	G	A	0.335499	-0.012928	0.002141	5.30E-10	-0.010385	0.003648	0.004426	-0.013637	0.002676	3.53E-07	3.98E-08	0.472145	
10	NRBF2	rs868798	63,135,250	G	A	0.378823	0.020655	0.002081	2.20E-25	0.016726	0.003546	2.43E-06	0.022316	0.002602	1.02E-17	1.55E-21	0.203746	
10	NRBF2	rs12416113	63,136,717	A	T	0.378648	0.020678	0.002082	2.00E-25	0.016721	0.003547	2.47E-06	0.022346	0.002602	9.42E-18	1.45E-21	0.201049	
10	NRBF2	rs10761720	63,139,023	A	G	0.333595	-0.01276	0.002143	8.90E-10	-0.009642	0.00365	0.008265	-0.013794	0.002679	2.67E-07	5.33E-08	0.359152	
10	NRBF2	rs61853336	63,140,115	A	G	0.378808	0.020732	0.002081	1.60E-25	0.016824	0.003546	2.12E-06	0.022371	0.002602	8.48E-18	1.13E-21	0.207176	
10	NRBF2	rs7070052	63,144,054	A	G	0.378833	0.020685	0.002081	1.90E-25	0.016802	0.003545	2.18E-06	0.022303	0.002601	1.04E-17	1.43E-21	0.210893	
10	NRBF2	rs7073746	63,144,311	G	A	0.31595	-0.013801	0.002172	5.60E-11	-0.011217	0.00369	0.002378	-0.014754	0.002718	5.83E-08	3.94E-09	0.440158	
10	NRBF2	rs7916224	63,144,843	T	C	0.387862	0.021228	0.002072	1.10E-26	0.017573	0.00353	6.55E-07	0.022686	0.00259	2.08E-18	9.10E-23	0.242929	
10	NRBF2	rs4746994	63,145,564	A	T	0.378912	0.020633	0.002079	2.20E-25	0.016784	0.003543	2.20E-06	0.02225	0.002599	1.18E-17	1.63E-21	0.213526	
10	NRBF2	rs10733787	63,147,078	T	A	0.387956	0.021196	0.002071	1.10E-26	0.017551	0.003529	6.71E-07	0.022667	0.002589	2.13E-18	9.55E-23	0.242414	
10	NRBF2	rs12240740	63,147,478	C	A	0.387955	0.021193	0.002071	1.10E-26	0.017548	0.003529	6.74E-07	0.022664	0.002589	2.15E-18	9.68E-23	0.242384	
10	NRBF2	rs931972	63,150,467	C	G	0.333128	-0.012445	0.002142	2.40E-09	-0.009455	0.00365	0.009598	-0.01368	0.002678	5.97E-07	1.38E-07	0.38593	
10	NRBF2	rs12415984	63,150,528	A	G	0.378921	0.020609	0.002079	2.30E-25	0.016755	0.003543	2.29E-06	0.022225	0.002598	1.26E-17	1.80E-21	0.213041	
10	NRBF2	rs13095	63,154,612	C	G	0.315794	-0.013677	0.002168	7.10E-11	-0.010974	0.003685	0.002911	-0.014696	0.002714	6.30E-08	5.11E-09	0.416043	
10	NRBF2 *	rs7897470	63,156,304	G	T	0.365628	0.01952	0.002111	1.70E-22	0.015364	0.003597	1.97E-05	0.021317	0.002638	6.79E-16	7.26E-19	0.18204	
10	NRBF2 *	rs1009984	63,156,709	T	G	0.387644	0.021076	0.002072	2.00E-26	0.017629	0.00353	6.03E-07	0.022425	0.002589	4.90E-18	1.96E-22	0.273287	
10	NRBF2 *	rs11814792	63,157,799	T	C	0.377611	0.020729	0.00208	1.70E-25	0.016863	0.003545	2.00E-06	0.022355	0.0026	8.62E-18	1.09E-21	0.21166	
10	NRBF2 *	rs10733788	63,158,105	C	C	0.387588	0.021143	0.002072	1.50E-26	0.017621	0.00353	6.08E-07	0.022556	0.002589	3.16E-18	1.28E-22	0.259645	
10	NRBF2 *	rs61853339	63,158,919	C	T	0.378023	0.020713	0.002079	1.80E-25	0.016919	0.003543	1.82E-06	0.022294	0.002599	1.00E-17	1.16E-21	0.221096	
10	NRBF2 *	rs12413415	63,159,751	C	T	0.375092	0.020559	0.002084	4.60E-25	0.01616	0.003551	5.41E-06	0.022427	0.002604	7.60E-18	2.50E-21	0.154653	
10	JMID1C *	rs11817689	63,164,457	C	T	0.379445	0.020668	0.002078	1.90E-25	0.016666	0.003541	2.56E-06	0.022379	0.002598	7.37E-18	1.18E-21	0.19326	
10	JMID1C *	rs4747045	63,166,722	T	C	0.378325	0.020741	0.002079	1.30E-25	0.016615	0.003541	2.75E-06	0.022496	0.002598	5.09E-18	8.77E-22	0.180533	
10	JMID1C	rs1935	63,168,063	G	C	0.312463	-0.013819	0.002176	3.80E-11	-0.011143	0.003697	0.002585	-0.01488	0.002723	4.76E-08	3.50E-09	0.415647	
10	JMID1C	rs1904296	63,173,019	C	G	0.387688	0.020804	0.002075	6.80E-26	0.017039	0.003534	1.45E-06	0.02241	0.002593	5.85E-18	5.43E-22	0.220478	
10	JMID1C	rs4466712	63,173,508	C	G	0.376858	0.020684	0.00208	1.60E-25	0.016636	0.003544	2.72E-06	0.022438	0.0026	6.52E-18	1.11E-21	0.186878	
10	JMID1C	rs10995453	63,174,571	T	C	0.386111	0.021103	0.002073	1.70E-26	0.017386	0.003532	8.73E-07	0.022652	0.002591	2.44E-18	1.41E-22	0.229347	
10	JMID1C	rs10822145	63,174,788	T	C	0.314433	-0.01352	0.002172	8.10E-11	-0.010721	0.003692	0.0037	-0.01467	0.002718	6.88E-08	6.94E-09	0.389097	
10	JMID1C	rs10995455	63,176,601	A	G	0.244485	-0.015565	0.002352	1.30E-11	-0.013118	0.004001	0.001049	-0.016787	0.002943	1.20E-08	4.00E-10	0.460117	
10	JMID1C	rs907	63,176,919	A	G	0.386553	0.021078	0.002076	1.70E-26	0.017401	0.003537	8.82E-07	0.02263	0.002594	2.87E-18	1.67E-22	0.233167	
10	JMID1C	rs10761721	63,178,644	T	G	0.386112	0.0211	0.002073	1.70E-26	0.017393	0.003532	8.60E-07	0.022635	0.002591	2.55E-18	1.45E-22	0.231316	
10	JMID1C	rs7289170	63,180,529	G	A	0.37655	0.020638	0.00208	2.50E-25	0.016768	0.003544	2.27E-06	0.022367	0.0026	8.33E-18	1.19E-21	0.202804	
10	JMID1C	rs10995459	63,183,050	A	G	0.385965	0.021008	0.002073	3.00E-26	0.017332	0.003532	9.44E-07	0.022592	0.002591	3.00E-18	1.86E-22	0.229842	
10	JMID1C	rs61853340	63,184,415	C	G	0.371879	0.020449	0.002096	1.50E-24	0.015978	0.003567	7.58E-06	0.022521	0.002621	9.01E-18	4.09E-21	0.193909	
10	JMID1C	rs10740107	63,184,557	T	A	0.376366	0.02042	0.002082	9.90E-25	0.01695	0.003547	1.80E-06	0.021971	0.002602	3.25E-17	3.64E-21	0.253747	
10	JMID1C	rs3211105	63,185,604	G	A	0.386251	0.021115	0.002072	1.60E-26	0.017556	0.003531	6.73E-07	0.022634	0.00259	2.49E-18	1.11E-22	0.24611	
10	JMID1C	rs10733789	63,188,924	C	T	0.244806	-0.015964	0.002352	5.20E-12	-0.01351	0.004001	0.000737	-0.017228	0.002943	4.93E-09	1.21E-10	0.454084	
10	JMID1C	rs10822146	63,191,707	A	G	0.332428	-0.012641	0.002142	8.40E-10	-0.009378	0.00365	0.010209	-0.013844	0.002677	2.37E-07	5.73E-08	0.323811	
10	JMID1C	rs10761722	63,195,287	C	G	0.386096	0.021176	0.002074	1.30E-26	0.017707	0.003534	5.55E-07	0.022672	0.002591	2.26E-18	8.42E-23	0.257287	
10	JMID1C	rs10761723	63,195,821	T	C	0.314325	-0.013588	0.002172	6.90E-11	-0.010706	0.003694	0.003764	-0.014808	0.002718	5.22E-08	5.39E-09	0.371023	
10	JMID1C	rs61854565	63,196,847	T	A	0.37715	0.02062	0.002078	2.30E-25	0.016687	0.003541	2.49E-06	0.022363	0.002597	7.63E-18	1.19E-21	0.196097	
10	JMID1C	rs10465990	63,200,776	A	G	0.330739	-0.01276	0.002145	6.30E-10	-0.00936	0.003653	0.010424	-0.014046	0.002682	1.66E-07	4.15E-08	0.301155	
10	JMID1C	rs7099425	63,200,957	C	T	0.377573	0.020592	0.002079	3.00E-25	0.01682	0.003543	2.09E-06	0.022253	0.002598	1.14E-17	1.50E-21	0.216232	
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CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
10	JMJD1C	rs10761728	63,235,808	C	T	0.386827	0.021158	0.002069	1.20E-26	0.017494	0.003527	7.17E-07	0.022729	0.002586	1.60E-18	7.67E-23	0.231341	
10	JMJD1C	rs10761729	63,235,844	C	G	0.314289	-0.013678	0.002173	5.10E-11	-0.010845	0.003694	0.003338	-0.014895	0.002718	4.37E-08	4.07E-09	0.377283	
10	JMJD1C	rs4439410	63,239,012	C	G	0.377168	0.020675	0.002077	1.70E-25	0.016661	0.00354	2.56E-06	0.022451	0.002596	5.54E-18	8.91E-22	0.187172	
10	JMJD1C	rs7082066	63,239,211	A	G	0.38676	0.021123	0.00207	1.40E-26	0.017414	0.003527	8.07E-07	0.022701	0.002587	1.78E-18	9.54E-23	0.226798	
10	JMJD1C	rs7082090	63,239,252	A	G	0.377168	0.020675	0.002077	1.70E-25	0.016661	0.00354	2.56E-06	0.022451	0.002596	5.54E-18	8.91E-22	0.187172	
10	JMJD1C	rs4399232	63,239,730	T	C	0.314323	-0.013657	0.002172	5.30E-11	-0.010714	0.003694	0.003737	-0.014905	0.002718	4.28E-08	4.41E-09	0.360819	
10	JMJD1C	rs9414780	63,241,673	A	C	0.377168	0.020675	0.002077	1.70E-25	0.016661	0.00354	2.56E-06	0.022451	0.002596	5.54E-18	8.91E-22	0.187172	
10	JMJD1C	rs7902343	63,245,639	T	C	0.285398	-0.014842	0.002239	1.20E-11	-0.012259	0.00381	0.001298	-0.015933	0.002801	1.31E-08	5.29E-10	0.437189	
10	JMJD1C	rs6479891	63,246,696	T	C	0.376988	0.020618	0.002077	2.50E-25	0.016455	0.003539	3.38E-06	0.022475	0.002596	5.12E-18	1.08E-21	0.170203	
10	JMJD1C	rs10995477	63,250,912	C	T	0.285933	-0.014565	0.002233	2.20E-11	-0.011734	0.003798	0.002014	-0.015827	0.002794	1.51E-08	9.12E-10	0.385377	
10	JMJD1C	rs7081614	63,252,088	C	T	0.386534	0.021147	0.002071	1.40E-26	0.017526	0.00353	6.99E-07	0.022722	0.002588	1.73E-18	8.09E-23	0.235171	
10	JMJD1C	rs4400684	63,252,927	G	A	0.285483	-0.01437	0.002236	4.00E-11	-0.011321	0.003803	0.002925	-0.015739	0.002797	1.89E-08	1.59E-09	0.349409	
10	JMJD1C	rs4454603	63,252,990	T	C	0.285949	-0.014545	0.002233	2.50E-11	-0.011783	0.003799	0.001933	-0.015773	0.002794	1.69E-08	9.78E-10	0.397487	
10	JMJD1C	rs4403688	63,253,156	G	A	0.386525	0.021137	0.002071	1.40E-26	0.017488	0.00353	7.40E-07	0.022727	0.002588	1.70E-18	8.39E-23	0.231305	
10	JMJD1C	rs4595427	63,253,184	C	A	0.285941	-0.014538	0.002233	2.50E-11	-0.011751	0.003799	0.001988	-0.015768	0.002794	1.71E-08	1.01E-09	0.39434	
10	JMJD1C	rs4450077	63,253,976	G	C	0.304125	-0.013365	0.002195	4.80E-10	-0.009956	0.00374	0.007783	-0.014703	0.002743	8.47E-08	1.66E-08	0.306013	
10	JMJD1C	rs4469770	63,254,152	G	A	0.304032	-0.013418	0.002195	4.20E-10	-0.010196	0.003741	0.006438	-0.014667	0.002744	9.20E-08	1.52E-08	0.335079	
10	JMJD1C	rs4405189	63,254,175	G	A	0.285773	-0.014466	0.002234	3.00E-11	-0.011728	0.003799	0.00203	-0.015668	0.002795	2.12E-08	1.27E-09	0.403544	
10	JMJD1C	rs1904297	63,255,428	G	A	0.386456	0.021197	0.002071	1.10E-26	0.017474	0.003531	7.60E-07	0.022827	0.002588	1.22E-18	6.21E-23	0.221451	
10	JMJD1C	rs7070693	63,256,402	A	G	0.386464	0.021165	0.002071	1.30E-26	0.017488	0.003531	7.44E-07	0.022767	0.002588	1.50E-18	7.46E-23	0.227869	
10	JMJD1C	rs7088799	63,256,414	G	T	0.2858	-0.014605	0.002232	2.00E-11	-0.011727	0.003795	0.00201	-0.015898	0.002792	1.28E-08	7.72E-10	0.376127	
10	JMJD1C	rs7896910	63,256,961	A	G	0.246182	-0.015898	0.002343	4.10E-12	-0.013402	0.003986	0.000778	-0.01718	0.002932	4.76E-09	1.23E-10	0.445211	
10	JMJD1C	rs10761730	63,257,293	C	T	0.377359	0.020668	0.002082	2.60E-25	0.016767	0.003547	2.31E-06	0.022429	0.002602	7.03E-18	1.02E-21	0.197199	
10	JMJD1C	rs10822150	63,257,736	G	A	0.386435	0.021088	0.002071	2.00E-26	0.017323	0.00353	9.40E-07	0.022738	0.002588	1.66E-18	1.03E-22	0.216114	
10	JMJD1C	rs9415680	63,261,130	A	G	0.37621	0.020394	0.00208	5.10E-25	0.016197	0.003545	4.97E-06	0.022386	0.002599	7.60E-18	2.30E-21	0.159158	
10	JMJD1C	rs7098181	63,267,383	T	G	0.286104	-0.014055	0.00223	7.30E-11	-0.010834	0.003792	0.004284	-0.015627	0.002791	2.22E-08	2.64E-09	0.308702	
10	JMJD1C	rs10761731	63,267,850	T	A	0.286083	-0.014071	0.00223	7.00E-11	-0.010891	0.003791	0.004079	-0.015624	0.002792	2.24E-08	2.54E-09	0.314742	
10	JMJD1C	rs10761732	63,268,497	C	T	0.385896	0.020893	0.002072	3.50E-26	0.01703	0.003532	1.45E-06	0.022672	0.002589	2.13E-18	2.00E-22	0.197657	
10	JMJD1C	rs7916282	63,272,051	A	T	0.389165	0.020389	0.002115	3.70E-24	0.016154	0.003602	7.42E-06	0.022284	0.002644	3.71E-17	1.62E-20	0.170067	
10	JMJD1C	rs7909555	63,273,348	T	C	0.387977	0.02031	0.00207	8.20E-25	0.016544	0.003529	2.80E-06	0.021978	0.002587	2.07E-17	3.57E-21	0.214216	
10	JMJD1C	rs9415682	63,274,057	G	T	0.37674	0.020637	0.002079	2.40E-25	0.0165	0.003543	3.26E-06	0.022516	0.002599	4.80E-18	9.77E-22	0.170926	
10	JMJD1C	rs10761733	63,275,024	T	C	0.404064	0.019895	0.002075	1.30E-23	0.016439	0.003536	3.38E-06	0.021499	0.002593	1.20E-16	2.42E-20	0.248488	
10	JMJD1C	rs10822151	63,276,907	G	C	0.375624	0.020475	0.00208	4.20E-25	0.016323	0.003545	4.21E-06	0.022445	0.0026	6.34E-18	1.64E-21	0.16377	
10	JMJD1C	rs9787438	63,278,270	C	G	0.286588	-0.014131	0.002229	6.80E-11	-0.010882	0.00379	0.004101	-0.015703	0.00279	1.86E-08	2.14E-09	0.305613	
10	JMJD1C	rs10740109	63,280,379	A	C	0.302162	-0.01297	0.002201	1.70E-09	-0.009256	0.003748	0.013558	-0.014637	0.002753	1.07E-07	3.43E-08	0.247172	
10	JMJD1C	rs10995489	63,281,085	A	G	0.303985	-0.013356	0.002204	6.20E-10	-0.00911	0.003754	0.015241	-0.015331	0.002755	2.69E-08	9.92E-09	0.18155	
10	JMJD1C	rs10761734	63,281,453	C	T	0.385292	0.021027	0.002072	2.20E-26	0.017213	0.003532	1.11E-06	0.02278	0.002589	1.48E-18	1.08E-22	0.203643	
10	JMJD1C	rs10740110	63,283,461	A	G	0.375653	0.020512	0.00208	3.70E-25	0.016322	0.003545	4.21E-06	0.02249	0.0026	5.42E-18	1.41E-21	0.160576	
10	JMJD1C	rs10761735	63,284,158	A	G	0.379157	0.020275	0.002083	1.20E-24	0.016213	0.003551	5.05E-06	0.022201	0.002602	1.52E-17	4.63E-21	0.173713	
10	JMJD1C	rs9414786	63,284,562	T	A	0.375653	0.020512	0.00208	3.70E-25	0.016322	0.003545	4.21E-06	0.02249	0.0026	5.42E-18	1.41E-21	0.160576	
10	JMJD1C	rs4417159	63,285,938	T	A	0.385289	0.021023	0.002072	2.30E-26	0.017213	0.003532	1.11E-06	0.022773	0.002589	1.51E-18	1.11E-22	0.204145	
10	JMJD1C	rs10995493	63,287,266	C	T	0.385291	0.021023	0.002072	2.30E-26	0.017213	0.003532	1.11E-06	0.022774	0.002589	1.50E-18	1.10E-22	0.204072	
10	JMJD1C	rs10761736	63,288,009	A	T	0.385332	0.02105	0.002072	2.00E-26	0.017269	0.003532	1.03E-06	0.022788	0.002589	1.44E-18	9.81E-23	0.207612	
10	JMJD1C	rs7080386	63,288,546	A	C	0.286588	-0.014131	0.002229	6.80E-11	-0.010882	0.00379	0.004101	-0.015703	0.00279	1.86E-08	2.14E-09	0.305613	
10	JMJD1C	rs7074351	63,290,343	A	T	0.375698	0.020511	0.00208	3.60E-25	0.016408	0.003545	3.75E-06	0.02244	0.0026	6.43E-18	1.49E-21	0.170031	
10	JMJD1C	rs7075195	63,290,899	G	A	0.287063	-0.014414	0.002228	2.90E-11	-0.011373	0.003788	0.002688	-0.015885	0.002788	1.24E-08	9.81E-10	0.337318	
10	JMJD1C	rs4486510	63,291,134	C	G	0.375141	0.020493	0.002081	4.00E-25	0.016128	0.003546	5.51E-06	0.022574	0.002601	4.18E-18	1.41E-21	0.142677	
10	JMJD1C	rs10761737	63,292,445	C	T	0.286924	-0.014521	0.002229	2.20E-11	-0.01153	0.003789	0.002351	-0.015984	0.002789	1.02E-08	7.17E-10	0.34368	
10	JMJD1C	rs6479892	63,292,472	A	G	0.37566	0.020513	0.00208	3.70E-25	0.016321	0.003545	4.21E-06	0.02249	0.0026	5.42E-18	1.41E-21	0.160517	
10	JMJD1C	rs7084707	63,292,782	T	C	0.28709	-0.014435	0.002228	2.80E-11	-0.011427	0.003788	0.002566	-0.015888	0.002788	1.24E-08	9.35E-10	0.342804	
10	JMJD1C	rs7913332	63,293,890	A	T	0.385297	0.021022	0.002072	2.30E-26	0.017204	0.003532	1.13E-06	0.022775	0.002589	1.50E-18	1.11E-22	0.203302	
10	JMJD1C	rs7093899	63,294,576	A	G	0.385293	0.021014	0.002072	2.40E-26	0.017205	0.003532	1.13E-06	0.022768	0.002589	1.54E-18	1.14E-22	0.203933	
10	JMJD1C	rs7907462	63,295,773	T	C	0.385807	0.021059	0.002073	2.00E-26	0.017145	0.003533	1.24E-06	0.022902	0.002591	1.01E-18	8.25E-23	0.188774	
10	JMJD1C	rs9414788	63,296,952	A	G	0.375644	0.020536	0.00208	3.40E-25	0.016348	0.003545	4.06E-06	0.022522	0.0026	4.91E-18	1.23E-21	0.16027	
10	JMJD1C	rs10822153	63,297,053	A	C	0.287218	-0.014393	0.002227	3.00E-11	-0.011414	0.003788	0.002591	-0.01586	0.002787	1.30E-08	9.92E-10	0.344477	
10	JMJD1C	rs12773283	63,298,464	C	T	0.375649	0.020528	0.00208	3.50E-25	0.016348	0.003545	4.06E-06	0.022504	0.0026	5.21E-18	1.31E-21	0.1	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	JMJD1C	rs9414793	63,315,349	G	A	0.375653	0.020543	0.002081	3.30E-25	0.016395	0.003546	3.83E-06	0.022502	0.0026	5.26E-18	1.25E-21	0.164837	
10	JMJD1C	rs7090111	63,318,234	G	C	0.287005	-0.014286	0.002228	4.20E-11	-0.011421	0.003787	0.002574	-0.015658	0.002788	2.00E-08	1.50E-09	0.367621	
10	JMJD1C	rs7899715	63,318,695	T	C	0.375718	0.020489	0.002081	4.40E-25	0.016362	0.003546	4.01E-06	0.022454	0.0026	6.18E-18	1.53E-21	0.165901	
10	JMJD1C	rs4518976	63,319,017	C	T	0.380359	0.020935	0.002086	6.70E-26	0.016967	0.003555	1.84E-06	0.022722	0.002606	3.00E-18	3.54E-22	0.19164	
10	JMJD1C	rs7808405	63,319,637	A	T	0.305138	-0.013249	0.00219	5.50E-10	-0.009886	0.003729	0.008044	-0.01467	0.002738	8.59E-08	1.74E-08	0.301076	
10	JMJD1C	rs10822156	63,320,967	C	T	0.287154	-0.014293	0.002227	4.00E-11	-0.011465	0.003787	0.002477	-0.01567	0.002787	1.94E-08	1.40E-09	0.371142	
10	JMJD1C	rs10740112	63,322,315	G	A	0.38531	0.021021	0.002072	2.50E-26	0.017235	0.003532	1.08E-06	0.022759	0.00259	1.60E-18	1.14E-22	0.207173	
10	JMJD1C	rs10740113	63,322,516	T	C	0.38531	0.021021	0.002072	2.50E-26	0.017235	0.003532	1.08E-06	0.022759	0.00259	1.60E-18	1.14E-22	0.207173	
10	JMJD1C	rs10740114	63,322,659	A	G	0.38531	0.021021	0.002072	2.50E-26	0.017235	0.003532	1.08E-06	0.022759	0.00259	1.60E-18	1.14E-22	0.207173	
10	JMJD1C	rs10761742	63,325,288	G	A	0.287261	-0.014331	0.002227	3.60E-11	-0.011396	0.003787	0.002628	-0.015763	0.002787	1.59E-08	1.23E-09	0.352948	
10	JMJD1C	rs4525102	63,326,513	C	T	0.375647	0.020581	0.002081	2.80E-25	0.016421	0.003546	3.69E-06	0.022549	0.0026	4.50E-18	1.03E-21	0.163403	
10	JMJD1C	rs7899503	63,327,708	C	G	0.375642	0.020577	0.002081	2.80E-25	0.016421	0.003546	3.69E-06	0.022542	0.0026	4.62E-18	1.06E-21	0.163907	
10	JMJD1C	rs12767177	63,327,882	C	G	0.386159	0.02087	0.002074	6.40E-26	0.016799	0.003534	2.04E-06	0.022732	0.002592	1.89E-18	2.48E-22	0.175834	
10	JMJD1C	rs7092504	63,329,679	A	G	0.375645	0.020564	0.002081	3.00E-25	0.016421	0.003546	3.69E-06	0.022523	0.0026	4.92E-18	1.13E-21	0.165214	
10	JMJD1C	rs10822157	63,329,720	A	G	0.385299	0.02104	0.002072	2.20E-26	0.017254	0.003532	1.05E-06	0.02278	0.00259	1.50E-18	1.04E-22	0.207038	
10	JMJD1C	rs10995505	63,331,399	G	A	0.305245	-0.013234	0.00219	5.60E-10	-0.009829	0.00373	0.008427	-0.014706	0.002738	7.99E-08	1.69E-08	0.291757	
10	JMJD1C	rs4133250	63,332,645	G	A	0.375642	0.020552	0.002081	3.20E-25	0.016393	0.003546	3.83E-06	0.022519	0.0026	4.99E-18	1.18E-21	0.16358	
10	JMJD1C	rs7918743	63,333,302	T	C	0.385276	0.021052	0.002072	2.10E-26	0.017261	0.003532	1.04E-06	0.022803	0.00259	1.38E-18	9.50E-23	0.205658	
10	JMJD1C	rs7902187	63,333,375	C	T	0.385276	0.021052	0.002072	2.10E-26	0.017261	0.003532	1.04E-06	0.022803	0.00259	1.38E-18	9.50E-23	0.205658	
10	JMJD1C	rs10822158	63,334,623	G	A	0.287066	-0.014241	0.002228	4.80E-11	-0.01134	0.003788	0.002767	-0.015662	0.002788	2.00E-08	1.60E-09	0.35812	
10	JMJD1C	rs10995506	63,334,706	A	G	0.375644	0.020553	0.002081	3.20E-25	0.016395	0.003546	3.82E-06	0.022519	0.0026	4.99E-18	1.18E-21	0.163714	
10	JMJD1C	rs10740115	63,335,230	C	G	0.286679	-0.014384	0.00223	3.30E-11	-0.011328	0.003791	0.00282	-0.015893	0.002791	1.27E-08	1.05E-09	0.332244	
10	JMJD1C	rs10740116	63,335,232	C	T	0.286679	-0.014384	0.00223	3.30E-11	-0.011328	0.003791	0.00282	-0.015893	0.002791	1.27E-08	1.05E-09	0.332244	
10	JMJD1C	rs12219332	63,335,932	G	C	0.375681	0.020524	0.002081	3.60E-25	0.016395	0.003546	3.84E-06	0.022482	0.002601	5.68E-18	1.35E-21	0.16634	
10	JMJD1C	rs10761743	63,336,258	C	T	0.385386	0.020956	0.002073	3.60E-26	0.017213	0.003533	1.12E-06	0.022682	0.00259	2.12E-18	1.56E-22	0.211879	
10	JMJD1C	rs10822159	63,336,490	T	C	0.286946	-0.014245	0.002228	4.80E-11	-0.011294	0.003788	0.002878	-0.015665	0.002789	1.99E-08	1.65E-09	0.352746	
10	JMJD1C	rs10740117	63,338,517	G	A	0.37563	0.020548	0.002081	3.40E-25	0.01641	0.003546	3.75E-06	0.022509	0.0026	5.17E-18	1.20E-21	0.165455	
10	JMJD1C	rs6479894	63,338,981	T	C	0.375631	0.020548	0.002081	3.40E-25	0.016411	0.003546	3.75E-06	0.022509	0.0026	5.17E-18	1.20E-21	0.165517	
10	JMJD1C	rs10733790	63,340,574	G	C	0.372021	0.02065	0.002089	2.90E-25	0.016828	0.003561	2.33E-06	0.022365	0.002611	1.12E-17	1.63E-21	0.20976	
10	JMJD1C	rs10761744	63,341,266	C	G	0.37563	0.020553	0.002081	3.40E-25	0.016411	0.003546	3.75E-06	0.022517	0.0026	5.01E-18	1.16E-21	0.164909	
10	JMJD1C	rs10761745	63,341,311	G	C	0.375834	0.020307	0.002083	1.50E-24	0.01659	0.00355	3.01E-06	0.022033	0.002604	2.75E-17	5.07E-21	0.216236	
10	JMJD1C	rs10740118	63,341,447	C	G	0.28715	-0.014276	0.002228	4.50E-11	-0.011573	0.003787	0.002253	-0.015561	0.002788	2.45E-08	1.61E-09	0.396333	
10	JMJD1C	rs7091664	63,342,040	G	A	0.37563	0.020553	0.002081	3.40E-25	0.016411	0.003546	3.75E-06	0.022517	0.0026	5.01E-18	1.16E-21	0.164909	
10	JMJD1C	rs7896518	63,344,740	G	A	0.286969	-0.014295	0.002228	4.20E-11	-0.011337	0.003788	0.002774	-0.015714	0.002789	1.79E-08	1.44E-09	0.352013	
10	JMJD1C	rs10761746	63,345,134	A	G	0.385265	0.021057	0.002072	2.10E-26	0.017275	0.003532	1.02E-06	0.022813	0.00259	1.33E-18	9.00E-23	0.206065	
10	JMJD1C	rs7081275	63,346,791	G	T	0.375704	0.020512	0.002081	4.20E-25	0.016388	0.003547	3.88E-06	0.022475	0.0026	5.79E-18	1.39E-21	0.166291	
10	JMJD1C	rs10761747	63,348,396	C	G	0.305241	-0.013285	0.00219	5.00E-10	-0.009867	0.00373	0.008174	-0.014766	0.002738	7.09E-08	1.46E-08	0.289668	
10	JMJD1C	rs7895348	63,349,781	C	A	0.375644	0.020575	0.002081	2.90E-25	0.016392	0.003546	3.85E-06	0.022565	0.0026	4.26E-18	1.02E-21	0.160333	
10	JMJD1C	rs7073932	63,350,160	C	T	0.385274	0.021074	0.002072	1.90E-26	0.017253	0.003532	1.06E-06	0.02285	0.00259	1.17E-18	8.18E-23	0.20129	
10	JMJD1C	rs10761748	63,350,216	T	G	0.385274	0.021074	0.002072	1.90E-26	0.017253	0.003532	1.06E-06	0.02285	0.00259	1.17E-18	8.18E-23	0.20129	
10	JMJD1C	rs10822160	63,353,036	G	T	0.28236	-0.014159	0.002248	1.10E-10	-0.010758	0.003815	0.004822	-0.015802	0.002815	2.04E-08	2.71E-09	0.287391	
10	JMJD1C	rs7912797	63,353,620	G	A	0.305242	-0.013288	0.00219	4.80E-10	-0.009928	0.00373	0.007792	-0.014743	0.002738	7.42E-08	1.46E-08	0.297967	
10	JMJD1C	rs7913278	63,353,774	G	A	0.386125	0.02111	0.002072	1.60E-26	0.017388	0.003532	8.68E-07	0.022838	0.002589	1.22E-18	7.04E-23	0.213338	
10	JMJD1C	rs10761749	63,354,049	C	T	0.41859	0.018909	0.002061	1.30E-21	0.014674	0.003516	3.03E-05	0.020923	0.002574	4.58E-16	7.42E-19	0.151517	
10	JMJD1C	rs9415692	63,355,392	A	G	0.374543	0.020625	0.002083	2.60E-25	0.016695	0.003551	2.63E-06	0.022517	0.002603	5.36E-18	8.84E-22	0.185995	
10	JMJD1C	rs7098614	63,355,667	T	C	0.304997	-0.013194	0.002191	6.10E-10	-0.009569	0.003732	0.010364	-0.014766	0.002739	7.19E-08	1.83E-08	0.261579	
10	JMJD1C	rs7082926	63,355,771	T	G	0.384565	0.021131	0.002074	1.90E-26	0.017317	0.003537	9.97E-07	0.022946	0.002592	8.99E-19	5.96E-23	0.199263	
10	JMJD1C	rs7083356	63,356,028	T	A	0.384339	0.02121	0.002074	1.10E-26	0.017466	0.003536	7.99E-07	0.022975	0.002591	7.94E-19	4.26E-23	0.208855	
10	JMJD1C	rs10822161	63,358,443	A	G	0.287071	-0.014284	0.002228	4.30E-11	-0.011415	0.003788	0.002594	-0.015674	0.002788	1.94E-08	1.47E-09	0.365244	
10	JMJD1C	rs9415693	63,360,127	C	T	0.375865	0.020569	0.002081	3.30E-25	0.016301	0.003547	4.37E-06	0.022618	0.002601	3.63E-18	9.82E-22	0.150945	
10	JMJD1C	rs12355784	63,361,805	A	C	0.274842	-0.013151	0.002267	5.50E-09	-0.011234	0.003874	0.003746	-0.014226	0.00283	5.07E-07	4.85E-08	0.532818	
10	JMJD1C	rs9629895	63,363,027	A	C	0.385324	0.020975	0.002072	3.10E-26	0.017096	0.003532	1.32E-06	0.022772	0.002589	1.53E-18	1.32E-22	0.194935	
10	JMJD1C	rs10822162	63,364,320	A	G	0.385323	0.020959	0.002072	3.40E-26	0.017056	0.003532	1.40E-06	0.022772	0.002589	1.53E-18	1.39E-22	0.191785	
10	JMJD1C	rs10822163	63,364,338	G	C	0.287421	-0.014179	0.002228	6.10E-11	-0.011304	0.003788	0.002851	-0.015593	0.002788	2.29E-08	1.88E-09	0.361812	
10	JMJD1C	rs10740119	63,365,477	T	G	0.384448	0.021125	0.002074	1.70E-26	0.01723	0.003535	1.11E-06	0.022953	0.002591	8.52E-19	6.29E-23	0.191633	
10	JMJD1C	rs6479896	63,367,072	C	T	0.287088	-0.014314	0.002228	4.00E-11	-0.011289	0.003788	0.002895	-0.015796	0.002789	1.51E-08	1.27E-09	0.33	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	JMJD1C	rs9415699	63,383,798	C	T	0.375663	0.020487	0.00208	4.20E-25	0.016227	0.003546	4.80E-06	0.022514	0.0026	5.00E-18	1.47E-21	0.15274	
10	JMJD1C	rs9415700	63,385,805	T	C	0.303647	0.018087	0.002195	4.70E-19	0.014312	0.003741	0.000132	0.020039	0.002743	2.87E-13	1.71E-15	0.216978	
10	JMJD1C	rs10822165	63,387,199	T	C	0.385309	0.020988	0.002072	2.70E-26	0.017091	0.003532	1.33E-06	0.022789	0.002589	1.43E-18	1.24E-22	0.193189	
10	JMJD1C	rs10995527	63,387,659	A	G	0.294799	-0.014451	0.002221	2.20E-11	-0.011034	0.003777	0.003497	-0.016233	0.00278	5.36E-09	5.50E-10	0.26756	
10	JMJD1C	rs9414802	63,391,622	C	T	0.312448	0.018716	0.002179	2.70E-20	0.01536	0.003718	3.64E-05	0.020442	0.002722	6.21E-14	1.12E-16	0.270087	
10	JMJD1C	rs9415701	63,391,749	C	T	0.302801	0.018236	0.002197	3.00E-19	0.01447	0.003746	0.000113	0.020211	0.002745	1.87E-13	9.68E-16	0.216358	
10	JMJD1C	rs4746125	63,393,125	A	G	0.306156	0.018357	0.002194	2.10E-19	0.014279	0.003742	0.000137	0.020496	0.002741	7.98E-14	5.02E-16	0.180148	
10	JMJD1C	rs10740122	63,395,451	C	A	0.384017	0.021096	0.002075	2.00E-26	0.017231	0.003538	1.13E-06	0.022935	0.002592	9.47E-19	7.10E-23	0.193427	
10	JMJD1C	rs10822167	63,398,991	C	T	0.38584	0.021095	0.002073	1.70E-26	0.017451	0.003534	8.05E-07	0.022779	0.002591	1.55E-18	8.29E-23	0.224002	
10	JMJD1C	rs4745706	63,399,820	C	T	0.370986	0.020711	0.002098	4.30E-25	0.016832	0.003575	2.54E-06	0.022641	0.002623	6.35E-18	1.01E-21	0.190141	
10	JMJD1C	rs12415038	63,401,098	G	A	0.376284	0.020612	0.002081	2.40E-25	0.016769	0.003547	2.30E-06	0.022436	0.002601	6.64E-18	6.92E-22	0.197546	
10	JMJD1C	rs9415705	63,401,790	G	T	0.375194	0.020695	0.00208	1.70E-25	0.016654	0.003545	2.68E-06	0.022621	0.002599	3.39E-18	5.73E-22	0.17459	
10	JMJD1C	rs10740123	63,404,755	A	G	0.31356	0.018799	0.002175	1.40E-20	0.015318	0.003709	3.67E-05	0.020552	0.002718	4.14E-14	7.57E-17	0.255038	
10	JMJD1C	rs10822168	63,405,424	A	G	0.286482	-0.014309	0.002231	3.90E-11	-0.011424	0.003792	0.002597	-0.015758	0.002792	1.69E-08	1.29E-09	0.357292	
10	JMJD1C	rs10822170	63,411,395	G	T	0.386688	0.020971	0.002076	4.80E-26	0.01725	0.003539	1.11E-06	0.022709	0.002594	2.18E-18	1.59E-22	0.213488	
10	JMJD1C	rs10761755	63,412,212	G	A	0.386149	0.021126	0.002071	1.40E-26	0.017583	0.003531	6.49E-07	0.022738	0.002588	1.66E-18	7.23E-23	0.239084	
10	JMJD1C	rs10761756	63,412,568	T	C	0.287061	-0.014208	0.002228	5.40E-11	-0.011381	0.003788	0.00267	-0.015601	0.002788	2.26E-08	1.74E-09	0.369553	
10	JMJD1C	rs10761757	63,412,790	C	G	0.386148	0.021127	0.002071	1.40E-26	0.017583	0.003531	6.49E-07	0.02274	0.002588	1.65E-18	7.18E-23	0.238893	
10	JMJD1C	rs10761758	63,412,987	T	A	0.286346	-0.014364	0.002232	3.20E-11	-0.011317	0.003794	0.002866	-0.015856	0.002793	1.40E-08	1.17E-09	0.335321	
10	JMJD1C	rs10761759	63,414,032	G	T	0.314112	0.018986	0.00218	7.30E-21	0.015909	0.003718	1.90E-05	0.02049	0.002723	5.49E-14	5.34E-17	0.320197	
10	JMJD1C	rs61853587	63,414,817	C	G	0.303618	0.018576	0.002194	6.70E-20	0.014895	0.003742	6.93E-05	0.020503	0.002741	7.84E-14	2.59E-16	0.296181	
10	JMJD1C	rs7909269	63,418,006	A	G	0.287054	-0.014295	0.002228	4.30E-11	-0.011421	0.003788	0.002581	-0.015705	0.002788	1.82E-08	1.37E-09	0.362378	
10	JMJD1C	rs10761760	63,419,392	C	A	0.28423	-0.014065	0.002244	8.40E-11	-0.01134	0.003813	0.002953	-0.015392	0.002808	4.32E-08	3.60E-09	0.392149	
10	JMJD1C	rs10761761	63,419,398	T	A	0.38955	0.021006	0.002076	3.60E-26	0.017841	0.003541	4.78E-07	0.022371	0.002594	6.82E-18	2.17E-22	0.302144	
10	JMJD1C	rs10995530	63,419,654	G	A	0.313316	0.019	0.002177	6.80E-21	0.015768	0.003715	2.21E-05	0.020646	0.00272	3.32E-14	3.76E-17	0.289388	
10	JMJD1C	rs11818194	63,420,692	A	G	0.364685	0.020359	0.002145	1.10E-23	0.014695	0.00366	6.01E-05	0.023184	0.002679	5.32E-18	1.75E-20	0.061323	
10	JMJD1C	rs6479901	63,421,016	C	A	0.385363	0.021234	0.002073	9.30E-27	0.017671	0.003534	5.81E-07	0.022875	0.002589	1.07E-18	4.21E-23	0.234906	
10	JMJD1C	rs7077580	63,421,125	A	G	0.287052	-0.01429	0.002228	4.30E-11	-0.011407	0.003788	0.002611	-0.015705	0.002788	1.82E-08	1.38E-09	0.360854	
10	JMJD1C	rs10740124	63,426,034	C	T	0.313227	0.019015	0.002177	6.80E-21	0.015709	0.003714	2.37E-05	0.0207	0.00272	2.84E-14	3.44E-17	0.278289	
10	JMJD1C	rs9415706	63,426,587	T	C	0.30363	0.018579	0.002194	6.70E-20	0.014928	0.003742	6.69E-05	0.020489	0.002742	8.15E-14	2.60E-16	0.230579	
10	JMJD1C	rs72837019	63,427,258	C	T	0.313227	0.019015	0.002177	6.80E-21	0.015709	0.003714	2.37E-05	0.0207	0.00272	2.84E-14	2.78289	0.23447	
10	JMJD1C	rs61853589	63,427,351	A	T	0.304181	0.018601	0.002195	5.10E-20	0.014844	0.003743	7.39E-05	0.020548	0.002742	7.06E-14	2.48E-16	0.218987	
10	JMJD1C	rs9414803	63,428,309	A	G	0.303627	0.018576	0.002194	6.80E-20	0.014928	0.003742	6.69E-05	0.020483	0.002742	8.27E-14	2.64E-16	0.231031	
10	JMJD1C	rs9415707	63,428,530	C	T	0.304458	0.018455	0.002192	9.60E-20	0.014831	0.003737	7.31E-05	0.020327	0.00274	1.23E-13	4.24E-16	0.2356	
10	JMJD1C	rs10761764	63,429,143	C	G	0.313375	0.018966	0.002178	8.40E-21	0.015826	0.003715	2.07E-05	0.020551	0.00272	4.37E-14	3.61E-17	0.304846	
10	JMJD1C	rs10761765	63,429,213	A	G	0.313227	0.019009	0.002177	6.90E-21	0.015702	0.003714	2.39E-05	0.020695	0.00272	2.88E-14	3.52E-17	0.278096	
10	JMJD1C	rs12413029	63,429,366	C	T	0.303629	0.018574	0.002194	6.80E-20	0.01492	0.003742	6.74E-05	0.020483	0.002742	8.27E-14	2.66E-16	0.230368	
10	JMJD1C	rs9415708	63,430,282	C	G	0.303629	0.018574	0.002194	6.80E-20	0.01492	0.003742	6.74E-05	0.020483	0.002742	8.27E-14	2.66E-16	0.230368	
10	JMJD1C	rs7924036	63,431,885	G	T	0.332597	0.019054	0.002144	1.10E-21	0.016511	0.003649	6.13E-06	0.020546	0.002681	1.90E-14	6.35E-18	0.372805	
10	JMJD1C	rs10761767	63,432,671	T	C	0.312746	0.018993	0.002177	7.10E-21	0.015461	0.003714	3.17E-05	0.020792	0.002719	2.17E-14	3.48E-17	0.246724	
10	JMJD1C	rs7917169	63,433,181	T	C	0.313731	0.01881	0.002176	1.30E-20	0.015314	0.003711	3.72E-05	0.020589	0.002718	3.78E-14	7.00E-17	0.2515	
10	JMJD1C	rs10761768	63,434,369	C	A	0.313817	0.018878	0.002175	1.00E-20	0.015285	0.003708	3.81E-05	0.020697	0.002717	2.70E-14	5.14E-17	0.239063	
10	JMJD1C	rs72837025	63,434,731	C	A	0.304502	0.018471	0.002192	8.80E-20	0.01483	0.003737	7.32E-05	0.020345	0.00274	1.17E-13	4.04E-16	0.234012	
10	JMJD1C	rs12784772	63,435,695	A	T	0.304456	0.018511	0.002192	7.50E-20	0.01484	0.003737	7.23E-05	0.02041	0.002739	9.73E-14	3.33E-16	0.229377	
10	JMJD1C	rs77494594	63,437,549	C	A	0.303649	0.018638	0.002194	5.00E-20	0.014883	0.003741	7.01E-05	0.020615	0.002741	5.71E-14	1.92E-16	0.216518	
10	JMJD1C	rs10437345	63,443,186	C	T	0.303644	0.018642	0.002194	4.90E-20	0.014906	0.003741	6.84E-05	0.020599	0.002741	5.99E-14	1.96E-16	0.21963	
10	JMJD1C	rs2616631	63,448,154	A	T	0.303178	0.018569	0.002194	6.60E-20	0.01463	0.00374	9.27E-05	0.020626	0.002741	5.57E-14	2.44E-16	0.196034	
10	JMJD1C	rs2466128	63,448,561	C	T	0.303178	0.018569	0.002194	6.60E-20	0.01463	0.00374	9.27E-05	0.020626	0.002741	5.57E-14	2.44E-16	0.196034	
10	JMJD1C	rs2719815	63,450,534	C	G	0.303178	0.018569	0.002194	6.60E-20	0.01463	0.00374	9.27E-05	0.020626	0.002741	5.57E-14	2.44E-16	0.196034	
10	JMJD1C	rs2616630	63,453,579	C	A	0.303178	0.018569	0.002194	6.60E-20	0.01463	0.00374	9.27E-05	0.020626	0.002741	5.57E-14	2.44E-16	0.196034	
10	JMJD1C	rs2616629	63,454,056	C	T	0.303178	0.018569	0.002194	6.60E-20	0.01463	0.00374	9.27E-05	0.020626	0.002741	5.57E-14	2.44E-16	0.196034	
10	JMJD1C	rs10822172	63,455,478	T	C	0.313077	0.019009	0.002178	6.90E-21	0.01536	0.003714	3.58E-05	0.020857	0.00272	1.84E-14	3.31E-17	0.232455	
10	JMJD1C	rs12573212	63,458,665	A	C	0.312682	0.018978	0.002177	7.70E-21	0.01549	0.003714	3.07E-05	0.020772	0.00272	2.32E-14	3.61E-17	0.251234	
10	JMJD1C	rs7074735	63,459,519	T	A	0.312922	0.019005	0.002177	7.00E-21	0.015497	0.003713	3.03E-05	0.02082	0.002719	2.00E-14	3.08E-17	0.247388	
10	JMJD1C	rs7075205	63,459,834	T	C	0.312752	0.019031	0.002177	6.20E-21	0.015482	0.003713	3.09E-05	0.020845	0.00272	1.87E-14	2.94E-17	0.243887	
10	JMJD1C	rs10995540	63,460,170	C	G	0.312752	0.019031	0.002177	6.20E-21	0.015482	0.003713	3.09E-05	0.020845	0.00272	1.87E-14	2		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	JMJD1C *	rs2393976	63,493,679	C	G	0.304255	0.018448	0.002193	9.90E-20	0.014299	0.003739	0.000132	0.020644	0.00274	5.15E-14	3.15E-16	0.171054	
10	REEP3 *	rs7910662	63,493,940	C	T	0.312456	0.018998	0.002178	7.30E-21	0.015254	0.003716	4.09E-05	0.020909	0.002721	1.61E-14	3.30E-17	0.219533	
10	REEP3 *	rs10822175	63,495,414	A	T	0.307833	0.019168	0.002196	6.10E-21	0.016852	0.003745	6.90E-06	0.020398	0.002744	1.10E-13	4.00E-17	0.44499	
10	REEP3 *	rs4746149	63,497,633	C	T	0.30318	0.01865	0.002194	4.80E-20	0.014711	0.003741	8.47E-05	0.020697	0.002741	4.56E-14	1.84E-16	0.196835	
10	REEP3 *	rs72837056	63,500,718	G	T	0.302734	0.018681	0.002196	4.80E-20	0.014783	0.003744	7.94E-05	0.020675	0.002744	5.09E-14	1.93E-16	0.204259	
10	REEP3 *	rs2893924	63,501,594	A	G	0.312757	0.019045	0.002177	5.80E-21	0.015514	0.003713	2.98E-05	0.020849	0.002719	1.84E-14	2.79E-17	0.246353	
10	REEP3 *	rs2393981	63,501,605	A	G	0.312757	0.019045	0.002177	5.80E-21	0.015514	0.003713	2.98E-05	0.020849	0.002719	1.84E-14	2.79E-17	0.246353	
10	REEP3 *	rs9971294	63,503,108	A	G	0.312757	0.019045	0.002177	5.80E-21	0.015514	0.003713	2.98E-05	0.020849	0.002719	1.84E-14	2.79E-17	0.246353	
10	REEP3 *	rs80026135	63,505,240	G	C	0.302698	0.018668	0.002198	5.10E-20	0.014793	0.003748	7.98E-05	0.020644	0.002746	5.82E-14	2.21E-16	0.207821	
10	REEP3 *	rs11815969	63,506,095	T	C	0.303188	0.018616	0.002194	5.50E-20	0.014706	0.003741	8.53E-05	0.02065	0.002741	5.18E-14	2.10E-16	0.199869	
10	REEP3 *	rs7078456	63,509,719	C	T	0.303353	0.0186	0.002194	6.10E-20	0.014757	0.00374	8.04E-05	0.020608	0.002741	5.81E-14	2.22E-16	0.206995	
10	REEP3 *	rs7083823	63,510,912	G	C	0.313412	0.018855	0.002178	1.30E-20	0.015583	0.003715	2.77E-05	0.020483	0.002721	5.37E-14	7.46E-17	0.287217	
10	REEP3 *	rs7097698	63,513,635	G	A	0.312812	0.01913	0.002178	4.40E-21	0.015656	0.003714	2.52E-05	0.020902	0.002721	1.64E-14	2.12E-17	0.254508	
10	REEP3 *	rs7068144	63,514,500	C	G	0.312809	0.019132	0.002178	4.40E-21	0.015667	0.003714	2.49E-05	0.0209	0.002721	1.65E-14	2.11E-17	0.255689	
10	REEP3 *	rs72837070	63,514,919	C	T	0.303244	0.01869	0.002195	4.40E-20	0.01485	0.003741	7.28E-05	0.020686	0.002743	4.83E-14	1.69E-16	0.208361	
10	REEP3 *	rs61853635	63,516,750	G	T	0.30325	0.018687	0.002195	4.40E-20	0.014857	0.003741	7.23E-05	0.02068	0.002743	4.92E-14	1.70E-16	0.209371	
10	REEP3 *	rs7082076	63,517,185	C	G	0.31428	0.019174	0.00218	4.60E-21	0.015719	0.00372	2.41E-05	0.020953	0.002723	1.49E-14	1.85E-17	0.256193	
10	REEP3 *	rs4745729	63,517,323	G	A	0.303231	0.018675	0.002195	4.70E-20	0.01486	0.003742	7.21E-05	0.020661	0.002743	5.21E-14	1.80E-16	0.211161	
10	REEP3 *	rs10740133	63,517,676	C	T	0.312798	0.019112	0.002178	4.70E-21	0.015676	0.003714	2.47E-05	0.020868	0.002721	1.81E-14	2.29E-17	0.259425	
10	REEP3 *	rs12416349	63,517,783	T	C	0.303082	0.01922	0.002214	1.20E-20	0.01477	0.00377	9.03E-05	0.021605	0.002769	6.29E-15	2.77E-17	0.143906	
10	REEP3 *	rs7358191	63,519,028	A	C	0.312798	0.019112	0.002178	4.70E-21	0.015676	0.003714	2.47E-05	0.020868	0.002721	1.81E-14	2.29E-17	0.259425	
10	REEP3 *	rs7358152	63,519,138	T	C	0.312798	0.019112	0.002178	4.70E-21	0.015676	0.003714	2.47E-05	0.020868	0.002721	1.81E-14	2.29E-17	0.259425	
10	REEP3 *	rs10822179	63,520,404	T	C	0.312798	0.019112	0.002178	4.70E-21	0.015676	0.003714	2.47E-05	0.020868	0.002721	1.81E-14	2.29E-17	0.259425	
10	REEP3	rs10761780	63,524,272	C	T	0.303317	0.018719	0.002195	3.90E-20	0.014879	0.003741	7.05E-05	0.020737	0.002743	4.21E-14	1.43E-16	0.206696	
10	REEP3	rs10761781	63,524,843	T	C	0.303231	0.018704	0.002195	4.20E-20	0.014859	0.003742	7.22E-05	0.020713	0.002743	4.53E-14	1.57E-16	0.207021	
10	REEP3	rs12412946	63,529,792	G	T	0.295529	0.018355	0.002228	4.20E-19	0.015353	0.003795	5.26E-05	0.019979	0.002786	7.77E-13	1.91E-15	0.325843	
10	REEP3	rs12414188	63,529,854	G	A	0.30254	0.0187	0.002198	5.10E-20	0.014918	0.003746	6.88E-05	0.02068	0.002747	5.41E-14	1.79E-16	0.214809	
10	REEP3	rs7087279	63,532,176	T	A	0.303234	0.018667	0.002195	4.70E-20	0.014914	0.003741	6.78E-05	0.020614	0.002743	5.91E-14	1.92E-16	0.219119	
10	REEP3	rs59035163	63,532,283	G	C	0.303234	0.018667	0.002195	4.70E-20	0.014914	0.003741	6.78E-05	0.020614	0.002743	5.91E-14	1.92E-16	0.219119	
10	REEP3	rs12413081	63,533,959	T	C	0.303234	0.018667	0.002195	4.70E-20	0.014914	0.003741	6.78E-05	0.020614	0.002743	5.91E-14	1.92E-16	0.219119	
10	REEP3	rs16918567	63,534,910	C	A	0.303091	0.018573	0.002195	6.50E-20	0.014912	0.003741	6.80E-05	0.020486	0.002744	8.63E-14	2.29E-16	0.229608	
10	REEP3	rs16918573	63,541,045	A	T	0.300757	0.018618	0.002199	5.50E-20	0.015055	0.00375	6.01E-05	0.020526	0.002748	8.43E-14	2.43E-16	0.239233	
10	REEP3	rs16918575	63,541,565	G	A	0.300757	0.018614	0.002199	5.60E-20	0.015055	0.00375	6.01E-05	0.020521	0.002748	8.55E-14	2.46E-16	0.239695	
10	REEP3	rs12414796	63,543,327	A	G	0.30072	0.01862	0.0022	5.50E-20	0.015022	0.00375	6.24E-05	0.020552	0.002748	7.87E-14	2.35E-16	0.234218	
10	REEP3	rs61853639	63,545,353	T	G	0.301286	0.018649	0.002198	5.00E-20	0.014842	0.003747	7.55E-05	0.020676	0.002747	5.42E-14	1.96E-16	0.209251	
10	REEP3	rs4746195	63,547,893	G	A	0.301325	0.018654	0.002198	4.60E-20	0.014921	0.003746	6.87E-05	0.020639	0.002746	5.95E-14	1.96E-16	0.218347	
10	REEP3	rs4469774	63,550,017	T	G	0.302383	0.018541	0.002198	1.10E-19	0.015064	0.003747	5.87E-05	0.020422	0.002747	1.10E-13	3.10E-16	0.248754	
10	REEP3	rs61853642	63,554,019	A	G	0.285222	0.018181	0.002233	2.10E-18	0.014421	0.003804	0.000151	0.020401	0.002791	2.78E-13	1.88E-15	0.204957	
10	REEP3	rs9919429	63,554,059	G	A	0.313114	0.018514	0.002176	7.90E-20	0.01596	0.003703	1.65E-05	0.020263	0.002722	1.03E-13	8.62E-17	0.349175	
10	REEP3	rs12163188	63,554,951	C	G	0.313261	0.018432	0.002177	1.00E-19	0.015969	0.003703	1.64E-05	0.020149	0.002723	1.41E-13	1.17E-16	0.363062	
10	REEP3	rs2393984	63,555,211	G	A	0.313115	0.01851	0.002176	8.00E-20	0.01596	0.003703	1.65E-05	0.020258	0.002722	1.04E-13	8.74E-17	0.349757	
10	REEP3	rs6479905	63,555,471	G	A	0.311128	0.018762	0.002182	5.30E-20	0.016712	0.003717	7.03E-06	0.020165	0.002728	1.49E-13	5.52E-17	0.453858	
10	REEP3	rs12411988	63,555,637	C	G	0.28541	0.018125	0.002232	2.60E-18	0.014256	0.003803	0.000179	0.020406	0.00279	2.72E-13	2.17E-15	0.192267	
10	REEP3	rs12412012	63,556,003	T	C	0.285335	0.018157	0.002232	2.30E-18	0.014414	0.003803	0.000152	0.020372	0.00279	2.98E-13	2.02E-15	0.206529	
10	REEP3	rs7919685	63,556,040	T	G	0.313232	0.018486	0.002176	8.60E-20	0.015961	0.003702	1.64E-05	0.020225	0.002722	1.13E-13	9.46E-17	0.35352	
10	REEP3	rs12247907	63,557,285	C	G	0.313228	0.018507	0.002176	7.90E-20	0.016014	0.003702	1.54E-05	0.020225	0.002722	1.13E-13	8.90E-17	0.359486	
10	REEP3	rs7070761	63,557,296	T	A	0.313228	0.018507	0.002176	7.90E-20	0.016014	0.003702	1.54E-05	0.020225	0.002722	1.13E-13	8.90E-17	0.359486	
10	REEP3	rs10761785	63,559,006	G	T	0.314762	0.018506	0.002175	8.30E-20	0.016327	0.003701	1.04E-05	0.019981	0.00272	2.12E-13	1.13E-16	0.426286	
10	REEP3	rs61579729	63,559,553	G	A	0.285333	0.018187	0.002232	2.00E-18	0.014495	0.003803	0.00014	0.020365	0.00279	3.04E-13	1.90E-15	0.21338	
10	REEP3	rs7898861	63,559,918	C	T	0.312129	0.018533	0.002181	8.60E-20	0.015995	0.003711	1.65E-05	0.020287	0.002729	1.09E-13	9.18E-17	0.351465	
10	REEP3	rs16918599	63,560,319	C	T	0.285308	0.018166	0.002232	2.20E-18	0.014488	0.003804	0.000141	0.020343	0.00279	3.22E-13	2.04E-15	0.214467	
10	REEP3	rs16918600	63,560,690	A	C	0.285308	0.018166	0.002232	2.20E-18	0.014488	0.003804	0.000141	0.020343	0.00279	3.22E-13	2.04E-15	0.214467	
10	REEP3	rs11812934	63,560,970	A	G	0.285312	0.018163	0.002232	2.20E-18	0.014481	0.003804	0.000142	0.020343	0.00279	3.22E-13	2.05E-15	0.213928	
10	REEP3	rs16918601	63,561,291	A	C	0.285325	0.018205	0.002233	1.90E-18	0.014559	0.003805	0.000131	0.020378	0.002792	3.00E-13	1.77E-15	0.217491	
10	REEP3	rs12245149	63,561,387	A	C	0.31321	0.01852	0.002177	7.90E-20	0.016078	0.003704	1.44E-05	0.02022	0.002723	1.17E-13	8.63E-17	0.367613	
10	REEP3	rs12245367	63,561,704	T	C	0.312772	0.018594	0.002183	8.10E-20	0.016004	0.003714	1.66E-05	0.020324	0.002731	1.03E-13	8.71E-17	0.348756	
10																		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
10	REEP3	rs7911761	63,578,993	G	C	0.305712	0.017896	0.002202	3.00E-18	0.014371	0.003744	0.000125	0.020208	0.002755	2.32E-13	1.32E-15	0.209205	
10	REEP3	rs11817901	63,580,123	A	G	0.286856	0.018038	0.002243	7.40E-18	0.013407	0.00382	0.000452	0.020716	0.002805	1.59E-13	3.04E-15	0.123019	
10	REEP3	rs12768534	63,581,137	A	G	0.305691	0.017899	0.002202	3.00E-18	0.014332	0.003744	0.00013	0.020227	0.002755	2.20E-13	1.30E-15	0.20471	
10	REEP3	rs16918638	63,583,371	C	T	0.28803	0.01811	0.002241	6.10E-18	0.013556	0.003816	0.000385	0.020766	0.002803	1.33E-13	2.19E-15	0.127798	
10	REEP3	rs61853658	63,590,037	T	C	0.282026	0.017247	0.00226	2.70E-16	0.012784	0.003847	0.000896	0.019916	0.002826	1.90E-12	6.58E-14	0.135168	
10	REEP3	rs11817169	63,596,549	G	A	0.283402	0.017348	0.002262	2.60E-16	0.012643	0.003853	0.001037	0.020112	0.002828	1.19E-12	4.75E-14	0.118063	
10	REEP3	rs4746244	63,599,941	T	C	0.281532	0.0172	0.002269	4.90E-16	0.012602	0.003861	0.001106	0.019839	0.002837	2.82E-12	1.18E-13	0.130956	
10	REEP3	rs11818738	63,604,971	C	A	0.285279	0.016969	0.002273	9.80E-16	0.010978	0.003871	0.00458	0.020435	0.002843	6.80E-13	1.07E-13	0.048922	F
10	REEP3 *	rs2565187	63,632,093	C	T	0.232748	0.015054	0.002399	3.70E-11	0.010399	0.004082	0.010868	0.017846	0.003001	2.82E-09	8.17E-10	0.141616	
10	REEP3 *	rs2565186	63,632,270	A	G	0.232722	0.015044	0.002399	3.80E-11	0.010355	0.004082	0.011211	0.017862	0.003001	2.73E-09	8.14E-10	0.138441	
10	REEP3 *	rs1268639	63,632,720	A	G	0.232879	0.015128	0.002398	3.10E-11	0.01058	0.004079	0.009519	0.017866	0.002999	2.65E-09	6.85E-10	0.150147	
10	REEP3 *	rs1255495	63,634,690	G	A	0.233126	0.015003	0.002393	4.10E-11	0.010338	0.004072	0.011148	0.017789	0.002994	2.89E-09	8.56E-10	0.140352	
10	IDE *	rs2798253	92,443,148	C	G	0.344555	0.011747	0.002129	2.50E-08	0.010356	0.003628	0.004321	0.012427	0.002661	3.06E-06	3.13E-07	0.645183	
10	IDE *	rs6583813	92,450,182	C	T	0.342857	0.011577	0.002125	4.80E-08	0.009716	0.00362	0.007296	0.012552	0.002656	2.33E-06	5.277746	0.527746	
10	IDE	rs3781241	92,456,753	T	C	0.346128	0.011851	0.002127	2.00E-08	0.010157	0.003623	0.005063	0.012782	0.002659	1.55E-06	1.88E-07	0.559165	
10	IDE	rs2149632	92,472,490	T	C	0.342758	0.011732	0.002123	2.70E-08	0.010128	0.003614	0.00509	0.012576	0.002654	2.19E-06	2.62E-07	0.5852	
10	IDE	rs10882067	92,484,511	T	C	0.341226	0.011759	0.002127	2.40E-08	0.01051	0.003621	0.003714	0.012371	0.00266	3.37E-06	2.98E-07	0.678865	
10	IDE	rs11187022	92,495,286	T	C	0.340745	0.011821	0.002131	2.20E-08	0.010275	0.003627	0.004632	0.012601	0.002665	2.30E-06	2.53E-07	0.605245	
10	IDE	rs34459034	92,499,489	G	A	0.437561	0.012424	0.002049	1.30E-09	0.011078	0.003489	0.001505	0.013466	0.002562	1.51E-07	6.50E-09	0.581265	
10	IDE	rs10786048	92,500,211	C	T	0.342477	0.011877	0.002126	1.80E-08	0.010332	0.003621	0.004337	0.012629	0.002658	2.06E-06	2.14E-07	0.609026	
10	IDE	rs10882071	92,500,348	T	C	0.343097	0.012119	0.002128	1.20E-08	0.010761	0.003626	0.003009	0.012662	0.002661	1.98E-06	1.48E-07	0.672479	
10	IDE	rs10882072	92,500,955	C	A	0.343726	0.01202	0.002129	1.30E-08	0.010476	0.003625	0.003865	0.012737	0.002661	1.73E-06	1.63E-07	0.615123	
10	IDE	rs11187030	92,501,246	C	T	0.343131	0.011769	0.002129	2.50E-08	0.010068	0.003625	0.005497	0.012578	0.002662	2.33E-06	2.99E-07	0.576778	
10	IDE	rs11187033	92,502,602	T	A	0.342469	0.011886	0.002127	1.70E-08	0.010381	0.003622	0.004169	0.012644	0.002659	2.01E-06	2.02E-07	0.614448	
10	IDE	rs10509645	92,518,109	C	A	0.343156	0.011724	0.002127	2.70E-08	0.010176	0.003621	0.00496	0.012453	0.00266	2.90E-06	3.36E-07	0.612453	
10	IDE	rs10882074	92,521,928	T	G	0.339449	0.012591	0.002141	4.70E-09	0.011161	0.003649	0.00223	0.013309	0.002676	6.71E-07	3.96E-08	0.634939	
10	IDE	rs7073833	92,526,663	T	C	0.344303	0.011946	0.002127	2.00E-08	0.011285	0.003623	0.001846	0.012308	0.002659	3.72E-06	1.73E-07	0.819968	
10	IDE	rs12220493	92,551,152	C	T	0.344404	0.012074	0.002125	1.40E-08	0.011086	0.003619	0.002197	0.012678	0.002657	1.86E-06	1.05E-07	0.723028	
10	IDE	rs2421943	92,552,058	G	A	0.344437	0.012044	0.002125	1.50E-08	0.011093	0.003619	0.002182	0.012632	0.002657	2.03E-06	1.13E-07	0.731879	
10	IDE	rs7078418	92,560,777	C	T	0.347022	0.011966	0.002134	1.80E-08	0.010681	0.003632	0.003288	0.012796	0.002669	1.66E-06	1.35E-07	0.638984	
10	IDE	rs10882083	92,562,216	C	G	0.344102	0.011974	0.002126	1.70E-08	0.011142	0.00362	0.002097	0.012545	0.002659	2.41E-06	1.28E-07	0.75463	
10	IDE	rs11187072	92,564,652	C	T	0.344756	0.012653	0.002134	3.00E-09	0.011354	0.003635	0.001792	0.013511	0.002667	4.14E-07	2.03E-08	0.632379	
10	IDE	rs7076966	92,565,754	C	T	0.344526	0.012194	0.002125	1.10E-08	0.011092	0.003619	0.002187	0.012875	0.002657	1.29E-06	6.91366	0.691366	
10	IDE *	rs11187078	92,580,948	C	G	0.344603	0.012512	0.002123	3.90E-09	0.011058	0.003613	0.002216	0.013396	0.002655	4.61E-07	2.74E-08	0.602176	
10	IDE *	rs2901597	92,582,906	C	T	0.344645	0.012466	0.002124	4.30E-09	0.011035	0.003615	0.002277	0.013332	0.002657	5.31E-07	3.22E-08	0.60866	
10	KIF11 *	rs7921210	92,587,812	G	A	0.345009	0.012496	0.002121	4.30E-09	0.011002	0.003609	0.002307	0.013423	0.002652	4.25E-07	2.63E-08	0.588771	
10	KIF11 *	rs7922041	92,588,443	G	A	0.437341	0.01234	0.002037	1.30E-09	0.010914	0.003465	0.001642	0.013587	0.002548	9.86E-08	4.67E-09	0.534302	
10	KIF11 *	rs12355158	92,590,924	G	A	0.334702	0.01303	0.002147	1.40E-09	0.010573	0.003653	0.003814	0.014404	0.002684	8.25E-08	8.50E-09	0.398166	
10	KIF11	rs3824735	92,594,447	T	G	0.33626	0.012973	0.002139	1.60E-09	0.011103	0.00364	0.002299	0.014088	0.002675	1.42E-07	9.04E-09	0.508738	
10	KIF11	rs11187090	92,600,915	C	T	0.336294	0.012948	0.002138	1.60E-09	0.011081	0.003639	0.002339	0.014081	0.002674	1.43E-07	9.27E-09	0.506439	
10	KIF11	rs10882085	92,605,125	C	T	0.336297	0.012952	0.002138	1.60E-09	0.011094	0.003639	0.002309	0.014081	0.002674	1.43E-07	9.17E-09	0.508466	
10	KIF11	rs11187094	92,608,421	G	A	0.4282	0.012377	0.002043	1.20E-09	0.010406	0.003477	0.002772	0.013838	0.002555	6.25E-08	4.85E-09	0.426402	
10	KIF11	rs11187096	92,609,831	G	T	0.336278	0.012939	0.002138	1.60E-09	0.011087	0.003639	0.002324	0.01407	0.002674	1.46E-07	9.42E-09	0.508985	
10	KIF11	rs11187098	92,615,134	C	C	0.336601	0.012951	0.002138	1.50E-09	0.011031	0.003639	0.002447	0.01412	0.002674	1.32E-07	8.93E-09	0.494004	
10	KIF11	rs11187099	92,615,240	T	C	0.336285	0.012959	0.002138	1.50E-09	0.011076	0.003639	0.002348	0.014109	0.002674	1.35E-07	8.80E-09	0.501858	
10	KIF11	rs10882092	92,619,466	G	A	0.336489	0.013062	0.002139	1.10E-09	0.011279	0.00364	0.00195	0.014183	0.002675	1.17E-07	6.44E-09	0.520242	
10	KIF11	rs11187105	92,624,670	C	T	0.428725	0.012281	0.002042	1.60E-09	0.010516	0.003475	0.002482	0.013669	0.002554	8.92E-08	6.20E-09	0.464705	
10	KIF11	rs1573051	92,627,577	T	C	0.336277	0.012956	0.002138	1.50E-09	0.011076	0.003639	0.002348	0.014106	0.002674	1.36E-07	8.85E-09	0.502227	
10	KIF11	rs11187107	92,631,940	G	A	0.336411	0.012858	0.002139	2.00E-09	0.01081	0.00364	0.002994	0.014093	0.002675	1.40E-07	1.14E-08	0.467339	
10	KIF11	rs10882095	92,634,645	T	G	0.336228	0.012799	0.002139	2.40E-09	0.010765	0.00364	0.003115	0.014027	0.002675	1.61E-07	1.35E-08	0.470308	
10	KIF11	rs1972360	92,636,831	C	T	0.337842	0.012842	0.002139	2.20E-09	0.010497	0.003641	0.003952	0.014257	0.002676	1.01E-07	1.07E-08	0.405411	
10	KIF11	rs10882096	92,641,629	G	T	0.336465	0.012821	0.002139	2.30E-09	0.010878	0.00364	0.002812	0.013979	0.002674	1.76E-07	1.34E-08	0.492419	
10	KIF11	rs11187114	92,646,480	A	T	0.336702	0.013162	0.00214	1.10E-09	0.0112	0.003643	0.00212	0.014332	0.002676	8.73E-08	5.25E-09	0.488539	
10	KIF11	rs11187117	92,652,401	A	C	0.33634	0.012861	0.002139	2.40E-09	0.010916	0.003641	0.002725	0.014003	0.002674	1.68E-07	1.24E-08	0.494488	
10	KIF11	rs1044153	92,655,321	A	C	0.335999	0.012838	0.002139	2.50E-09	0.010994	0.003641	0.002544	0.013923	0.002676	1.99E-07	1.38E-08	0.516876	
10	KIF11 *	rs2153827	92,664,316	T	G	0.336141	0.01349	0.002146	4.60E-10	0.012709	0.003652	0.000504	0.013994	0.002684	1.89E-07	2.93E-09	0.776704	
10	KIF11 *	rs35978445	92,664,665															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	CYP26A1 *	rs10882141	93,084,327	G	A	0.1563	0.01699	0.00279	3.20E-10	0.017621	0.004744	0.000205	0.0173	0.003491	7.35E-07	4.69E-09	0.956411	
10	CYP26A1 *	rs913423	93,085,279	G	A	0.1612	0.016716	0.002748	2.10E-10	0.016925	0.004677	0.000299	0.017288	0.003436	4.95E-07	4.56E-09	0.950081	
10	CYP26A1 *	rs10786069	93,085,789	C	T	0.162262	0.016136	0.002744	6.00E-10	0.015269	0.004669	0.001081	0.017186	0.003433	5.66E-07	1.72E-08	0.740851	
10	CYP26A1 *	rs7080494	93,086,336	G	A	0.150755	0.015689	0.002883	6.80E-09	0.017117	0.004904	0.000485	0.015825	0.003606	1.16E-05	1.49E-07	0.83191	
10	WDR11 *	rs2246958	121,129,610	C	T	0.377593	-0.012378	0.002094	5.90E-09	-0.005603	0.00357	0.0116523	-0.015638	0.002616	2.31E-09	5.04E-09	0.02337	F
10	WDR11 *	rs2246730	121,131,141	C	T	0.37611	-0.012773	0.002098	2.80E-09	-0.005918	0.003577	0.098076	-0.016151	0.002621	7.36E-10	1.44E-09	0.021044	F
10	WDR11 *	rs1873446	121,131,995	C	T	0.375804	-0.012729	0.002095	2.70E-09	-0.005852	0.003573	0.10149	-0.016027	0.002617	9.42E-10	1.88E-09	0.021622	F
10	WDR11 *	rs1907239	121,135,315	A	C	0.367314	0.013564	0.002092	4.60E-11	0.006904	0.003557	0.052296	0.016787	0.002617	1.47E-10	1.78E-10	0.025254	F
10	WDR11 *	rs2502666	121,138,399	A	G	0.365909	0.01354	0.002096	5.00E-11	0.007333	0.003563	0.039605	0.016581	0.002623	2.66E-10	2.51E-10	0.036603	F
10	WDR11 *	rs1907240	121,138,445	G	A	0.414321	-0.014861	0.002048	7.30E-13	-0.00927	0.003493	0.00797	-0.017235	0.002558	1.66E-11	4.08E-12	0.065812	
10	WDR11 *	rs1907241	121,138,470	G	T	0.41381	-0.014996	0.002048	4.40E-13	-0.009352	0.003493	0.00743	-0.017398	0.002558	1.07E-11	2.49E-12	0.063087	
10	WDR11 *	rs2257129	121,139,183	T	C	0.411379	-0.015291	0.00205	1.20E-13	-0.00905	0.003496	0.009662	-0.018088	0.00256	1.68E-12	5.11E-13	0.03703	F
10	WDR11 *	rs2263985	121,143,992	C	T	0.411401	-0.015451	0.002051	6.60E-14	-0.009167	0.003498	0.008794	-0.018234	0.002562	1.14E-12	3.22E-13	0.036528	F
10	WDR11 *	rs2451876	121,144,368	T	C	0.411309	-0.01542	0.00205	7.50E-14	-0.009085	0.003497	0.009403	-0.018242	0.002561	1.11E-12	3.32E-13	0.034688	F
10	WDR11 *	rs2263983	121,145,186	T	C	0.411304	-0.015404	0.00205	8.00E-14	-0.009066	0.003497	0.009557	-0.018229	0.002561	1.15E-12	3.49E-13	0.03455	F
10	WDR11 *	rs2220607	121,146,746	C	A	0.412846	-0.015443	0.002049	7.30E-14	-0.009101	0.003495	0.009241	-0.018254	0.00256	1.04E-12	3.06E-13	0.034644	F
10	WDR11 *	rs2172073	121,150,111	C	A	0.413019	-0.015392	0.002049	7.50E-14	-0.009003	0.003495	0.010019	-0.018273	0.00256	9.81E-13	3.11E-13	0.032398	F
10	WDR11 *	rs1907256	121,150,416	A	G	0.370804	0.01372	0.002089	1.40E-11	0.006513	0.003553	0.066819	0.017297	0.002613	3.74E-11	5.71E-11	0.014498	F
10	WDR11 *	rs2263997	121,151,174	A	C	0.367349	0.013522	0.002102	3.50E-11	0.006491	0.003577	0.069609	0.017081	0.00263	8.59E-11	1.33E-10	0.017087	F
10	WDR11 *	rs7098433	121,153,961	C	T	0.413124	-0.015398	0.002048	7.30E-14	-0.008685	0.003493	0.01293	-0.018435	0.002559	6.06E-13	2.43E-13	0.024355	F
10	WDR11 *	rs17101518	121,155,455	G	A	0.366237	-0.015318	0.002094	4.70E-13	-0.0112	0.003569	0.001706	-0.016664	0.002617	1.97E-10	1.13E-11	0.216865	
10	WDR11 *	rs58846742	121,155,542	C	G	0.31695	-0.013711	0.002166	2.00E-10	-0.010178	0.003693	0.005873	-0.014603	0.002707	7.01E-08	1.07E-08	0.333856	
10	WDR11 *	rs72631105	121,155,831	A	G	0.352253	0.013566	0.002112	4.80E-11	0.005578	0.003596	0.120879	0.017537	0.00264	3.17E-11	7.82E-11	0.007361	F
10	WDR11 *	rs56351107	121,155,983	G	C	0.366083	-0.015331	0.002093	4.00E-13	-0.011241	0.003568	0.001638	-0.016646	0.002616	2.03E-10	1.12E-11	0.221787	
10	WDR11 *	rs17101521	121,156,039	C	T	0.365157	-0.015285	0.002097	5.30E-13	-0.011394	0.003573	0.001437	-0.016488	0.00262	3.21E-10	1.56E-11	0.250273	
10	WDR11 *	rs56132357	121,156,071	A	T	0.315682	-0.013723	0.002172	2.20E-10	-0.010304	0.003703	0.005403	-0.014497	0.002714	9.41E-08	1.33E-08	0.361127	
10	WDR11 *	rs59313277	121,156,141	T	G	0.365925	-0.015244	0.002094	5.60E-13	-0.011113	0.003569	0.001857	-0.016602	0.002617	2.30E-10	1.42E-11	0.214807	
10	WDR11 *	rs73366917	121,156,240	A	G	0.365546	-0.015248	0.002094	5.70E-13	-0.011104	0.003571	0.001881	-0.016605	0.002617	2.30E-10	1.44E-11	0.214021	
10	WDR11 *	rs17101524	121,156,265	A	C	0.366083	-0.015331	0.002093	4.00E-13	-0.011241	0.003568	0.001638	-0.016646	0.002616	2.03E-10	1.12E-11	0.221787	
10	WDR11 *	rs4752500	121,156,448	T	A	0.368429	-0.015245	0.002097	5.60E-13	-0.011615	0.003576	0.001167	-0.016291	0.00262	5.17E-10	2.05E-11	0.291434	
10	WDR11 *	rs1907266	121,156,628	T	C	0.412902	-0.015306	0.002048	1.00E-13	-0.008643	0.003493	0.013368	-0.018306	0.002558	8.69E-13	3.57E-13	0.025654	F
10	WDR11 *	rs7920116	121,156,957	C	T	0.366083	-0.015331	0.002093	4.00E-13	-0.011241	0.003568	0.001638	-0.016646	0.002616	2.03E-10	1.12E-11	0.221787	
10	WDR11 *	rs7903585	121,157,114	G	A	0.364527	-0.015293	0.002097	5.70E-13	-0.011423	0.003573	0.001396	-0.016513	0.002621	3.07E-10	1.45E-11	0.250786	
10	WDR11 *	rs7903948	121,157,125	A	G	0.365959	-0.015362	0.002094	3.60E-13	-0.011313	0.003568	0.001528	-0.016679	0.002616	1.88E-10	9.79E-12	0.225183	
10	WDR11 *	rs7903733	121,157,208	G	A	0.31696	-0.013719	0.002166	2.00E-10	-0.010169	0.003693	0.005914	-0.014616	0.002707	6.81E-08	1.05E-08	0.331465	
10	WDR11 *	rs7904102	121,157,377	G	C	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs58960052	121,157,487	A	G	0.31696	-0.013719	0.002166	2.00E-10	-0.010169	0.003693	0.005914	-0.014616	0.002707	6.81E-08	1.05E-08	0.331465	
10	WDR11 *	rs59754371	121,157,811	C	T	0.365384	-0.015176	0.002096	7.10E-13	-0.010109	0.003572	0.002043	-0.016516	0.002619	2.96E-10	1.99E-11	0.21449	
10	WDR11 *	rs57615383	121,157,842	A	G	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs112209982	121,158,067	A	G	0.361999	-0.01505	0.002106	1.50E-12	-0.010914	0.00359	0.002374	-0.016424	0.002632	4.49E-10	3.43E-11	0.215769	
10	WDR11 *	rs58324269	121,158,215	G	A	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs60809052	121,158,221	C	T	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs58217496	121,158,313	C	T	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs60711290	121,158,469	T	G	0.366077	-0.015336	0.002093	3.90E-13	-0.011217	0.003568	0.001674	-0.016667	0.002615	1.92E-10	1.09E-11	0.217909	
10	WDR11 *	rs57142282	121,158,561	T	C	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs17101530	121,158,601	C	T	0.366124	-0.015333	0.002093	4.00E-13	-0.011264	0.003568	0.001599	-0.016634	0.002616	2.09E-10	1.13E-11	0.224816	
10	WDR11 *	rs73366943	121,158,995	G	A	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs17101534	121,159,361	C	T	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs11199803	121,159,565	G	A	0.36608	-0.015338	0.002093	3.80E-13	-0.011235	0.003567	0.001644	-0.016656	0.002615	1.97E-10	1.10E-11	0.220351	
10	WDR11 *	rs11199804	121,159,660	G	C	0.366079	-0.015338	0.002093	3.90E-13	-0.011235	0.003567	0.001644	-0.016657	0.002615	1.97E-10	1.09E-11	0.220325	
10	WDR11 *	rs11199805	121,159,692	T	C	0.366079	-0.015338	0.002093	3.90E-13	-0.011235	0.003567	0.001644	-0.016657	0.002615	1.97E-10	1.09E-11	0.220325	
10	WDR11 *	rs11199806	121,159,795	A	G	0.366083	-0.015334	0.002093	3.90E-13	-0.011235	0.003567	0.001644	-0.016651	0.002616	2.00E-10	1.11E-11	0.220769	
10	WDR11 *	rs7917346	121,160,328	G	A	0.366201	-0.015287	0.002093	4.50E-13	-0.011145	0.003568	0.001793	-0.016633	0.002616	2.11E-10	1.27E-11	0.21474	
10	WDR11 *	rs7902796	121,160,495	C	T	0.316963	-0.013713	0.002166	2.00E-10	-0.010169	0.003693	0.005914	-0.014609	0.002707	6.91E-08	1.07E-08	0.33226	
10	WDR11 *	rs7902919	121,160,588	C	T	0.366082	-0.01533	0.002093	4.00E-13	-0.011234	0.003567	0.001646	-0.016646	0.002616	2.03E-10	1.13E-11	0.221146	
10	WDR11 *	rs7917833	121,160,641	A	C	0.366087	-0.015347	0.002093	3.70E-13									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	WDR11 *	rs7915733	121,165,125	A	C	0.366102	-0.015353	0.002093	3.70E-13	-0.011242	0.003568	0.001634	-0.016671	0.002616	1.90E-10	1.05E-11	0.219682	
10	WDR11 *	rs10788141	121,165,340	G	T	0.41299	-0.015327	0.002048	9.40E-14	-0.008613	0.003492	0.013672	-0.018346	0.002558	7.73E-13	3.25E-13	0.024578	F
10	WDR11 *	rs1907272	121,165,648	A	G	0.316659	-0.013822	0.002168	1.50E-10	-0.0104	0.003695	0.004904	-0.014684	0.002709	6.07E-08	7.93E-09	0.349783	
10	WDR11 *	rs1907273	121,165,771	C	T	0.316965	-0.013765	0.002166	1.70E-10	-0.010243	0.003694	0.005572	-0.014641	0.002707	6.48E-08	9.49E-09	0.368845	
10	WDR11 *	rs1907274	121,165,824	T	G	0.366098	-0.015366	0.002093	3.50E-13	-0.01129	0.003568	0.001561	-0.016662	0.002616	1.95E-10	1.03E-11	0.224598	
10	WDR11 *	rs7096589	121,165,945	G	A	0.316965	-0.013765	0.002166	1.70E-10	-0.010243	0.003694	0.005572	-0.014641	0.002707	6.48E-08	9.49E-09	0.368845	
10	WDR11 *	rs7080940	121,166,105	A	T	0.316965	-0.013765	0.002166	1.70E-10	-0.010243	0.003694	0.005572	-0.014641	0.002707	6.48E-08	9.49E-09	0.368845	
10	WDR11 *	rs6585704	121,166,509	G	A	0.317029	-0.013736	0.002167	1.90E-10	-0.010197	0.003694	0.005789	-0.014623	0.002707	6.74E-08	1.02E-08	0.3339	
10	WDR11 *	rs7920839	121,166,658	T	C	0.317029	-0.013736	0.002167	1.90E-10	-0.010197	0.003694	0.005789	-0.014623	0.002707	6.74E-08	1.02E-08	0.3339	
10	WDR11 *	rs7921081	121,166,703	T	G	0.316987	-0.013688	0.002167	2.10E-10	-0.010174	0.003694	0.005903	-0.014559	0.002707	7.70E-08	1.18E-08	0.338349	
10	WDR11 *	rs17559591	121,166,830	G	A	0.316987	-0.013688	0.002167	2.10E-10	-0.010174	0.003694	0.005903	-0.014559	0.002707	7.70E-08	1.18E-08	0.338349	
10	WDR11 *	rs7921353	121,166,901	A	G	0.318635	-0.013659	0.002168	2.10E-10	-0.010307	0.003697	0.005314	-0.014435	0.002709	1.01E-07	1.40E-08	0.367752	
10	WDR11 *	rs7893136	121,166,946	T	C	0.316987	-0.013688	0.002167	2.10E-10	-0.010174	0.003694	0.005903	-0.014559	0.002707	7.70E-08	1.18E-08	0.338349	
10	WDR11 *	rs6585705	121,167,044	C	T	0.316541	-0.013783	0.002168	1.60E-10	-0.010403	0.003696	0.004896	-0.014625	0.002709	6.84E-08	8.90E-09	0.356821	
10	WDR11 *	rs6585706	121,167,075	G	A	0.316056	-0.013836	0.00217	1.50E-10	-0.01038	0.0037	0.005036	-0.014708	0.002712	5.97E-08	7.99E-09	0.345315	
10	WDR11 *	rs6585707	121,167,285	G	C	0.316987	-0.013688	0.002167	2.10E-10	-0.010174	0.003694	0.005903	-0.014559	0.002707	7.70E-08	1.18E-08	0.338349	
10	WDR11 *	rs6585708	121,167,429	T	C	0.366079	-0.015355	0.002094	3.60E-13	-0.011279	0.003568	0.00158	-0.016645	0.002616	2.05E-10	1.10E-11	0.225168	
10	WDR11 *	rs7897890	121,168,240	T	C	0.316421	-0.013675	0.002168	2.20E-10	-0.009846	0.003696	0.007739	-0.014732	0.002709	5.49E-08	1.09E-08	0.286305	
10	WDR11 *	rs11199811	121,169,559	A	C	0.316649	-0.013701	0.002168	2.00E-10	-0.009849	0.003697	0.007742	-0.01478	0.002708	4.96E-08	9.84E-09	0.281886	
10	WDR11 *	rs10886862	121,169,894	C	T	0.412673	-0.015338	0.002049	8.50E-14	-0.008332	0.003495	0.017139	-0.018519	0.00256	4.89E-13	2.53E-13	0.018715	F
10	WDR11 *	rs35326857	121,169,898	G	T	0.370227	-0.013933	0.002089	5.20E-12	0.006637	0.003554	0.06182	0.017594	0.002614	1.75E-11	2.54E-11	0.01302	F
10	WDR11 *	rs10886863	121,169,979	T	C	0.412673	-0.015338	0.002049	8.50E-14	-0.008332	0.003495	0.017139	-0.018519	0.00256	4.89E-13	2.53E-13	0.018715	F
10	WDR11 *	rs10886864	121,170,023	C	T	0.412673	-0.015338	0.002049	8.50E-14	-0.008332	0.003495	0.017139	-0.018519	0.00256	4.89E-13	2.53E-13	0.018715	F
10	WDR11 *	rs7071036	121,171,054	C	T	0.365856	-0.015349	0.002094	3.70E-13	-0.010993	0.00357	0.002085	-0.016809	0.002617	1.38E-10	9.64E-12	0.188828	
10	WDR11 *	rs7071062	121,171,098	C	T	0.365856	-0.015349	0.002094	3.70E-13	-0.010993	0.00357	0.002085	-0.016809	0.002617	1.38E-10	9.64E-12	0.188828	
10	WDR11 *	rs11199812	121,171,431	A	G	0.316321	-0.013986	0.002169	9.10E-11	-0.010229	0.003699	0.005706	-0.015001	0.00271	3.20E-08	4.88E-09	0.298082	
10	WDR11 *	rs7873449	121,172,138	T	G	0.362501	-0.015457	0.002102	3.20E-13	-0.011021	0.003582	0.002102	-0.016812	0.002628	1.63E-10	1.14E-11	0.19234	
10	WDR11 *	rs754227	121,172,490	C	T	0.368819	-0.015353	0.002096	3.40E-13	-0.012214	0.003575	0.000638	-0.016094	0.002619	8.24E-10	1.84E-11	0.381268	
10	WDR11 *	rs74764497	121,173,614	A	G	0.235262	-0.013066	0.002397	4.40E-08	-0.009335	0.004087	0.022395	-0.014199	0.002995	2.16E-06	9.70E-07	0.337045	
10	WDR11 *	rs3962120	121,177,844	A	C	0.362974	-0.015777	0.002127	1.10E-13	-0.012797	0.00363	0.000426	-0.016617	0.002657	4.11E-10	6.41E-12	0.395749	
10	WDR11 *	rs191959515	121,178,085	T	C	0.324645	-0.015664	0.002186	6.10E-13	-0.011857	0.003731	0.001489	-0.016783	0.002729	7.99E-10	1.28E-11	0.286611	
10	WDR11 *	rs12218818	121,178,570	T	G	0.232703	-0.013019	0.002406	4.40E-08	-0.009883	0.004101	0.015982	-0.013926	0.003006	3.67E-06	1.20E-06	0.426574	
10	WDR11 *	rs7085142	121,179,860	C	T	0.421187	0.011083	0.002054	1.70E-08	0.006674	0.003493	0.056068	0.01358	0.00257	1.29E-07	1.40E-07	0.111312	
10	WDR11 *	rs10788142	121,181,315	C	T	0.378037	0.012474	0.002086	5.90E-10	0.009276	0.00355	0.009002	0.01421	0.002609	5.23E-08	1.19E-08	0.262713	
10	WDR11 *	rs1907279	121,181,633	C	G	0.423925	0.010688	0.002051	4.40E-08	0.006321	0.003488	0.069981	0.013137	0.002565	3.10E-07	3.91E-07	0.115433	
10	WDR11 *	rs1907282	121,182,017	A	G	0.386105	0.012711	0.002074	1.90E-10	0.009614	0.003531	0.006492	0.014377	0.002593	3.02E-08	0.276838	0.159609	
10	WDR11 *	rs1907284	121,182,265	G	T	0.38664	0.012705	0.002075	2.10E-10	0.009668	0.003533	0.006219	0.01431	0.002594	3.55E-08	0.289544	0.129419	
10	WDR11 *	rs6585711	121,182,277	A	G	0.430483	0.011307	0.002041	6.80E-09	0.007044	0.003474	0.042591	0.01366	0.002553	9.01E-08	7.81E-08	0.289544	
10	WDR11 *	rs3943077	121,185,572	G	A	0.387965	0.012762	0.002084	2.20E-10	0.009828	0.00355	0.005642	0.014222	0.002605	4.90E-08	7.32E-09	0.318248	
10	WDR11 *	rs7088428	121,185,738	G	T	0.386523	0.012669	0.002076	2.30E-10	0.009571	0.003536	0.006814	0.014339	0.002596	3.38E-08	6.05E-09	0.277049	
10	WDR11 *	rs17101591	121,187,689	T	C	0.226733	-0.013433	0.002411	2.70E-08	-0.012882	0.004111	0.001733	-0.0129	0.003013	1.88E-05	7.70E-07	0.997149	
10	WDR11 *	rs12221113	121,187,774	G	T	0.226801	-0.013551	0.00241	1.90E-08	-0.012925	0.004109	0.001665	-0.013068	0.003012	1.45E-05	5.80E-07	0.977642	
10	WDR11 *	rs10788144	121,188,708	T	C	0.402414	0.01036	0.002068	4.80E-08	0.008797	0.003519	0.012455	0.011585	0.002586	7.57E-06	1.53E-06	0.523223	
10	WDR11 *	rs7089185	121,189,319	A	G	0.402107	0.010429	0.00206	3.60E-08	0.008711	0.003506	0.012992	0.011718	0.002577	5.52E-06	1.48E-06	0.489588	
10	WDR11 *	rs1907287	121,189,936	A	G	0.401295	0.010462	0.002061	3.40E-08	0.008672	0.003507	0.01342	0.011829	0.002578	4.54E-06	1.26E-06	0.468199	
10	WDR11 *	rs2901288	121,192,680	A	G	0.401824	0.01048	0.00206	3.50E-08	0.008691	0.003506	0.013194	0.011848	0.002577	4.34E-06	1.19E-06	0.468167	
10	FGFR2 *	rs7077138	121,195,851	A	T	0.402355	0.010465	0.002061	3.50E-08	0.008651	0.003507	0.013642	0.011829	0.002578	4.53E-06	1.28E-06	0.465272	
10	FGFR2 *	rs7067847	121,197,234	T	C	0.401856	0.010395	0.002061	4.50E-08	0.008542	0.003507	0.014876	0.011785	0.002578	4.92E-06	1.49E-06	0.456274	
10	FGFR2 *	rs7082125	121,199,983	T	G	0.40187	0.010573	0.002062	2.90E-08	0.008786	0.00351	0.012321	0.011885	0.00258	4.14E-06	1.07E-06	0.476768	
10	FGFR2 *	rs12358575	121,203,420	T	C	0.333027	0.011974	0.002142	1.50E-09	0.011039	0.003645	0.002466	0.012665	0.002679	2.31E-06	1.43E-07	0.719207	
10	FGFR2 *	rs11199828	121,205,116	A	G	0.326972	0.011816	0.0022	4.70E-09	0.010711	0.003744	0.004238	0.01254	0.002752	5.29E-06	5.19E-07	0.693941	
10	FGFR2 *	rs10788149	121,207,656	G	A	0.320097	0.012729	0.002162	4.10E-10	0.008471	0.003682	0.021449	0.014957	0.002703	3.21E-08	1.59E-08	0.155633	
10	FGFR2 *	rs10749408	121,208,012	C	T	0.319561	0.012846	0.002165	2.70E-10	0.008341	0.003687	0.023717	0.015224	0.002707	1.91E-08	1.04E-08	0.13239	
10	FGFR2 *	rs2172071	121,208,516	C	T	0.318456	0.01287	0.002169	2.90E-10	0.008746	0.003693	0.01789	0.01506	0.002711	2.85E-08	1.21E-08	0.168128	
10	FGFR2 *	rs11199830	121,208,601	T	C	0.337058	-0.011887	0.002136	6.40E-09	-0.010745	0.003644	0.003203	-0.012126	0.002668	5.58E-06	4.23E-07	0.759862	
10	FGFR2 *	rs11592107	121,209,450	A	G	0.31848	0.012841	0.002169	3.20E-10	0.008698	0.003693							

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
10	FGFR2 *	rs11199837	121,227,134	A	T	0.497244	-0.012679	0.002019	1.90E-10	-0.010026	0.003444	0.003608	-0.013752	0.002523	5.12E-08	5.09E-09	0.382759	
10	FGFR2 *	rs1907232	121,227,612	A	G	0.49589	-0.012451	0.002019	3.60E-10	-0.009794	0.003442	0.004446	-0.013572	0.002522	7.59E-08	9.01E-09	0.375822	
10	FGFR2 *	rs1907233	121,227,775	T	C	0.336266	-0.012051	0.002137	5.60E-09	-0.012141	0.003641	0.00086	-0.011794	0.002671	1.02E-05	2.24E-07	0.938622	
10	FGFR2 *	rs11199838	121,228,771	A	G	0.335557	-0.011969	0.002136	7.00E-09	-0.011926	0.003641	0.001062	-0.011784	0.00267	1.03E-05	2.76E-07	0.975024	
10	FGFR2 *	rs4752518	121,229,421	T	C	0.300187	0.011296	0.002209	4.70E-08	0.008362	0.003768	0.026485	0.012759	0.002759	3.81E-06	1.94E-06	0.346494	
10	FGFR2 *	rs11597855	121,229,534	T	C	0.497233	-0.012671	0.002019	2.00E-10	-0.009914	0.003443	0.003998	-0.013786	0.002523	4.75E-08	5.19E-09	0.364427	
10	FGFR2 *	rs4500422	121,230,633	A	G	0.486826	-0.011866	0.002027	2.90E-09	-0.009695	0.003456	0.005048	-0.012744	0.002532	4.93E-07	6.19E-08	0.476736	
10	FGFR2 *	rs11199840	121,230,824	G	A	0.486911	-0.01186	0.002027	3.00E-09	-0.009714	0.003458	0.004979	-0.012726	0.002532	5.13E-07	6.35E-08	0.482201	
10	FGFR2 *	rs11199842	121,230,972	C	T	0.486499	-0.01185	0.002031	2.90E-09	-0.009852	0.003464	0.004471	-0.012563	0.002537	7.49E-07	8.31E-08	0.527852	
10	FGFR2 *	rs11199843	121,230,977	C	T	0.487033	-0.011842	0.002033	3.20E-09	-0.009909	0.003467	0.004276	-0.012541	0.002539	7.99E-07	8.49E-08	0.540325	
10	FGFR2 *	rs10886874	121,232,008	A	G	0.494283	-0.011936	0.002036	1.50E-09	-0.009707	0.00347	0.005173	-0.01283	0.002544	4.67E-07	6.01E-08	0.46795	
10	FGFR2 *	rs4294510	121,232,748	A	G	0.485714	-0.0119	0.002027	2.70E-09	-0.00969	0.003456	0.005062	-0.012858	0.002533	3.94E-07	5.00E-08	0.45973	
10	FGFR2 *	rs11199844	121,232,928	T	C	0.325298	-0.011522	0.002161	3.60E-08	-0.011859	0.003683	0.00129	-0.011219	0.0027	3.30E-05	1.00E-06	0.888606	
10	FGFR2 *	rs11199845	121,232,961	T	C	0.325307	-0.011514	0.002161	3.70E-08	-0.011854	0.003683	0.001295	-0.011208	0.0027	3.36E-05	1.02E-06	0.887429	
10	FGFR2 *	rs10886876	121,233,331	G	C	0.48679	-0.012133	0.002026	1.30E-09	-0.010019	0.003455	0.003742	-0.013017	0.002532	2.79E-07	2.72E-08	0.484044	
10	FGFR2 *	rs11199848	121,235,094	G	A	0.486815	-0.011942	0.002029	2.40E-09	-0.009667	0.003458	0.0052	-0.012894	0.002535	3.72E-07	4.84E-08	0.451746	
10	FGFR2 *	rs12217412	121,235,456	C	T	0.489431	-0.011968	0.002031	2.20E-09	-0.009783	0.003463	0.004744	-0.012824	0.002538	4.43E-07	5.28E-08	0.47869	
10	FGFR2 *	rs12220647	121,235,627	A	C	0.324427	-0.011475	0.002165	4.00E-08	-0.011695	0.003689	0.001529	-0.011229	0.002706	3.36E-05	1.19E-06	0.918808	
10	FGFR2 *	rs11199850	121,236,106	T	C	0.485005	-0.011821	0.00203	3.30E-09	-0.009516	0.00346	0.005964	-0.01284	0.002537	4.26E-07	6.25E-08	0.438469	
10	FGFR2 *	rs878409	121,240,036	A	G	0.496526	-0.012597	0.002023	2.00E-10	-0.010052	0.003451	0.003597	-0.013699	0.002528	6.11E-08	6.03E-09	0.39398	
10	FGFR2 *	rs12245393	121,240,386	T	C	0.496533	-0.012575	0.002024	2.10E-10	-0.00998	0.003452	0.003848	-0.013692	0.002528	6.23E-08	6.52E-09	0.3856	
10	FGFR2 *	rs5016035	121,241,124	G	T	0.494008	-0.012048	0.002055	1.50E-09	-0.007737	0.003505	0.027282	-0.014059	0.002566	4.41E-08	2.67E-08	0.145573	
11	ARNTL	rs7947951	13,334,483	G	A	0.364561	0.013195	0.002085	3.00E-10	0.00948	0.003546	0.007519	0.014828	0.002619	1.54E-08	3.07E-09	0.225029	
11	ARNTL	rs10832027	13,335,636	A	G	0.363532	0.012943	0.002082	6.10E-10	0.009384	0.00354	0.008047	0.014518	0.002615	2.89E-08	6.02E-09	0.243385	
11	ARNTL	rs2896635	13,338,198	A	T	0.363716	0.013249	0.002088	2.30E-10	0.009407	0.003548	0.008038	0.014989	0.002622	1.12E-08	2.40E-09	0.205875	
11	ARNTL	rs1037169	13,339,458	C	T	0.359407	0.012875	0.002109	1.30E-09	0.008677	0.003588	0.015631	0.014665	0.002647	3.11E-08	1.17E-08	0.1793	
11	ARNTL	rs6486122	13,339,977	T	C	0.367095	0.01331	0.002079	1.80E-10	0.009018	0.003536	0.010788	0.01524	0.00261	5.38E-09	1.52E-09	0.156822	
11	ARNTL	rs10766078	13,341,701	G	A	0.391291	0.012363	0.002091	2.90E-09	0.00754	0.003555	0.006085	0.013729	0.002625	1.74E-07	2.67E-08	0.368387	
11	ARNTL	rs3816360	13,346,203	C	T	0.36725	0.011416	0.002086	4.20E-08	0.009941	0.003551	0.005139	0.011975	0.002617	4.83E-06	5.67E-07	0.64483	
11	DAGLA *	rs7925523	61,675,020	A	G	0.25368	-0.018955	0.002314	2.00E-16	-0.023658	0.003961	2.40E-09	-0.016325	0.002894	1.74E-08	2.22E-15	0.13497	
11	DAGLA *	rs60399071	61,675,683	A	G	0.25381	-0.018948	0.002314	2.00E-16	-0.023611	0.003962	2.61E-09	-0.016378	0.002895	1.57E-08	2.17E-15	0.140481	
11	DAGLA *	rs151242175	61,679,851	T	C	0.253266	-0.018954	0.002319	2.30E-16	-0.023096	0.003973	6.29E-09	-0.016703	0.002901	8.71E-09	2.89E-15	0.193717	
11	DAGLA *	rs151702847	61,679,884	A	T	0.25327	-0.018953	0.002319	2.30E-16	-0.023096	0.003973	6.29E-09	-0.016703	0.002901	8.71E-09	2.89E-15	0.193739	
11	DAGLA	rs11230779	61,682,061	A	G	0.491985	-0.011698	0.002039	1.60E-09	-0.010794	0.003477	0.001917	-0.01228	0.002557	1.60E-06	7.95E-08	0.730764	
11	DAGLA	rs59200224	61,682,665	G	A	0.253782	-0.018925	0.002317	2.40E-16	-0.023297	0.003967	4.39E-09	-0.016521	0.002898	1.22E-08	2.83E-15	0.167754	
11	DAGLA	rs59371352	61,682,823	A	G	0.253964	-0.018855	0.00232	3.50E-16	-0.023515	0.003972	3.31E-09	-0.016369	0.002903	1.76E-08	3.06E-15	0.146358	
11	DAGLA	rs72918042	61,684,076	G	C	0.253791	-0.018923	0.002317	2.40E-16	-0.023311	0.003967	4.30E-09	-0.016509	0.002898	1.25E-08	2.84E-15	0.166117	
11	DAGLA	rs61898525	61,686,132	G	A	0.492001	-0.011504	0.002038	2.60E-09	-0.010462	0.003476	0.002621	-0.01216	0.002555	1.97E-06	1.30E-07	0.693836	
11	DAGLA	rs4963308	61,688,954	A	G	0.253788	-0.018909	0.002317	2.60E-16	-0.023239	0.003968	4.86E-09	-0.016529	0.002899	1.21E-08	3.10E-15	0.172101	
11	DAGLA	rs883724	61,690,385	T	C	0.253407	-0.018678	0.002319	6.20E-16	-0.023025	0.00397	6.84E-09	-0.016304	0.002901	1.95E-08	6.88E-15	0.171655	
11	DAGLA	rs11827215	61,691,123	A	G	0.254143	-0.018652	0.002316	6.60E-16	-0.022859	0.003966	8.47E-09	-0.016353	0.002896	1.68E-08	7.31E-15	0.185273	
11	DAGLA	rs60507107	61,696,297	T	C	0.253738	-0.018779	0.002318	4.30E-16	-0.023142	0.00397	5.71E-09	-0.01639	0.0029	1.62E-08	4.81E-15	0.169584	
11	DAGLA	rs17827816	61,697,053	T	C	0.440031	-0.012289	0.002057	5.40E-10	-0.012674	0.003511	0.000309	-0.011933	0.002578	3.74E-06	3.31E-08	0.865009	
11	DAGLA	rs198453	61,697,078	C	T	0.492521	-0.011522	0.002035	2.60E-09	-0.010815	0.003473	0.001853	-0.011946	0.00225	2.84E-06	1.34E-07	0.792821	
11	DAGLA	rs2097853	61,698,795	T	G	0.253895	-0.018736	0.002318	5.20E-16	-0.02316	0.00397	5.56E-09	-0.01631	0.0029	1.90E-08	5.48E-15	0.163497	
11	DAGLA	rs81659	61,699,580	G	A	0.466171	-0.013097	0.002048	2.30E-11	-0.013703	0.003494	8.87E-05	-0.013062	0.002567	3.69E-07	1.09E-09	0.882489	
11	DAGLA	rs58217294	61,702,031	A	T	0.253919	-0.018718	0.002318	5.60E-16	-0.023063	0.003971	6.50E-09	-0.016325	0.0029	1.85E-08	6.23E-15	0.170548	
11	DAGLA	rs12274157	61,710,175	C	A	0.254064	-0.018733	0.00232	5.70E-16	-0.022954	0.003974	7.86E-09	-0.016382	0.002901	1.67E-08	6.79E-15	0.181676	
11	DAGLA	rs731842	61,712,719	C	T	0.254175	-0.018721	0.002319	5.70E-16	-0.022986	0.003973	7.44E-09	-0.016371	0.002901	1.71E-08	6.55E-15	0.178674	
11	DAGLA	rs2107617	61,714,167	G	C	0.304592	-0.016173	0.00206	9.40E-14	-0.01825	0.003769	1.31E-06	-0.015236	0.002763	3.59E-08	2.03E-12	0.518951	
11	DAGLA	rs17156244	61,714,923	G	T	0.254257	-0.018728	0.002319	5.50E-16	-0.02315	0.003972	5.77E-09	-0.016311	0.0029	1.91E-08	5.70E-15	0.164379	
11	DAGLA	rs198435	61,715,852	C	G	0.251225	-0.018412	0.002331	2.00E-15	-0.021973	0.003992	3.78E-08	-0.016502	0.002916	1.55E-08	2.91E-14	0.268367	
11	DAGLA	rs2903825	61,721,496	T	C	0.261475	-0.019259	0.0023	5.50E-17	-0.024448	0.00394	5.62E-10	-0.016466	0.002876	1.06E-08	3.30E-16	0.101744	
11	DAGLA	rs9735635	61,723,408	A	C	0.260873	-0.019369	0.002301	3.80E-17	-0.024629	0.003943	4.32E-10	-0.016555	0.002878	9.05E-09	2.20E-16	0.098109	
11	DAGLA	rs4963243	61,726,855	A	G	0.261874	-0.019318	0.002297	3.40E-17	-0.024625	0.003935	4.03E-10	-0.016485	0.002873	9.84E-09	0.094765	0.094765	
11	DAGLA	rs2240287	61,738,111	A	G	0.264282	-0.019152	0.002294	5.90E-17	-0.02388	0.003929	1.26E-09	-0.016705	0.002869	5.97E-09	4.17E-16	0.140305	
11	DAGLA	rs2240286	61,738,98															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	FADS1	rs174545	61,801,834	C	G	0.41451	-0.022521	0.002048	2.00E-28	-0.023236	0.003495	3.08E-11	-0.022117	0.002567	7.43E-18	1.95E-26	0.796266	
11	FADS1	rs174546	61,802,358	C	T	0.41455	-0.022623	0.002049	1.20E-28	-0.023474	0.003496	1.95E-11	-0.022174	0.002568	6.15E-18	1.03E-26	0.764472	
11	FADS1	rs174547	61,803,311	T	C	0.414437	-0.022392	0.002049	4.30E-28	-0.023113	0.003496	3.94E-11	-0.02197	0.002569	1.27E-17	4.20E-26	0.792214	
11	FADS1	rs174548	61,803,876	C	G	0.422251	-0.022649	0.002044	7.70E-29	-0.022699	0.003487	7.80E-11	-0.022641	0.002563	1.06E-18	7.07E-27	0.989227	
11	FADS1	rs174549	61,803,910	G	A	0.422738	-0.022561	0.002045	1.40E-28	-0.022683	0.00349	8.29E-11	-0.022489	0.002563	1.84E-18	1.29E-26	0.964137	
11	FADS1	rs174550	61,804,006	T	C	0.414484	-0.022624	0.002048	1.10E-28	-0.02347	0.003496	1.96E-11	-0.022164	0.002567	6.32E-18	1.06E-26	0.763306	
11	FADS1	rs174553	61,807,686	A	G	0.41481	-0.022755	0.002049	6.20E-29	-0.02342	0.003495	2.15E-11	-0.022406	0.002568	2.77E-18	5.18E-27	0.815219	
11	FADS1	rs72643557	61,811,955	T	C	0.411304	-0.022877	0.002058	6.80E-29	-0.024503	0.003513	3.20E-12	-0.022025	0.002578	1.39E-17	3.92E-27	0.569644	
11	FADS1	rs174554	61,811,991	A	G	0.41483	-0.022766	0.002048	5.80E-29	-0.023391	0.003495	2.27E-11	-0.022433	0.002567	2.52E-18	8.25E-27	0.82526	
11	FADS1	rs174555	61,812,288	T	C	0.422113	-0.02281	0.002044	3.60E-29	-0.022694	0.003487	7.91E-11	-0.02292	0.002563	4.00E-19	2.74E-27	0.958319	
11	FADS1	rs174556	61,813,163	C	T	0.422159	-0.022835	0.002044	3.10E-29	-0.022741	0.003487	7.24E-11	-0.022934	0.002563	3.82E-19	2.39E-27	0.964342	
11	FADS1	rs174559	61,814,184	G	A	0.423855	-0.022676	0.002044	8.50E-29	-0.022701	0.003488	7.82E-11	-0.022681	0.002562	8.96E-19	6.00E-27	0.996292	
11	FADS1	rs174560	61,814,292	T	C	0.422145	-0.022875	0.002045	2.60E-29	-0.022858	0.003488	5.81E-11	-0.022934	0.002563	3.82E-19	1.93E-27	0.985873	
11	FADS1, MIR1908	rs174561	61,815,236	T	C	0.422119	-0.022866	0.002045	2.60E-29	-0.022905	0.003488	5.34E-11	-0.022897	0.002563	4.43E-19	2.06E-27	0.998525	
11	FADS2	rs174562	61,817,672	A	G	0.414053	-0.022854	0.002051	4.50E-29	-0.02357	0.003498	1.66E-11	-0.022459	0.00257	2.52E-18	3.66E-27	0.79815	
11	FADS2	rs174564	61,820,833	A	G	0.413123	-0.022466	0.002053	4.10E-28	-0.023105	0.003503	4.36E-11	-0.022081	0.002574	1.00E-17	6.37E-26	0.813756	
11	FADS2	rs28456	61,822,009	A	G	0.420836	-0.022439	0.002051	4.10E-28	-0.022201	0.003498	2.28E-10	-0.02259	0.002571	1.62E-18	3.07E-26	0.928726	
11	FADS2	rs174565	61,824,164	C	G	0.415066	-0.022175	0.002052	2.00E-27	-0.022478	0.003502	1.41E-10	-0.021298	0.002572	1.62E-17	1.87E-25	0.899191	
11	FADS2	rs174566	61,824,890	A	G	0.413124	-0.022458	0.002053	4.30E-28	-0.023058	0.003503	4.76E-11	-0.022092	0.002574	9.65E-18	3.87E-26	0.824088	
11	FADS2	rs174567	61,825,533	A	G	0.416035	-0.02298	0.00205	2.40E-29	-0.023754	0.003498	1.16E-11	-0.022594	0.00257	1.55E-18	1.59E-27	0.789235	
11	FADS2	rs174568	61,826,344	C	T	0.415059	-0.022792	0.00205	5.20E-29	-0.023513	0.003497	1.82E-11	-0.022391	0.002569	3.07E-18	4.87E-27	0.795899	
11	FADS2	rs99780	61,829,161	C	T	0.413192	-0.022661	0.00205	1.60E-28	-0.023225	0.003498	3.25E-11	-0.022311	0.00257	4.09E-18	1.14E-26	0.833175	
11	FADS2	rs174570	61,829,740	C	T	0.415197	-0.022426	0.002049	5.50E-28	-0.022752	0.003495	7.80E-11	-0.022171	0.002568	6.23E-18	4.07E-26	0.893466	
11	FADS2	rs1535	61,830,500	A	G	0.41312	-0.0227	0.00205	1.30E-28	-0.023185	0.003497	3.48E-11	-0.022402	0.002569	2.96E-18	8.83E-27	0.856809	
11	FADS2	rs174574	61,832,870	C	A	0.413183	-0.022574	0.002051	2.60E-28	-0.023151	0.003499	3.80E-11	-0.022194	0.002571	6.30E-18	2.03E-26	0.825551	
11	FADS2	rs2524296	61,833,906	T	C	0.438675	0.019521	0.002036	5.50E-22	0.016522	0.003477	2.05E-06	0.020414	0.00255	1.25E-15	1.51E-19	0.366768	
11	FADS2	rs2845574	61,834,400	T	C	0.443484	0.019984	0.002026	4.10E-23	0.017129	0.003459	7.47E-07	0.020727	0.002538	3.37E-16	1.57E-20	0.401646	
11	FADS2	rs2845573	61,834,436	G	A	0.448876	0.019498	0.002026	6.20E-22	0.016902	0.003457	1.03E-06	0.020181	0.002539	1.96E-15	1.22E-19	0.444664	
11	FADS2	rs199649489	61,834,989	A	C	0.431714	-0.021627	0.002083	3.00E-25	-0.023592	0.003559	3.51E-11	-0.020682	0.002609	2.33E-15	6.45E-24	0.509659	
11	FADS2	rs2727270	61,835,765	T	C	0.445756	0.020377	0.002025	4.50E-24	0.017279	0.003456	5.85E-07	0.021305	0.002537	4.86E-17	1.84E-21	0.347837	
11	FADS2	rs2727271	61,835,886	T	A	0.445796	0.020228	0.002025	1.00E-23	0.017383	0.003456	5.00E-07	0.021027	0.002538	1.23E-16	3.95E-21	0.3954	
11	FADS2	rs174576	61,836,038	C	A	0.412736	-0.022529	0.002051	3.40E-28	-0.022822	0.003499	7.18E-11	-0.022292	0.002571	4.50E-18	2.72E-26	0.902921	
11	FADS2	rs2524299	61,837,310	T	A	0.446028	0.020279	0.002024	6.20E-24	0.017262	0.003455	5.95E-07	0.021153	0.002537	7.88E-17	3.01E-21	0.363975	
11	FADS2	rs174577	61,837,342	C	A	0.412863	-0.02254	0.002051	3.20E-28	-0.022751	0.003499	8.16E-11	-0.022368	0.00257	3.42E-18	2.35E-26	0.929588	
11	FADS2	rs2072113	61,837,495	T	C	0.445745	0.020424	0.002025	3.10E-24	0.017305	0.003457	5.66E-07	0.021356	0.002538	4.13E-17	1.51E-21	0.344819	
11	FADS2	rs2072114	61,837,743	G	A	0.445701	0.020243	0.002025	9.00E-24	0.017385	0.003456	5.00E-07	0.021008	0.002537	1.30E-16	4.18E-21	0.3982	
11	FADS2	rs174578	61,838,027	T	A	0.413088	-0.022469	0.002051	4.70E-28	-0.022938	0.003499	5.74E-11	-0.022222	0.002571	5.86E-18	2.83E-26	0.868942	
11	FADS2	rs174580	61,839,170	A	G	0.412469	-0.022497	0.002052	4.30E-28	-0.022841	0.003502	7.13E-11	-0.022259	0.002573	5.31E-18	3.18E-26	0.893553	
11	FADS2	rs174581	61,839,211	G	A	0.412598	-0.022468	0.002053	5.00E-28	-0.022925	0.003502	6.11E-11	-0.022174	0.002573	7.17E-18	3.68E-26	0.862869	
11	FADS2	rs2727265	61,841,532	A	C	0.446293	0.020549	0.002037	3.80E-24	0.017552	0.00348	4.66E-07	0.021432	0.002557	4.76E-17	1.44E-21	0.368663	
11	FADS2	rs174583	61,842,278	C	T	0.412122	-0.022541	0.002051	3.70E-28	-0.02287	0.0035	6.61E-11	-0.022317	0.002571	4.22E-18	2.36E-26	0.898695	
11	FADS2	rs174584	61,843,278	G	A	0.411812	-0.022568	0.002053	3.60E-28	-0.022884	0.003502	6.63E-11	-0.022331	0.002573	4.19E-18	2.35E-26	0.898688	
11	FADS2	rs2526680	61,843,744	T	C	0.448202	0.020368	0.002028	5.80E-24	0.017189	0.003461	6.93E-07	0.021434	0.002542	3.59E-17	1.60E-21	0.322875	
11	FADS2	rs2845572	61,847,123	A	G	0.444651	0.02039	0.002029	5.60E-24	0.01678	0.00346	1.26E-06	0.021604	0.002543	2.07E-17	1.66E-21	0.261261	
11	FADS2	rs2851682	61,848,540	G	A	0.44508	0.020166	0.002026	1.40E-23	0.016334	0.003456	2.32E-06	0.021496	0.002539	2.69E-17	1.22E-25	0.286521	
11	FADS2	rs2727263	61,850,540	T	C	0.446077	0.020325	0.002034	1.10E-23	0.016906	0.003467	1.10E-06	0.02141	0.00255	4.85E-17	3.37E-21	0.295396	
11	FADS2	rs174592	61,851,136	A	G	0.409028	-0.022738	0.002052	1.00E-28	-0.022989	0.003499	5.21E-11	-0.022564	0.002573	1.87E-18	8.34E-27	0.922133	
11	FADS2	rs174594	61,852,357	A	C	0.408949	-0.02298	0.002055	2.80E-29	-0.023108	0.003506	4.53E-11	-0.022863	0.002576	7.45E-19	2.93E-27	0.955004	
11	FADS2	rs72643559	61,852,802	C	T	0.405256	-0.022672	0.002066	2.40E-28	-0.022667	0.003527	1.34E-10	-0.022762	0.002589	1.57E-18	1.78E-26	0.982686	
11	FADS2	rs174598	61,853,722	G	A	0.410336	-0.022739	0.002053	1.10E-28	-0.022971	0.003504	5.71E-11	-0.02255	0.002572	1.93E-18	9.42E-27	0.922796	
11	FADS2	rs174599	61,854,084	G	C	0.40819	-0.023001	0.002055	2.40E-29	-0.023118	0.003506	4.44E-11	-0.022871	0.002576	7.08E-19	2.73E-27	0.954707	
11	FADS2	rs174600	61,854,755	T	C	0.40972	-0.022767	0.002056	1.10E-28	-0.022735	0.003508	9.39E-11	-0.022649	0.002577	1.61E-18	1.28E-26	0.984338	
11	FADS2	rs174601	61,855,668	C	T	0.404479	-0.022591	0.002057	2.20E-28	-0.02263	0.003511	1.20E-10	-0.022499	0.002577	2.70E-18	2.71E-26	0.975995	
11	FADS2 *	rs174626	61,869,585	G	C	0.318597	0.012161	0.00216	3.00E-08	0.016824	0.003681	4.95E-06	0.009615	0.00271	0.000391	5.39E-08	0.114792	
11	FADS3	rs174453	61,878,495	G	C	0.300852	0.01416	0.00223	9.80E-11	0.017118	0.0038	6.73E-06	0.012905	0.002797	4.02E-06	3.71E-07	0.371807	
11	FADS3	rs174634	61,879,915	G	C	0.308624	0.013824	0.002209	1.90E-10	0.017411	0.003762	3.74E-06	0.012086	0.002771	1.31E-05	1.65E-09	0.254377	
11	FADS3	rs174635	61,879,955	T	G	0.308624	0.013817	0.002209	1.90E-10	0.017408	0.003762	3.						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	RAB31L1	rs174474	61,904,793	C	T	0.33178	0.013299	0.002176	8.70E-10	0.016846	0.003705	5.54E-06	0.011675	0.002731	1.93E-05	3.49E-09	0.261282	
11	RAB31L1	rs174479	61,911,282	G	T	0.338242	0.01211	0.002117	6.00E-09	0.01515	0.003616	2.82E-05	0.010451	0.002652	8.19E-05	6.53E-08	0.294664	
11	MTNR1B *	rs4331050	92,962,848	T	G	0.438187	0.011082	0.002041	2.40E-08	0.014781	0.003493	2.35E-05	0.010259	0.002555	5.98E-05	4.07E-08	0.296106	
11	MTNR1B *	rs10466351	92,964,815	T	C	0.439258	0.011355	0.002017	9.90E-09	0.014723	0.003455	2.06E-05	0.010524	0.002523	3.06E-05	1.90E-08	0.326339	
11	MTNR1B *	rs10830962	92,965,261	G	C	0.4398	0.011284	0.002018	1.20E-08	0.014834	0.003455	1.78E-05	0.010375	0.002524	3.99E-05	2.13E-08	0.297368	
11	MTNR1B *	rs7941837	92,966,500	T	A	0.440235	0.011553	0.002023	6.10E-09	0.014474	0.003465	2.98E-05	0.010995	0.002531	1.42E-05	1.30E-08	0.417463	
11	MTNR1B *	rs7945617	92,967,121	C	T	0.473221	0.011063	0.002015	3.00E-08	0.013709	0.003447	7.04E-05	0.010742	0.002522	2.07E-05	4.22E-08	0.487285	
11	MTNR1B	rs10830963	92,975,544	G	C	0.433009	0.011228	0.002021	1.40E-08	0.014945	0.003454	1.53E-05	0.010176	0.002531	5.88E-05	2.66E-08	0.265391	
11	BUD13 *	rs191081678	116,505,105	T	G	0.011733	0.067045	0.009378	4.30E-13	0.062644	0.016143	0.000105	0.070395	0.0117	1.83E-09	7.40E-12	0.697432	
11	BUD13 *	rs79859462	116,509,279	A	G	0.022096	0.041627	0.006861	6.30E-10	0.051551	0.011913	1.53E-05	0.034391	0.00852	5.48E-05	2.49E-08	0.241338	
11	BUD13 *	rs188115846	116,511,441	A	G	0.020428	0.045352	0.007149	8.80E-11	0.061416	0.01233	6.45E-07	0.034416	0.008909	0.000113	2.36E-09	0.075921	
11	BUD13 *	rs140673349	116,525,979	A	G	0.015876	0.070755	0.008097	1.20E-18	0.070869	0.013822	3.00E-07	0.072203	0.010148	1.16E-12	1.98E-17	0.937991	
11	BUD13 *	rs61904846	116,578,975	A	G	0.062763	-0.023472	0.004138	2.20E-08	-0.015311	0.007041	0.029681	-0.02786	0.005194	8.34E-08	5.32E-08	0.151459	
11	BUD13 *	rs144641996	116,579,022	T	A	0.035715	0.039107	0.005469	1.20E-12	0.031891	0.009425	0.00072	0.041156	0.006819	1.63E-09	4.02E-11	0.425825	
11	BUD13 *	rs61904847	116,583,168	C	T	0.059354	-0.023627	0.004245	3.40E-08	-0.016162	0.007223	0.025277	-0.028018	0.005328	1.48E-07	8.11E-08	0.186532	
11	BUD13 *	rs7951761	116,597,136	A	G	0.462336	-0.011914	0.002047	1.80E-09	-0.010859	0.003479	0.001806	-0.012355	0.002571	1.56E-06	7.72E-08	0.729413	
11	BUD13 *	rs114594921	116,602,565	C	T	0.05087	0.035141	0.004651	4.20E-14	0.028567	0.007804	0.000254	0.038942	0.005884	3.77E-11	3.80E-13	0.288416	
11	BUD13 *	rs74733106	116,608,826	T	G	0.055847	0.033749	0.004371	3.00E-14	0.026323	0.007459	0.00042	0.038118	0.005478	3.57E-12	6.04E-14	0.202446	
11	BUD13 *	rs116585768	116,615,113	A	G	0.058332	0.038901	0.00432	4.10E-19	0.030843	0.007359	2.81E-05	0.044249	0.005419	3.39E-16	5.13E-19	0.142425	
11	BUD13 *	rs11216040	116,617,822	A	G	0.084316	0.023625	0.00361	1.50E-11	0.026295	0.006133	1.83E-05	0.022284	0.004536	9.16E-07	5.86E-10	0.599031	
11	BUD13 *	rs10891999	116,618,165	T	A	0.146169	0.031653	0.00287	7.10E-29	0.029699	0.004874	1.14E-09	0.032843	0.003606	8.90E-20	0.604069	0.729413	
11	BUD13 *	rs12365864	116,618,319	G	A	0.084762	0.023408	0.003599	2.10E-11	0.026513	0.006118	1.49E-05	0.021911	0.004521	1.28E-06	6.64E-10	0.545203	
11	BUD13 *	rs11216043	116,619,262	C	T	0.144987	0.031383	0.002877	3.90E-28	0.030235	0.004887	6.32E-10	0.032177	0.003616	5.98E-19	3.11E-26	0.749352	
11	BUD13 *	rs148093284	116,620,192	C	T	0.030113	0.050089	0.005953	1.20E-18	0.054966	0.010017	4.18E-08	0.045888	0.00752	1.08E-09	2.38E-15	0.468638	
11	BUD13 *	rs12365322	116,620,253	G	T	0.08574	0.023361	0.00358	2.00E-11	0.026394	0.006087	1.47E-05	0.021759	0.004496	1.32E-06	6.75E-10	0.540275	
11	BUD13 *	rs182744169	116,620,615	C	T	0.012911	0.065367	0.008944	2.60E-13	0.052724	0.01519	0.000522	0.074808	0.011239	2.91E-11	5.79E-13	0.242491	
11	BUD13 *	rs61904858	116,621,390	G	A	0.086701	0.023667	0.003558	8.40E-12	0.02783	0.006054	4.35E-06	0.02151	0.004466	1.49E-06	2.36E-10	0.400868	
11	BUD13 *	rs11216045	116,621,694	C	T	0.146128	0.030893	0.002868	1.80E-27	0.029664	0.00487	1.15E-09	0.031676	0.003604	1.60E-18	1.48E-25	0.739782	
11	BUD13 *	rs11216046	116,621,984	T	G	0.084395	0.023277	0.003614	3.50E-11	0.026088	0.006127	2.09E-05	0.021771	0.004545	1.70E-06	1.21E-09	0.571543	
11	BUD13 *	rs79801428	116,623,547	A	G	0.083375	-0.030684	0.003707	7.80E-18	-0.023065	0.006317	0.000263	-0.03385	0.004649	3.46E-13	3.93E-15	0.169106	
11	BUD13 *	rs11216048	116,624,342	G	A	0.087691	-0.029759	0.003597	1.10E-17	-0.023415	0.006115	0.00013	-0.032565	0.004518	5.90E-13	3.41E-15	0.228734	
11	BUD13 *	rs11216049	116,624,458	C	T	0.087925	-0.029439	0.003592	2.20E-17	-0.023004	0.006107	0.000167	-0.032216	0.00451	9.53E-13	6.93E-15	0.224937	
11	BUD13 *	rs11216050	116,624,597	T	C	0.088408	-0.029259	0.00358	2.40E-17	-0.022301	0.006086	0.00025	-0.032445	0.004496	5.58E-13	6.00E-15	0.180047	
11	BUD13 *	rs112305884	116,625,067	T	C	0.089849	-0.02789	0.003544	3.20E-16	-0.021278	0.006022	0.000413	-0.030873	0.004452	4.23E-12	7.02E-14	0.200077	
11	BUD13 *	rs112494128	116,625,184	T	C	0.089951	-0.027751	0.00354	4.20E-16	-0.021332	0.006015	0.000393	-0.030618	0.004447	6.01E-12	9.47E-14	0.214434	
11	BUD13 *	rs7114844	116,625,470	A	G	0.142306	0.030543	0.002877	1.70E-26	0.019363	0.004935	8.82E-05	0.036318	0.003595	5.84E-24	3.17E-26	0.005503	F
11	BUD13 *	rs4340085	116,625,592	T	C	0.09037	-0.028166	0.00353	1.40E-16	-0.021541	0.006003	0.000335	-0.031002	0.004433	2.79E-12	3.84E-14	0.204849	
11	BUD13 *	rs7114993	116,625,593	T	G	0.141913	0.030693	0.00288	1.20E-26	0.019616	0.004941	7.27E-05	0.036437	0.0036	4.74E-24	2.14E-26	0.005948	F
11	BUD13 *	rs2156122	116,625,906	A	C	0.142753	0.031567	0.00287	2.90E-28	0.020781	0.004925	2.48E-05	0.03714	0.003586	4.23E-25	7.02E-28	0.007264	F
11	BUD13 *	rs77984767	116,626,027	G	A	0.091242	-0.027047	0.003512	1.40E-15	-0.020697	0.005972	0.000533	-0.029805	0.004409	1.43E-11	2.95E-13	0.219848	
11	BUD13 *	rs77623050	116,626,231	T	C	0.089209	-0.027516	0.003553	9.70E-16	-0.020871	0.006048	0.000562	-0.030343	0.004459	1.05E-11	2.30E-13	0.207504	
11	BUD13 *	rs78485217	116,626,244	A	T	0.088343	-0.027123	0.003574	4.10E-15	-0.020014	0.006081	0.001002	-0.030436	0.004486	1.21E-11	4.50E-13	0.167805	
11	BUD13 *	rs10892000	116,628,145	G	T	0.147743	0.029775	0.002839	8.80E-26	0.019259	0.004869	7.72E-05	0.035042	0.003548	5.62E-23	2.63E-25	0.00882	F
11	BUD13 *	rs11216054	116,628,234	C	A	0.147757	0.029822	0.002839	7.50E-26	0.01934	0.004869	7.19E-05	0.035074	0.003548	5.13E-23	2.25E-25	0.009028	F
11	BUD13 *	rs61270867	116,628,783	G	A	0.173975	-0.014196	0.002677	2.00E-08	-0.009795	0.004552	0.031435	-0.016441	0.003361	1.02E-06	6.31E-07	0.240193	
11	BUD13 *	rs11216055	116,629,871	T	C	0.093757	-0.02789	0.003447	6.60E-17	-0.021317	0.005872	0.000285	-0.030657	0.004324	1.39E-12	1.67E-14	0.200216	
11	BUD13 *	rs11216056	116,629,912	A	C	0.093796	-0.027828	0.003446	7.40E-17	-0.021161	0.005871	0.000315	-0.03062	0.004323	1.46E-12	1.92E-14	0.194481	
11	BUD13 *	rs11216057	116,630,051	T	C	0.093745	-0.027776	0.003445	7.90E-17	-0.021323	0.005869	0.000282	-0.030439	0.004321	1.93E-12	2.27E-14	0.211009	
11	BUD13 *	rs77649044	116,630,336	C	T	0.093772	-0.027729	0.003443	8.60E-17	-0.021505	0.005867	0.000249	-0.030255	0.004319	2.56E-12	2.66E-14	0.229703	
11	BUD13 *	rs76055915	116,630,355	T	C	0.093778	-0.027725	0.003443	8.60E-17	-0.021505	0.005867	0.000249	-0.030243	0.004318	2.60E-12	2.71E-14	0.230314	
11	BUD13 *	rs74424292	116,630,372	T	A	0.093778	-0.027725	0.003443	8.60E-17	-0.021505	0.005867	0.000249	-0.030243	0.004318	2.60E-12	2.71E-14	0.230314	
11	BUD13 *	rs11216059	116,631,270	A	C	0.094112	-0.028604	0.003436	8.30E-18	-0.021951	0.005856	0.000179	-0.031366	0.004309	3.52E-13	2.79E-15	0.195313	
11	BUD13 *	rs11216060	116,631,550	A	G	0.094719	-0.028628	0.003429	9.20E-18	-0.0214	0.005847	0.000254	-0.031692	0.004299	1.75E-13	1.94E-15	0.156074	
11	BUD13 *	rs11216061	116,632,035	C	T	0.094057	-0.029151	0.003436	2.10E-18	-0.02227	0.005857	0.000145	-0.03199	0.004309	1.19E-13	7.84E-16	0.181306	
11	BUD13 *	rs11216062	116,632,051	A	C	0.094069	-0.02916	0.003436	2.00E-18	-0.022297	0.005857	0.000142	-0.031988	0.004309	1.19E-13	7.70E-16	0.18255	
11	BUD13 *	rs11216063	116,632,059	A	T	0.094069	-0.02916	0.003436	2.00E-18	-0.022297	0.005857	0.00014						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	BUD13 *	rs1145184	116,642,465	A	G	0.137782	0.038777	0.002949	5.60E-41	0.043657	0.005013	3.27E-18	0.03615	0.003703	1.74E-22	6.89E-38	0.228373	
11	BUD13 *	rs117239953	116,642,471	C	T	0.092413	-0.036699	0.003462	2.60E-27	-0.031255	0.005903	1.22E-07	-0.03863	0.004342	6.05E-19	5.26E-24	0.314209	
11	BUD13 *	rs116859831	116,642,711	C	T	0.092593	-0.036894	0.003459	1.20E-27	-0.031248	0.005897	1.19E-07	-0.038899	0.004337	3.19E-19	2.74E-24	0.295947	
11	BUD13 *	rs78642155	116,643,375	C	G	0.092071	-0.036888	0.003471	1.70E-27	-0.031803	0.00591	7.54E-08	-0.038753	0.004353	5.83E-19	3.19E-24	0.34373	
11	BUD13 *	rs116948654	116,643,602	C	T	0.092151	-0.036958	0.003471	1.50E-27	-0.031587	0.005912	9.35E-08	-0.038991	0.004354	3.63E-19	2.46E-24	0.313272	
11	BUD13 *	rs117689643	116,643,612	T	G	0.092152	-0.036942	0.003471	1.50E-27	-0.031595	0.005912	9.28E-08	-0.038959	0.004355	3.88E-19	2.61E-24	0.315866	
11	BUD13 *	rs191049803	116,643,878	A	G	0.020271	-0.043066	0.007086	1.70E-09	-0.026744	0.012122	0.02739	-0.053943	0.008869	1.22E-09	8.14E-10	0.070173	
11	BUD13 *	rs1145185	116,643,982	A	G	0.137591	0.039408	0.002927	7.00E-43	0.044767	0.004986	2.90E-19	0.036639	0.003671	1.99E-23	7.31E-40	0.189245	
11	BUD13 *	rs78221557	116,644,811	A	G	0.213083	0.020975	0.002491	3.60E-18	0.013538	0.00424	0.001414	0.025438	0.003126	4.25E-16	2.55E-17	0.023897	F
11	BUD13 *	rs71480306	116,644,840	C	T	0.142479	0.040242	0.002871	1.60E-46	0.045494	0.004897	1.63E-20	0.037456	0.0036	2.53E-25	5.58E-43	0.185918	
11	BUD13 *	rs11216072	116,645,635	C	T	0.026342	-0.046482	0.006278	1.10E-13	-0.045506	0.010712	2.18E-05	-0.04898	0.007868	4.97E-10	4.65E-13	0.793767	
11	BUD13 *	rs2212428	116,645,870	T	C	0.091969	-0.038609	0.003485	1.00E-29	-0.032139	0.005935	6.27E-08	-0.041112	0.004373	5.76E-21	2.77E-26	0.22358	
11	BUD13 *	rs1002037	116,646,019	C	G	0.096533	-0.038849	0.003424	1.80E-31	-0.031501	0.005824	6.50E-08	-0.041642	0.004299	3.71E-22	1.89E-27	0.16125	
11	BUD13 *	rs71480307	116,646,156	A	G	0.142197	0.040604	0.002869	2.60E-47	0.046195	0.004892	3.83E-21	0.037688	0.003598	1.21E-25	6.45E-44	0.161235	
11	BUD13 *	rs35165288	116,646,608	C	T	0.142828	0.040256	0.002864	1.20E-46	0.045831	0.004884	6.79E-21	0.037311	0.00359	2.89E-25	2.68E-43	0.159863	
11	BUD13 *	rs1124874	116,647,291	A	G	0.089403	-0.037843	0.00353	6.10E-28	-0.030195	0.006011	5.19E-07	-0.041061	0.004429	1.94E-20	7.14E-25	0.145603	
11	BUD13 *	rs117338034	116,648,026	G	T	0.089375	-0.037898	0.003531	5.10E-28	-0.032023	0.006013	5.19E-07	-0.041144	0.00443	1.69E-20	6.21E-25	0.142935	
11	BUD13 *	rs1240771	116,648,172	G	A	0.229039	0.020168	0.002382	2.90E-18	0.013635	0.004054	0.000773	0.023998	0.00299	1.06E-15	3.58E-17	0.039677	F
11	BUD13 *	rs73580632	116,648,184	T	C	0.08936	-0.0379	0.003531	5.40E-28	-0.030182	0.006013	5.29E-07	-0.041149	0.004431	1.69E-20	6.35E-25	0.14201	
11	BUD13 *	rs1261672	116,648,243	G	A	0.228515	0.020454	0.002384	1.00E-18	0.01418	0.004059	0.00048	0.024157	0.002991	6.95E-16	1.52E-17	0.047845	F
11	BUD13 *	rs1240772	116,648,412	C	G	0.320621	0.022181	0.00218	4.70E-25	0.015964	0.003713	1.73E-05	0.025731	0.002735	5.37E-21	5.81E-24	0.034187	F
11	BUD13 *	rs513533	116,648,641	G	A	0.115595	0.050273	0.003143	3.50E-59	0.055146	0.005353	7.37E-25	0.048375	0.003944	1.52E-34	1.93E-56	0.308491	
11	BUD13 *	rs516043	116,648,867	G	C	0.115658	0.050099	0.003142	8.00E-59	0.055162	0.005351	6.91E-25	0.048087	0.003943	3.61E-34	4.28E-56	0.287162	
11	BUD13 *	rs516226	116,648,938	T	C	0.294324	0.015669	0.002244	3.10E-12	0.020115	0.003805	1.27E-07	0.013942	0.002823	7.98E-07	4.29E-12	0.192534	
11	BUD13 *	rs499790	116,649,022	T	C	0.11564	0.050106	0.003142	7.90E-59	0.055139	0.005351	7.16E-25	0.048119	0.003943	3.26E-34	4.01E-56	0.290892	
11	BUD13 *	rs504268	116,649,487	T	C	0.115643	0.050165	0.003142	5.70E-59	0.055238	0.00535	5.88E-25	0.048156	0.003943	2.90E-34	2.93E-56	0.286617	
11	BUD13 *	rs544479	116,649,681	C	T	0.115647	0.050098	0.003142	8.00E-59	0.055163	0.005351	6.84E-25	0.048088	0.003943	3.54E-34	4.16E-56	0.287084	
11	BUD13 *	rs506222	116,649,717	C	A	0.115649	0.050102	0.003142	7.90E-59	0.055162	0.005351	6.85E-25	0.048095	0.003943	3.46E-34	4.07E-56	0.287616	
11	BUD13 *	rs1240773	116,649,810	T	G	0.229195	0.020549	0.002378	5.60E-19	0.014558	0.004052	0.00033	0.0241	0.002983	6.93E-16	1.07E-17	0.057956	
11	BUD13 *	rs549125	116,650,209	G	C	0.119566	0.052693	0.003097	9.50E-67	0.058505	0.005271	1.38E-28	0.050345	0.003887	2.53E-38	6.74E-64	0.121783	
11	BUD13 *	rs533668	116,650,418	G	T	0.119567	0.052734	0.003097	7.50E-67	0.058631	0.005271	1.05E-28	0.050345	0.003887	2.53E-38	5.15E-64	0.205844	
11	BUD13 *	rs573985	116,650,599	A	G	0.119403	0.05282	0.003099	7.30E-67	0.058549	0.005275	1.38E-28	0.050537	0.003889	1.42E-38	3.81E-64	0.221512	
11	BUD13 *	rs575906	116,650,841	G	A	0.11976	0.052755	0.003095	7.80E-67	0.058521	0.005267	1.20E-28	0.050446	0.003885	1.65E-38	3.86E-64	0.217245	
11	BUD13 *	rs143762798	116,650,954	A	G	0.020602	-0.059091	0.007063	3.50E-17	-0.069681	0.011965	5.91E-09	-0.053699	0.008888	1.57E-09	5.11E-16	0.283597	
11	BUD13 *	rs562756	116,651,258	C	G	0.119498	0.052619	0.003098	2.10E-66	0.059481	0.005273	1.77E-29	0.04976	0.003889	1.88E-37	6.47E-64	0.137874	
11	BUD13 *	rs491022	116,651,271	C	T	0.137703	0.042459	0.002951	7.30E-48	0.050059	0.004998	1.39E-23	0.039006	0.003715	9.26E-26	1.88E-46	0.075932	
11	BUD13 *	rs563796	116,651,394	G	A	0.120426	0.05289	0.003085	2.10E-67	0.058967	0.005252	3.23E-29	0.050431	0.003872	9.79E-39	6.22E-65	0.190807	
11	BUD13 *	rs563917	116,651,439	T	C	0.120453	0.052917	0.003085	1.70E-67	0.058941	0.005251	3.33E-29	0.050477	0.003872	8.20E-39	5.37E-65	0.194495	
11	BUD13 *	rs492182	116,651,447	A	G	0.120478	0.052999	0.003084	9.90E-68	0.058947	0.005251	3.26E-29	0.050601	0.003871	5.25E-39	3.37E-65	0.200708	
11	BUD13 *	rs565607	116,651,613	T	C	0.120405	0.05302	0.003085	8.40E-68	0.058903	0.005254	3.85E-29	0.05068	0.003871	4.01E-39	3.03E-65	0.207604	
11	BUD13 *	rs567576	116,651,842	G	A	0.120325	0.053064	0.003083	5.50E-68	0.058694	0.005249	5.39E-29	0.050911	0.003868	1.60E-39	1.70E-65	0.232588	
11	BUD13 *	rs567599	116,651,848	T	G	0.120344	0.053057	0.003082	5.70E-68	0.058572	0.005249	6.95E-29	0.05098	0.003868	1.24E-39	1.70E-65	0.244257	
11	BUD13 *	rs3017237	116,651,908	C	G	0.120503	0.053001	0.00308	6.30E-68	0.058687	0.005244	4.82E-29	0.05082	0.003865	1.86E-39	1.77E-65	0.227146	
11	BUD13 *	rs480028	116,652,053	G	C	0.120539	0.052992	0.003079	6.20E-68	0.058644	0.005242	5.06E-29	0.050833	0.003863	1.68E-39	1.68E-65	0.23026	
11	BUD13 *	rs480878	116,652,137	A	G	0.121032	0.052671	0.003075	2.30E-67	0.058353	0.005236	8.23E-29	0.050463	0.003859	4.86E-39	7.82E-65	0.225132	
11	BUD13 *	rs499563	116,652,244	T	C	0.120678	0.053169	0.003077	1.90E-68	0.059038	0.005242	2.18E-29	0.050869	0.00386	1.31E-39	5.65E-66	0.209525	
11	BUD13 *	rs79770434	116,652,448	T	C	0.086129	-0.039718	0.003597	1.60E-29	-0.033553	0.006126	4.42E-08	-0.042206	0.004513	9.20E-21	3.13E-26	0.255464	
11	BUD13 *	rs483747	116,652,450	C	T	0.120572	0.052997	0.003078	5.60E-68	0.058693	0.00524	4.41E-29	0.050815	0.003863	1.74E-39	1.52E-65	0.22662	
11	BUD13 *	rs141584077	116,652,587	T	A	0.112751	0.049626	0.003196	1.90E-55	0.051828	0.005449	2.01E-21	0.049211	0.004008	1.31E-34	4.23E-53	0.698851	
11	BUD13 *	rs523980	116,652,589	T	A	0.107612	0.049013	0.003275	1.30E-51	0.050244	0.005574	2.10E-19	0.048976	0.00441	1.06E-32	3.33E-49	0.854685	
11	BUD13 *	rs485638	116,652,656	C	G	0.120568	0.053	0.003078	5.50E-68	0.058688	0.00524	4.46E-29	0.050822	0.003863	1.70E-39	1.50E-65	0.226966	
11	BUD13 *	rs143547828	116,652,846	G	A	0.016874	-0.04409	0.007858	4.00E-08	-0.0526	0.013469	9.50E-05	-0.039732	0.009826	5.32E-05	1.37E-07	0.440208	
11	BUD13 *	rs117742492	116,652,940	A	G	0.085981	-0.039827	0.003602	1.20E-29	-0.033597	0.006132	4.38E-08	-0.042409	0.004521	7.00E-21	2.37E-26	0.247409	
11	BUD13 *	rs528647	116,653,104	T	C	0.120559	0.053022	0.003078	4.90E-68	0.058709	0.005241	4.27E-29	0.050844	0.003862	1.56E-39	1.32E-65	0.226989	
11	BUD13 *	rs528732	116,653,127	A	G	0.120559	0.053022	0.003078	4.90E-68	0.058709	0.005241	4.27E-29	0.050844	0.003862	1.56E-39	1.32E-65	0.226989	
11	BUD13 *	rs3017778	116,653,214	T	C	0.120521	0.052994	0.003079	6.10E-68	0.058578	0.005242	5.85E-29	0.050861	0.003863	1.51E-39	1.74E-65		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	BUD13 *	rs1944153	116,661,504	C	T	0.1921	0.018541	0.002548	4.40E-14	0.008503	0.004353	0.050796	0.024188	0.003191	3.59E-14	4.93E-14	0.00367	F
11	BUD13 *	rs78198334	116,661,566	C	G	0.08789	-0.044794	0.003539	3.70E-38	-0.039903	0.006032	3.84E-11	-0.04699	0.004438	3.61E-26	1.41E-34	0.343925	
11	BUD13 *	rs118175510	116,661,831	C	T	0.082295	0.069136	0.003679	1.70E-80	0.074919	0.006239	3.53E-33	0.067635	0.004627	2.36E-48	1.92E-78	0.348383	
11	BUD13 *	rs79291519	116,662,593	T	C	0.086556	-0.044939	0.003562	9.00E-38	-0.039463	0.006079	8.77E-11	-0.047438	0.004464	2.42E-26	2.13E-34	0.290277	
11	BUD13 *	rs75942205	116,662,878	C	T	0.086822	-0.044791	0.003556	1.20E-37	-0.039612	0.006062	6.61E-11	-0.047139	0.004459	4.32E-26	2.87E-34	0.317179	
11	BUD13 *	rs61659529	116,662,911	G	A	0.086809	-0.044772	0.003557	1.20E-37	-0.039452	0.006065	8.06E-11	-0.047185	0.004459	3.88E-26	3.13E-34	0.304299	
11	BUD13 *	rs486915	116,663,571	T	A	0.368282	-0.045286	0.002128	9.40E-105	-0.04218	0.003626	3.03E-31	-0.047392	0.002669	1.70E-70	1.37E-98	0.24699	
11	BUD13 *	rs76547220	116,663,833	G	T	0.086847	-0.044807	0.003556	1.10E-37	-0.039688	0.006064	6.18E-11	-0.047104	0.004459	4.69E-26	2.92E-34	0.324488	
11	BUD13 *	rs567209	116,664,111	T	C	0.167767	0.028697	0.002709	2.20E-27	0.035867	0.004628	9.62E-15	0.025104	0.003393	1.44E-13	1.18E-25	0.060737	
11	BUD13 *	rs12802672	116,664,246	G	A	0.093193	0.022919	0.003472	1.30E-10	0.022481	0.00591	0.000144	0.022303	0.004357	3.14E-07	1.47E-09	0.980617	
11	BUD13 *	rs2105609	116,664,370	A	G	0.086847	-0.044807	0.003556	1.10E-37	-0.039688	0.006064	6.18E-11	-0.047108	0.004459	4.67E-26	2.90E-34	0.324238	
11	BUD13 *	rs2105610	116,664,409	C	T	0.086446	-0.044469	0.003565	4.10E-37	-0.039109	0.006075	1.25E-10	-0.046906	0.004471	1.03E-25	1.27E-33	0.301294	
11	BUD13 *	rs77226464	116,664,718	T	C	0.086951	-0.044651	0.003555	1.60E-37	-0.039406	0.006062	8.26E-11	-0.046985	0.004457	6.01E-26	4.96E-34	0.313764	
11	BUD13 *	rs190069353	116,664,907	A	C	0.086823	-0.044761	0.003557	1.30E-37	-0.039659	0.006065	6.42E-11	-0.047036	0.00446	5.73E-26	3.69E-34	0.32713	
11	BUD13 *	rs117014628	116,664,914	T	C	0.086842	-0.044727	0.003557	1.40E-37	-0.039693	0.006065	6.16E-11	-0.046971	0.00446	6.56E-26	4.06E-34	0.333614	
11	BUD13 *	rs1240776	116,665,564	T	C	0.374673	-0.046239	0.002077	1.90E-114	-0.043642	0.003538	6.45E-35	-0.047714	0.002606	7.71E-75	1.44E-106	0.354046	
11	BUD13 *	rs12803249	116,665,701	G	A	0.167771	0.028689	0.002709	2.40E-27	0.035805	0.004627	1.06E-14	0.025071	0.003393	1.53E-13	1.38E-25	0.061395	
11	BUD13 *	rs1240777	116,665,759	C	T	0.200308	0.018757	0.002505	1.20E-14	0.008339	0.004281	0.051425	0.024564	0.003136	5.05E-15	7.20E-15	0.002243	F
11	BUD13 *	rs1240778	116,665,773	C	A	0.37099	0.030684	0.002104	6.90E-51	0.027411	0.003589	2.33E-14	0.032769	0.002636	1.98E-35	6.17E-47	0.228917	
11	BUD13 *	rs10892010	116,665,939	A	A	0.24787	0.020086	0.002354	7.20E-18	0.021261	0.004008	1.15E-07	0.019088	0.002953	1.06E-10	6.57E-16	0.662539	
11	BUD13 *	rs79063991	116,666,103	T	C	0.086841	-0.044715	0.003557	1.50E-37	-0.039697	0.006065	6.15E-11	-0.046939	0.00446	7.14E-26	4.36E-34	0.336064	
11	BUD13 *	rs61906081	116,666,342	A	G	0.167784	0.028643	0.002708	2.90E-27	0.035805	0.004627	1.06E-14	0.025007	0.003392	1.75E-13	1.58E-25	0.059863	
11	BUD13 *	rs118103820	116,666,399	G	A	0.086841	-0.044715	0.003557	1.50E-37	-0.039697	0.006065	6.15E-11	-0.046939	0.00446	7.14E-26	4.40E-34	0.336064	
11	BUD13 *	rs6589557	116,667,044	T	C	0.423955	0.031979	0.002032	1.00E-57	0.036384	0.003467	9.80E-26	0.029476	0.002546	5.94E-31	9.69E-54	0.108292	
11	BUD13 *	rs140973748	116,667,081	C	T	0.086847	-0.044718	0.003557	1.50E-37	-0.03971	0.006065	6.06E-11	-0.04694	0.00446	7.10E-26	4.32E-34	0.336837	
11	BUD13 *	rs35933073	116,667,129	A	C	0.167803	0.028638	0.002708	2.80E-27	0.035805	0.004627	1.06E-14	0.024999	0.003392	1.77E-13	1.59E-25	0.059664	
11	BUD13 *	rs6589558	116,667,225	A	G	0.423956	0.031981	0.002032	1.00E-57	0.036384	0.003467	9.80E-26	0.029478	0.002546	5.89E-31	9.60E-54	0.108394	
11	BUD13 *	rs1784125	116,667,245	C	G	0.200296	0.018829	0.002505	9.30E-15	0.008436	0.00428	0.048757	0.024615	0.003136	4.42E-15	6.04E-15	0.002306	F
11	BUD13 *	rs12787592	116,667,257	C	G	0.167815	0.02861	0.002708	3.20E-27	0.035712	0.004627	1.24E-14	0.025002	0.003392	1.76E-13	1.84E-25	0.06195	
11	BUD13 *	rs143380339	116,667,386	A	C	0.086847	-0.044718	0.003557	1.50E-37	-0.03971	0.006065	6.06E-11	-0.04694	0.00446	7.10E-26	4.32E-34	0.336837	
11	BUD13 *	rs1784126	116,667,498	T	G	0.372679	-0.045838	0.002078	1.60E-112	-0.043024	0.00354	6.06E-34	-0.047443	0.002607	5.71E-74	9.82E-105	0.314824	
11	BUD13 *	rs57258844	116,667,690	C	G	0.093354	0.023254	0.003467	5.80E-11	0.022026	0.005899	0.00019	0.023016	0.004352	1.26E-07	7.94E-10	0.892518	
11	BUD13 *	rs1784127	116,667,859	A	G	0.373001	-0.045854	0.002078	1.40E-112	-0.04306	0.00354	5.17E-34	-0.047461	0.002606	4.75E-74	7.00E-105	0.316635	
11	BUD13 *	rs1784128	116,667,972	A	G	0.373009	-0.045873	0.002078	1.20E-112	-0.04306	0.00354	5.17E-34	-0.047492	0.002606	3.87E-74	5.70E-105	0.313296	
11	BUD13 *	rs1632755	116,668,134	C	A	0.200355	0.01883	0.002505	9.20E-15	0.008408	0.004281	0.049545	0.024631	0.003137	4.27E-15	5.92E-15	0.002246	F
11	BUD13 *	rs112464350	116,668,341	A	C	0.093366	0.023277	0.003467	5.60E-11	0.022049	0.005898	0.000187	0.023049	0.004352	1.21E-07	7.50E-10	0.891413	
11	BUD13 *	rs1787682	116,668,486	G	C	0.200298	0.018822	0.002505	9.50E-15	0.008432	0.00428	0.048868	0.024606	0.003136	4.52E-15	6.19E-15	0.002313	F
11	BUD13 *	rs150937658	116,668,605	G	A	0.099706	-0.040712	0.003385	1.10E-32	-0.049259	0.005763	1.34E-17	-0.035758	0.004248	4.08E-17	5.69E-32	0.059367	
11	BUD13 *	rs9681206	116,668,801	T	C	0.249787	0.019396	0.002346	7.30E-17	0.020385	0.003995	3.41E-07	0.01857	0.002944	2.92E-10	5.07E-15	0.714589	
11	BUD13 *	rs112550319	116,669,092	G	C	0.093391	0.023354	0.003466	8.40E-11	0.022085	0.005898	0.000182	0.023123	0.004352	1.10E-07	6.67E-10	0.887357	
11	BUD13 *	rs1784131	116,669,151	C	T	0.200053	0.018775	0.002506	1.20E-14	0.008321	0.004282	0.052019	0.024588	0.003139	4.94E-15	7.12E-15	0.002194	F
11	BUD13 *	rs11216085	116,669,432	C	T	0.249832	0.019436	0.002346	6.80E-17	0.0204	0.003995	3.36E-07	0.018608	0.002944	2.68E-10	4.60E-15	0.717996	
11	BUD13 *	rs2846015	116,669,722	T	C	0.200294	0.018828	0.002505	9.40E-15	0.008438	0.00428	0.048711	0.024615	0.003136	4.42E-15	6.04E-15	0.002308	F
11	BUD13 *	rs3016354	116,670,075	C	T	0.200299	0.018805	0.002504	9.90E-15	0.008438	0.00428	0.048711	0.024583	0.003136	4.78E-15	6.52E-15	0.002354	F
11	BUD13 *	rs3017337	116,670,090	T	C	0.200451	0.019006	0.002505	5.10E-15	0.008677	0.004281	0.042692	0.024782	0.003137	2.90E-15	3.57E-15	0.002418	F
11	BUD13 *	rs7925553	116,670,267	G	A	0.168007	0.028588	0.002706	3.00E-27	0.035792	0.004624	1.04E-14	0.024915	0.003388	2.02E-13	1.78E-25	0.057779	
11	BUD13 *	rs144188664	116,670,317	T	A	0.086857	-0.044742	0.003557	1.40E-37	-0.039772	0.006065	5.67E-11	-0.046964	0.00446	6.79E-26	3.87E-34	0.339397	
11	BUD13 *	rs1784133	116,670,700	T	C	0.200298	0.018801	0.002504	1.00E-14	0.008438	0.00428	0.048711	0.024576	0.003136	4.87E-15	6.64E-15	0.002365	F
11	BUD13 *	rs1787686	116,670,755	A	G	0.285803	-0.035278	0.002227	4.50E-59	-0.033978	0.003794	3.61E-19	-0.03627	0.002794	1.67E-38	9.62E-55	0.626711	
11	BUD13 *	rs2846016	116,670,822	T	C	0.200028	0.018936	0.002506	6.90E-15	0.008674	0.004282	0.042844	0.024669	0.003138	4.01E-15	4.93E-15	0.0026	F
11	BUD13 *	rs36195057	116,671,530	A	G	0.249949	0.01946	0.002345	6.40E-17	0.020466	0.003994	3.06E-07	0.01863	0.002943	2.52E-10	3.95E-15	0.711364	
11	BUD13 *	rs1787692	116,671,779	G	T	0.459499	0.01424	0.002039	4.10E-13	0.012456	0.003479	0.000346	0.015686	0.002556	8.70E-10	1.10E-11	0.454331	
11	BUD13 *	rs148462279	116,672,020	G	A	0.086862	-0.04471	0.003557	1.60E-37	-0.039656	0.006066	6.46E-11	-0.046971	0.00446	6.70E-26	4.34E-34	0.331293	
11	BUD13 *	rs75930640	116,672,095	T	G	0.200295	0.018786	0.002504	1.10E-14	0.008406	0.00428	0.04956	0.024572	0.003136	4.92E-15	6.80E-15	0.002324	F
11	BUD13 *	rs144256947	116,672,308	C	T	0.086781	-0.044836	0.003559	1.10E-37	-0.039993	0.00607	4.59E-11	-0.046985	0.004463	6.87E-26	3.18E-34	0.35339	
11	BUD13 *	rs113264811	116,672,394	T	C	0.202092	0.018975	0.002498	5.20E-15	0.008522	0.00427	0.045983</						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	BUD13 *	rs74792494	116,678,691	C	A	0.197707	0.017477	0.002518	5.30E-13	0.006556	0.004301	0.127447	0.02379	0.003154	4.79E-14	1.38E-13	0.001238	F
11	BUD13 *	rs1787687	116,679,179	G	A	0.200327	0.018702	0.002503	1.30E-14	0.008227	0.004278	0.05448	0.024563	0.003135	4.91E-15	7.36E-15	0.002077	F
11	BUD13 *	rs35963862	116,679,180	C	T	0.168425	0.028314	0.002702	7.00E-27	0.03562	0.004614	1.22E-14	0.024603	0.003385	3.79E-13	3.88E-25	0.054227	
11	BUD13 *	rs17830617	116,679,254	A	G	0.086984	-0.044827	0.003559	1.20E-27	-0.039067	0.006068	1.25E-10	-0.047447	0.004463	2.31E-26	2.89E-34	0.265923	
11	BUD13 *	rs61906104	116,679,398	G	A	0.172544	0.027914	0.002683	1.30E-26	0.036711	0.004578	1.12E-15	0.023501	0.003363	2.89E-12	2.70E-25	0.020068	M
11	BUD13 *	rs11216091	116,679,966	G	A	0.021647	-0.04918	0.006909	1.40E-12	-0.039029	0.011747	0.000897	-0.055606	0.008677	1.52E-10	4.84E-12	0.256317	
11	BUD13 *	rs12417015	116,680,059	G	A	0.197485	0.017341	0.002519	8.10E-13	0.006579	0.004302	0.126229	0.023553	0.003155	8.73E-14	2.47E-13	0.001472	F
11	BUD13 *	rs1787717	116,682,049	T	C	0.370368	-0.046005	0.002085	1.30E-112	-0.042375	0.00355	8.44E-33	-0.048023	0.002615	2.96E-75	7.03E-105	0.002026	
11	BUD13 *	rs12806224	116,682,098	C	T	0.172344	0.027844	0.002685	1.80E-26	0.036675	0.004585	1.31E-15	0.023412	0.003364	3.57E-12	3.88E-25	0.019713	M
11	BUD13 *	rs113194822	116,682,143	A	G	0.092659	0.024964	0.003483	2.80E-12	0.021546	0.005912	0.00027	0.025632	0.004378	4.93E-09	4.73E-11	0.578693	
11	BUD13 *	rs12805061	116,682,308	G	A	0.172636	0.027869	0.002682	1.60E-26	0.036546	0.004578	1.51E-15	0.023476	0.003361	2.97E-12	3.73E-25	0.021407	M
11	BUD13 *	rs11826999	116,683,062	A	G	0.172746	0.027691	0.002682	3.50E-26	0.036314	0.004578	2.27E-15	0.023332	0.003361	4.03E-12	7.52E-25	0.0223	M
11	BUD13 *	rs71480312	116,683,372	A	C	0.098841	0.022904	0.00338	3.60E-11	0.019887	0.005742	0.000537	0.023488	0.004247	3.27E-08	5.68E-10	0.614073	
11	BUD13 *	rs117341026	116,684,410	A	G	0.085867	-0.046117	0.003588	3.90E-39	-0.039433	0.006105	1.09E-10	-0.049121	0.004504	1.16E-27	1.29E-35	0.201585	
11	BUD13 *	rs7932330	116,684,491	G	A	0.246739	0.019103	0.002361	3.20E-16	0.01826	0.004027	5.87E-06	0.01916	0.002961	1.00E-10	2.76E-14	0.857046	
11	BUD13 *	rs35681250	116,684,670	T	A	0.172969	0.027785	0.002684	2.60E-26	0.036684	0.00458	1.21E-15	0.023264	0.003363	4.77E-12	4.76E-25	0.018212	M
11	BUD13 *	rs3016357	116,684,699	T	C	0.291665	-0.036286	0.002239	6.80E-62	-0.034609	0.003816	1.28E-19	-0.037468	0.002809	1.49E-40	3.15E-57	0.54632	
11	BUD13 *	rs1145213	116,684,706	G	A	0.294972	-0.034466	0.002238	5.10E-56	-0.032717	0.003813	1.01E-17	-0.035687	0.002807	5.56E-37	8.46E-52	0.530544	
11	BUD13 *	rs77835865	116,684,713	G	A	0.172759	0.027863	0.002682	1.80E-26	0.036661	0.004579	1.24E-15	0.023392	0.003361	3.56E-12	3.67E-25	0.019513	M
11	BUD13 *	rs956832572	116,684,717	T	A	0.014421	0.076593	0.008452	1.70E-20	0.082195	0.014185	7.04E-09	0.072938	0.010692	9.34E-12	4.02E-18	0.602288	
11	BUD13 *	rs61906112	116,685,049	A	T	0.172696	0.027931	0.002683	1.40E-26	0.036624	0.00458	1.34E-15	0.023532	0.003362	2.67E-12	3.00E-25	0.021244	M
11	BUD13 *	rs17092638	116,685,520	G	C	0.172711	0.028169	0.002684	5.60E-27	0.036797	0.004581	1.01E-15	0.023816	0.003363	1.48E-12	1.26E-25	0.022387	M
11	BUD13 *	rs1145212	116,686,149	A	G	0.452218	0.028035	0.002046	2.10E-44	0.021863	0.003485	3.64E-10	0.031359	0.002566	2.69E-34	1.08E-41	0.028258	F
11	BUD13 *	rs2156120	116,686,439	G	A	0.249736	0.019987	0.002351	6.90E-18	0.020845	0.004005	1.99E-07	0.019241	0.002949	7.05E-11	7.49E-16	0.747186	
11	BUD13 *	rs1145211	116,686,500	A	C	0.283594	-0.035657	0.00224	6.90E-60	-0.034958	0.003817	5.57E-20	-0.036435	0.002809	2.00E-38	1.81E-55	0.755294	
11	BUD13 *	rs17092642	116,686,532	C	T	0.172644	0.028327	0.002686	3.20E-27	0.03689	0.004585	9.05E-16	0.024009	0.003367	1.03E-12	7.96E-26	0.023577	M
11	BUD13 *	rs947990	116,686,598	T	G	0.061881	-0.043759	0.004182	2.60E-25	-0.039947	0.007167	2.55E-08	-0.047282	0.00523	1.66E-19	3.21E-25	0.408375	
11	BUD13 *	rs11216093	116,687,166	C	A	0.250409	0.020244	0.002352	3.00E-18	0.021328	0.004008	1.06E-07	0.019344	0.002949	5.59E-11	3.24E-16	0.690132	
11	BUD13 *	rs61906115	116,687,529	A	T	0.168313	0.028847	0.002708	1.20E-27	0.035886	0.004628	9.27E-15	0.025214	0.003392	1.10E-13	8.75E-26	0.062894	
11	BUD13 *	rs12799766	116,687,711	A	G	0.168341	0.028894	0.002708	9.70E-28	0.035916	0.004626	8.67E-15	0.025269	0.003392	9.78E-14	7.29E-26	0.063484	
11	BUD13 *	rs12799441	116,687,799	T	A	0.168457	0.028936	0.002708	8.10E-28	0.036006	0.004625	7.34E-15	0.025306	0.003391	8.91E-14	5.64E-26	0.062115	
11	BUD13 *	rs12799449	116,687,809	G	A	0.168489	0.029034	0.002708	5.80E-28	0.036146	0.004626	5.83E-15	0.025397	0.003392	7.35E-14	3.72E-26	0.060691	
11	BUD13 *	rs1145210	116,688,286	T	C	0.202354	-0.01427	0.002543	1.40E-09	-0.013891	0.004324	0.001321	-0.014951	0.003193	2.88E-06	9.94E-08	0.84353	
11	BUD13 *	rs77277788	116,688,720	T	C	0.092413	0.024128	0.00348	1.20E-11	0.022093	0.005941	0.000202	0.024066	0.00436	3.47E-08	2.40E-10	0.788863	
11	BUD13 *	rs11824135	116,688,837	T	G	0.201712	0.014496	0.002545	1.80E-09	0.007495	0.004343	0.0844	0.018611	0.003189	5.51E-09	9.10E-09	0.039136	F
11	BUD13 *	rs12828763	116,688,947	G	A	0.212414	0.016637	0.002479	3.70E-12	0.009211	0.004229	0.029435	0.020742	0.003107	2.55E-11	1.96E-11	0.028031	
11	BUD13 *	rs3016360	116,689,027	C	T	0.212893	0.016804	0.002476	3.40E-12	0.009821	0.004226	0.020157	0.020588	0.003102	3.31E-11	1.83E-11	0.040001	
11	BUD13 *	rs1787716	116,689,458	A	G	0.198765	0.02032	0.002519	1.40E-16	0.010894	0.004307	0.011459	0.025749	0.003153	3.31E-16	1.34E-16	0.005399	F
11	BUD13 *	rs1787715	116,689,609	T	C	0.198759	0.020311	0.002519	1.40E-16	0.010908	0.004307	0.011346	0.025731	0.003153	3.47E-16	1.39E-16	0.005502	F
11	BUD13 *	rs1623797	116,689,731	T	C	0.432325	-0.041455	0.002047	1.20E-96	-0.039429	0.003487	1.30E-29	-0.042886	0.002569	1.59E-62	5.09E-89	0.424749	
11	BUD13 *	rs34937367	116,689,808	C	T	0.198884	0.020267	0.002519	1.60E-16	0.010942	0.004307	0.011089	0.025653	0.003153	4.28E-16	1.67E-16	0.005868	F
11	BUD13 *	rs74330350	116,689,812	G	A	0.198884	0.020267	0.002519	1.60E-16	0.010942	0.004307	0.011089	0.025653	0.003153	4.28E-16	1.67E-16	0.005868	F
11	BUD13 *	rs79280888	116,689,813	G	A	0.198884	0.020267	0.002519	1.60E-16	0.010942	0.004307	0.011089	0.025653	0.003153	4.28E-16	1.67E-16	0.005868	F
11	BUD13 *	rs1787714	116,689,894	A	G	0.246483	-0.046709	0.002367	2.00E-90	-0.044158	0.004045	1.05E-27	-0.048378	0.002964	7.54E-60	1.85E-84	0.400087	
11	BUD13 *	rs1787713	116,689,895	G	C	0.246483	-0.046709	0.002367	2.00E-90	-0.044158	0.004045	1.05E-27	-0.048378	0.002964	7.54E-60	1.85E-84	0.400087	
11	BUD13 *	rs12291024	116,689,951	G	T	0.365896	0.029873	0.002098	6.20E-49	0.034681	0.003581	3.72E-22	0.027345	0.002629	2.67E-25	1.40E-44	0.098655	
11	BUD13 *	rs1787711	116,690,062	G	A	0.1988	0.020189	0.002518	2.00E-16	0.010684	0.004306	0.013104	0.025651	0.003152	4.25E-16	1.92E-16	0.005048	F
11	BUD13 *	rs3017232	116,690,167	T	C	0.19912	0.020365	0.002516	1.10E-16	0.010939	0.004302	0.011021	0.025779	0.00315	2.92E-16	1.14E-16	0.0054	
11	BUD13 *	rs3017231	116,690,232	A	G	0.198807	0.020186	0.002518	2.00E-16	0.010729	0.004305	0.012715	0.025625	0.003152	4.54E-16	2.00E-16	0.00526	F
11	BUD13 *	rs3017230	116,690,245	C	G	0.198808	0.020183	0.002518	2.10E-16	0.010725	0.004305	0.012748	0.025621	0.003152	4.59E-16	2.03E-16	0.005259	F
11	BUD13 *	rs3017229	116,690,251	A	G	0.248185	-0.047109	0.002358	2.10E-92	-0.044342	0.00403	4.00E-28	-0.048815	0.002953	2.55E-61	2.43E-86	0.370625	
11	BUD13 *	rs3017228	116,690,276	G	A	0.198808	0.020183	0.002518	2.10E-16	0.010725	0.004305	0.012748	0.025621	0.003152	4.59E-16	2.03E-16	0.005259	F
11	BUD13 *	rs1787710	116,690,486	A	G	0.198817	0.020133	0.002518	2.50E-16	0.010705	0.004305	0.012916	0.025555	0.003152	5.44E-16	2.43E-16	0.005397	F
11	BUD13 *	rs76483212	116,690,550	A	G	0.092287	0.025038	0.003474	1.70E-12	0.022081	0.00593	0.000198	0.025494	0.004353	4.85E-09	3.47E-11	0.642758	
11	BUD13 *	rs1787709	116,690,612	G	C	0.198803	0.020111	0.002518	2.60E-16	0.01066	0.004305	0.013298	0.02554	0.003152	5.64E-16	2.58E-16	0.005303	F
11	BUD13 *	rs1784123	116,690,665	C	T	0.198802	0.02014	0.002518	2.40E-16	0.010726	0.004305</							

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
11	BUD13 *	rs12420888	116,693,106	G	C	0.364412	0.030597	0.002098	3.90E-51	0.035034	0.003579	1.34E-22	0.028252	0.00263	6.88E-27	1.35E-46	0.12677	
11	BUD13 *	rs1787701	116,693,276	C	C	0.336204	-0.056918	0.002155	6.70E-160	-0.052318	0.00367	4.70E-46	-0.05938	0.002704	8.24E-107	1.50E-149	0.121413	
11	BUD13 *	rs117889337	116,693,777	T	C	0.083099	-0.048255	0.003654	2.20E-41	-0.042189	0.006208	1.12E-11	-0.050693	0.004591	2.62E-28	3.18E-37	0.270753	
11	BUD13 *	rs1787699	116,693,837	G	A	0.247427	-0.047746	0.002362	1.30E-94	-0.044702	0.004032	1.58E-28	-0.049563	0.00296	7.03E-63	2.69E-88	0.331106	
11	BUD13 *	rs1787698	116,693,846	T	C	0.247423	-0.047737	0.002362	1.30E-94	-0.044699	0.004032	1.59E-28	-0.049553	0.00296	7.43E-63	2.87E-88	0.331863	
11	BUD13 *	rs1784118	116,694,339	T	C	0.25018	-0.048027	0.002351	1.70E-96	-0.04554	0.004015	8.71E-30	-0.049555	0.002946	1.92E-63	4.16E-90	0.420186	
11	BUD13 *	rs12293222	116,694,593	A	G	0.2862	0.027336	0.00224	2.30E-34	0.020038	0.003837	1.81E-07	0.03088	0.002802	3.31E-28	5.11E-33	0.022524	F
11	BUD13 *	rs111226221	116,694,718	T	C	0.09199	0.024518	0.003481	5.10E-12	0.021191	0.005944	0.000366	0.025174	0.004361	8.04E-09	1.01E-10	0.589017	
11	BUD13 *	rs117607796	116,694,887	A	C	0.083537	-0.048237	0.003646	1.40E-41	-0.042908	0.006193	4.41E-12	-0.0503	0.004581	5.08E-28	2.46E-37	0.337204	
11	BUD13 *	rs116978945	116,694,974	T	C	0.09078	0.021894	0.003503	1.20E-09	0.01884	0.005982	0.001643	0.022481	0.004389	3.07E-07	1.41E-08	0.623585	
11	BUD13 *	rs111218525	116,695,822	T	C	0.206192	0.029528	0.002505	1.80E-33	0.034081	0.004276	1.66E-15	0.027021	0.003138	7.71E-18	1.28E-30	0.183162	
11	BUD13 *	rs59854309	116,696,047	T	C	0.255655	-0.049216	0.002359	1.50E-100	-0.046914	0.004029	2.66E-31	-0.050552	0.002955	1.44E-65	9.92E-94	0.466532	
11	BUD13 *	rs60954647	116,696,217	T	C	0.409064	-0.029074	0.002086	7.40E-45	-0.026137	0.003569	2.52E-13	-0.030722	0.00261	6.04E-32	1.86E-42	0.299756	
11	BUD13 *	rs1784106	116,696,733	A	C	0.2523	-0.048608	0.002347	7.20E-99	-0.045651	0.004007	4.99E-30	-0.050343	0.002941	1.17E-65	1.49E-92	0.345142	
11	BUD13 *	rs78888567	116,696,897	A	G	0.059574	0.023701	0.003419	1.10E-11	0.020451	0.005831	0.000456	0.024426	0.004286	1.23E-08	1.88E-10	0.582786	
11	BUD13 *	rs4938300	116,696,903	T	C	0.203052	0.032364	0.002509	1.00E-39	0.035701	0.004284	8.34E-17	0.030671	0.003142	1.78E-22	1.73E-36	0.343875	
11	BUD13 *	rs10892017	116,697,165	C	G	0.35991	0.03328	0.002092	1.50E-60	0.036876	0.003571	5.65E-25	0.031447	0.002621	4.00E-33	3.82E-55	0.22028	
11	BUD13 *	rs11605568	116,697,452	A	G	0.359857	0.033226	0.002092	2.20E-60	0.036717	0.00357	8.85E-25	0.031446	0.002621	4.03E-33	6.02E-55	0.233929	
11	BUD13 *	rs11606013	116,697,509	T	G	0.359918	0.033202	0.002091	2.70E-60	0.036742	0.00357	8.11E-25	0.031393	0.002621	5.04E-33	6.89E-55	0.227056	
11	BUD13 *	rs140078194	116,697,574	A	C	0.086781	-0.047121	0.003582	1.30E-40	-0.042622	0.006088	2.64E-12	-0.048983	0.0045	1.44E-27	4.18E-37	0.400794	
11	BUD13 *	rs11608173	116,697,648	A	T	0.359919	0.03319	0.002091	2.90E-60	0.036744	0.00357	8.07E-25	0.031375	0.002621	5.47E-33	7.43E-55	0.225331	
11	BUD13 *	rs1787689	116,697,666	G	A	0.44294	-0.043047	0.002032	1.50E-104	-0.04193	0.003463	1.06E-33	-0.04386	0.002549	2.77E-66	7.87E-97	0.653546	
11	BUD13 *	rs1787690	116,697,800	T	G	0.25204	-0.048536	0.002343	6.50E-99	-0.046146	0.004003	1.05E-30	-0.049843	0.002934	1.10E-64	2.95E-92	0.45629	
11	BUD13 *	rs1787691	116,697,997	A	G	0.442317	-0.042988	0.002032	2.20E-104	-0.041747	0.003461	1.86E-33	-0.0439	0.002549	1.98E-66	9.87E-97	0.616541	
11	BUD13 *	rs947986	116,698,488	A	G	0.250751	-0.048508	0.002347	1.30E-98	-0.046276	0.00401	9.12E-31	-0.049743	0.00294	3.66E-64	8.48E-92	0.485677	
11	BUD13 *	rs3017338	116,698,629	A	G	0.442256	-0.04233	0.002035	7.10E-101	-0.041288	0.003466	1.09E-32	-0.043017	0.002553	1.15E-63	3.28E-93	0.687946	
11	BUD13 *	rs1145191	116,700,002	G	C	0.444809	-0.042246	0.002028	3.40E-101	-0.040692	0.003453	5.15E-32	-0.043192	0.002544	1.33E-64	1.78E-93	0.560021	
11	BUD13 *	rs150808564	116,700,125	T	C	0.041694	-0.053439	0.005034	9.70E-27	-0.046626	0.008564	5.31E-08	-0.056367	0.00632	4.97E-19	1.94E-24	0.360059	
11	BUD13 *	rs1145193	116,700,226	G	A	0.446025	-0.042602	0.002027	5.00E-103	-0.041229	0.003452	7.57E-33	-0.043495	0.002543	1.57E-65	3.15E-95	0.597027	
11	BUD13 *	rs1145194	116,700,252	A	C	0.249592	-0.048825	0.002354	5.70E-99	-0.045748	0.004024	6.44E-30	-0.050576	0.002948	6.42E-66	1.05E-92	0.333151	
11	BUD13 *	rs11601168	116,700,422	A	T	0.0782	-0.047151	0.003736	1.00E-36	-0.047613	0.006412	1.17E-13	-0.048485	0.004669	3.10E-25	4.03E-36	0.912435	
11	BUD13 *	rs1145195	116,700,534	A	G	0.444967	-0.042229	0.002027	3.90E-101	-0.040459	0.003453	1.12E-31	-0.04328	0.002544	7.27E-65	2.11E-93	0.510741	
11	BUD13 *	rs11601584	116,700,568	C	T	0.348663	0.034619	0.002097	3.90E-65	0.037799	0.003577	4.56E-26	0.033083	0.002629	2.76E-36	2.27E-59	0.288034	
11	BUD13 *	rs61905066	116,700,892	G	A	0.206955	0.014072	0.002491	1.50E-08	0.006355	0.004252	0.134973	0.018366	0.003122	4.14E-09	9.99E-09	0.022802	F
11	BUD13 *	rs1892948	116,701,373	T	C	0.206218	0.014127	0.002495	1.40E-08	0.006457	0.004257	0.129364	0.018382	0.003126	4.21E-09	9.83E-09	0.023985	F
11	BUD13 *	rs1145196	116,701,489	T	C	0.445207	-0.042348	0.002028	1.10E-101	-0.040979	0.003454	1.95E-32	-0.043177	0.002544	1.49E-64	7.58E-94	0.608302	
11	BUD13 *	rs1240783	116,701,809	C	T	0.445166	-0.04235	0.002028	1.00E-101	-0.040899	0.003454	2.60E-32	-0.043223	0.002544	1.12E-64	7.62E-94	0.587971	
11	BUD13 *	rs11216100	116,701,814	G	C	0.34438	0.03543	0.002106	3.30E-67	0.039143	0.003592	1.29E-27	0.033516	0.002641	7.09E-37	1.71E-61	0.206938	
11	BUD13 *	rs879858	116,702,404	A	G	0.206078	0.014268	0.002498	1.00E-08	0.006266	0.004263	0.141639	0.018681	0.00313	2.47E-09	6.27E-09	0.018927	F
11	BUD13 *	rs947989	116,702,805	A	C	0.451764	-0.042593	0.00206	7.50E-100	-0.041705	0.003508	1.50E-32	-0.04309	0.002585	2.58E-62	9.96E-92	0.75077	
11	BUD13 *	rs882398	116,703,122	C	T	0.206833	0.01414	0.002497	1.40E-08	0.006042	0.004261	0.156158	0.018451	0.003129	3.82E-09	1.03E-08	0.018928	F
11	BUD13 *	rs77206548	116,703,747	A	G	0.086875	-0.04726	0.003582	7.50E-41	-0.042811	0.006086	2.07E-12	-0.049203	0.004501	8.70E-28	2.00E-37	0.398409	
11	BUD13 *	rs11216103	116,703,772	A	G	0.203353	0.013741	0.002515	4.20E-08	0.005452	0.00429	0.203787	0.018374	0.003152	5.73E-09	1.87E-08	0.015235	F
11	BUD13 *	rs1240782	116,703,868	A	G	0.352128	-0.029015	0.002128	9.20E-45	-0.027751	0.003629	2.15E-14	-0.029803	0.002669	6.32E-29	1.65E-40	0.648608	
11	BUD13 *	rs1240781	116,704,101	T	C	0.244663	-0.048004	0.002374	4.30E-94	-0.044882	0.004058	2.10E-28	-0.0496	0.002974	2.05E-62	1.04E-87	0.348338	
11	BUD13 *	rs1268832	116,704,513	T	G	0.30517	-0.022316	0.00221	2.60E-25	-0.019396	0.003765	2.62E-07	-0.023808	0.002772	9.30E-18	1.65E-22	0.3453	
11	BUD13 *	rs4938301	116,704,757	A	G	0.205953	0.030148	0.002497	1.20E-34	0.033582	0.004426	3.37E-15	0.028216	0.003131	2.12E-19	7.39E-32	0.310204	
11	BUD13 *	rs1263058	116,704,839	A	G	0.306974	-0.020921	0.002203	1.30E-22	-0.017865	0.003751	1.94E-06	-0.022509	0.002765	4.09E-16	4.78E-20	0.318933	
11	BUD13 *	rs76124005	116,704,898	G	T	0.087378	-0.047212	0.003573	5.10E-41	-0.043567	0.006071	7.46E-13	-0.048748	0.004489	1.93E-27	1.61E-37	0.492608	
11	BUD13 *	rs12574790	116,704,971	T	C	0.016037	-0.051192	0.008081	3.50E-11	-0.029072	0.013938	0.037024	-0.060444	0.01007	2.00E-09	1.70E-09	0.068091	
11	BUD13 *	rs74939223	116,705,164	G	A	0.087386	-0.047386	0.003574	3.00E-41	-0.044197	0.006073	3.53E-13	-0.048715	0.00449	2.14E-27	8.55E-38	0.549732	
11	BUD13 *	rs59873384	116,705,494	T	C	0.087304	-0.047353	0.003575	3.20E-41	-0.043938	0.006075	4.93E-13	-0.048794	0.004491	1.84E-27	1.03E-37	0.520374	
11	BUD13 *	rs12802944	116,705,684	C	T	0.204405	0.031761	0.002505	3.20E-38	0.034713	0.004279	5.18E-16	0.029927	0.003139	1.59E-21	9.16E-35	0.367128	
11	BUD13 *	rs1263056	116,705,699	A	G	0.343391	-0.057338	0.002148	4.60E-162	-0.05413	0.003662	2.12E-49	-0.059024	0.002693	2.13E-106	1.81E-152	0.281706	
11	BUD13 *	rs1263055	116,706,327	A	G	0.252239	-0.048448	0.002351	2.10E-97	-0.045541	0.004017	9.38E-30	-0.050091	0.002945	7.79E-65	1.84E-91	0.360991	
11	BUD13 *	rs11216105	116,706,725	A	G	0.252338	-0.048474	0.002352	1.40E-97	-0.045712	0.004019	6.02E-30	-0.050122	0.0				

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	BUD13 *	rs4938302	116,713,788	C	T	0.494431	0.03087	0.002004	1.50E-54	0.026223	0.003418	1.77E-14	0.033168	0.002513	9.88E-40	2.47E-51	0.101599	
11	BUD13 *	rs4938303	116,714,271	C	T	0.494376	0.031	0.002003	4.60E-55	0.026193	0.003415	1.81E-14	0.033413	0.002511	2.38E-40	6.14E-52	0.088559	
11	BUD13 *	rs79886324	116,714,728	A	G	0.08676	-0.048138	0.003576	2.00E-42	-0.042979	0.006079	1.61E-12	-0.050665	0.004492	1.78E-29	3.29E-39	0.309179	
11	BUD13 *	rs2000571	116,714,817	A	G	0.309528	0.07648	0.002174	5.80E-279	0.075849	0.003709	6.98E-93	0.076752	0.002724	1.37E-174	6.45E-264	0.844424	
11	BUD13 *	rs17119918	116,714,897	A	G	0.108109	-0.050076	0.00325	1.60E-54	-0.058557	0.005553	5.79E-26	-0.045482	0.004071	5.96E-29	5.59E-52	0.057582	
11	BUD13 *	rs34100096	116,714,909	A	G	0.102854	0.023918	0.003302	3.20E-14	0.026977	0.005638	1.74E-06	0.022736	0.004137	3.97E-08	2.95E-12	0.544243	
11	BUD13 *	rs117785509	116,715,515	A	G	0.086813	-0.048255	0.003577	1.20E-42	-0.043508	0.006079	8.56E-13	-0.050592	0.004492	2.20E-29	2.18E-39	0.348662	
11	BUD13 *	rs7350481	116,715,567	T	C	0.235046	0.114039	0.002363	0	0.113609	0.004032	1.29E-174	0.114831	0.002962	0	0	0.807026	
11	BUD13 *	rs7926828	116,715,707	C	T	0.31287	0.080359	0.002166	8.89999999	0.080764	0.003699	1.28E-105	0.080096	0.002714	2.79E-191	2.65E-293	0.884327	
11	BUD13 *	rs151061355	116,716,138	A	G	0.087558	-0.048498	0.003562	2.10E-43	-0.043096	0.00605	1.10E-12	-0.051206	0.004477	2.90E-30	3.71E-40	0.281223	
11	BUD13 *	rs142290703	116,716,430	A	G	0.087781	-0.048494	0.003554	1.50E-43	-0.044013	0.006036	3.18E-13	-0.050641	0.004465	3.87E-30	3.37E-40	0.377358	
11	BUD13 *	rs17119920	116,717,173	G	C	0.100811	0.022453	0.003327	1.40E-12	0.025132	0.005687	1.00E-05	0.021592	0.004165	2.22E-07	8.40E-11	0.615593	
11	BUD13 *	rs76542665	116,717,237	A	C	0.100822	0.02245	0.003326	1.40E-12	0.025137	0.005687	1.00E-05	0.021578	0.004165	2.25E-07	8.49E-11	0.613691	
11	BUD13 *	rs4938304	116,717,709	T	C	0.079032	-0.049432	0.003708	8.30E-41	-0.050973	0.006356	1.11E-15	-0.050246	0.004635	2.41E-27	3.30E-40	0.926276	
11	BUD13 *	rs79408961	116,717,877	T	C	0.054199	0.092107	0.004433	8.10E-98	0.092939	0.007566	1.20E-34	0.091364	0.005556	1.05E-60	3.29E-92	0.866665	
11	BUD13 *	rs4938305	116,717,913	T	C	0.31138	0.082515	0.002177	1.48219693	0.083222	0.00372	8.68E-111	0.082041	0.002726	7.06E-199	4.75E-306	0.797878	
11	BUD13 *	rs1262892	116,718,188	A	G	0.101132	0.022425	0.003319	1.30E-12	0.024713	0.005673	1.34E-05	0.021658	0.004156	1.91E-07	9.59E-11	0.664015	
11	BUD13 *	rs180378	116,718,193	A	G	0.312344	0.082302	0.002174	1.38338380	0.082972	0.003715	1.98E-110	0.081774	0.002723	5.29E-198	8.09E-305	0.794852	
11	BUD13 *	rs180377	116,718,411	T	C	0.312293	0.082382	0.002175	4.94065645	0.083032	0.003715	1.46E-110	0.081881	0.002724	1.74E-198	1.95E-305	0.802833	
11	BUD13 *	rs56881207	116,718,802	T	C	0.101503	0.02228	0.003311	1.50E-12	0.024203	0.005662	1.94E-05	0.021768	0.004145	1.54E-07	1.10E-10	0.728483	
11	BUD13 *	rs10892020	116,718,936	G	C	0.311179	0.082429	0.002178	2.32210853	0.083302	0.003722	7.42E-111	0.081974	0.002727	1.27E-198	1.27E-305	0.773553	
11	BUD13 *	rs12419326	116,719,152	A	G	0.101589	0.022091	0.003309	2.20E-12	0.024022	0.005658	2.21E-05	0.021591	0.004142	1.90E-07	1.54E-10	0.728874	
11	BUD13 *	rs180376	116,719,323	C	G	0.328725	-0.034774	0.002153	2.30E-60	-0.033267	0.003676	1.52E-19	-0.035395	0.002698	2.81E-39	6.94E-56	0.640739	
11	BUD13 *	rs118046012	116,719,812	A	G	0.08617	-0.049043	0.003583	7.10E-44	-0.044575	0.006078	2.32E-13	-0.051272	0.004505	5.58E-30	1.54E-40	0.376028	
11	BUD13 *	rs6589563	116,720,071	A	G	0.102721	0.021877	0.003291	3.10E-12	0.025347	0.005626	6.72E-06	0.020482	0.00412	6.78E-07	1.68E-10	0.485407	
11	BUD13 *	rs180375	116,720,324	T	C	0.328837	-0.034786	0.002152	2.00E-60	-0.033417	0.003674	9.98E-20	-0.035367	0.002697	3.08E-39	5.03E-56	0.66869	
11	BUD13 *	rs116962103	116,720,402	A	G	0.021708	-0.060662	0.006912	2.40E-18	-0.052258	0.011732	8.54E-06	-0.066039	0.00869	3.10E-14	1.41E-17	0.345187	
11	BUD13 *	rs117305246	116,720,548	A	G	0.037117	0.030678	0.005335	9.00E-09	0.036293	0.009142	7.26E-05	0.027626	0.006672	3.50E-05	7.15E-08	0.443379	
11	BUD13 *	rs12421490	116,720,725	G	T	0.101942	0.021802	0.003301	3.50E-12	0.023932	0.005644	2.26E-05	0.021191	0.004134	3.01E-07	2.45E-10	0.695208	
11	BUD13 *	rs180373	116,720,837	A	C	0.166361	-0.059389	0.002706	7.70E-112	-0.064593	0.004617	1.99E-44	-0.05706	0.003392	1.92E-63	1.15E-104	0.188533	
11	BUD13 *	rs147232672	116,721,147	A	C	0.011591	0.100011	0.00938	9.00E-27	0.095987	0.016081	2.45E-09	0.104987	0.011726	3.66E-19	7.20E-26	0.651143	
11	BUD13 *	rs180372	116,721,218	A	G	0.327948	-0.034663	0.002153	7.20E-60	-0.033314	0.003675	1.32E-19	-0.035273	0.002699	5.39E-39	1.16E-55	0.667482	
11	BUD13 *	rs180371	116,721,487	A	G	0.417373	-0.047287	0.002041	3.50E-122	-0.04512	0.003474	1.54E-38	-0.048328	0.002562	2.51E-79	1.20E-114	0.457336	
11	BUD13 *	rs143315658	116,721,532	C	T	0.086597	-0.049058	0.003573	3.70E-44	-0.045039	0.006063	1.15E-13	-0.051044	0.004493	7.05E-30	9.74E-41	0.426186	
11	BUD13 *	rs180370	116,721,649	T	C	0.327948	-0.034663	0.002153	7.20E-60	-0.033314	0.003675	1.32E-19	-0.035273	0.002699	5.39E-39	1.16E-55	0.667482	
11	BUD13 *	rs74680844	116,721,744	C	G	0.164827	-0.059942	0.002715	7.00E-113	-0.065863	0.004629	6.88E-46	-0.057058	0.003404	5.41E-63	1.13E-105	0.125465	
11	BUD13 *	rs79100692	116,722,391	A	G	0.164515	-0.06002	0.002718	5.10E-113	-0.066469	0.004635	1.34E-46	-0.056844	0.003407	1.94E-62	7.92E-106	0.094369	
11	BUD13 *	rs79826170	116,723,038	C	T	0.101881	0.021779	0.003303	3.90E-12	0.023767	0.005647	2.60E-05	0.021204	0.004136	3.00E-07	0.714211		
11	BUD13 *	rs12420920	116,723,315	A	G	0.164519	-0.060021	0.002718	4.90E-113	-0.066469	0.004635	1.34E-46	-0.056848	0.003407	1.91E-62	7.82E-106	0.094415	
11	BUD13 *	rs12421191	116,723,578	T	C	0.164519	-0.060021	0.002718	4.90E-113	-0.066469	0.004635	1.34E-46	-0.056848	0.003407	1.91E-62	7.82E-106	0.094415	
11	BUD13 *	rs75779227	116,724,640	T	C	0.101878	0.021681	0.003303	4.80E-12	0.023615	0.005647	2.93E-05	0.021137	0.004136	3.28E-07	3.40E-10	0.723279	
11	BUD13 *	rs180365	116,725,458	T	C	0.294316	-0.064884	0.002233	2.70E-191	-0.062129	0.003815	1.38E-59	-0.066276	0.002797	4.55E-124	2.93E-180	0.380757	
11	BUD13 *	rs61905078	116,725,593	C	A	0.163696	-0.059222	0.002726	8.80E-110	-0.064233	0.004655	2.86E-43	-0.056923	0.003415	2.53E-62	2.13E-102	0.205436	
11	BUD13 *	rs11216118	116,725,679	T	G	0.076683	0.120009	0.003787	4.20E-225	0.114919	0.006486	3.47E-70	0.123463	0.004736	1.00E-149	1.91E-216	0.287389	
11	BUD13 *	rs180364	116,726,036	G	A	0.255941	-0.063216	0.002322	5.50E-170	-0.06466	0.003954	4.68E-60	-0.062712	0.002914	1.11E-102	2.24E-159	0.691826	
11	BUD13 *	rs78347254	116,726,040	A	G	0.100877	0.022433	0.003323	1.40E-12	0.023541	0.005683	3.47E-05	0.022363	0.00416	7.78E-08	9.94E-11	0.867206	
11	BUD13 *	rs146714678	116,726,114	G	T	0.092445	-0.056345	0.003485	1.20E-60	-0.061324	0.005945	6.41E-25	-0.053247	0.004369	3.93E-34	4.32E-56	0.273555	
11	BUD13 *	rs75662937	116,726,178	T	C	0.034707	0.169538	0.005482	7.00E-217	0.165706	0.009395	1.44E-69	0.171757	0.006854	1.64E-138	1.25E-204	0.602876	
11	BUD13 *	rs144027752	116,726,289	A	G	0.010044	0.100184	0.010034	7.50E-24	0.107595	0.017236	4.45E-10	0.0931	0.012531	1.14E-13	3.57E-21	0.496381	
11	BUD13 *	rs180363	116,727,173	C	T	0.25436	-0.064507	0.002322	5.60E-177	-0.066649	0.003953	1.01E-63	-0.063629	0.002914	1.20E-105	5.41E-166	0.538627	
11	BUD13 *	rs78484485	116,727,349	A	G	0.252718	-0.064819	0.002326	1.00E-177	-0.06757	0.003959	2.88E-65	-0.06347	0.00292	1.09E-104	1.42E-166	0.404543	
11	BUD13 *	rs10892023	116,727,532	T	C	0.308705	0.084227	0.002183	0	0.084841	0.003728	1.34E-114	0.083909	0.002734	9.36E-207	1.00000023069254E-317	0.840231	
11	BUD13 *	rs180361	116,727,933	T	C	0.328489	-0.034512	0.002154	2.50E-59	-0.03322	0.003675	1.67E-19	-0.035108	0.002699	1.23E-38	3.32E-55	0.678832	
11	BUD13 *	rs139628269	116,727,934	A	G	0.014219	-0.046737	0.008488	1.00E-08	-0.042156	0.014344	0.003303	-0.051396	0.010695	1.57E-06	0.6056		
11	BUD13 *	rs139283556	116,728,079	T	C	0.012975	0.087542	0.008847	2.60E-23	0.103904	0.015537	2.35E-11	0.079741	0.010924	3.01E-13	2.03279	0.6056	
11	BUD13 *	rs180360	116,728,272	G	A	0.253689	-0.064743	0.002324	1.10E-177	-0.067417	0.00							

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	BUD13 *	rs1013526	116,735,178	G	A	0.099896	0.021641	0.003337	9.30E-12	0.024267	0.005704	2.12E-05	0.020705	0.00418	7.41E-07	5.50E-10	0.614559	
11	BUD13 *	rs1974718	116,736,050	G	A	0.204235	0.106542	0.002482	0	0.108348	0.004222	3.77E-145	0.106396	0.003116	1.88E-255	0	0.709924	
11	BUD13 *	rs1558860	116,736,652	A	C	0.203988	0.106932	0.002482	0	0.108706	0.004222	4.33E-146	0.106807	0.003116	2.35E-257	0	0.717472	
11	BUD13 *	rs1558861	116,736,721	C	T	0.204011	0.106781	0.002482	0	0.108849	0.004221	1.47E-146	0.106503	0.003116	5.79E-256	0	0.654795	
11	BUD13 *	rs180351	116,736,925	T	C	0.353005	-0.01447	0.002111	4.70E-12	-0.014389	0.003603	6.58E-05	-0.014554	0.002645	3.83E-08	9.16E-11	0.970397	
11	BUD13 *	rs114554198	116,736,935	T	C	0.010498	0.072555	0.009873	4.90E-14	0.070078	0.016755	2.92E-05	0.0748	0.001242	1.72E-09	2.06E-12	0.820841	
11	BUD13 *	rs77032561	116,738,180	C	T	0.100673	0.021486	0.003327	1.40E-11	0.025211	0.005687	9.43E-06	0.019895	0.004166	1.82E-06	6.03E-10	0.450872	
11	BUD13 *	rs180350	116,739,332	T	C	0.279208	-0.069664	0.002253	7.50E-216	-0.066779	0.003849	2.17E-67	-0.071624	0.002821	4.08E-142	4.66E-206	0.309912	
11	BUD13 *	rs10466588	116,739,533	G	A	0.100732	0.021417	0.003326	1.50E-11	0.025232	0.005684	9.16E-06	0.019769	0.004165	2.11E-06	4.38E-254	0.194265	
11	BUD13 *	rs61905084	116,739,578	C	T	0.340718	-0.072263	0.002128	1.10E-261	-0.076483	0.003628	1.42E-98	-0.070638	0.002668	2.20E-154	2.04E-249	0.194265	
11	BUD13 *	rs9326246	116,741,017	C	G	0.203904	0.10709	0.002485	0	0.10871	0.004227	8.94E-146	0.107195	0.003119	1.07E-258	0	0.773064	
11	BUD13 *	rs180349	116,741,111	A	T	0.2044	0.107046	0.002483	0	0.108476	0.004223	1.93E-145	0.107158	0.003117	6.55E-259	0	0.801731	
11	BUD13 *	rs17092646	116,741,248	C	G	0.100482	0.021065	0.003331	3.80E-11	0.02519	0.005692	9.75E-06	0.019209	0.004172	4.20E-06	1.39E-09	0.396681	
11	BUD13 *	rs180348	116,741,279	A	G	0.067651	-0.045568	0.004004	5.10E-30	-0.043372	0.006832	2.24E-10	-0.04731	0.005018	4.44E-21	8.81E-29	0.642251	
11	BUD13 *	rs10466533	116,741,412	G	A	0.101202	0.020682	0.003322	7.50E-11	0.024777	0.005676	1.29E-05	0.018821	0.004161	6.17E-06	2.62E-09	0.397382	
11	BUD13 *	rs1216125	116,741,558	A	G	0.259053	-0.062508	0.002287	8.00E-171	-0.067536	0.003901	4.18E-67	-0.060715	0.002866	1.59E-99	2.97E-163	0.158817	
11	BUD13 *	rs180346	116,741,943	C	A	0.278643	-0.069343	0.002249	2.00E-214	-0.066557	0.003843	3.76E-67	-0.071245	0.002817	4.27E-141	8.42E-205	0.325057	
11	BUD13 *	rs117788500	116,742,318	C	G	0.0841	-0.04886	0.003622	1.70E-42	-0.047167	0.006156	1.92E-14	-0.049457	0.004548	1.67E-27	3.80E-39	0.764836	
11	BUD13 *	rs180344	116,742,468	C	T	0.355801	-0.014557	0.002103	2.80E-12	-0.014236	0.003592	7.47E-05	-0.014899	0.002635	1.60E-08	4.41E-11	0.881595	
11	BUD13 *	rs17518841	116,744,528	A	G	0.08444	-0.048741	0.003613	1.50E-42	-0.046982	0.006139	2.06E-14	-0.049373	0.004539	1.61E-27	3.93E-39	0.754201	
11	BUD13 *	rs4983808	116,745,386	T	C	0.098139	0.020533	0.003367	1.80E-10	0.023618	0.005759	4.16E-05	0.019415	0.004215	4.16E-06	5.50E-09	0.555997	
11	BUD13 *	rs180340	116,745,686	C	T	0.357534	-0.015236	0.002102	2.30E-13	-0.015119	0.00359	2.56E-05	-0.015508	0.002634	4.04E-09	4.19E-12	0.93036	
11	BUD13 *	rs75197796	116,746,360	C	A	0.098311	0.020234	0.003364	3.20E-10	0.022907	0.005753	6.91E-05	0.019371	0.004211	4.29E-06	9.18E-09	0.620019	
11	BUD13 *	rs11216126	116,746,524	C	A	0.256185	-0.064978	0.002291	1.70E-183	-0.069303	0.003907	2.35E-70	-0.063554	0.002872	2.07E-108	2.31E-175	0.235809	
11	BUD13 *	rs180339	116,747,066	T	C	0.4409	-0.058774	0.002028	9.70E-190	-0.060534	0.00346	1.72E-68	-0.058299	0.002543	2.84E-116	2.36E-181	0.602682	
11	BUD13 *	rs45539536	116,747,179	T	C	0.084521	-0.048657	0.003612	2.10E-42	-0.046677	0.006137	2.97E-14	-0.04942	0.004538	1.39E-27	4.87E-39	0.719269	
11	BUD13	rs11556024	116,748,335	A	G	0.097253	0.020003	0.003389	5.00E-10	0.022332	0.005794	0.000117	0.019452	0.004244	4.64E-06	1.63E-08	0.688519	
11	BUD13	rs34637368	116,748,889	A	G	0.249804	-0.063956	0.002332	3.10E-172	-0.067782	0.003974	3.41E-65	-0.062508	0.002925	2.74E-101	4.15E-163	0.285117	
11	BUD13	rs77684111	116,749,413	A	G	0.097128	0.019808	0.003392	8.10E-10	0.021717	0.0058	0.000183	0.019495	0.004246	4.47E-06	2.39E-08	0.757255	
11	BUD13	rs12161219	116,749,540	A	C	0.2515	-0.065082	0.002314	1.10E-180	-0.068843	0.003941	2.88E-68	-0.063856	0.002904	3.91E-107	5.24E-172	0.308316	
11	BUD13	rs57950207	116,749,954	C	T	0.084697	-0.048705	0.00361	1.90E-42	-0.047101	0.006134	1.68E-14	-0.049251	0.004535	1.93E-27	3.86E-39	0.778128	
11	BUD13	rs2849179	116,750,080	T	C	0.353371	-0.015247	0.002104	2.10E-13	-0.015265	0.003593	2.18E-05	-0.015391	0.002636	5.41E-09	4.78E-12	0.977505	
11	BUD13	rs17440396	116,751,054	A	G	0.08343	-0.048276	0.003637	3.40E-41	-0.04691	0.006178	3.28E-14	-0.048587	0.004569	2.22E-26	8.43E-38	0.827214	
11	BUD13	rs74368849	116,751,583	A	G	0.066662	0.154432	0.004054	0	0.148172	0.006975	4.29E-100	0.158641	0.005059	8.79E-216	2.8999999999901e-312	0.224332	
11	BUD13	rs112064363	116,751,626	A	G	0.098154	0.019249	0.003374	1.90E-09	0.020577	0.005768	0.000363	0.019196	0.004225	5.62E-06	5.68E-08	0.846857	
11	BUD13	rs180329	116,752,242	A	G	0.355089	-0.01519	0.002103	2.90E-13	-0.014793	0.003592	3.86E-05	-0.015605	0.002635	3.26E-09	5.02E-12	0.855368	
11	BUD13	rs180327	116,752,943	C	T	0.305067	0.092403	0.002181	0	0.095471	0.00371	6.09E-146	0.091655	0.002737	1.01E-245	0	0.407886	
11	BUD13	rs6589564	116,753,437	C	G	0.201823	0.110152	0.002493	0	0.111895	0.004241	2.55E-153	0.110318	0.00313	5.18E-272	0	0.764814	
11	BUD13	rs180326	116,753,987	G	T	0.203657	0.10937	0.002484	0	0.111935	0.004225	1.46E-154	0.108943	0.003118	2.33E-267	0	0.56887	
11	BUD13	rs7930786	116,754,011	C	G	0.202038	0.110238	0.002494	0	0.112129	0.004241	6.04E-154	0.110346	0.003131	4.93E-272	0	0.735209	
11	BUD13	rs117728849	116,754,200	T	C	0.100348	0.021555	0.003333	1.20E-11	0.025891	0.005694	5.52E-06	0.019525	0.004175	2.96E-06	5.76E-10	0.367264	
11	BUD13	rs12421652	116,755,159	T	G	0.252849	-0.065229	0.002309	3.10E-182	-0.069068	0.003937	7.28E-69	-0.063926	0.002896	6.26E-108	2.14E-173	0.292635	
11	BUD13	rs77112220	116,755,510	T	C	0.08445	-0.048711	0.003613	1.80E-42	-0.046824	0.006139	2.51E-14	-0.049416	0.004539	1.42E-27	4.22E-39	0.734319	
11	BUD13	rs79869230	116,755,799	A	T	0.09958	0.020171	0.003354	2.90E-10	0.023417	0.005739	4.54E-05	0.01889	0.004198	6.90E-06	9.72E-09	0.524394	
11	BUD13	rs182500870	116,755,846	A	T	0.011254	0.164775	0.009527	7.90E-71	0.161228	0.016398	8.73E-23	0.169346	0.011886	5.10E-46	8.41E-66	0.688552	
11	BUD13	rs180322	116,756,019	C	T	0.357922	-0.045983	0.002089	2.00E-110	-0.047731	0.003559	5.78E-41	-0.045688	0.00262	4.55E-68	7.86E-106	0.643912	
11	BUD13	rs4983809	116,756,339	T	C	0.253068	-0.065348	0.002309	6.50E-183	-0.069002	0.003934	7.81E-69	-0.064169	0.002896	1.01E-108	3.70E-174	0.322476	
11	BUD13	rs171685786	116,756,907	C	T	0.043656	-0.054491	0.004916	7.10E-29	-0.052075	0.008343	4.47E-10	-0.055494	0.006179	2.84E-19	1.06E-26	0.741904	
11	BUD13	rs2075295	116,757,685	C	T	0.441017	-0.058745	0.002028	1.30E-189	-0.060689	0.00346	7.96E-69	-0.058158	0.002542	9.17E-116	3.54E-181	0.555586	
11	BUD13	rs17519093	116,759,189	A	G	0.084652	-0.048388	0.003609	5.10E-42	-0.047196	0.006131	1.45E-14	-0.04874	0.004533	6.27E-27	1.08E-38	0.839567	
11	BUD13	rs75955612	116,759,802	T	A	0.042431	0.093782	0.004992	7.10E-82	0.097694	0.008577	5.08E-30	0.091377	0.006234	1.32E-48	1.48E-75	0.55136	
11	BUD13	rs918143	116,759,884	T	C	0.354601	-0.014459	0.002103	3.50E-12	-0.014493	0.003592	5.51E-05	-0.014651	0.002634	2.72E-08	5.55E-11	0.971831	
11	BUD13	rs3741301	116,760,675	C	T	0.281319	-0.069256	0.002242	2.80E-215	-0.066154	0.003833	1.11E-66	-0.071474	0.002806	4.91E-143	2.86E-206	0.262719	
11	BUD13	rs3741300	116,760,974	A	G	0.357036	-0.014324	0.002099	5.60E-12	-0.014003	0.003587	9.55E-05	-0.014747	0.002629	2.07E-08	7.18E-11	0.867107	
11	BUD13	rs3825041	116,760,991	T	C	0.200343	0.110418	0.0025	0	0.112256	0.004252	1.61E-153	0.110532	0.003139	1.44E-271	0	0.744283	
11	BUD13	rs189069311	116,761,070	T	A	0.098008	0.020112	0.003381	4.80E-10	0.023447	0.005782	5.07E-05	0.018959	0.004232	7.58E-06	1.18E-08	0.531122	
11	BUD13	rs139872819																

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	BUD13	rs6589565	116,769,521	A	G	0.20142	0.111161	0.002497	0	0.112991	0.004245	5.29E-156	0.111305	0.003136	6.86E-276	0	0.749393	
11	BUD13	rs623908	116,769,652	G	A	0.303581	-0.070305	0.002185	8.10E-236	-0.073459	0.003731	3.11E-86	-0.069484	0.002737	4.07E-142	7.46E-225	0.39029	
11	BUD13	rs4938311	116,769,888	T	C	0.107569	0.021604	0.003232	2.90E-12	0.024942	0.005519	6.29E-06	0.020805	0.004049	2.84E-07	6.80E-11	0.545629	
11	BUD13	rs1263151	116,770,312	T	C	0.384682	-0.021727	0.002064	1.40E-26	-0.021872	0.003521	5.39E-10	-0.02205	0.002588	1.70E-17	7.27E-25	0.967586	
11	BUD13	rs181315084	116,770,469	C	T	0.012889	0.090921	0.008881	9.00E-25	0.108017	0.015563	4.06E-12	0.082625	0.010977	5.43E-14	1.73E-23	0.182432	
11	BUD13	rs117579298	116,771,384	G	A	0.040977	-0.03782	0.005062	2.70E-14	-0.037577	0.008636	1.37E-05	-0.037878	0.006345	2.44E-09	1.41E-12	0.977632	
11	BUD13	rs664059	116,771,421	T	C	0.493229	-0.012112	0.002011	2.60E-09	-0.011184	0.003438	0.00115	-0.01262	0.002518	5.48E-07	1.77E-08	0.736025	
11	BUD13	rs79110162	116,772,295	G	A	0.040973	-0.03779	0.005062	2.70E-14	-0.037595	0.008636	1.36E-05	-0.03781	0.006345	2.61E-09	1.49E-12	0.983947	
11	BUD13	rs656417	116,772,720	T	G	0.491433	-0.013235	0.002014	6.80E-11	-0.012009	0.003442	0.000488	-0.013977	0.002522	3.05E-08	4.85E-10	0.644736	
11	BUD13 *	rs12422067	116,773,572	G	A	0.069937	-0.053403	0.003946	2.60E-44	-0.059915	0.006726	5.51E-19	-0.050983	0.004949	7.49E-25	5.34E-41	0.284808	
11	BUD13 *	rs2041967	116,774,433	G	A	0.410447	-0.053451	0.002042	2.60E-155	-0.055367	0.003479	5.63E-57	-0.052751	0.002561	3.22E-94	7.32E-148	0.544826	
11	BUD13 *	rs7118999	116,774,559	T	C	0.385423	-0.021849	0.002062	6.70E-27	-0.02173	0.003516	6.57E-10	-0.022417	0.002585	4.53E-18	2.39E-25	0.874891	
11	BUD13 *	rs45443305	116,774,966	A	C	0.106166	0.020716	0.003246	2.30E-11	0.022898	0.00555	3.74E-05	0.020506	0.004065	4.63E-07	6.00E-10	0.728113	
11	BUD13 *	rs11216135	116,775,346	G	C	0.301197	-0.07035	0.00219	9.70E-235	-0.074355	0.003737	4.78E-88	-0.068893	0.002744	5.27E-139	1.49E-223	0.238733	
11	ZPR1 *	rs11602073	116,776,142	T	C	0.30077	-0.06964	0.00219	3.20E-230	-0.073228	0.003737	1.88E-85	-0.068404	0.002745	5.25E-137	5.71E-219	0.298097	
11	ZPR1 *	rs11216136	116,776,404	G	T	0.303284	-0.070052	0.002185	2.90E-234	-0.073263	0.00373	7.67E-86	-0.069116	0.002737	1.38E-140	6.20E-223	0.370123	
11	ZPR1 *	rs2160669	116,776,891	C	T	0.202746	0.113139	0.002489	0	0.113033	0.00423	3.32E-157	0.111585	0.003126	6.65E-279	0	0.783111	
11	ZPR1 *	rs78296522	116,778,060	A	C	0.040974	-0.03784	0.005062	2.50E-14	-0.03756	0.008636	1.38E-05	-0.037894	0.006345	2.40E-09	1.40E-12	0.97513	
11	ZPR1 *	rs964184	116,778,201	G	C	0.203203	0.11138	0.002487	0	0.113289	0.004226	2.89E-158	0.11151	0.003124	5.75E-279	0	0.734971	
11	ZPR1	rs75198889	116,779,090	A	G	0.066151	0.168349	0.004041	0	0.160924	0.006979	1.41E-117	0.172001	0.005032	5.89E-256	0	0.197935	
11	ZPR1	rs113932726	116,779,922	T	C	0.065412	0.169207	0.004064	0	0.162763	0.007006	2.57E-119	0.172349	0.005065	1.02E-253	0	0.267495	
11	ZPR1	rs11604424	116,780,399	C	T	0.35356	0.081153	0.002096	0	0.084229	0.003573	8.67E-123	0.080696	0.002628	4.73E-207	0	0.425711	
11	ZPR1	rs200405951	116,780,493	G	C	0.011093	0.151555	0.009583	8.70E-59	0.132555	0.016414	7.06E-16	0.159698	0.011986	1.84E-40	1.94E-53	0.181703	
11	ZPR1	rs1942478	116,780,747	G	T	0.302799	-0.070365	0.002185	1.00E-235	-0.074828	0.00373	1.77E-89	-0.068711	0.002738	7.11E-139	7.50E-225	0.186165	
11	ZPR1	rs9633942	116,781,154	C	T	0.025074	-0.051973	0.006451	1.70E-15	-0.041644	0.011244	0.000214	-0.058142	0.007995	3.69E-13	3.45E-15	0.231756	
11	ZPR1	rs4417316	116,781,585	T	C	0.300735	-0.070025	0.002186	3.50E-233	-0.073782	0.003731	5.71E-87	-0.068693	0.00274	1.21E-138	4.06E-222	0.271595	
11	ZPR1	rs6589566	116,781,707	G	A	0.203118	0.111405	0.002488	0	0.113155	0.004227	8.65E-158	0.111645	0.003125	1.69E-279	0	0.773918	
11	ZPR1	rs190443984	116,781,741	A	G	0.014925	-0.046627	0.008314	8.30E-09	-0.066594	0.013976	1.92E-06	-0.037532	0.010508	0.000357	1.99E-08	0.096507	
11	ZPR1	rs7483863	116,781,775	A	G	0.203118	0.111405	0.002488	0	0.113155	0.004227	8.65E-158	0.111645	0.003125	1.69E-279	0	0.773918	
11	ZPR1	rs2075290	116,782,580	C	T	0.221253	0.099984	0.002411	0	0.10044	0.004103	2.64E-132	0.10084	0.003027	3.29E-243	0	0.937447	
11	ZPR1	rs76836072	116,783,046	T	C	0.041031	-0.038082	0.005058	1.80E-14	-0.037501	0.008631	1.41E-05	-0.038273	0.006339	1.61E-09	9.68E-13	0.942555	
11	ZPR1	rs603446	116,783,719	T	C	0.279084	-0.070529	0.002235	9.00E-225	-0.067869	0.003822	1.69E-70	-0.072519	0.002797	4.31E-148	3.99E-215	0.326186	
11	ZPR1	rs74662600	116,784,243	A	G	0.105011	0.020875	0.003264	2.40E-11	0.022697	0.005582	4.84E-05	0.020927	0.004085	3.08E-07	5.16E-10	0.798056	
11	ZPR1	rs139678706	116,784,368	A	G	0.018691	-0.072632	0.007442	1.50E-22	-0.07062	0.012639	2.36E-08	-0.074785	0.009353	1.35E-15	2.17E-21	0.791093	
11	ZPR1	rs10750096	116,786,072	C	A	0.203153	0.111554	0.002488	0	0.113552	0.004228	7.74E-159	0.111646	0.003125	1.70E-279	0	0.716952	
11	ZPR1	rs3741298	116,786,845	C	T	0.362877	0.079486	0.002081	0	0.084043	0.003548	5.61E-124	0.078186	0.00261	4.15E-197	1.89000020379804e-317	0.183552	
11	ZPR1	rs3741297	116,786,951	T	C	0.065051	0.173463	0.004071	0	0.168408	0.007022	4.97E-127	0.175997	0.005074	1.44E-263	0	0.381037	
11	ZPR1	rs2075294	116,787,406	T	G	0.116451	0.017959	0.003118	1.70E-09	0.022519	0.005334	2.45E-05	0.016346	0.003902	2.84E-05	2.09E-08	0.350327	
11	APOA5	rs33984246	116,789,734	G	A	0.117192	0.018104	0.003109	1.30E-09	0.023679	0.005322	8.72E-06	0.015869	0.003891	4.58E-05	1.23E-08	0.236133	
11	APOA5	rs2266788	116,789,970	G	A	0.20309	0.111804	0.002489	0	0.113642	0.004229	5.84E-159	0.111978	0.003126	7.29E-281	0	0.75172	
11	APOA5	rs34089864	116,790,052	A	G	0.117187	0.018145	0.003109	1.20E-09	0.023722	0.005322	8.41E-06	0.0159	0.003891	4.43E-05	1.15E-08	0.235407	
11	APOA5	rs2075291	116,790,676	A	C	0.065115	0.174037	0.004067	0	0.169471	0.007016	7.90E-129	0.176306	0.005068	4.11E-265	0	0.429702	
11	APOA5	rs13135507	116,790,772	T	C	0.104021	0.022608	0.003287	1.30E-12	0.026042	0.005629	3.77E-06	0.021988	0.004112	9.11E-08	1.39E-11	0.560854	
11	APOA5	rs2072560	116,791,110	T	C	0.202119	0.11195	0.002497	0	0.113691	0.004245	6.41E-158	0.112167	0.003137	5.76E-280	0	0.772796	
11	APOA5	rs651821	116,791,863	C	T	0.270777	0.144797	0.002259	0	0.144692	0.003868	3.28E-306	0.145701	0.002827	0	0	0.833168	
11	APOA5 *	rs34003087	116,792,880	T	C	0.040528	-0.036267	0.005106	3.40E-13	-0.036652	0.008748	2.82E-05	-0.035993	0.006386	1.78E-08	1.95E-11	0.951449	
11	APOA5 *	rs662799	116,792,991	G	A	0.271039	0.144432	0.002257	0	0.144473	0.003863	4.71E-306	0.14531	0.002824	0	0	0.861133	
11	APOA5 *	rs17120035	116,793,135	T	C	0.081843	-0.047485	0.003676	6.60E-39	-0.047122	0.006262	5.52E-14	-0.048558	0.004611	6.67E-26	4.19E-37	0.853466	
11	APOA5 *	rs7103224	116,793,250	A	G	0.081813	-0.047508	0.003676	6.40E-39	-0.047023	0.006265	6.35E-14	-0.048646	0.004611	5.52E-26	3.98E-37	0.834724	
11	APOA5 *	rs10750097	116,793,324	G	A	0.434506	0.028127	0.002052	2.00E-43	0.029328	0.003507	6.51E-17	0.027898	0.002569	1.95E-27	1.63E-41	0.742175	
11	APOA5 *	rs1787680	116,794,060	A	T	0.265736	-0.072262	0.002313	1.90E-219	-0.070714	0.003954	1.78E-71	-0.073668	0.002896	1.11E-142	1.07E-210	0.546812	
11	APOA5 *	rs9804646	116,794,363	T	C	0.219393	-0.064245	0.002471	8.90E-154	-0.06536	0.004211	2.77E-54	-0.064155	0.003099	3.65E-95	4.01E-146	0.817693	
11	APOA5 *	rs35904674	116,795,383	T	C	0.054167	-0.042559	0.004454	6.40E-23	-0.04859	0.007589	1.58E-10	-0.040953	0.005587	2.39E-13	2.70E-21	0.417779	
11	APOA5 *	rs117730008	116,795,625	A	G	0.045823	0.035093	0.004848	6.70E-14	0.039301	0.008335	2.45E-06	0.032661	0.006051	6.92E-08	7.02E-12	0.519177	
11	APOA5 *	rs1273666	116,796,367	A	G	0.157721	0.103413	0.002787	2.00E-307	0.107395	0.004726	2.97E-114	0.102066	0.003505	2.33E-186	5.28E-297	0.365086	
11	APOA5 *	rs75919952	116,796,829	T	C	0.041463	-0.036925	0.005057	9.50E-14	-0.036508	0.008649	2.46E-05	-0.037232	0.006331	4.20E-09	4.18E-12	0.94618	
11	APOA5 *	rs35606865	116,798,127	C	T	0.053783	-0.042034	0.00447	2.80E-22	-0.04854	0.00761	1.85E						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	APOA4 *	rs80220270	116,810,245	C	A	0.05164	-0.028575	0.004547	9.20E-11	-0.024957	0.007711	0.001215	-0.030736	0.005718	7.82E-08	2.82E-09	0.54722	
11	APOA4 *	rs1263173	116,810,292	A	G	0.305405	-0.031848	0.002174	4.10E-49	-0.028864	0.003716	8.45E-15	-0.0333	0.002723	2.34E-34	2.64E-46	0.335553	
11	APOA4 *	rs1263174	116,810,527	T	G	0.309223	-0.031659	0.002172	1.00E-48	-0.02831	0.003713	2.56E-14	-0.033196	0.002719	3.06E-34	1.03E-45	0.288464	
11	APOA4 *	rs75145979	116,810,778	A	C	0.050397	-0.027418	0.004606	9.20E-10	-0.023318	0.007809	0.002838	-0.030073	0.005793	2.13E-07	1.63E-08	0.487276	
11	APOA4 *	rs6589572	116,810,847	G	A	0.305668	0.071943	0.002178	3.50E-246	0.069513	0.003712	3.34E-78	0.073193	0.002732	4.86E-158	9.63E-233	0.424487	
11	APOA4 *	rs79538491	116,811,203	G	A	0.060764	0.049382	0.004227	5.50E-33	0.046517	0.007261	1.54E-10	0.051058	0.00528	4.30E-22	6.03E-30	0.613018	
11	APOA4 *	rs7927820	116,811,440	G	A	0.304529	0.072257	0.002177	1.70E-248	0.069833	0.00371	5.72E-79	0.073479	0.00273	1.84E-159	6.30E-235	0.428646	
11	APOA4 *	rs76636922	116,812,279	A	G	0.335215	-0.03152	0.002132	2.90E-51	-0.032725	0.003638	2.49E-19	-0.031008	0.002673	4.47E-31	1.62E-47	0.703675	
11	APOA4 *	rs2727793	116,812,658	T	C	0.304171	-0.031308	0.002185	2.90E-47	-0.028991	0.003733	8.51E-15	-0.032441	0.002736	2.15E-32	2.38E-44	0.456015	
11	APOA4 *	rs75318540	116,813,146	T	C	0.219074	-0.026043	0.002447	2.50E-27	-0.032098	0.004192	2.00E-14	-0.022471	0.003061	2.20E-13	3.68E-25	0.063659	
11	APOA4 *	rs7396835	116,813,312	T	C	0.305116	0.071808	0.002172	1.30E-246	0.069511	0.003701	1.20E-78	0.072987	0.002724	4.67E-158	3.33E-233	0.449504	
11	APOA4 *	rs7396851	116,813,448	T	C	0.304777	0.072059	0.002174	6.40E-248	0.069608	0.003705	1.05E-78	0.073329	0.002726	2.88E-159	1.80E-234	0.418591	
11	APOA4 *	rs79841374	116,813,844	T	C	0.334365	-0.031757	0.002133	6.80E-52	-0.033379	0.003638	4.82E-20	-0.031012	0.002674	4.62E-31	3.29E-48	0.600134	
11	APOA4 *	rs2727791	116,813,846	G	C	0.30671	-0.032229	0.00218	3.10E-50	-0.029663	0.003723	1.69E-15	-0.033375	0.002731	2.63E-34	6.08E-47	0.42144	
11	APOA4 *	rs2849167	116,814,028	A	G	0.306606	-0.032344	0.002181	1.80E-50	-0.029839	0.003725	1.20E-15	-0.033452	0.002732	2.01E-34	3.30E-47	0.434233	
11	APOA4 *	rs2542063	116,814,051	A	G	0.307049	-0.03227	0.00218	2.70E-50	-0.029706	0.003723	1.56E-15	-0.033446	0.002731	1.91E-34	4.06E-47	0.418208	
11	APOA4 *	rs77535577	116,814,675	A	G	0.333435	-0.032148	0.002142	1.10E-52	-0.033827	0.003652	2.10E-20	-0.031457	0.002685	1.16E-31	3.67E-49	0.601058	
11	APOA4 *	rs6589573	116,815,050	C	G	0.307214	0.072697	0.002194	1.80E-247	0.071167	0.003738	9.63E-81	0.07338	0.002751	1.21E-156	6.98E-234	0.633568	
11	APOA4 *	rs7107757	116,815,572	T	C	0.356781	0.06161	0.002108	1.50E-192	0.060675	0.003588	4.19E-64	0.061982	0.002646	2.65E-121	5.33E-182	0.769384	
11	APOA4 *	rs9735326	116,818,049	C	A	0.326213	0.067975	0.002162	1.30E-222	0.067009	0.003686	8.25E-74	0.068332	0.002711	4.22E-140	1.90E-210	0.772364	
11	APOA4 *	rs184316726	116,818,292	C	A	0.047382	-0.025811	0.004739	1.50E-08	-0.019557	0.00805	0.015147	-0.029672	0.005955	6.40E-07	2.13E-07	0.312448	
11	APOA4 *	rs1263176	116,819,407	T	C	0.368407	0.059686	0.002094	1.10E-182	0.059736	0.003564	5.32E-63	0.059563	0.002628	1.27E-113	3.12E-173	0.968896	
11	APOA4 *	rs1268354	116,819,862	C	T	0.368755	0.059646	0.002094	1.20E-182	0.059742	0.003563	4.88E-63	0.059484	0.002628	2.32E-113	5.02E-173	0.953569	
11	APOA4 *	rs1263177	116,819,996	C	T	0.367218	0.059945	0.002098	9.20E-184	0.059962	0.003572	3.42E-63	0.059855	0.002632	2.20E-114	3.49E-174	0.980752	
11	APOA4 *	rs5104	116,821,618	C	T	0.31976	0.069993	0.002163	1.10E-235	0.0685	0.003687	5.36E-77	0.070743	0.002713	8.12E-150	2.50E-223	0.62409	
11	APOA4 *	rs6413456	116,821,733	A	G	0.033241	-0.070575	0.0056	1.00E-38	-0.042536	0.009547	8.48E-06	-0.068971	0.007023	3.49E-35	2.44E-38	0.000179	F
11	APOA4 *	rs5103	116,821,836	G	A	0.048866	-0.026172	0.004667	7.40E-09	-0.022774	0.007927	0.004077	-0.028834	0.005865	8.98E-07	9.10E-08	0.538846	
11	APOA4 *	rs5100	116,821,978	G	A	0.372586	0.059559	0.002091	1.10E-182	0.059033	0.003559	9.66E-62	0.059718	0.002624	1.42E-114	6.29E-173	0.876905	
11	APOA4 *	rs5096	116,822,379	G	A	0.372562	0.059535	0.002091	1.80E-182	0.059003	0.003559	1.14E-61	0.059698	0.002624	1.66E-114	8.66E-173	0.875112	
11	APOA4 *	rs2239013	116,822,637	T	C	0.040771	-0.06963	0.005088	3.80E-45	-0.051199	0.008652	3.35E-09	-0.081447	0.006389	3.48E-37	1.27E-43	0.00493	F
11	APOA4 *	rs5093	116,822,638	A	G	0.217399	-0.026595	0.002467	5.80E-28	-0.032594	0.004225	1.27E-14	-0.022974	0.003086	1.01E-13	1.10E-25	0.065977	
11	APOA4 *	rs5092	116,822,748	C	T	0.372187	0.059347	0.002093	6.50E-181	0.058788	0.003563	4.12E-61	0.059541	0.002626	9.78E-114	1.83E-171	0.865003	
11	APOA4 *	rs1268833	116,824,150	G	A	0.3724	0.059371	0.002092	2.00E-181	0.058635	0.003564	9.10E-61	0.05963	0.002624	2.83E-114	1.17E-171	0.82223	
11	APOA4 *	rs10892035	116,824,222	A	G	0.371801	0.05934	0.002093	4.80E-181	0.058542	0.003566	1.60E-60	0.059655	0.002625	2.74E-114	1.99E-171	0.801466	
11	APOA4 *	rs182352602	116,824,894	A	G	0.211429	-0.026031	0.002495	2.20E-26	-0.032445	0.004281	3.63E-14	-0.022322	0.003117	8.35E-13	2.46E-24	0.055939	
11	APOA4 *	rs7111242	116,825,064	A	G	0.320577	0.069253	0.002171	6.60E-229	0.06739	0.003705	7.08E-74	0.070242	0.002721	7.68E-147	3.04E-217	0.534964	
11	APOA4 *	rs2126311	116,825,327	G	A	0.372313	0.059597	0.002092	1.20E-182	0.059166	0.003568	1.07E-61	0.059724	0.002623	1.14E-114	5.59E-173	0.899626	
11	APOA4 *	rs2098453	116,825,964	C	T	0.371794	0.059796	0.002094	1.70E-183	0.059269	0.00357	7.72E-62	0.059928	0.002625	2.69E-115	9.55E-174	0.881619	
11	APOA4 *	rs7123326	116,825,965	A	G	0.048967	-0.026212	0.004661	6.70E-09	-0.022999	0.007934	0.003761	-0.028688	0.00585	9.56E-07	8.99E-08	0.56389	
11	APOA4 *	rs2727789	116,826,171	G	T	0.373345	0.059546	0.002093	3.80E-182	0.05917	0.003569	1.09E-61	0.059668	0.002624	2.06E-114	1.03E-172	0.910463	
11	APOA4 *	rs2849176	116,826,205	T	C	0.372385	0.05974	0.002093	3.20E-183	0.0594	0.00357	4.10E-62	0.059806	0.002625	7.13E-115	1.35E-173	0.927026	
11	APOA4 *	rs2849174	116,826,350	A	G	0.049553	-0.025748	0.004635	1.10E-08	-0.022607	0.007889	0.004175	-0.028309	0.005817	1.16E-06	1.19E-07	0.560733	
11	APOA4 *	rs2542050	116,826,401	C	A	0.371801	0.059838	0.002093	6.80E-184	0.059275	0.00357	7.43E-62	0.060001	0.002624	1.23E-115	4.21E-174	0.869778	
11	APOC3 *	rs2849173	116,826,605	G	C	0.371832	0.059787	0.002093	1.60E-183	0.059273	0.003571	7.79E-62	0.059927	0.002624	2.32E-115	8.31E-174	0.882613	
11	APOC3 *	rs2071523	116,826,628	C	T	0.371858	0.059785	0.002093	1.50E-183	0.059253	0.003571	8.54E-62	0.05993	0.002624	2.15E-115	8.45E-174	0.878567	
11	APOC3 *	rs2071522	116,826,822	T	C	0.371856	0.059741	0.002093	3.10E-183	0.059196	0.003571	1.13E-61	0.0599	0.002624	2.90E-115	1.51E-173	0.873755	
11	APOC3 *	rs2542051	116,827,022	C	A	0.372009	0.059737	0.002093	3.30E-183	0.059178	0.003571	1.27E-61	0.059899	0.002624	2.84E-115	1.66E-173	0.87067	
11	APOC3 *	rs2071521	116,827,132	G	A	0.371961	0.059769	0.002093	1.80E-183	0.059249	0.00357	8.46E-62	0.059918	0.002624	2.26E-115	8.80E-174	0.88005	
11	APOC3 *	rs7101528	116,827,949	A	G	0.049198	-0.026291	0.004652	6.00E-09	-0.023343	0.007922	0.003222	-0.028613	0.005837	9.66E-07	7.88E-08	0.592314	
11	APOC3 *	rs2727788	116,828,247	A	C	0.049766	-0.025871	0.004626	9.40E-09	-0.023162	0.007877	0.003289	-0.028159	0.005805	1.25E-06	1.03E-07	0.609644	
11	APOC3 *	rs595049	116,828,729	C	A	0.373684	0.059759	0.002086	1.90E-184	0.059205	0.003559	4.35E-62	0.060021	0.002615	1.50E-116	3.03E-175	0.853375	
11	APOC3 *	rs734104	116,830,144	C	T	0.292958	0.056551	0.002222	8.40E-147	0.056614	0.003794	2.66E-50	0.056338	0.002783	4.90E-91	4.89E-138	0.953177	
11	APOC3 *	rs5128	116,832,924	G	C	0.290699	0.057287	0.00221	2.80E-152	0.057015	0.003775	1.69E-51	0.057352	0.002769	2.87E-95	1.89E-143	0.942727	
11	APOA1 *	rs10750098	116,834,852	G	T	0.290169	0.057113	0.002217	4.30E-150	0.057496	0.003786	4.73E-52	0.056784	0.002778	7.91E-93	1.44E-141	0.879486	
11	APOA1 *	rs12718462	116,835,003	C	T	0.044319	-0.0641	0.004883	1.20E-41	-0.042818	0.008311	2.63E-07	-0.077462	0.006129	1.42E-36	3.58E-41	0.000799	F
11	APOA1 *	rs12721025	116,835,331	A	G	0.047623	-0.062235	0.004753	3.30E-41	-0.039827	0.008084	8.53E-07	-0.075315	0.005967	1.77			

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	SIK3	rs11216161	116,850,485	C	T	0.400907	-0.02002	0.002051	1.30E-22	-0.016149	0.003507	4.19E-06	-0.021454	0.002567	6.72E-17	1.68E-20	0.222153	
11	SIK3	rs10047459	116,851,110	T	C	0.400431	-0.019946	0.002048	1.80E-22	-0.016138	0.003502	4.12E-06	-0.02132	0.002564	9.77E-17	2.40E-20	0.232514	
11	SIK3	rs10047462	116,851,325	T	G	0.483333	-0.035692	0.002006	3.70E-73	-0.030372	0.003428	8.48E-19	-0.03841	0.002512	9.86E-53	1.53E-68	0.058581	
11	SIK3	rs689243	116,851,977	C	G	0.230871	-0.032403	0.002385	2.00E-42	-0.027331	0.004078	2.13E-11	-0.034711	0.002986	3.30E-31	7.87E-40	0.144248	
11	SIK3	rs139952838	116,852,044	T	C	0.028147	0.085984	0.006049	3.00E-47	0.094756	0.010213	1.83E-20	0.081307	0.007626	1.66E-26	4.22E-44	0.291357	
11	SIK3	rs888245	116,853,021	G	C	0.050178	0.052996	0.004585	3.60E-32	0.058646	0.007854	8.56E-14	0.052009	0.005736	1.29E-19	0.494967		
11	SIK3	rs888246	116,853,516	T	C	0.050163	0.053315	0.004586	1.50E-32	0.058633	0.007855	8.71E-14	0.052597	0.005736	5.01E-20	4.36E-31	0.534869	
11	SIK3	rs12099358	116,855,332	A	C	0.050316	0.052723	0.004579	5.30E-32	0.058106	0.007784	1.31E-13	0.051853	0.005728	1.49E-19	1.91E-30	0.519625	
11	SIK3	rs112618266	116,855,993	T	C	0.079106	-0.054575	0.003707	2.30E-52	-0.046398	0.006307	1.96E-13	-0.06061	0.004654	9.89E-39	2.62E-49	0.06982	
11	SIK3	rs640621	116,856,053	G	C	0.234787	-0.034203	0.002368	1.60E-47	-0.029809	0.004046	1.81E-13	-0.036235	0.002966	2.69E-34	6.21E-45	0.200161	
11	SIK3	rs78857232	116,856,749	T	C	0.050131	0.052678	0.004586	7.80E-32	0.058343	0.007853	1.14E-13	0.051718	0.005737	2.10E-19	2.34E-30	0.495774	
11	SIK3	rs1035237	116,857,134	C	G	0.48463	-0.036075	0.002014	3.70E-74	-0.030745	0.003442	4.38E-19	-0.038856	0.002522	1.58E-53	1.29E-69	0.057298	
11	SIK3	rs11216162	116,857,561	A	G	0.088874	0.023431	0.003519	3.30E-11	0.028316	0.006018	2.58E-06	0.021436	0.004406	1.16E-06	1.13E-10	0.356319	
11	SIK3	rs12225230	116,857,914	C	G	0.088856	0.023511	0.003519	2.80E-11	0.02856	0.006019	2.12E-06	0.02146	0.004405	1.13E-06	9.09E-11	0.341118	
11	SIK3	rs6589574	116,859,922	A	G	0.311738	0.04859	0.002187	1.20E-112	0.048224	0.003735	4.31E-38	0.048196	0.00274	3.33E-69	4.18E-104	0.995054	
11	SIK3	rs567312	116,860,022	A	G	0.233558	-0.034059	0.002373	5.50E-47	-0.0303	0.004052	7.86E-14	-0.035779	0.002973	2.52E-33	2.75E-42	0.275627	
11	SIK3	rs4938315	116,860,489	A	G	0.483229	-0.035864	0.002014	3.10E-73	-0.030612	0.003442	6.20E-19	-0.038597	0.002523	8.43E-53	9.63E-69	0.061311	
11	SIK3	rs2075292	116,861,796	T	G	0.482565	-0.036247	0.002017	1.00E-74	-0.030579	0.003448	7.78E-19	-0.039167	0.002525	3.35E-54	4.84E-70	0.04451	F
11	SIK3	rs117010832	116,861,803	A	G	0.138539	-0.022473	0.002934	4.70E-15	-0.032775	0.005025	7.18E-11	-0.016016	0.003669	1.29E-05	4.23E-14	0.007091	M
11	SIK3	rs484646	116,862,140	G	A	0.23489	-0.034253	0.002367	1.00E-47	-0.030069	0.004045	1.11E-13	-0.036197	0.002965	3.08E-34	4.38E-45	0.221726	
11	SIK3	rs6589575	116,862,594	T	C	0.483917	-0.036067	0.002013	4.00E-74	-0.0307	0.00344	4.80E-19	-0.038858	0.002521	1.46E-53	1.30E-69	0.055787	
11	SIK3	rs2080586	116,862,600	C	T	0.049964	0.053495	0.004593	1.00E-32	0.058705	0.007864	8.67E-14	0.052765	0.005747	4.55E-20	3.94E-31	0.541956	
11	SIK3	rs476399	116,863,012	C	T	0.234847	-0.034261	0.002367	9.90E-48	-0.029993	0.004044	1.26E-13	-0.036239	0.002965	2.57E-34	4.14E-45	0.212877	
11	SIK3	rs718847	116,863,430	T	C	0.483294	-0.03603	0.002013	4.40E-74	-0.030498	0.00344	8.05E-19	-0.038925	0.002521	1.03E-53	1.53E-69	0.048196	F
11	SIK3	rs17120099	116,864,744	C	A	0.07917	-0.054366	0.003706	5.00E-52	-0.046433	0.006304	1.84E-13	-0.060312	0.004652	2.13E-38	5.28E-49	0.076501	
11	SIK3	rs6589576	116,865,072	G	C	0.483799	-0.036099	0.002013	2.50E-74	-0.030811	0.003439	3.50E-19	-0.038856	0.002521	1.44E-53	9.40E-70	0.059212	
11	SIK3	rs573549	116,865,963	G	A	0.235447	-0.03446	0.002368	2.60E-48	-0.030319	0.004047	7.07E-14	-0.036393	0.002966	1.42E-34	1.30E-45	0.226054	
11	SIK3	rs77009426	116,867,798	T	C	0.032086	-0.034628	0.005718	1.10E-09	-0.030269	0.009713	0.00184	-0.039829	0.007185	3.03E-08	4.28E-72	0.165E-09	
11	SIK3	rs17120101	116,867,872	T	C	0.032572	-0.048072	0.005657	1.40E-18	-0.05375	0.009577	2.04E-08	-0.046439	0.00712	7.18E-11	8.38E-17	0.54009	
11	SIK3	rs11216168	116,870,837	A	G	0.050131	0.052911	0.004586	4.30E-32	0.058676	0.007854	8.31E-14	0.051886	0.005737	1.60E-19	1.31E-30	0.485076	
11	SIK3	rs533556	116,870,856	C	A	0.235769	-0.034008	0.002363	3.20E-47	-0.030204	0.004038	7.79E-14	-0.035728	0.002959	1.54E-33	1.26E-44	0.269729	
11	SIK3	rs17120111	116,873,302	T	C	0.049657	0.053945	0.004609	6.00E-33	0.05824	0.007886	1.59E-13	0.053594	0.005769	1.63E-20	2.60E-31	0.634449	
11	SIK3	rs11216169	116,873,673	C	T	0.049658	0.0534	0.004611	3.00E-32	0.057524	0.00789	3.22E-13	0.053076	0.00577	3.83E-20	1.21E-30	0.649161	
11	SIK3	rs9919599	116,874,768	G	C	0.483271	-0.035745	0.002017	2.80E-72	-0.030881	0.003445	3.34E-19	-0.038344	0.002527	5.85E-52	3.59E-68	0.080721	
11	SIK3	rs17120119	116,876,566	G	C	0.077172	-0.052772	0.003751	3.80E-48	-0.045919	0.006381	6.45E-13	-0.058229	0.00471	4.49E-35	3.66E-45	0.120625	
11	SIK3	rs77682889	116,876,596	T	C	0.030388	0.077014	0.005819	3.20E-41	0.085772	0.009848	3.23E-18	0.072136	0.007326	7.59E-23	2.99E-38	0.266589	
11	SIK3	rs12278117	116,877,453	A	G	0.077168	-0.052819	0.003751	3.20E-48	-0.04605	0.006381	5.56E-13	-0.058229	0.00471	4.49E-35	3.16E-45	0.124653	
11	SIK3	rs12279433	116,877,505	T	G	0.078525	-0.054068	0.003719	3.00E-51	-0.046951	0.006327	1.21E-13	-0.059725	0.004668	1.95E-37	3.17E-48	0.104246	
11	SIK3	rs12279464	116,877,766	T	C	0.077168	-0.052819	0.003751	3.20E-48	-0.04605	0.006381	5.56E-13	-0.058229	0.00471	4.49E-35	3.16E-45	0.124653	
11	SIK3	rs12292614	116,877,799	G	A	0.077168	-0.052819	0.003751	3.20E-48	-0.04605	0.006381	5.56E-13	-0.058229	0.00471	4.49E-35	3.16E-45	0.124653	
11	SIK3	rs12286581	116,878,028	C	T	0.077168	-0.052818	0.003751	3.20E-48	-0.046048	0.006381	5.58E-13	-0.058229	0.00471	4.49E-35	3.17E-45	0.124591	
11	SIK3	rs61907566	116,878,189	G	C	0.232396	-0.034285	0.00238	5.00E-47	-0.031016	0.004063	2.37E-14	-0.035787	0.002982	3.74E-33	1.15E-44	0.343796	
11	SIK3	rs75294669	116,878,356	A	C	0.077168	-0.052818	0.003751	3.20E-48	-0.046048	0.006381	5.58E-13	-0.058229	0.00471	4.49E-35	3.17E-45	0.124591	
11	SIK3	rs76523703	116,878,793	G	T	0.049702	0.05291	0.004609	9.80E-32	0.057443	0.007884	3.33E-13	0.052312	0.005769	1.28E-19	4.13E-30	0.599424	
11	SIK3	rs11216172	116,879,162	A	G	0.360064	-0.018413	0.002099	9.90E-18	-0.016019	0.003581	7.81E-06	-0.018784	0.002632	9.89E-13	3.91E-16	0.533782	
11	SIK3	rs6589577	116,879,261	T	C	0.483247	-0.035836	0.002018	1.40E-72	-0.031091	0.003446	1.95E-19	-0.038377	0.002528	5.12E-52	1.85E-68	0.088216	
11	SIK3	rs543819	116,879,357	G	A	0.083267	-0.054403	0.003629	2.00E-54	-0.047465	0.006177	1.62E-14	-0.060232	0.004554	6.72E-40	1.54E-51	0.096195	
11	SIK3	rs7396061	116,880,158	C	A	0.316747	-0.032643	0.002169	1.30E-50	-0.030943	0.003691	5.44E-17	-0.033146	0.002723	4.77E-34	3.70E-48	0.631071	
11	SIK3	rs74341458	116,880,833	A	G	0.04956	0.053252	0.004615	4.40E-32	0.057397	0.007894	3.72E-13	0.052916	0.005777	5.50E-20	1.99E-30	0.646918	
11	SIK3	rs482371	116,881,447	C	T	0.228907	-0.033256	0.002395	1.20E-43	-0.029836	0.004089	3.06E-13	-0.034657	0.003	7.82E-31	2.87E-41	0.341714	
11	SIK3	rs7124741	116,881,503	T	A	0.482895	-0.035836	0.002016	9.90E-73	-0.031071	0.003444	1.94E-19	-0.038391	0.002525	3.71E-52	1.34E-68	0.086472	
11	SIK3	rs12275565	116,882,836	G	A	0.082161	-0.053069	0.003653	2.70E-51	-0.046836	0.006212	4.93E-14	-0.058433	0.004586	3.83E-37	2.55E-48	0.133115	
11	SIK3	rs12416987	116,883,549	C	T	0.078562	-0.054053	0.003718	2.70E-51	-0.046872	0.006324	1.30E-13	-0.05974	0.004667	1.81E-37	3.15E-48	0.101589	
11	SIK3	rs1269329	116,884,325	C	T	0.234812	-0.033981	0.002375	2.30E-46	-0.030714	0.004056	3.84E-14	-0.035486	0.002976	9.65E-33	4.74E-44	0.342881	
11	SIK3	rs139733873	116,884,844	G	A	0.01235	0.100452	0.009079	1.60E-28	0.094289	0.015569	1.43E-09	0.105181	0.011348	2.01E-20	2.571866	0.571866	
11	SIK3	rs11827828	116,884,868	A	G	0.049707	0.05285	0.004608	1.10E-31	0.057455	0.007884	3.29E-13	0.052212	0.005768	1.49E-19			

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	SIK3	rs11820814	116,894,984	C	T	0.049547	0.053421	0.004617	2.60E-32	0.057868	0.007898	2.46E-13	0.052796	0.005779	6.85E-20	1.65E-30	0.604335	
11	SIK3	rs74881320	116,895,209	C	A	0.083827	-0.054508	0.003613	4.10E-55	-0.047409	0.006149	1.31E-14	-0.060381	0.004535	2.11E-40	3.96E-52	0.089542	
11	SIK3	rs11216178	116,895,674	T	G	0.049504	0.053382	0.004619	3.30E-32	0.057734	0.007903	2.87E-13	0.052839	0.005782	6.71E-20	1.88E-30	0.617164	
11	SIK3	rs10892044	116,896,183	C	T	0.049537	0.053451	0.004617	2.60E-32	0.057968	0.007899	2.25E-13	0.052789	0.005779	7.01E-20	1.59E-30	0.596743	
11	SIK3	rs2270392	116,896,972	C	T	0.121645	-0.044208	0.003069	2.90E-51	-0.037402	0.005215	7.72E-13	-0.05001	0.003856	2.02E-38	2.04E-48	0.051918	
11	SIK3	rs11884008	116,898,027	C	G	0.116791	-0.043482	0.003121	3.80E-48	-0.03619	0.005301	9.03E-12	-0.049363	0.003921	2.62E-36	2.89E-45	0.045746	F
11	SIK3	rs190051172	116,898,198	G	C	0.083832	-0.05448	0.003613	4.70E-55	-0.047409	0.006149	1.31E-14	-0.06033	0.004535	2.42E-40	4.56E-52	0.09079	
11	SIK3	rs609177	116,899,801	G	A	0.235379	-0.034058	0.002376	1.00E-46	-0.031447	0.004058	9.62E-15	-0.035178	0.002977	3.44E-32	4.28E-44	0.458391	
11	SIK3	rs72645460	116,900,659	A	G	0.480473	-0.03597	0.002021	6.10E-73	-0.031522	0.003452	7.12E-20	-0.038335	0.002532	9.70E-52	1.29E-68	0.111479	
11	SIK3	rs1076485	116,901,725	C	T	0.443023	-0.034656	0.00203	2.00E-66	-0.030378	0.003464	1.91E-18	-0.036666	0.002545	4.97E-47	1.64E-62	0.143451	
11	SIK3	rs17120131	116,901,770	C	T	0.084129	-0.054644	0.00361	1.50E-55	-0.047404	0.006143	1.24E-14	-0.060609	0.004531	9.11E-41	1.63E-52	0.083652	
11	SIK3	rs518181	116,902,071	A	C	0.227929	-0.033537	0.002401	3.10E-44	-0.030687	0.0041	7.53E-14	-0.03465	0.003007	1.11E-30	1.02E-41	0.435803	
11	SIK3	rs17120132	116,902,602	A	T	0.084215	-0.054621	0.003607	1.30E-55	-0.047157	0.006141	1.67E-14	-0.060706	0.004528	5.94E-41	1.42E-52	0.075739	
11	SIK3	rs11216180	116,902,662	T	A	0.049553	0.053639	0.004616	1.60E-32	0.058283	0.0079	1.68E-13	0.052913	0.005777	5.55E-20	9.19E-31	0.583258	
11	SIK3	rs17120136	116,903,045	G	T	0.082173	-0.053337	0.003653	5.90E-52	-0.046778	0.006208	5.11E-14	-0.058951	0.004589	9.80E-38	6.81E-49	0.114841	
11	SIK3	rs17120139	116,903,485	G	A	0.480128	-0.036215	0.002022	7.00E-74	-0.031453	0.003452	8.64E-20	-0.038796	0.002533	6.60E-53	1.07E-69	0.086312	
11	SIK3	rs78694306	116,903,528	T	G	0.077817	-0.053144	0.003735	2.20E-49	-0.045479	0.006357	8.76E-13	-0.059027	0.004688	2.57E-36	2.87E-46	0.086307	
11	SIK3	rs11216181	116,903,758	T	A	0.046186	0.054973	0.004786	9.70E-32	0.060888	0.008176	9.96E-14	0.053641	0.005994	3.80E-19	3.69E-30	0.474688	
11	SIK3	rs78832854	116,903,759	A	T	0.080857	-0.047844	0.003678	1.50E-41	-0.03977	0.006257	2.14E-10	-0.053662	0.004617	3.48E-31	7.97E-39	0.07406	
11	SIK3	rs115971514	116,903,783	C	G	0.077817	-0.053144	0.003735	2.20E-49	-0.045479	0.006357	8.76E-13	-0.059027	0.004688	2.57E-36	2.87E-46	0.086307	
11	SIK3	rs12280030	116,904,480	A	T	0.084	-0.05454	0.003609	2.00E-55	-0.047368	0.006143	1.31E-14	-0.060456	0.004529	1.32E-40	2.48E-52	0.086364	
11	SIK3	rs7111854	116,906,110	T	A	0.121833	-0.044267	0.003066	1.30E-51	-0.037386	0.005211	7.56E-13	-0.050124	0.003852	1.15E-38	1.14E-48	0.049357	F
11	SIK3	rs12273762	116,906,347	A	T	0.084	-0.05454	0.003609	2.00E-55	-0.047368	0.006143	1.31E-14	-0.060456	0.004529	1.32E-40	2.48E-52	0.086364	
11	SIK3	rs9651681	116,907,349	C	T	0.084213	-0.054619	0.003607	1.30E-55	-0.047153	0.006141	1.68E-14	-0.060707	0.004528	5.94E-41	1.43E-52	0.075636	
11	SIK3	rs4938317	116,907,559	C	T	0.049549	0.053663	0.004616	1.50E-32	0.058274	0.0079	1.69E-13	0.052962	0.005777	5.15E-20	8.61E-31	0.587282	
11	SIK3	rs3184536	116,908,097	G	A	0.08407	-0.054554	0.00361	2.40E-55	-0.047342	0.006145	1.38E-14	-0.060477	0.004531	1.35E-40	2.67E-52	0.085382	
11	SIK3	rs10790166	116,908,783	G	A	0.246185	-0.015676	0.002333	1.90E-12	-0.01109	0.003976	0.005302	-0.018331	0.002926	3.85E-10	6.15E-11	0.142451	
11	SIK3	rs75920871	116,909,379	T	A	0.049634	0.055092	0.004623	3.80E-34	0.059025	0.007921	9.59E-14	0.055257	0.005781	1.27E-21	1.26E-32	0.700858	
11	SIK3	rs11216183	116,910,829	A	C	0.075074	-0.055931	0.00379	7.20E-53	-0.048765	0.006453	4.33E-14	-0.061812	0.004757	1.43E-38	8.53E-50	0.103625	
11	SIK3	rs191330880	116,911,276	A	G	0.020925	-0.040175	0.007062	1.20E-08	-0.051007	0.012015	2.21E-05	-0.031183	0.008866	0.000439	2.51E-07	0.184294	
11	SIK3	rs7123336	116,912,103	C	T	0.162967	-0.013866	0.002713	3.40E-08	-0.007345	0.00463	0.112673	-0.018235	0.003401	8.40E-08	1.62E-07	0.058018	
11	SIK3	rs11216185	116,912,258	G	T	0.079281	-0.054206	0.003701	3.50E-52	-0.04629	0.006298	2.06E-13	-0.060298	0.004645	1.70E-38	4.71E-49	0.073436	
11	SIK3	rs983567	116,912,884	C	T	0.162954	-0.013973	0.002714	2.80E-08	-0.007529	0.004632	0.104092	-0.018307	0.003402	7.54E-08	1.37E-07	0.060751	
11	SIK3	rs7115583	116,913,660	T	G	0.117027	-0.043737	0.003119	7.30E-49	-0.036239	0.005301	8.42E-12	-0.049651	0.003917	8.93E-37	9.25E-46	0.041891	F
11	SIK3	rs11216186	116,913,976	C	T	0.098755	-0.05317	0.003355	7.00E-60	-0.046689	0.005717	3.32E-16	-0.058125	0.004208	2.35E-43	1.22E-56	0.107149	
11	SIK3	rs10892045	116,914,108	A	C	0.046234	0.05475	0.00478	1.40E-31	0.059336	0.008218	5.40E-13	0.054042	0.005967	1.43E-19	7.40E-30	0.602152	
11	SIK3	rs79711490	116,914,625	T	C	0.098755	-0.053172	0.003355	6.90E-60	-0.046689	0.005717	3.32E-16	-0.058129	0.004208	2.33E-43	1.20E-56	0.107054	
11	SIK3	rs11216187	116,916,432	T	C	0.049518	0.053515	0.004619	2.40E-32	0.057692	0.007903	3.00E-13	0.053068	0.005781	4.56E-20	6.36E-76	0.063776	
11	SIK3	rs12277181	116,916,604	A	G	0.098874	-0.053074	0.003355	1.50E-59	-0.046435	0.005714	4.66E-16	-0.05812	0.00421	2.61E-43	1.89E-56	0.099702	
11	SIK3	rs12277092	116,916,611	T	C	0.098761	-0.053175	0.003355	7.00E-60	-0.046687	0.005716	3.31E-16	-0.058129	0.004208	2.33E-43	1.20E-56	0.106972	
11	SIK3	rs7928298	116,916,811	T	A	0.073643	-0.034638	0.003881	6.90E-21	-0.036045	0.006575	4.30E-08	-0.035713	0.004884	2.74E-13	7.31E-19	0.967595	
11	SIK3	rs12418208	116,916,917	T	C	0.096076	-0.053824	0.003403	1.20E-59	-0.046415	0.005801	1.29E-15	-0.059413	0.004267	5.09E-44	1.01E-56	0.071102	
11	SIK3	rs12418209	116,916,925	T	C	0.096076	-0.053824	0.003403	1.20E-59	-0.046415	0.005801	1.29E-15	-0.059413	0.004267	5.09E-44	1.01E-56	0.071102	
11	SIK3	rs1006176	116,917,417	C	T	0.098963	-0.053142	0.003351	6.60E-60	-0.046392	0.005708	4.61E-16	-0.058194	0.004203	1.52E-43	1.09E-56	0.095923	
11	SIK3	rs76136280	116,917,775	T	C	0.049545	0.053615	0.004617	1.80E-32	0.057994	0.0079	2.21E-13	0.053092	0.005779	4.30E-20	6.16E-48	0.061486	
11	SIK3	rs1135663	116,918,121	T	C	0.085557	-0.050857	0.003616	1.30E-47	-0.04611	0.006131	5.67E-14	-0.05425	0.004549	9.32E-33	6.71E-44	0.286233	
11	SIK3	rs79530380	116,918,472	A	T	0.041004	0.061124	0.005103	3.30E-34	0.061285	0.008759	2.72E-12	0.062711	0.006376	8.43E-23	2.30E-32	0.895239	
11	SIK3	rs78692246	116,920,591	A	G	0.099548	-0.052762	0.003341	2.40E-59	-0.046373	0.005693	3.97E-16	-0.057569	0.004191	6.68E-43	4.11E-56	0.113261	
11	SIK3	rs141203891	116,921,220	C	T	0.101217	-0.077721	0.009962	5.90E-16	-0.056878	0.016919	0.000779	-0.092076	0.012518	1.98E-13	6.27E-15	0.094441	
11	SIK3	rs7934763	116,921,641	G	T	0.049868	0.052225	0.004604	4.60E-31	0.057807	0.00787	2.14E-13	0.050951	0.005765	1.03E-18	2.10E-29	0.48215	
11	SIK3	rs7948838	116,922,245	G	A	0.136934	-0.04439	0.002914	2.30E-56	-0.03829	0.004953	1.13E-14	-0.04928	0.00366	2.80E-41	4.56E-53	0.074352	
11	SIK3	rs12225187	116,922,515	A	G	0.203038	-0.029943	0.0025	4.20E-33	-0.027552	0.004272	1.16E-10	-0.03112	0.003132	3.06E-23	3.36E-31	0.500569	
11	SIK3	rs12288386	116,922,907	T	C	0.099234	-0.052671	0.003345	4.70E-59	-0.046348	0.005697	4.33E-16	-0.057457	0.004197	1.28E-42	8.51E-56	0.116412	
11	SIK3	rs10892047	116,922,977	T	C	0.099147	-0.052825	0.003348	2.50E-59	-0.046189	0.005701	5.67E-16	-0.057818	0.004201	4.74E-43	4.14E-56	0.100576	
11	SIK3	rs117287138	116,924,163	A	G	0.049773	0.052353	0.004609	4.00E-31	0.057796	0.007881	2.34E-13	0.051174	0.00577	7.79E-19	1.74E-29	0.497801	
11	SIK3	rs56314469	116,924,187	A	G	0.049773	0.052353	0.004609	4.00E-31	0.057796	0.007881	2.34E-13	0.051174					

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	SIK3	rs12418735	116,934,046	G	T	0.099345	-0.05265	0.003343	5.60E-59	-0.046422	0.005692	3.67E-16	-0.057345	0.004195	1.67E-42	9.44E-56	0.122385	
11	SIK3	rs77204473	116,934,348	G	T	0.064702	-0.050016	0.004068	3.50E-36	-0.037862	0.006926	4.69E-08	-0.057472	0.005104	2.25E-29	9.57E-35	0.02267	F
11	SIK3	rs562179	116,934,488	C	T	0.436613	-0.028154	0.002033	2.20E-44	-0.022749	0.003466	5.44E-11	-0.030881	0.002549	9.58E-34	5.94E-42	0.058761	
11	SIK3	rs79207844	116,934,725	A	G	0.064224	-0.050644	0.004082	7.60E-37	-0.03802	0.00695	4.58E-08	-0.058376	0.005122	4.67E-30	1.97E-35	0.018401	F
11	SIK3	rs12275490	116,934,980	A	G	0.064224	-0.050644	0.004082	7.60E-37	-0.03802	0.00695	4.58E-08	-0.058376	0.005122	4.67E-30	1.97E-35	0.018401	F
11	SIK3	rs144015791	116,935,158	T	G	0.049871	0.052237	0.004604	4.40E-31	0.057816	0.00787	2.12E-13	0.050966	0.005765	1.00E-18	2.03E-29	0.48259	
11	SIK3	rs2513095	116,935,553	C	T	0.471999	-0.034572	0.002021	1.60E-67	-0.029919	0.00345	4.51E-18	-0.037121	0.002532	1.29E-48	1.01E-63	0.092429	
11	SIK3	rs2513094	116,935,696	C	T	0.266294	-0.019319	0.002272	1.40E-18	-0.015238	0.003872	8.40E-05	-0.021687	0.002849	2.82E-14	1.13E-16	0.179773	
11	SIK3	rs2513093	116,935,971	G	A	0.47179	-0.034693	0.00202	7.40E-68	-0.030086	0.003449	2.86E-18	-0.037222	0.002531	6.68E-49	0.095292	0.095292	
11	SIK3	rs12273769	116,936,457	G	T	0.099344	-0.052675	0.003343	4.80E-59	-0.046445	0.005692	3.54E-16	-0.057372	0.004194	1.51E-42	8.27E-56	0.12224	
11	SIK3	rs12294657	116,936,652	C	G	0.099347	-0.052662	0.003343	5.00E-59	-0.046398	0.005692	3.78E-16	-0.057372	0.004194	1.51E-42	8.82E-56	0.12064	
11	SIK3	rs77920516	116,936,711	C	T	0.088573	0.034964	0.003551	5.40E-23	0.039599	0.006048	6.06E-11	0.031788	0.004455	1.00E-12	4.31E-21	0.298436	
11	SIK3	rs473172	116,937,254	G	A	0.471799	-0.034683	0.00202	5.10E-68	-0.030052	0.003449	3.11E-18	-0.037224	0.002531	6.63E-49	3.60E-64	0.093655	
11	SIK3	rs77136879	116,937,737	T	C	0.099362	-0.052652	0.003342	5.10E-59	-0.046284	0.005691	4.39E-16	-0.05741	0.004194	1.33E-42	9.01E-56	0.115516	
11	SIK3	rs142440762	116,938,378	A	G	0.143256	-0.021071	0.002885	4.20E-14	-0.015006	0.004922	0.002305	-0.024772	0.003617	7.74E-12	6.26E-13	0.109814	
11	SIK3	rs61907600	116,938,632	G	A	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.005764	1.05E-18	2.13E-29	0.480438	
11	SIK3	rs7480278	116,939,073	G	T	0.099367	-0.052652	0.003342	5.10E-59	-0.046236	0.00569	4.69E-16	-0.057445	0.004194	1.18E-42	8.53E-56	0.112829	
11	SIK3	rs61624438	116,939,229	A	C	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.005764	1.05E-18	2.13E-29	0.480438	
11	SIK3	rs80015203	116,940,190	G	A	0.099367	-0.052652	0.003342	5.10E-59	-0.046236	0.00569	4.69E-16	-0.057445	0.004194	1.18E-42	8.53E-56	0.112829	
11	SIK3	rs117877581	116,940,238	G	T	0.099499	-0.052794	0.003342	2.30E-59	-0.046544	0.005688	2.93E-16	-0.057516	0.004194	9.43E-43	4.29E-56	0.12056	
11	SIK3	rs116597701	116,940,771	G	C	0.09785	-0.052009	0.003367	1.30E-56	-0.044789	0.00573	5.68E-15	-0.057069	0.004227	1.71E-41	1.42E-53	0.084588	
11	SIK3	rs145705809	116,940,967	A	C	0.013056	0.122973	0.008835	6.00E-45	0.108537	0.015133	7.68E-13	0.128263	0.011051	4.14E-31	3.77E-41	0.292454	
11	SIK3	rs473188	116,941,313	G	C	0.471501	-0.034667	0.00202	5.30E-68	-0.03005	0.003448	3.10E-18	-0.037202	0.002531	7.02E-49	3.79E-64	0.094529	
11	SIK3	rs78066444	116,941,342	C	A	0.098231	-0.052266	0.003363	1.30E-57	-0.045022	0.005727	4.00E-15	-0.057496	0.00422	3.09E-42	1.84E-54	0.079516	
11	SIK3	rs17120157	116,941,912	C	T	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs75410648	116,942,722	T	C	0.099382	-0.052594	0.003342	6.50E-59	-0.046372	0.00569	3.82E-16	-0.057299	0.004194	1.87E-42	1.10E-55	0.122146	
11	SIK3	rs510988	116,943,088	T	C	0.471476	-0.034677	0.00202	4.80E-68	-0.030039	0.003448	3.18E-18	-0.037226	0.002531	6.13E-49	3.41E-64	0.092938	
11	SIK3	rs12292858	116,943,263	C	A	0.136821	-0.044485	0.002914	1.40E-56	-0.038596	0.004951	6.69E-15	-0.049224	0.00366	3.46E-41	3.38E-53	0.084312	
11	SIK3	rs10892048	116,943,880	G	A	0.201426	-0.029527	0.002509	4.90E-32	-0.027063	0.004288	2.85E-10	-0.030858	0.003143	1.00E-22	2.62E-30	0.475318	
11	SIK3	rs12421902	116,943,930	G	A	0.097567	-0.052547	0.003375	1.10E-57	-0.045971	0.005747	1.32E-15	-0.057225	0.004234	1.41E-41	2.79E-54	0.114918	
11	SIK3	rs11216193	116,944,883	T	C	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs11216194	116,945,022	C	G	0.099037	-0.052229	0.003354	1.40E-57	-0.046467	0.00571	4.25E-16	-0.056587	0.004209	3.68E-41	2.37E-54	0.153716	
11	SIK3	rs11216195	116,945,175	A	G	0.097251	-0.052838	0.003382	5.60E-58	-0.045717	0.005757	2.11E-15	-0.057995	0.004244	1.77E-42	5.64E-55	0.086039	
11	SIK3	rs11216196	116,945,176	G	T	0.097251	-0.052838	0.003382	5.60E-58	-0.045717	0.005757	2.11E-15	-0.057995	0.004244	1.77E-42	5.64E-55	0.086039	
11	SIK3	rs10892049	116,945,500	C	G	0.13681	-0.044482	0.002914	1.40E-56	-0.038617	0.004951	6.52E-15	-0.049209	0.00366	3.70E-41	3.52E-53	0.085427	
11	SIK3	rs10892050	116,945,678	A	C	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs75958227	116,945,875	A	G	0.139683	-0.021605	0.002916	3.10E-14	-0.030867	0.005001	6.93E-10	-0.015537	0.003646	2.05E-05	6.07E-13	0.013263	M
11	SIK3	rs7924318	116,945,914	G	C	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.005764	1.05E-18	2.13E-29	0.480438	
11	SIK3	rs11216197	116,946,062	G	A	0.099608	-0.052308	0.003341	2.20E-58	-0.046139	0.005691	5.41E-16	-0.057012	0.004191	4.21E-42	3.48E-55	0.123903	
11	SIK3	rs191655881	116,946,939	C	A	0.13681	-0.044482	0.002914	1.40E-56	-0.038617	0.004951	6.52E-15	-0.049209	0.00366	3.70E-41	3.52E-53	0.085427	
11	SIK3	rs111327557	116,947,068	T	C	0.049596	0.051339	0.004621	8.20E-30	0.057236	0.007889	4.17E-13	0.04952	0.005791	1.28E-17	4.88E-28	0.430463	
11	SIK3	rs146056222	116,947,627	G	A	0.13681	-0.044482	0.002914	1.40E-56	-0.038617	0.004951	6.52E-15	-0.049209	0.00366	3.70E-41	3.52E-53	0.085427	
11	SIK3	rs61907604	116,947,691	G	A	0.187438	-0.018228	0.002567	7.90E-14	-0.011809	0.004382	0.007052	-0.022345	0.003217	3.91E-12	8.85E-13	0.052597	
11	SIK3	rs112704540	116,947,811	G	A	0.187175	-0.018257	0.002568	7.00E-14	-0.012039	0.004382	0.006019	-0.022294	0.003218	4.43E-12	8.66E-13	0.05927	
11	SIK3	rs146503809	116,948,352	G	A	0.027303	0.073468	0.006146	1.00E-33	0.082064	0.010419	3.52E-15	0.068804	0.00773	5.89E-19	2.12E-31	0.3067	
11	SIK3	rs4316540	116,948,525	T	C	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.005764	1.05E-18	2.13E-29	0.480438	
11	SIK3	rs12293755	116,948,548	T	A	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs1241658	116,948,901	A	G	0.470865	-0.034031	0.002021	1.90E-65	-0.029314	0.00345	2.07E-17	-0.036601	0.002533	2.71E-47	9.43E-62	0.088655	
11	SIK3	rs6589580	116,949,157	A	G	0.187175	-0.018257	0.002568	7.00E-14	-0.012039	0.004382	0.006019	-0.022294	0.003218	4.43E-12	8.66E-13	0.05927	
11	SIK3	rs12419047	116,949,190	A	G	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs12421834	116,949,307	C	A	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs61907605	116,949,355	A	T	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.005764	1.05E-18	2.13E-29	0.480438	
11	SIK3	rs12420518	116,949,372	C	T	0.13681	-0.044482	0.002914	1.40E-56	-0.038617	0.004951	6.52E-15	-0.049209	0.00366	3.70E-41	3.52E-53	0.085427	
11	SIK3	rs12419437	116,949,974	A	G	0.099365	-0.052654	0.003342	5.10E-59	-0.046259	0.00569	4.54E-16	-0.057437	0.004194	1.21E-42	8.46E-56	0.11382	
11	SIK3	rs1473324	116,951,202	G	T	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.005764	1.05E-18	2.13E-29	0.480438	
11	SIK3	rs1473325	116,951,318	T	C	0.049874	0.052211	0.004604	4.70E-31	0.057816	0.00787	2.12E-13	0.050932	0.00				

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
11	SIK3	rs193291566	116,957,830	G	T	0.010257	-0.078839	0.009939	2.30E-16	-0.057098	0.016861	0.000712	-0.093614	0.012498	7.16E-14	2.12E-15	0.081882	
11	SIK3	rs878692	116,958,223	A	C	0.099292	-0.052589	0.003346	9.80E-59	-0.045849	0.005697	8.84E-16	-0.057536	0.004199	1.09E-42	1.47E-55	0.098664	
11	SIK3	rs6589582	116,958,484	C	A	0.204519	-0.030008	0.002493	2.40E-33	-0.027291	0.004259	1.53E-10	-0.031452	0.003122	7.66E-24	1.11E-31	0.430795	
11	SIK3	rs1240857	116,958,726	T	G	0.09928	-0.052595	0.003346	9.80E-59	-0.045853	0.005697	8.82E-16	-0.057537	0.004199	1.10E-42	1.48E-55	0.098795	
11	SIK3	rs7120706	116,959,371	C	T	0.204516	-0.030002	0.002493	2.50E-33	-0.027291	0.004259	1.53E-10	-0.031443	0.003122	7.87E-24	1.14E-31	0.43177	
11	SIK3	rs7120963	116,959,545	C	T	0.204516	-0.030002	0.002493	2.50E-33	-0.027291	0.004259	1.53E-10	-0.031443	0.003122	7.87E-24	1.14E-31	0.43177	
11	SIK3	rs11216199	116,960,300	T	C	0.099244	-0.05253	0.003347	1.40E-58	-0.045725	0.005699	1.08E-15	-0.057505	0.0042	1.25E-42	2.05E-55	0.096135	
11	SIK3	rs11216200	116,961,127	T	C	0.136764	-0.044458	0.002916	1.80E-56	-0.0384	0.004956	9.73E-15	-0.049261	0.003662	3.30E-41	4.66E-53	0.077979	
11	SIK3	rs7112967	116,961,196	T	C	0.049881	0.052158	0.004603	5.30E-31	0.057836	0.007869	2.07E-13	0.0508	0.005764	1.29E-18	2.53E-29	0.470721	
11	SIK3	rs10892051	116,962,002	A	C	0.099232	-0.052601	0.003347	9.70E-59	-0.045804	0.005699	9.67E-16	-0.057562	0.0042	1.05E-42	1.55E-55	0.096765	
11	SIK3	rs117157737	116,962,297	T	G	0.017142	-0.060706	0.007763	1.40E-15	-0.066913	0.013339	5.37E-07	-0.055805	0.009694	8.80E-09	2.18E-13	0.500573	
11	SIK3	rs56134734	116,962,339	A	G	0.049886	0.052049	0.004603	6.90E-31	0.057817	0.007869	2.11E-13	0.050636	0.005764	1.65E-18	3.29E-29	0.46161	
11	SIK3	rs61905677	116,962,939	G	T	0.049886	0.052049	0.004603	6.90E-31	0.057817	0.007869	2.11E-13	0.050636	0.005764	1.65E-18	3.29E-29	0.46161	
11	SIK3	rs493134	116,962,963	T	C	0.471246	-0.03475	0.00202	2.40E-68	-0.030041	0.00345	3.26E-18	-0.037366	0.002531	2.80E-49	1.59E-64	0.086868	
11	SIK3	rs10502222	116,963,014	T	C	0.184921	-0.032306	0.002593	6.60E-36	-0.027994	0.004433	2.79E-10	-0.034622	0.003248	1.67E-26	4.58E-34	0.227781	
11	SIK3	rs145388534	116,963,492	T	C	0.012734	0.055926	0.008965	1.40E-10	0.055084	0.015385	0.000346	0.054363	0.011201	1.23E-06	1.26E-08	0.96974	
11	SIK3	rs10892052	116,963,597	A	G	0.184909	-0.032296	0.002594	6.80E-36	-0.027978	0.004433	2.86E-10	-0.034621	0.003248	1.68E-26	4.73E-34	0.226715	
11	SIK3	rs61905678	116,964,069	T	C	0.04989	0.051993	0.004603	7.80E-31	0.057817	0.007869	2.11E-13	0.050551	0.005763	1.87E-18	3.73E-29	0.456347	
11	SIK3	rs61905679	116,964,071	T	C	0.04989	0.051993	0.004603	7.80E-31	0.057817	0.007869	2.11E-13	0.050551	0.005763	1.87E-18	3.73E-29	0.456347	
11	SIK3	rs1815789	116,964,237	C	T	0.186956	-0.018142	0.00257	1.20E-13	-0.011925	0.004386	0.006571	-0.022152	0.003222	6.39E-12	1.34E-12	0.060226	
11	SIK3	rs1815788	116,964,255	C	T	0.186921	-0.018137	0.00257	1.20E-13	-0.011937	0.004386	0.006509	-0.022125	0.003221	6.75E-12	1.41E-12	0.061208	
11	SIK3	rs61905680	116,965,315	A	G	0.04989	0.051993	0.004603	7.80E-31	0.057817	0.007869	2.11E-13	0.050551	0.005763	1.87E-18	3.73E-29	0.456347	
11	SIK3	rs76930628	116,965,385	T	A	0.020545	-0.051917	0.007092	1.90E-13	-0.050972	0.011999	2.18E-05	-0.054159	0.008931	1.37E-09	1.25E-12	0.831255	
11	SIK3	rs61905681	116,965,493	C	A	0.04989	0.051993	0.004603	7.80E-31	0.057817	0.007869	2.11E-13	0.050551	0.005763	1.87E-18	3.73E-29	0.456347	
11	SIK3	rs21513097	116,965,496	G	A	0.265664	-0.019571	0.002275	4.80E-19	-0.015584	0.003876	5.87E-05	-0.021897	0.002854	1.76E-14	5.07E-17	0.189618	
11	SIK3	rs77320801	116,965,633	T	C	0.049883	0.052054	0.004603	7.00E-31	0.057817	0.007869	2.11E-13	0.050633	0.005764	1.66E-18	3.31E-29	0.461468	
11	SIK3	rs78044162	116,966,373	T	C	0.136651	-0.044394	0.002917	3.30E-56	-0.038465	0.004958	9.02E-15	-0.049118	0.003664	6.25E-41	8.16E-53	0.084012	
11	SIK3	rs971422	116,966,657	C	T	0.136128	-0.044305	0.002924	5.70E-56	-0.038658	0.004967	7.46E-15	-0.048853	0.003673	2.56E-40	2.76E-52	0.098904	
11	SIK3	rs1241655	116,967,092	T	G	0.26627	-0.019272	0.002274	1.50E-18	-0.015164	0.003875	9.20E-05	-0.021654	0.002852	3.31E-14	1.45E-16	0.177396	
11	SIK3	rs12281729	116,967,414	C	A	0.09925	-0.052567	0.003348	1.20E-58	-0.045819	0.0057	9.52E-16	-0.057524	0.004201	1.24E-42	1.80E-55	0.09832	
11	SIK3	rs7941927	116,968,188	G	A	0.187004	-0.018109	0.00257	1.10E-13	-0.011852	0.004387	0.006911	-0.022171	0.003221	6.09E-12	1.34E-12	0.057962	
11	SIK3	rs149144614	116,968,288	A	G	0.044994	0.05395	0.004851	5.20E-30	0.060012	0.008294	4.82E-13	0.052238	0.006075	8.47E-18	3.75E-28	0.449562	
11	SIK3	rs12417152	116,968,577	C	G	0.099068	-0.052647	0.003352	1.10E-58	-0.046083	0.005706	6.98E-16	-0.0575	0.004206	1.68E-42	1.80E-55	0.107248	
11	SIK3	rs11823013	116,968,819	C	T	0.049878	0.052032	0.004604	7.20E-31	0.058205	0.007874	1.50E-13	0.050406	0.005763	2.34E-18	3.33E-29	0.424136	
11	SIK3	rs11216204	116,968,898	A	G	0.099049	-0.052726	0.003352	7.40E-59	-0.046166	0.005706	6.23E-16	-0.057573	0.004207	1.35E-42	1.29E-55	0.107571	
11	SIK3	rs1241657	116,969,045	T	C	0.312384	0.043217	0.002175	1.60E-90	0.043625	0.003708	6.47E-32	0.042399	0.002727	1.85E-54	2.87E-83	0.789889	
11	SIK3	rs12272305	116,969,222	A	G	0.095767	-0.052866	0.003411	2.80E-57	-0.045423	0.005805	5.33E-15	-0.058389	0.004282	2.73E-42	2.16E-54	0.07227	
11	SIK3	rs12279266	116,969,317	C	T	0.098479	-0.052358	0.003362	8.80E-58	-0.04605	0.00572	8.61E-16	-0.057152	0.004222	1.03E-41	1.34E-54	0.118358	
11	SIK3	rs59294170	116,970,730	T	A	0.049869	0.05217	0.004604	5.20E-31	0.05825	0.007874	1.44E-13	0.050596	0.005764	1.75E-18	2.40E-29	0.432774	
11	SIK3	rs12418324	116,971,960	C	C	0.099002	-0.05262	0.003352	1.30E-58	-0.046224	0.005706	5.75E-16	-0.057366	0.004207	2.72E-42	2.39E-55	0.116052	
11	SIK3	rs11216206	116,972,709	G	C	0.313021	-0.025507	0.002165	1.20E-33	-0.027704	0.003695	6.75E-14	-0.024128	0.002713	6.28E-19	4.14E-30	0.435325	
11	SIK3	rs17120197	116,974,388	C	T	0.050021	0.052217	0.004596	3.60E-31	0.057996	0.007868	1.76E-13	0.050782	0.00575	1.09E-18	1.84E-29	0.459146	
11	SIK3	rs74927399	116,975,550	C	T	0.099182	-0.052848	0.003349	3.50E-59	-0.046219	0.005701	5.46E-16	-0.057689	0.004203	7.79E-43	6.54E-56	0.105363	
11	SIK3	rs76949321	116,975,627	A	G	0.099182	-0.052848	0.003349	3.50E-59	-0.046219	0.005701	5.46E-16	-0.057689	0.004203	7.79E-43	6.54E-56	0.105363	
11	SIK3	rs11216209	116,977,470	C	T	0.099194	-0.052873	0.003349	3.00E-59	-0.046247	0.005701	5.21E-16	-0.057722	0.004203	6.94E-43	5.57E-56	0.105205	
11	SIK3	rs11216210	116,977,613	T	G	0.136911	-0.044114	0.002912	1.20E-55	-0.038179	0.004951	1.30E-14	-0.048779	0.003658	1.59E-40	2.97E-52	0.085055	
11	SIK3	rs7109876	116,977,932	A	C	0.050044	0.052215	0.004595	3.40E-31	0.057891	0.007866	1.93E-13	0.050828	0.005749	1.00E-18	1.84E-29	0.468516	
11	SIK3	rs509171	116,978,141	T	C	0.266412	-0.019118	0.002268	2.70E-18	-0.01541	0.003866	6.80E-05	-0.021293	0.002844	7.31E-14	2.37E-16	0.220269	
11	SIK3	rs11216212	116,979,635	A	T	0.099194	-0.052873	0.003349	3.00E-59	-0.046247	0.005701	5.21E-16	-0.057722	0.004203	6.94E-43	5.57E-56	0.105205	
11	SIK3	rs146178826	116,980,651	G	A	0.099194	-0.052873	0.003349	3.00E-59	-0.046247	0.005701	5.21E-16	-0.057722	0.004203	6.94E-43	5.57E-56	0.105205	
11	SIK3	rs7358350	116,980,892	C	T	0.136911	-0.044114	0.002912	1.20E-55	-0.038179	0.004951	1.30E-14	-0.048779	0.003658	1.59E-40	2.97E-52	0.085055	
11	SIK3	rs4938321	116,981,791	T	C	0.187309	-0.017942	0.002566	1.80E-13	-0.011851	0.004381	0.006845	-0.021857	0.003214	1.09E-11	2.35E-12	0.065551	
11	SIK3	rs11216215	116,981,971	A	T	0.099194	-0.052873	0.003349	3.00E-59	-0.046247	0.005701	5.21E-16	-0.057722	0.004203	6.94E-43	5.57E-56	0.105205	
11	SIK3	rs3863304	116,982,407	A	G	0.201331	-0.031038	0.002513	3.20E-35	-0.027706	0.004297	1.17E-10	-0.032751	0.003147	2.44E-25	2.80E-33	0.343487	
11	SIK3	rs3863305	116,982,408	T	C	0.201331	-0.031038	0.002513	3.20E-35	-0.027706	0.004297	1.17E-10	-0.032751	0.003147	2.44E-25	2.80E-33	0.343487	
11	SIK3	rs3863306	116,982,497	T	C	0.202624	-0.029578	0.002504	2.80E-32	-0.026184	0.004287	1.04E-09	-0.031289					

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	SIK3	rs80242245	116,991,529	G	C	0.09919	-0.05283	0.003349	3.80E-59	-0.046277	0.005701	4.99E-16	-0.05766	0.004203	8.60E-43	6.61E-56	0.108014	
11	SIK3	rs11216218	116,991,945	T	C	0.09919	-0.05283	0.003349	3.80E-59	-0.046277	0.005701	4.99E-16	-0.05766	0.004203	8.60E-43	6.61E-56	0.108014	
11	SIK3	rs11216219	116,992,039	T	C	0.09919	-0.05283	0.003349	3.80E-59	-0.046277	0.005701	4.99E-16	-0.05766	0.004203	8.60E-43	6.61E-56	0.108014	
11	SIK3	rs607273	116,992,102	A	T	0.311564	0.043694	0.002168	6.30E-93	0.043858	0.003701	2.30E-32	0.043106	0.002717	1.23E-56	6.98E-86	0.869821	
11	SIK3	rs12272973	116,992,331	C	A	0.099783	-0.053124	0.003351	9.20E-60	-0.04637	0.005704	4.53E-16	-0.058107	0.004205	2.17E-43	1.52E-56	0.097655	
11	SIK3	rs10128682	116,992,742	T	C	0.099326	-0.052966	0.003346	1.30E-59	-0.046203	0.005697	5.32E-16	-0.057921	0.004199	3.09E-43	2.54E-56	0.097765	
11	SIK3	rs6589583	116,993,050	T	C	0.266624	-0.019124	0.002266	2.50E-18	-0.015553	0.003864	5.76E-05	-0.021251	0.002841	7.80E-14	2.16E-16	0.234769	
11	SIK3	rs7130531	116,993,117	T	C	0.050073	0.052152	0.004593	4.00E-31	0.057626	0.007862	2.41E-13	0.050884	0.005747	8.99E-19	2.06E-29	0.488759	
11	SIK3	rs11216220	116,993,272	C	T	0.136909	-0.044044	0.002912	1.70E-55	-0.038177	0.00495	1.29E-14	-0.048684	0.003658	2.30E-40	4.24E-52	0.087804	
11	SIK3	rs75826529	116,994,384	A	T	0.099326	-0.052966	0.003346	1.30E-59	-0.046203	0.005697	5.32E-16	-0.057921	0.004199	3.09E-43	2.54E-56	0.097765	
11	SIK3	rs74460214	116,994,491	C	T	0.099326	-0.052966	0.003346	1.30E-59	-0.046203	0.005697	5.32E-16	-0.057921	0.004199	3.09E-43	2.54E-56	0.097765	
11	SIK3	rs79349393	116,994,651	G	A	0.099326	-0.052966	0.003346	1.30E-59	-0.046203	0.005697	5.32E-16	-0.057921	0.004199	3.09E-43	2.54E-56	0.097765	
11	SIK3	rs7931665	116,995,524	G	A	0.137027	-0.044196	0.002911	5.50E-56	-0.038206	0.004949	1.22E-14	-0.048925	0.003656	8.56E-41	1.50E-52	0.081522	
11	SIK3	rs7931770	116,995,574	T	C	0.47139	-0.034106	0.002015	3.10E-66	-0.029204	0.003443	2.31E-17	-0.036925	0.002524	2.07E-48	8.08E-63	0.07051	
11	SIK3	rs7121347	116,996,493	T	G	0.47139	-0.034106	0.002015	3.10E-66	-0.029204	0.003443	2.31E-17	-0.036925	0.002524	2.07E-48	8.08E-63	0.07051	
11	SIK3	rs11604866	116,996,798	T	C	0.099326	-0.052966	0.003346	1.30E-59	-0.046203	0.005697	5.32E-16	-0.057921	0.004199	3.09E-43	2.54E-56	0.097765	
11	SIK3	rs10892054	116,997,505	T	C	0.187344	-0.017988	0.002565	1.50E-13	-0.01198	0.00438	0.006245	-0.021854	0.003214	1.09E-11	2.17E-12	0.069161	
11	SIK3	rs10892055	116,997,655	A	G	0.187344	-0.017988	0.002565	1.50E-13	-0.01198	0.00438	0.006245	-0.021854	0.003214	1.09E-11	2.17E-12	0.069161	
11	SIK3	rs7950213	116,997,938	A	C	0.050082	0.052156	0.004593	3.90E-31	0.057626	0.007862	2.41E-13	0.050886	0.005747	8.86E-19	2.03E-29	0.488873	
11	SIK3	rs61905689	116,998,501	T	C	0.08775	0.024967	0.003537	2.30E-12	0.02905	0.006044	1.56E-06	0.02304	0.00443	2.03E-07	1.29E-11	0.422546	
11	SIK3	rs10892056	116,999,695	C	G	0.099326	-0.052966	0.003346	1.30E-59	-0.046203	0.005697	5.32E-16	-0.057921	0.004199	3.09E-43	2.54E-56	0.097765	
11	SIK3	rs10502224	116,999,764	G	A	0.137044	-0.044161	0.002912	6.90E-56	-0.038211	0.004949	1.22E-14	-0.04887	0.003657	1.07E-40	1.88E-52	0.083271	
11	SIK3	rs7930264	117,000,050	A	G	0.266695	-0.019082	0.002266	3.00E-18	-0.015378	0.003863	6.94E-05	-0.021282	0.002841	7.12E-14	2.36E-16	0.218224	
11	SIK3	rs17102233	117,000,507	G	A	0.050082	0.052156	0.004593	3.90E-31	0.057626	0.007862	2.41E-13	0.050886	0.005747	8.86E-19	2.03E-29	0.488873	
11	SIK3	rs10892057	117,001,318	C	A	0.13764	-0.044242	0.00291	3.70E-56	-0.038267	0.004947	1.08E-14	-0.048981	0.003655	6.63E-41	1.03E-52	0.081541	
11	SIK3	rs75858236	117,001,547	G	A	0.050086	0.052116	0.004593	4.40E-31	0.057465	0.007861	2.79E-13	0.050886	0.005747	8.86E-19	2.35E-29	0.499297	
11	SIK3	rs12278943	117,003,642	C	T	0.099193	-0.052852	0.003349	3.40E-59	-0.046277	0.005701	4.99E-16	-0.057695	0.004203	7.65E-43	5.88E-56	0.106945	
11	SIK3	rs7946390	117,004,436	G	A	0.137027	-0.044162	0.002911	6.50E-56	-0.038172	0.004949	1.28E-14	-0.048887	0.003656	9.80E-41	1.81E-52	0.08162	
11	SIK3	rs6589587	117,004,622	G	T	0.18736	-0.017962	0.002565	1.60E-13	-0.011987	0.004379	0.006212	-0.021823	0.003214	1.16E-11	2.30E-12	0.070207	
11	SIK3	rs11216224	117,005,208	C	T	0.13581	-0.04395	0.002925	7.00E-55	-0.037804	0.004976	3.15E-14	-0.048824	0.003672	2.63E-40	1.17E-51	0.074735	
11	SIK3	rs7114963	117,005,267	C	T	0.467103	-0.034175	0.002025	4.60E-66	-0.029776	0.003459	7.81E-18	-0.036597	0.002536	3.70E-47	4.90E-62	0.111731	
11	SIK3	rs1940625	117,005,726	G	A	0.137026	-0.044159	0.002911	6.60E-56	-0.038172	0.004949	1.28E-14	-0.048882	0.003656	9.96E-41	1.84E-52	0.081745	
11	SIK3	rs10892058	117,005,905	T	C	0.202853	-0.029308	0.002496	7.40E-32	-0.026651	0.004271	4.49E-10	-0.030694	0.003124	9.48E-23	3.85E-30	0.444837	
11	SIK3	rs10790169	117,006,443	C	A	0.471678	-0.034277	0.002014	5.80E-67	-0.029452	0.00344	1.16E-17	-0.036992	0.002523	1.31E-48	2.61E-63	0.077181	
11	SIK3	rs77250716	117,006,637	C	T	0.049578	0.052307	0.004617	5.80E-31	0.058448	0.007899	1.42E-13	0.050812	0.005779	1.56E-18	2.11E-29	0.435264	
11	SIK3	rs11216225	117,007,298	G	A	0.137026	-0.044159	0.002911	6.60E-56	-0.038172	0.004949	1.28E-14	-0.048882	0.003656	9.96E-41	1.84E-52	0.081745	
11	SIK3	rs11216226	117,007,350	G	C	0.099327	-0.052968	0.003346	1.30E-59	-0.046204	0.005697	5.31E-16	-0.057921	0.004199	3.09E-43	2.53E-56	0.097812	
11	SIK3	rs11216227	117,007,881	G	C	0.203019	-0.029417	0.002497	4.60E-32	-0.026842	0.004272	3.42E-10	-0.030744	0.003125	8.35E-23	2.60E-30	0.461041	
11	SIK3	rs12276805	117,008,043	C	T	0.097255	-0.054273	0.003385	8.40E-61	-0.046249	0.005758	1.01E-15	-0.059926	0.004249	4.01E-45	6.33E-58	0.055978	
11	SIK3	rs12271319	117,008,508	T	C	0.137029	-0.04416	0.002911	6.50E-56	-0.038172	0.004949	1.28E-14	-0.048885	0.003656	9.85E-41	1.82E-52	0.08162	
11	SIK3	rs12284696	117,008,803	G	A	0.136151	-0.044024	0.002922	3.40E-55	-0.038526	0.004966	9.02E-15	-0.048583	0.00367	5.82E-40	7.53E-52	0.103377	
11	SIK3	rs7931398	117,008,960	C	T	0.267274	-0.019114	0.002264	2.60E-18	-0.015275	0.003861	7.70E-05	-0.021391	0.002839	5.12E-14	1.88E-16	0.201887	
11	SIK3	rs117901629	117,008,963	A	G	0.099201	-0.052818	0.003349	3.90E-59	-0.04627	0.005701	5.04E-16	-0.057639	0.004203	9.31E-43	7.22E-56	0.108441	
11	SIK3	rs138181556	117,009,007	A	G	0.099197	-0.052849	0.003349	3.40E-59	-0.046248	0.005701	5.19E-16	-0.057695	0.004203	7.65E-43	6.12E-56	0.106059	
11	SIK3	rs7112937	117,009,740	C	T	0.137046	-0.044153	0.002911	6.70E-56	-0.03808	0.004948	1.47E-14	-0.048912	0.003656	8.86E-41	1.87E-52	0.078305	
11	SIK3	rs61905691	117,009,987	G	A	0.050086	0.052116	0.004593	4.40E-31	0.057465	0.007861	2.79E-13	0.050886	0.005747	8.86E-19	2.35E-29	0.499297	
11	SIK3	rs7127881	117,010,082	A	G	0.20683	-0.029425	0.002495	4.80E-32	-0.027599	0.004267	1.02E-10	-0.030503	0.003124	1.70E-22	1.62E-30	0.582989	
11	SIK3	rs58176010	117,010,731	A	G	0.019097	0.077242	0.007349	3.70E-27	0.076031	0.012693	2.16E-09	0.076936	0.009152	4.44E-17	7.28E-24	0.953878	
11	SIK3	rs10892059	117,010,929	A	G	0.203076	-0.029239	0.002494	9.30E-32	-0.026364	0.004265	6.52E-10	-0.030725	0.003123	8.14E-23	4.77E-30	0.409392	
11	SIK3	rs10892060	117,010,946	A	C	0.202724	-0.029091	0.002497	2.20E-31	-0.026268	0.004269	7.84E-10	-0.030547	0.003126	1.57E-22	1.10E-29	0.418657	
11	SIK3	rs4245168	117,011,922	A	C	0.471282	-0.034244	0.002013	6.50E-67	-0.029401	0.003437	1.26E-17	-0.037001	0.002522	1.07E-48	2.30E-63	0.074629	
11	SIK3	rs7125788	117,012,680	C	T	0.050082	0.052092	0.004593	4.70E-31	0.057465	0.007861	2.79E-13	0.050848	0.005747	9.43E-19	2.50E-29	0.496816	
11	SIK3	rs10790170	117,012,828	G	T	0.204073	-0.029795	0.002499	1.00E-32	-0.026387	0.004275	6.90E-10	-0.03167	0.003129	4.71E-24	2.99E-31	0.318614	
11	SIK3	rs61905705	117,013,060	T	A	0.050086	0.052062	0.004593	5.20E-31	0.057372	0.007861	3.03E-13	0.05085	0.005747	9.40E-19	2.70E-29	0.503038	
11	SIK3	rs61905706	117,013,061	T	G	0.050086	0.052062	0.004593	5.20E-31	0.057372	0.007861	3.03E-13	0.05085	0.005747	9.40E-19	2.70E-29	0.503038	
11	SIK3	rs374772197	117,013,968	C	T	0.049985	0.051996	0.004597	7.00E-31	0.057457	0.007873	3.04E-13	0.050					

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
11	SIK3	rs2186844	117,026,197	T	C	0.099165	-0.052788	0.003349	4.20E-59	-0.046032	0.0057	7.04E-16	-0.057713	0.004203	7.37E-43	7.95E-56	0.099075	
11	SIK3	rs10892065	117,026,308	C	T	0.203822	-0.029194	0.00249	9.80E-32	-0.026361	0.004258	6.14E-10	-0.030737	0.003117	6.58E-23	3.64E-30	0.406921	
11	SIK3	rs61905709	117,027,118	T	C	0.050085	0.052199	0.004592	3.60E-31	0.057407	0.00786	2.92E-13	0.051044	0.005745	6.80E-19	1.89E-29	0.513464	
11	SIK3	rs4936361	117,027,438	C	T	0.18157	-0.017254	0.002611	5.50E-12	-0.011215	0.004455	0.011843	-0.020975	0.003273	1.52E-10	0.077411	0.077473	
11	SIK3	rs4938235	117,027,763	A	G	0.050091	0.052278	0.004591	2.80E-31	0.057407	0.00786	2.92E-13	0.051161	0.005745	5.62E-19	1.56E-29	0.521179	
11	SIK3	rs7950364	117,028,170	G	C	0.471056	-0.034358	0.002013	2.70E-67	-0.029441	0.003438	1.17E-17	-0.037156	0.002522	4.38E-49	8.82E-64	0.070409	
11	SIK3	rs11216240	117,028,532	T	A	0.266697	-0.019182	0.002264	2.00E-18	-0.015342	0.003861	7.17E-05	-0.021411	0.002839	4.84E-14	1.66E-16	0.20537	
11	SIK3	rs11216241	117,028,533	C	A	0.266724	-0.019194	0.002264	1.80E-18	-0.015335	0.003861	7.21E-05	-0.021438	0.002839	4.47E-14	1.55E-16	0.202787	
11	SIK3	rs12289032	117,028,864	T	C	0.099174	-0.052813	0.003349	3.60E-59	-0.04603	0.0057	7.02E-16	-0.057757	0.004203	6.36E-43	6.85E-56	0.097743	
11	SIK3	rs7926104	117,029,066	A	G	0.203531	-0.029393	0.002492	4.40E-32	-0.026771	0.004264	3.53E-10	-0.030843	0.003119	5.02E-23	1.62E-30	0.440819	
11	SIK3	rs112120205	117,029,070	A	G	0.050091	0.052278	0.004591	2.80E-31	0.057407	0.00786	2.92E-13	0.051161	0.005745	5.62E-19	1.56E-29	0.521179	
11	SIK3	rs146943088	117,029,109	C	A	0.099174	-0.052813	0.003349	3.60E-59	-0.04603	0.0057	7.02E-16	-0.057757	0.004203	6.36E-43	6.85E-56	0.097743	
11	SIK3	rs11600552	117,030,231	C	T	0.26672	-0.019228	0.002264	1.60E-18	-0.015403	0.003861	6.70E-05	-0.02145	0.002839	4.34E-14	1.40E-16	0.20704	
11	SIK3	rs11216242	117,030,833	A	G	0.203542	-0.029409	0.002492	3.90E-32	-0.026781	0.004264	3.47E-10	-0.030862	0.003119	4.69E-23	1.49E-30	0.439825	
11	SIK3	rs7112191	117,031,340	A	G	0.050086	0.052223	0.004592	3.40E-31	0.057228	0.007862	3.51E-13	0.051183	0.005745	5.42E-19	1.81E-29	0.534787	
11	SIK3	rs199986368	117,031,627	C	T	0.015185	0.12726	0.00823	2.70E-55	0.112767	0.014181	1.92E-15	0.13392	0.010261	6.86E-39	1.91E-51	0.226844	
11	SIK3	rs7481286	117,031,656	T	G	0.099293	-0.052856	0.003346	1.90E-59	-0.045511	0.005694	1.39E-15	-0.058096	0.004201	1.86E-43	3.95E-56	0.075327	
11	SIK3	rs12804122	117,031,900	G	C	0.203528	-0.029169	0.002492	1.10E-31	-0.026615	0.004261	4.35E-10	-0.030579	0.00312	1.18E-22	4.66E-30	0.452908	
11	SIK3	rs4548653	117,032,600	A	G	0.18736	-0.018071	0.002564	1.10E-13	-0.012058	0.004378	0.005904	-0.021905	0.003213	9.59E-12	1.82E-12	0.069815	
11	SIK3	rs7941428	117,032,668	G	C	0.265022	-0.018245	0.002274	1.20E-16	-0.014219	0.003878	0.000247	-0.020401	0.00285	8.55E-13	9.04E-15	0.198956	
11	SIK3	rs4575311	117,033,641	A	G	0.203585	-0.029433	0.002492	3.20E-32	-0.026783	0.004263	3.45E-10	-0.030889	0.003118	4.22E-23	1.33E-30	0.437052	
11	SIK3	rs4938236	117,034,748	C	G	0.050086	0.052223	0.004592	3.40E-31	0.057228	0.007862	3.51E-13	0.051183	0.005745	5.42E-19	1.81E-29	0.534787	
11	SIK3	rs187437651	117,034,813	A	G	0.018519	0.080912	0.007494	1.00E-27	0.082464	0.012967	2.09E-10	0.079329	0.009324	1.86E-17	3.15E-25	0.844341	
11	SIK3	rs147518949	117,035,258	A	G	0.018519	0.080907	0.007494	1.00E-27	0.082447	0.012967	2.10E-10	0.079329	0.009324	1.86E-17	3.17E-25	0.845174	
11	SIK3	rs4938327	117,036,012	C	T	0.187417	-0.01806	0.002563	1.10E-13	-0.011966	0.004377	0.006279	-0.021946	0.003212	8.62E-12	1.73E-12	0.066027	
11	SIK3	rs3181	117,036,327	A	G	0.187432	-0.018036	0.002563	1.10E-13	-0.011948	0.004378	0.006365	-0.021927	0.003212	8.97E-12	1.82E-12	0.066089	
11	SIK3	rs10732856	117,036,397	C	T	0.471454	-0.034295	0.002012	3.50E-67	-0.029344	0.003436	1.41E-17	-0.037121	0.002521	4.81E-49	1.16E-63	0.068003	
11	SIK3	rs721783	117,036,733	T	C	0.187478	-0.018166	0.002563	7.70E-14	-0.012109	0.004377	0.00568	-0.022054	0.003211	6.79E-12	1.25E-12	0.06699	
11	SIK3	rs75216569	117,036,999	G	A	0.099315	-0.052818	0.003346	2.70E-59	-0.045741	0.005695	1.00E-15	-0.057917	0.0042	3.23E-43	4.98E-56	0.085292	
11	SIK3	rs7115242	117,037,567	A	G	0.312989	0.043102	0.002158	1.70E-91	0.042662	0.003681	5.06E-31	0.042859	0.002704	1.63E-56	1.98E-84	0.965602	
11	SIK3	rs7118591	117,037,741	A	C	0.187438	-0.018087	0.002563	9.80E-14	-0.011971	0.004377	0.006257	-0.021986	0.003211	7.89E-12	1.58E-12	0.065099	
11	SIK3	rs80273401	117,037,990	C	T	0.099315	-0.052818	0.003346	2.70E-59	-0.045741	0.005695	1.00E-15	-0.057917	0.0042	3.23E-43	4.98E-56	0.085292	
11	SIK3	rs61905712	117,038,577	A	G	0.05013	0.052106	0.004591	4.90E-31	0.057003	0.007861	4.30E-13	0.051085	0.005743	6.14E-19	2.50E-29	0.543279	
11	SIK3	rs61905713	117,038,713	T	C	0.049881	0.051708	0.004603	1.40E-30	0.057345	0.007877	3.47E-13	0.050296	0.00576	2.65E-18	8.59E-29	0.470093	
11	SIK3	rs147501797	117,038,982	A	G	0.034507	-0.038398	0.005502	7.10E-13	-0.025002	0.009333	0.007405	-0.046833	0.006919	1.34E-11	3.11E-12	0.060252	
11	SIK3	rs12273536	117,040,255	T	C	0.096592	-0.052722	0.003388	2.30E-57	-0.047589	0.005767	1.64E-16	-0.056684	0.004253	1.75E-40	4.36E-54	0.204309	
11	SIK3	rs12273535	117,040,296	T	C	0.096592	-0.052722	0.003388	2.30E-57	-0.047589	0.005767	1.64E-16	-0.056684	0.004253	1.75E-40	4.36E-54	0.204309	
11	SIK3	rs77999164	117,041,401	T	C	0.096603	-0.052738	0.003388	2.00E-57	-0.047671	0.005766	1.45E-16	-0.056659	0.004253	1.90E-40	4.20E-54	0.209639	
11	SIK3	rs11216244	117,042,014	T	C	0.264023	-0.018635	0.002271	2.50E-17	-0.015679	0.003873	5.22E-05	-0.020342	0.002848	9.45E-13	2.29E-15	0.331987	
11	SIK3	rs11216245	117,042,486	T	C	0.264023	-0.018635	0.002271	2.50E-17	-0.015679	0.003873	5.22E-05	-0.020342	0.002848	9.45E-13	2.29E-15	0.331987	
11	SIK3	rs80143284	117,042,854	A	C	0.096731	-0.052816	0.003386	1.00E-57	-0.047437	0.005763	1.95E-16	-0.05692	0.004249	7.07E-41	2.11E-54	0.185367	
11	SIK3	rs12279066	117,043,193	G	C	0.263875	-0.018626	0.002272	2.60E-17	-0.015642	0.003875	5.49E-05	-0.020341	0.002848	9.62E-13	2.45E-15	0.328544	
11	SIK3	rs17120241	117,044,304	C	T	0.050114	0.052112	0.004591	4.50E-31	0.0573	0.007861	3.25E-13	0.050961	0.005743	7.48E-19	2.31E-29	0.514972	
11	SIK3	rs1255583	117,044,501	G	A	0.471212	-0.034422	0.002013	1.30E-67	-0.029486	0.003439	1.07E-17	-0.037231	0.002522	2.77E-49	5.09E-64	0.069375	
11	SIK3	rs2000614	117,045,026	T	C	0.471122	-0.034422	0.002013	1.30E-67	-0.029499	0.003439	1.02E-17	-0.03723	0.002521	2.72E-49	4.77E-64	0.069832	
11	SIK3	rs2000615	117,045,103	T	C	0.471122	-0.034422	0.002013	1.30E-67	-0.029499	0.003439	1.02E-17	-0.03723	0.002521	2.72E-49	4.77E-64	0.069832	
11	SIK3	rs2000616	117,045,813	T	C	0.471119	-0.034422	0.002013	1.30E-67	-0.029499	0.003439	1.02E-17	-0.03723	0.002521	2.71E-49	4.77E-64	0.069839	
11	SIK3	rs76972960	117,045,962	C	T	0.050114	0.052112	0.004591	4.50E-31	0.0573	0.007861	3.25E-13	0.050961	0.005743	7.48E-19	2.31E-29	0.514972	
11	SIK3	rs71050100	117,046,528	C	T	0.471116	-0.034418	0.002013	1.30E-67	-0.029486	0.003439	1.05E-17	-0.03723	0.002521	2.71E-49	4.91E-64	0.06937	
11	SIK3	rs61905716	117,048,351	T	C	0.050114	0.052119	0.004591	4.40E-31	0.05732	0.007861	3.19E-13	0.050961	0.005743	7.48E-19	2.26E-29	0.51364	
11	SIK3	rs12280172	117,048,557	A	G	0.097309	-0.051814	0.003378	8.90E-56	-0.045604	0.005744	2.14E-15	-0.056423	0.004242	2.54E-40	7.97E-53	0.129741	
11	SIK3	rs112151056	117,048,652	A	G	0.050114	0.052119	0.004591	4.40E-31	0.05732	0.007861	3.19E-13	0.050961	0.005743	7.48E-19	2.26E-29	0.51364	
11	SIK3	rs61905718	117,048,961	T	C	0.050114	0.052119	0.004591	4.40E-31	0.05732	0.007861	3.19E-13	0.050961	0.005743	7.48E-19	2.26E-29	0.51364	
11	SIK3	rs75890305	117,049,253	G	A	0.096622	-0.052741	0.003388	2.00E-57	-0.047526	0.005765	1.76E-16	-0.056742	0.004253	1.44E-40	3.85E-54	0.198248	
11	SIK3	rs142341972	117,049,453	T	C	0.140369	-0.022612	0.002905	2.20E-15	-0.031544	0.004994	2.76E-10	-0.016747	0.003627	3.94E-06	5.08E-14	0.016527	M
11	SIK3	rs11826651	117,049,977	A	T	0.05012	0.052087	0.00459	4.80E-31	0.057338	0.007861	3.14E-13	0.050898	0.005742	8.12E-19	2.41E-29	0.508273	
11																		

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	SIK3	rs11216252	117,057,507	A	G	0.096614	-0.052774	0.003388	1.80E-57	-0.047529	0.005765	1.75E-16	-0.056785	0.004253	1.28E-40	3.41E-54	0.196353	
11	SIK3	rs11216253	117,057,509	C	A	0.096614	-0.052774	0.003388	1.80E-57	-0.047529	0.005765	1.75E-16	-0.056785	0.004253	1.28E-40	3.41E-54	0.196353	
11	SIK3	rs4938330	117,057,798	G	C	0.226542	-0.017797	0.002392	4.40E-14	-0.014859	0.004075	0.000268	-0.019206	0.003001	1.60E-10	1.65E-12	0.390279	
11	SIK3	rs10892068	117,057,830	T	C	0.096719	-0.052863	0.003386	8.40E-58	-0.047441	0.005763	1.94E-16	-0.056981	0.00425	5.97E-41	1.77E-54	0.182761	
11	SIK3	rs9493680	117,058,538	C	T	0.187275	-0.027572	0.002626	5.50E-26	-0.024295	0.004498	6.79E-08	-0.029456	0.003285	3.19E-19	1.59E-24	0.354071	
11	SIK3	rs11216255	117,059,279	G	A	0.264157	-0.018526	0.002272	4.00E-17	-0.015515	0.003875	6.29E-05	-0.020268	0.002848	1.15E-12	3.30E-15	0.32294	
11	SIK3	rs4938331	117,059,966	A	C	0.206085	-0.030083	0.002483	4.70E-34	-0.026291	0.004247	6.21E-10	-0.032201	0.003109	4.11E-25	2.40E-32	0.261483	
11	SIK3	rs4938332	117,060,082	G	A	0.20618	-0.030189	0.002483	2.90E-34	-0.026522	0.004247	4.39E-10	-0.032236	0.003108	3.62E-25	1.51E-32	0.27759	
11	SIK3	rs4938333	117,060,172	G	A	0.050136	0.052161	0.004589	3.80E-31	0.057599	0.007857	2.39E-13	0.050873	0.005741	8.41E-19	1.91E-29	0.48945	
11	SIK3	rs4938334	117,060,326	C	G	0.206344	-0.030169	0.002484	3.40E-34	-0.026244	0.004247	6.65E-10	-0.032352	0.003109	2.51E-25	1.57E-32	0.245896	
11	SIK3	rs61903394	117,061,182	A	G	0.050133	0.052161	0.004589	3.80E-31	0.057621	0.007858	2.35E-13	0.050873	0.005741	8.41E-19	1.88E-29	0.488041	
11	SIK3	rs11216257	117,061,845	T	C	0.372653	-0.017185	0.002081	1.00E-16	-0.014014	0.003555	8.17E-05	-0.018618	0.002607	9.57E-13	3.55E-15	0.296273	
11	SIK3	rs6589590	117,065,365	C	A	0.207079	-0.029867	0.002478	1.00E-33	-0.025735	0.004236	1.27E-09	-0.032163	0.003103	3.85E-25	4.54E-32	0.220865	
11	SIK3	rs56751865	117,066,155	T	C	0.115631	-0.046567	0.003152	1.30E-52	-0.041069	0.00536	1.92E-14	-0.050555	0.003959	2.62E-37	6.92E-49	0.154566	
11	SIK3	rs112895963	117,066,443	T	A	0.049536	0.05256	0.004618	3.40E-31	0.058547	0.007901	1.32E-13	0.051138	0.00578	9.45E-19	1.20E-29	0.449164	
11	SIK3	rs79955870	117,066,645	T	C	0.09744	-0.05316	0.003383	1.40E-58	-0.048263	0.005758	5.50E-17	-0.05685	0.004246	7.78E-41	6.64E-55	0.23003	
11	SIK3	rs11216261	117,069,494	C	T	0.096501	-0.052811	0.003391	1.70E-57	-0.04753	0.00577	1.85E-16	-0.056783	0.004256	1.46E-40	4.12E-54	0.196819	
11	SIK3	rs12280210	117,069,733	C	T	0.134307	-0.043702	0.002937	8.60E-54	-0.039106	0.004995	5.15E-15	-0.04751	0.003688	6.28E-38	4.56E-50	0.175908	
11	SIK3	rs9971421	117,070,824	T	C	0.095217	-0.052817	0.003416	7.20E-57	-0.047371	0.005816	4.00E-16	-0.05697	0.004287	2.96E-40	1.78E-53	0.184011	
11	SIK3	rs61903398	117,070,897	T	C	0.049984	0.052274	0.004597	3.50E-31	0.057669	0.007867	2.39E-13	0.050988	0.005752	8.13E-19	1.85E-29	0.493011	
11	SIK3	rs144942164	117,071,184	C	T	0.039195	0.053234	0.005198	1.10E-25	0.057001	0.008884	1.45E-10	0.052743	0.006508	5.59E-16	6.32E-24	0.699053	
11	SIK3	rs7101763	117,071,269	T	G	0.184331	-0.017316	0.002583	1.50E-12	-0.012459	0.00441	0.004742	-0.020466	0.003236	2.61E-10	3.79E-11	0.143167	
11	SIK3	rs17120280	117,071,416	A	G	0.051316	0.050733	0.004545	8.30E-30	0.055541	0.007787	1.02E-12	0.049618	0.005685	2.73E-18	2.56E-28	0.539006	
11	SIK3	rs77182215	117,071,650	A	C	0.085276	0.039752	0.003611	1.80E-28	0.045355	0.006156	1.81E-13	0.035998	0.004529	1.98E-15	3.12E-26	0.220789	
11	SIK3	rs61903399	117,071,759	T	A	0.049536	0.052447	0.004619	3.90E-31	0.058894	0.007899	9.31E-14	0.050437	0.005782	2.85E-18	2.53E-29	0.387657	
11	SIK3	rs116582417	117,072,350	A	G	0.096369	-0.052842	0.003393	1.80E-57	-0.04788	0.005776	1.19E-16	-0.056668	0.004259	2.34E-40	4.26E-54	0.220684	
11	SIK3	rs1351452	117,072,638	C	A	0.47164	-0.034355	0.002015	2.40E-67	-0.029347	0.003442	1.58E-17	-0.037243	0.002524	3.26E-49	8.85E-64	0.064299	
11	SIK3	rs7109649	117,072,828	T	C	0.263868	-0.018446	0.002274	5.10E-17	-0.015574	0.003878	5.97E-05	-0.020112	0.002851	1.80E-12	4.91E-15	0.345769	
11	SIK3	rs1531706	117,073,236	A	C	0.263868	-0.018446	0.002274	5.10E-17	-0.015574	0.003878	5.97E-05	-0.020112	0.002851	1.80E-12	4.91E-15	0.345769	
11	SIK3	rs77400241	117,073,331	T	C	0.017171	-0.058432	0.007751	1.70E-14	-0.066042	0.013374	8.04E-07	-0.05263	0.009657	5.16E-08	1.80E-12	0.416186	
11	SIK3	rs7935913	117,073,632	A	G	0.263868	-0.018446	0.002274	5.10E-17	-0.015574	0.003878	5.97E-05	-0.020112	0.002851	1.80E-12	4.91E-15	0.345769	
11	SIK3	rs7935834	117,073,721	G	C	0.263868	-0.018446	0.002274	5.10E-17	-0.015574	0.003878	5.97E-05	-0.020112	0.002851	1.80E-12	4.91E-15	0.345769	
11	SIK3	rs1531707	117,073,996	A	G	0.263865	-0.01844	0.002274	5.20E-17	-0.015574	0.003878	5.97E-05	-0.020103	0.002851	1.84E-12	5.02E-15	0.346749	
11	SIK3	rs17120293	117,074,130	C	T	0.096387	-0.052765	0.003393	2.40E-57	-0.047767	0.005774	1.39E-16	-0.056612	0.004258	2.76E-40	5.81E-54	0.217625	
11	SIK3	rs191035489	117,074,759	T	C	0.011064	0.053975	0.009633	1.80E-08	0.074855	0.016721	7.69E-06	0.044479	0.011965	0.000203	4.44E-08	0.139567	
11	SIK3	rs4620758	117,075,002	A	G	0.184156	-0.017178	0.002584	2.30E-12	-0.012487	0.004411	0.004653	-0.020226	0.003238	4.32E-10	6.11E-11	0.157253	
11	SIK3	rs59511712	117,075,046	T	C	0.087487	0.024914	0.003544	3.40E-12	0.02819	0.006056	3.29E-06	0.023423	0.004439	1.34E-07	1.77E-11	0.525575	
11	SIK3	rs12274388	117,075,522	T	C	0.261618	-0.017794	0.002286	8.80E-16	-0.015106	0.003897	0.000107	-0.019302	0.002866	1.70E-11	7.71E-14	0.385735	
11	SIK3	rs7130213	117,075,936	A	C	0.183737	-0.017344	0.002587	1.40E-12	-0.012049	0.004419	0.006412	-0.020635	0.00324	1.97E-10	3.79E-11	0.117133	
11	SIK3	rs12274725	117,076,137	T	C	0.096362	-0.052858	0.003393	1.70E-57	-0.04788	0.005776	1.19E-16	-0.056695	0.004259	2.19E-40	4.00E-54	0.219333	
11	SIK3	rs7484045	117,076,174	T	C	0.263882	-0.018476	0.002274	4.60E-17	-0.015578	0.003878	5.95E-05	-0.020149	0.002851	1.64E-12	4.45E-15	0.342185	
11	SIK3	rs11216265	117,076,464	C	T	0.096362	-0.052858	0.003393	1.70E-57	-0.04788	0.005776	1.19E-16	-0.056695	0.004259	2.19E-40	4.00E-54	0.219333	
11	SIK3	rs12418036	117,076,590	A	G	0.096362	-0.052858	0.003393	1.70E-57	-0.04788	0.005776	1.19E-16	-0.056695	0.004259	2.19E-40	4.00E-54	0.219333	
11	SIK3	rs4938335	117,076,645	C	A	0.471269	-0.034387	0.002016	2.30E-67	-0.029163	0.003442	2.53E-17	-0.037365	0.002525	1.71E-49	7.40E-64	0.054726	
11	SIK3	rs4938336	117,077,726	G	A	0.049973	0.052104	0.004597	5.60E-31	0.057451	0.007868	2.97E-13	0.050814	0.005753	1.08E-18	3.03E-29	0.495983	
11	SIK3	rs10082609	117,078,358	T	C	0.256127	-0.017498	0.002303	4.40E-15	-0.014183	0.003928	0.000307	-0.019435	0.002888	1.76E-11	2.15E-13	0.28141	
11	SIK3	rs11216266	117,079,434	C	T	0.263861	-0.018443	0.002274	5.20E-17	-0.015548	0.003878	6.15E-05	-0.020115	0.002851	1.79E-12	5.01E-15	0.342621	
11	SIK3	rs10736487	117,079,516	G	A	0.472632	-0.033946	0.002015	7.60E-66	-0.028982	0.00344	3.81E-17	-0.036796	0.002524	4.43E-48	0.067068	0.283E-62	
11	SIK3	rs7106662	117,080,669	C	T	0.263863	-0.018445	0.002274	5.10E-17	-0.015548	0.003878	6.15E-05	-0.020117	0.002851	1.78E-12	4.98E-15	0.342389	
11	SIK3	rs10892070	117,080,817	A	G	0.220221	-0.029442	0.002437	8.00E-34	-0.026332	0.004167	2.71E-10	-0.031301	0.003051	1.16E-24	3.00E-32	0.336014	
11	SIK3	rs10082561	117,080,868	C	A	0.091322	-0.051554	0.003476	2.80E-52	-0.04473	0.005921	4.39E-14	-0.056179	0.00436	5.98E-38	3.59E-49	0.119459	
11	SIK3	rs4936362	117,081,484	T	C	0.049971	0.052008	0.004598	7.20E-31	0.057314	0.007871	3.42E-13	0.05076	0.005753	1.19E-18	3.83E-29	0.501385	
11	SIK3	rs11216267	117,081,676	T	C	0.207874	-0.029143	0.002474	2.70E-32	-0.025204	0.004227	2.55E-09	-0.031338	0.003099	5.16E-24	1.17E-30	0.241815	
11	SIK3	rs11216270	117,082,928	A	C	0.096355	-0.05292	0.003394	1.30E-57	-0.04793	0.005776	1.11E-16	-0.056763	0.004259	1.78E-40	3.04E-54	0.21838	
11	SIK3	rs1871756	117,082,929	A	G	0.184285	-0.017273	0.002583	1.70E-12	-0.012458	0.00441	0.004745	-0.020408	0.003236	2.95E-10	4.28E-11	0.146133	
11	SIK3	rs10892071	117,083,849	T	C	0.263865	-0.018422	0.002274	5.60E-17	-0.015516	0.003878	6.37E-05	-0.02					

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	SIK3	rs900012	117,095,719	A	G	0.468365	-0.033813	0.00202	4.10E-65	-0.029102	0.003451	3.55E-17	-0.036548	0.002529	2.77E-47	1.64E-61	0.081847	
11	SIK3	rs1320668	117,096,950	T	C	0.473357	-0.032576	0.002018	4.30E-61	-0.027715	0.003447	9.51E-16	-0.035333	0.002528	2.39E-44	3.52E-57	0.074752	
11	SIK3	rs61903426	117,097,552	T	C	0.054274	0.053517	0.004427	2.00E-34	0.059931	0.007583	2.84E-15	0.05166	0.005538	1.15E-20	3.47E-33	0.3784	
11	SIK3	rs7128071	117,098,082	A	G	0.052806	0.052837	0.00449	1.20E-32	0.060005	0.007698	6.73E-15	0.050519	0.005614	2.42E-19	1.66E-31	0.319395	
11	SIK3 *	rs10892073	117,098,674	T	C	0.20308	-0.028729	0.002501	5.30E-31	-0.024847	0.004275	6.32E-09	-0.030893	0.003133	6.56E-23	3.53E-29	0.253892	
11	SIK3 *	rs76567973	117,100,045	G	C	0.096151	-0.052785	0.003397	3.00E-57	-0.04826	0.005786	7.80E-17	-0.056524	0.004261	4.04E-40	4.83E-54	0.250081	
11	SIK3 *	rs78135964	117,100,961	T	G	0.096183	-0.052716	0.003396	3.50E-57	-0.048329	0.005784	6.83E-17	-0.056413	0.00426	5.48E-40	5.73E-54	0.26042	
11	SIK3 *	rs148233183	117,101,511	A	G	0.09622	-0.052657	0.003395	4.40E-57	-0.048051	0.005781	9.92E-17	-0.056463	0.004259	4.57E-40	6.91E-54	0.241359	
11	SIK3 *	rs4938338	117,102,178	A	C	0.05443	0.053531	0.004419	1.80E-34	0.059818	0.007565	2.75E-15	0.051695	0.005528	9.23E-21	2.72E-33	0.385937	
11	SIK3 *	rs4936363	117,102,219	T	C	0.054431	0.053529	0.004419	1.80E-34	0.059816	0.007565	2.76E-15	0.051695	0.005528	9.22E-21	2.72E-33	0.386101	
11	SIK3 *	rs76942203	117,102,531	A	G	0.096249	-0.052706	0.003394	3.40E-57	-0.048085	0.00578	9.35E-17	-0.056534	0.004258	5.00E-40	2.39E-54	0.239214	
11	SIK3 *	rs12269901	117,103,213	C	G	0.268995	-0.016757	0.002258	9.60E-15	-0.01403	0.003851	0.000272	-0.018378	0.002831	8.74E-11	9.23E-13	0.362975	
11	SIK3 *	rs149576335	117,104,420	A	G	0.096225	-0.052713	0.003394	3.20E-57	-0.048134	0.005782	8.85E-17	-0.056534	0.004259	3.56E-40	4.82E-54	0.242076	
11	SIK3 *	rs11216275	117,104,988	G	T	0.092008	0.027571	0.003466	5.10E-15	0.03073	0.005922	2.16E-07	0.026249	0.004341	1.52E-09	1.63E-14	0.541678	
11	SIK3 *	rs142395187	117,105,293	G	A	0.09562	-0.052983	0.003405	1.40E-57	-0.048029	0.005803	1.34E-16	-0.057037	0.00427	1.19E-40	2.44E-54	0.211213	
11	SIK3 *	rs4388921	117,106,062	C	T	0.188486	-0.015471	0.002564	1.10E-10	-0.009743	0.004382	0.026231	-0.019044	0.003211	3.09E-09	1.94E-09	0.086896	
11	SIK3 *	rs145671645	117,106,195	A	G	0.029016	-0.052523	0.005983	5.20E-20	-0.056921	0.010148	2.08E-08	-0.052577	0.007524	2.89E-12	3.66E-18	0.730978	
11	SIK3 *	rs10160799	117,107,172	A	G	0.473503	-0.032182	0.00202	1.70E-59	-0.026642	0.003448	1.16E-14	-0.035311	0.002531	3.51E-44	6.08E-56	0.042746	F
11	SIK3 *	rs181104223	117,107,559	C	A	0.02931	0.072169	0.005943	3.10E-35	0.07877	0.010041	4.55E-15	0.068663	0.00749	5.15E-20	2.44E-32	0.419773	
11	SIK3 *	rs12416941	117,108,647	A	G	0.096823	-0.051709	0.003387	2.40E-55	-0.045999	0.00577	1.64E-15	-0.055947	0.004249	1.49E-39	3.58E-52	0.165049	
11	SIK3 *	rs113784559	117,108,649	G	C	0.056715	0.047445	0.004332	2.20E-28	0.052895	0.007412	9.97E-13	0.045793	0.005422	3.17E-17	2.82E-27	0.439334	
11	SIK3 *	rs10750101	117,108,973	C	T	0.473643	-0.032204	0.002019	1.30E-59	-0.026938	0.003446	5.62E-15	-0.035204	0.002529	5.45E-44	4.62E-56	0.053134	
11	SIK3 *	rs12271161	117,109,195	A	G	0.15382	-0.015275	0.002777	8.20E-09	-0.009508	0.00474	0.044876	-0.018612	0.00348	9.10E-08	8.24E-08	0.12159	
11	SIK3 *	rs12271169	117,109,305	G	C	0.177765	-0.014967	0.002627	1.30E-09	-0.009356	0.004487	0.037084	-0.018319	0.00329	2.65E-08	2.12E-08	0.107223	
11	SIK3 *	rs4938339	117,109,878	T	C	0.056726	0.047479	0.004332	2.00E-28	0.052956	0.007411	9.35E-13	0.045827	0.005421	2.99E-17	2.49E-27	0.437535	
11	SIK3 *	rs4938340	117,109,906	A	G	0.057084	0.04686	0.00433	1.00E-27	0.052473	0.007407	1.45E-12	0.044896	0.00542	1.26E-16	1.59E-26	0.409053	
11	SIK3 *	rs10892074	117,109,925	T	G	0.202747	-0.027551	0.002503	1.30E-28	-0.023928	0.004274	2.21E-08	-0.02951	0.003137	5.36E-21	9.36E-27	0.29238	
11	SIK3 *	rs114221654	117,109,963	T	C	0.096823	-0.051709	0.003387	2.40E-55	-0.045999	0.00577	1.64E-15	-0.055947	0.004249	1.49E-39	3.58E-52	0.165049	
11	SIK3 *	rs61903427	117,110,070	C	G	0.056726	0.047479	0.004332	2.00E-28	0.052956	0.007411	9.35E-13	0.045827	0.005421	2.99E-17	2.49E-27	0.437535	
11	SIK3 *	rs7112111	117,110,142	G	T	0.1909	-0.016938	0.002554	2.50E-12	-0.009893	0.004366	0.023492	-0.021083	0.003198	4.49E-11	2.81E-11	0.038694	F
11	SIK3 *	rs4635117	117,110,285	A	G	0.298432	0.041235	0.002215	2.10E-80	0.039538	0.003782	1.49E-25	0.041662	0.002775	6.53E-51	2.04E-73	0.650691	
11	SIK3 *	rs148910068	117,110,595	T	C	0.018772	-0.041509	0.007401	1.50E-09	-0.014039	0.012449	0.259417	-0.057855	0.00935	6.29E-10	2.57E-09	0.004901	F
11	SIK3 *	rs6589595	117,110,619	A	G	0.056726	0.047479	0.004332	2.00E-28	0.052956	0.007411	9.35E-13	0.045827	0.005421	2.99E-17	2.49E-27	0.437535	
11	SIK3 *	rs116770907	117,110,799	T	C	0.096823	-0.051706	0.003387	2.40E-55	-0.045989	0.00577	1.67E-15	-0.055947	0.004249	1.49E-39	3.63E-52	0.164622	
11	SIK3 *	rs2127907	117,110,864	G	A	0.48826	-0.033596	0.002019	1.00E-64	-0.0276	0.003447	1.22E-15	-0.037026	0.00253	1.94E-48	3.83E-61	0.0275	F
11	SIK3 *	rs111677878	117,111,718	T	C	0.096807	-0.051714	0.003388	2.40E-55	-0.045996	0.005771	1.67E-15	-0.055966	0.00425	1.45E-39	3.53E-52	0.164153	
11	SIK3 *	rs7104023	117,111,886	T	A	0.190853	-0.016852	0.002555	3.20E-12	-0.009913	0.004368	0.023255	-0.020949	0.003199	5.98E-11	3.69E-11	0.041506	F
11	SIK3 *	rs10892075	117,112,105	T	C	0.153789	-0.015321	0.002778	7.40E-09	-0.009539	0.004743	0.044306	-0.018654	0.003481	8.57E-08	7.69E-08	0.121303	
11	SIK3 *	rs59700451	117,112,212	A	G	0.056723	0.047452	0.004332	2.10E-28	0.052943	0.007413	9.60E-13	0.045805	0.005421	3.08E-17	2.64E-27	0.437048	
11	SIK3 *	rs113979111	117,112,300	A	G	0.056723	0.047447	0.004332	2.10E-28	0.052947	0.007413	9.56E-13	0.045798	0.005421	3.12E-17	2.66E-27	0.43636	
11	SIK3 *	rs111560312	117,112,840	A	G	0.056722	0.047447	0.004332	2.10E-28	0.052947	0.007413	9.56E-13	0.045799	0.005421	3.11E-17	2.65E-27	0.436386	
11	SIK3 *	rs55703909	117,114,150	A	G	0.05672	0.047455	0.004332	2.10E-28	0.053	0.007414	9.12E-13	0.045781	0.005421	3.20E-17	2.61E-27	0.431867	
11	SIK3 *	rs74882651	117,114,475	A	G	0.096803	-0.051736	0.003388	2.20E-55	-0.04607	0.005772	1.51E-15	-0.055964	0.00425	1.48E-39	3.26E-52	0.167456	
11	SIK3 *	rs60834024	117,115,141	A	C	0.096815	-0.051709	0.003388	2.30E-55	-0.046096	0.00577	1.44E-15	-0.05592	0.00425	1.68E-39	3.53E-52	0.170391	
11	SIK3 *	rs61903429	117,115,968	A	C	0.056731	0.047513	0.004332	1.80E-28	0.053209	0.007414	7.45E-13	0.045768	0.005421	3.25E-17	2.17E-27	0.441779	
11	SIK3 *	rs11216277	117,116,330	A	G	0.293791	-0.027302	0.00221	1.90E-35	-0.024635	0.003758	5.74E-11	-0.028616	0.002776	6.80E-25	3.85E-33	0.394116	
11	SIK3 *	rs145335872	117,116,511	A	C	0.05509	-0.047813	0.004392	1.20E-28	-0.033859	0.007493	6.31E-06	-0.056211	0.005505	1.89E-24	8.39E-28	0.016235	F
11	SIK3 *	rs61903430	117,116,626	C	G	0.056731	0.047521	0.004332	1.70E-28	0.053209	0.007414	7.45E-13	0.045781	0.005421	3.19E-17	2.12E-27	0.418642	
11	SIK3 *	rs75904569	117,117,597	G	A	0.056728	0.047532	0.004332	1.70E-28	0.053225	0.007415	7.37E-13	0.045783	0.005421	3.17E-17	2.09E-27	0.417869	
11	SIK3 *	rs80197460	117,118,074	G	C	0.096829	-0.051672	0.003387	2.80E-55	-0.046319	0.005769	1.04E-15	-0.055752	0.00425	2.83E-39	4.30E-52	0.188039	
11	SIK3 *	rs10892076	117,118,220	A	G	0.292595	-0.02732	0.002214	1.70E-35	-0.024761	0.003765	4.96E-11	-0.028609	0.00278	8.40E-25	4.12E-33	0.410996	
11	SIK3 *	rs74428560	117,119,266	T	C	0.056735	0.04756	0.004332	1.50E-28	0.053235	0.007414	7.26E-13	0.045817	0.00542	3.00E-17	1.95E-27	0.419287	
11	SIK3 *	rs117300172	117,119,795	C	A	0.015625	0.073494	0.008075	4.00E-20	0.079296	0.013842	1.04E-08	0.069644	0.010095	5.45E-12	3.46E-18	0.573173	
11	SIK3 *	rs200802441	117,120,056	C	A	0.415143	-0.043219	0.002072	7.90E-100	-0.037187	0.003534	7.36E-26	-0.046969	0.002598	5.22E-73	9.53E-96	0.025756	F
11	SIK3 *	rs12366015	117,120,135	G	A	0.429145	-0.044402	0.002037	4.40E-109	-0.038902	0.003471	4.03E-29	-0.047843	0.002555	3.42E-78	3.74E-104	0.038055	F
11	PAFAH1B2 *	rs74955808	117,121,969	A	G	0.097078	-0.051324	0.003383	1.20E-54	-0.046193	0.005763	1.15E-15						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	PAFAH1B2	rs117588325	117,157,577	T	A	0.027918	0.072808	0.006093	4.10E-34	0.077342	0.010297	6.11E-14	0.069994	0.007677	8.19E-20	5.00E-31	0.56727	
11	PAFAH1B2	rs12420250	117,158,011	A	G	0.100664	-0.043109	0.003328	1.80E-40	-0.04112	0.005667	4.17E-13	-0.04528	0.004175	2.27E-27	1.07E-37	0.554609	
11	PAFAH1B2	rs78166985	117,159,069	T	A	0.100783	-0.043342	0.003326	6.90E-41	-0.040879	0.005661	5.35E-13	-0.04578	0.004174	5.93E-28	3.61E-38	0.48592	
11	PAFAH1B2	rs1871757	117,159,865	A	T	0.458214	-0.029646	0.002012	9.20E-51	-0.024607	0.003429	7.44E-13	-0.032384	0.002524	1.24E-37	1.19E-47	0.067738	
11	PAFAH1B2	rs200545029	117,159,917	C	T	0.100866	-0.043129	0.003324	1.50E-40	-0.040775	0.00566	6.11E-13	-0.04555	0.00417	9.65E-28	6.66E-38	0.497045	
11	PAFAH1B2	rs142017584	117,160,647	A	G	0.100962	-0.043231	0.003323	8.80E-41	-0.040685	0.005658	6.69E-13	-0.045718	0.004169	6.01E-28	4.55E-38	0.473886	
11	PAFAH1B2	rs3736120	117,161,409	T	G	0.330557	-0.022659	0.002133	9.40E-27	-0.01765	0.003634	1.21E-06	-0.02506	0.002676	8.22E-21	6.92E-25	0.100626	
11	PAFAH1B2	rs12281009	117,162,243	G	A	0.100962	-0.043231	0.003323	8.80E-41	-0.040685	0.005658	6.69E-13	-0.045718	0.004169	6.01E-28	4.55E-38	0.473886	
11	PAFAH1B2	rs7122944	117,163,903	T	G	0.494839	-0.032311	0.002007	6.80E-61	-0.026194	0.003424	2.10E-14	-0.035774	0.002515	7.23E-46	2.29E-57	0.02415	F
11	PAFAH1B2	rs10790175	117,164,013	C	T	0.357249	-0.014921	0.00209	7.50E-13	-0.010425	0.003561	0.00343	-0.016936	0.002622	1.08E-10	1.19E-11	0.140888	
11	PAFAH1B2	rs150984554	117,164,300	A	G	0.100074	-0.043854	0.003338	1.90E-41	-0.041306	0.005684	3.84E-13	-0.046475	0.004188	1.39E-28	1.46E-39	0.464171	
11	PAFAH1B2	rs12420127	117,164,603	G	A	0.100962	-0.043231	0.003323	8.80E-41	-0.040685	0.005658	6.69E-13	-0.045718	0.004169	6.01E-28	4.55E-38	0.473886	
11	PAFAH1B2	rs10892080	117,164,786	G	A	0.29771	-0.0278	0.002195	3.00E-37	-0.024011	0.003736	1.35E-10	-0.029707	0.002755	4.49E-27	6.10E-35	0.2198	
11	PAFAH1B2	rs149378955	117,164,863	A	G	0.045868	0.052712	0.0048	3.10E-29	0.059117	0.008199	5.81E-13	0.050772	0.006012	3.22E-17	1.68E-27	0.411776	
11	PAFAH1B2	rs7931335	117,166,089	T	C	0.458395	-0.02966	0.002012	8.00E-51	-0.024682	0.003428	6.24E-13	-0.032358	0.002524	1.35E-37	1.10E-47	0.071348	
11	PAFAH1B2	rs6589602	117,166,349	C	T	0.298814	-0.027997	0.002191	7.50E-38	-0.023889	0.003728	1.52E-10	-0.030109	0.002075	7.30E-28	1.13E-35	0.179357	
11	PAFAH1B2	rs7112513	117,166,645	G	A	0.495722	-0.031786	0.002005	5.20E-59	-0.02554	0.003422	8.75E-14	-0.035265	0.002513	1.09E-44	1.39E-55	0.022001	F
11	PAFAH1B2	rs77171490	117,168,025	A	T	0.100962	-0.043231	0.003323	8.80E-41	-0.040685	0.005658	6.69E-13	-0.045718	0.004169	6.01E-28	4.55E-38	0.473886	
11	PAFAH1B2	rs190482111	117,168,438	A	G	0.100956	-0.043252	0.003323	8.20E-41	-0.040731	0.005658	6.32E-13	-0.045729	0.004169	5.85E-28	4.19E-38	0.476944	
11	PAFAH1B2	rs10892082	117,168,609	G	T	0.49556	-0.032077	0.002006	4.60E-60	-0.025657	0.003423	6.95E-14	-0.035642	0.002514	1.40E-45	1.44E-56	0.018753	F
11	PAFAH1B2	rs116773440	117,168,745	C	A	0.100566	-0.0436	0.003332	3.00E-41	-0.041943	0.005681	1.61E-13	-0.045594	0.004177	1.06E-27	1.97E-38	0.604698	
11	PAFAH1B2	rs1060211	117,169,081	A	G	0.45836	-0.029684	0.002012	7.10E-51	-0.024663	0.003428	6.52E-13	-0.032413	0.002524	1.04E-37	8.87E-48	0.068698	
11	PAFAH1B2	rs77678768	117,169,789	C	G	0.100956	-0.043252	0.003323	8.20E-41	-0.040731	0.005658	6.32E-13	-0.045729	0.004169	5.85E-28	4.19E-38	0.476944	
11	PAFAH1B2	rs10750103	117,171,522	T	C	0.298159	-0.028007	0.002193	9.60E-38	-0.023891	0.003732	1.59E-10	-0.030099	0.002753	8.73E-28	1.41E-35	0.180713	
11	PAFAH1B2	rs4936367	117,171,661	A	G	0.495736	-0.031812	0.002005	4.30E-59	-0.025494	0.003422	9.73E-14	-0.035313	0.002513	8.43E-45	1.19E-55	0.020758	F
11	PAFAH1B2	rs10892083	117,171,864	C	G	0.208208	-0.028754	0.002472	7.10E-32	-0.023424	0.004221	2.92E-08	-0.031695	0.003097	1.50E-24	3.71E-30	0.114122	
11	PAFAH1B2	rs7123039	117,172,100	A	T	0.4584	-0.029674	0.002012	7.30E-51	-0.024647	0.003428	6.75E-13	-0.032397	0.002524	1.12E-37	9.87E-48	0.068672	
11	PAFAH1B2	rs7120449	117,172,183	C	T	0.458138	-0.02969	0.002012	6.60E-51	-0.024704	0.003428	5.99E-13	-0.032408	0.002524	1.10E-37	8.60E-48	0.070349	
11	PAFAH1B2	rs7120565	117,172,233	C	T	0.298803	-0.028078	0.002191	4.70E-38	-0.023927	0.003728	1.43E-10	-0.030197	0.00275	5.18E-28	7.57E-36	0.175926	
11	PAFAH1B2	rs56371319	117,172,251	A	C	0.057732	0.046333	0.004295	1.30E-27	0.051473	0.007348	2.56E-12	0.044923	0.005376	6.83E-17	1.52E-26	0.471899	
11	PAFAH1B2	rs4604928	117,173,487	A	C	0.495736	-0.031813	0.002005	4.30E-59	-0.025494	0.003422	9.73E-14	-0.035313	0.002513	8.42E-45	1.19E-55	0.020757	F
11	PAFAH1B2	rs7925256	117,174,619	T	C	0.285679	0.040251	0.002235	8.00E-75	0.038461	0.003824	8.97E-24	0.04073	0.002798	6.02E-48	1.06E-68	0.632122	
11	PAFAH1B2	rs1462228126	117,175,016	T	G	0.015459	0.070752	0.008151	2.60E-18	0.055905	0.01397	6.35E-05	0.079428	0.010191	6.82E-15	2.15E-17	0.173698	
11	PAFAH1B2	rs4938353	117,175,481	A	G	0.458385	-0.029664	0.002012	7.90E-51	-0.024631	0.003428	6.98E-13	-0.032388	0.002524	1.18E-37	1.07E-47	0.068419	
11	PAFAH1B2	rs10790176	117,177,136	T	G	0.458407	-0.029658	0.002012	8.20E-51	-0.024647	0.003428	6.75E-13	-0.032371	0.002524	1.29E-37	1.13E-47	0.069601	
11	PAFAH1B2	rs80353869	117,177,406	A	G	0.100739	-0.043493	0.003327	4.00E-41	-0.040604	0.005664	7.85E-13	-0.046133	0.004175	2.35E-28	2.09E-38	0.432001	
11	PAFAH1B2	rs10790177	117,177,701	G	A	0.357355	-0.014846	0.002091	9.70E-13	-0.010437	0.003562	0.003401	-0.016806	0.002622	1.51E-10	1.65E-11	0.149897	
11	SIDT2	rs12419178	117,180,202	T	C	0.10063	-0.043412	0.003329	6.10E-41	-0.040566	0.005668	8.55E-13	-0.046057	0.004177	3.07E-28	2.97E-38	0.435485	
11	SIDT2	rs76883864	117,181,009	T	C	0.100634	-0.043381	0.003328	6.80E-41	-0.040566	0.005668	8.55E-13	-0.046017	0.004177	3.40E-28	3.29E-38	0.438855	
11	SIDT2	rs7946257	117,182,449	G	A	0.35711	-0.014946	0.002091	6.60E-13	-0.010526	0.003564	0.003154	-0.016917	0.002623	1.16E-10	1.18E-11	0.088597	
11	SIDT2	rs2046150	117,182,717	A	C	0.102831	-0.042305	0.003297	7.10E-40	-0.039268	0.005609	2.65E-12	-0.045037	0.004139	1.55E-27	4.50E-37	0.407933	
11	SIDT2	rs4938355	117,182,959	G	A	0.056313	0.046904	0.004347	1.90E-27	0.052285	0.007444	2.25E-12	0.045312	0.005438	8.38E-17	1.63E-26	0.449396	
11	SIDT2	rs2046149	117,183,993	G	C	0.102834	-0.042306	0.003297	7.10E-40	-0.039263	0.005609	2.67E-12	-0.045037	0.004139	1.55E-27	4.07E-37	0.407532	
11	SIDT2	rs10892085	117,185,065	C	T	0.338577	-0.013703	0.002153	1.90E-10	-0.009273	0.003665	0.011417	-0.015806	0.002701	5.02E-09	1.50E-09	0.151336	
11	SIDT2	rs6589603	117,185,123	C	T	0.495351	-0.032052	0.002013	1.10E-59	-0.025598	0.003437	1.00E-13	-0.035652	0.002523	2.66E-45	3.90E-56	0.01839	F
11	SIDT2	rs11606672	117,185,343	T	C	0.102624	-0.042075	0.003301	2.00E-39	-0.038803	0.005613	4.94E-12	-0.044967	0.004146	2.22E-27	1.19E-36	0.37706	
11	SIDT2	rs7107152	117,185,364	G	A	0.357284	-0.015032	0.002091	4.70E-13	-0.010555	0.003564	0.003069	-0.017043	0.002623	8.47E-11	8.49E-12	0.14256	
11	SIDT2	rs2306472	117,187,346	T	C	0.100625	-0.042905	0.003329	4.20E-40	-0.040257	0.005666	1.25E-12	-0.045533	0.004178	1.25E-27	1.74E-37	0.453582	
11	SIDT2	rs546506427	117,188,416	C	T	0.102632	-0.042054	0.003301	2.20E-39	-0.038886	0.005613	4.43E-12	-0.044904	0.004145	2.59E-27	1.24E-36	0.388379	
11	SIDT2	rs90192	117,188,631	T	C	0.460852	-0.028556	0.002014	4.00E-47	-0.023924	0.003432	3.26E-12	-0.031036	0.002525	1.13E-34	4.47E-44	0.095064	
11	SIDT2	rs474339	117,188,836	A	G	0.35715	-0.014937	0.002091	6.60E-13	-0.010636	0.003563	0.002849	-0.016846	0.002623	1.39E-10	1.29E-11	0.160443	
11	SIDT2	rs7933134	117,189,078	T	C	0.102844	-0.042289	0.003297	7.50E-40	-0.039337	0.005608	2.40E-12	-0.044994	0.004139	1.70E-27	4.50E-37	0.416978	
11	SIDT2	rs12419470	117,191,059	T	G	0.102628	-0.042058	0.003301	2.20E-39	-0.038893	0.005613	4.39E-12	-0.044907	0.004145	2.57E-27	1.22E-36	0.388739	
11	SIDT2	rs61703672	117,191,109	T	C	0.102628	-0.042058	0.003301	2.20E-39	-0.038893	0.005613	4.39E-12	-0.044907	0.004145	2.57E-27	1.22E-36	0.388739	
11	SIDT2	rs140056851	117,191,110	G	T	0.045919	0.052311	0.004798	7.80E-29	0.059048	0.00819	5.84E-13	0.050249	0.006013	6.78E-17	3.53E-27	0.386449	
11	SIDT2	rs499713	117,191,															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
11	LOC100652768	rs474488	117,198,261	G	A	0.458068	-0.029744	0.002012	3.90E-51	-0.024848	0.003429	4.43E-13	-0.032426	0.002524	1.01E-37	5.88E-48	0.075137	
11	LOC100652768	rs7112573	117,198,307	C	T	0.102838	-0.042303	0.003297	7.50E-40	-0.039474	0.005607	2.00E-12	-0.044945	0.004139	1.97E-27	4.32E-37	0.432378	
11	LOC100652768	rs585849	117,198,345	G	A	0.356446	-0.015114	0.002094	3.70E-13	-0.010858	0.003567	0.002345	-0.017055	0.002626	8.63E-11	6.76E-12	0.161823	
11	LOC100652768	rs2269398	117,199,072	T	C	0.100823	-0.043147	0.003325	1.50E-40	-0.040745	0.005661	6.36E-13	-0.045597	0.004174	9.44E-28	6.77E-38	0.490301	
11	LOC100652768	rs17523113	117,199,185	A	G	0.044172	0.050209	0.004889	1.20E-27	0.058301	0.008367	3.34E-12	0.050242	0.006117	2.27E-16	6.46E-26	0.436846	
11	LOC100652768, TAGLN	rs2239678	117,199,880	T	C	0.100807	-0.043237	0.003325	1.00E-40	-0.040849	0.005661	5.58E-13	-0.045678	0.004173	7.56E-28	4.78E-38	0.492278	
11	LOC100652768, TAGLN	rs2170317	117,200,024	C	A	0.100859	-0.043303	0.003325	8.60E-41	-0.040947	0.005661	4.92E-13	-0.045723	0.004173	6.70E-28	3.75E-38	0.497061	
11	LOC100652768, TAGLN	rs664971	117,200,141	A	G	0.357093	-0.015164	0.002096	3.70E-13	-0.010937	0.003571	0.002204	-0.01706	0.002629	8.91E-11	6.59E-12	0.167351	
11	LOC100652768, TAGLN	rs664922	117,200,179	A	C	0.35695	-0.015221	0.002096	3.00E-13	-0.010928	0.003571	0.00222	-0.017166	0.002628	6.75E-11	0.159384	0.168976	
11	LOC100652768, TAGLN	rs664082	117,200,354	G	C	0.356269	-0.01514	0.002099	3.90E-13	-0.010923	0.003575	0.00226	-0.01703	0.002632	1.02E-10	7.68E-12	0.168976	
11	LOC100652768, TAGLN	rs494356	117,201,254	C	T	0.46968	-0.029088	0.002025	2.20E-48	-0.022929	0.003449	3.09E-11	-0.032487	0.002541	2.16E-37	8.07E-46	0.025695	F
11	LOC100652768, TAGLN	rs488962	117,201,809	C	T	0.357179	-0.01524	0.002096	2.70E-13	-0.010982	0.003571	0.002112	-0.017167	0.002628	6.74E-11	4.82E-12	0.163074	
11	TAGLN	rs634960	117,202,247	T	C	0.357161	-0.015181	0.002095	3.50E-13	-0.010839	0.00357	0.002407	-0.017142	0.002628	7.17E-11	5.78E-12	0.155062	
11	TAGLN	rs145613978	117,202,393	A	G	0.029271	0.069286	0.005964	2.60E-32	0.075289	0.010073	8.11E-14	0.066119	0.007518	1.52E-18	1.19E-29	0.465663	
11	TAGLN	rs12970	117,203,393	A	G	0.101119	-0.04268	0.003319	6.10E-40	-0.040299	0.005653	1.05E-12	-0.04514	0.004165	2.43E-27	2.84E-37	0.490476	
11	TAGLN	rs641620	117,203,513	T	C	0.437469	-0.02648	0.00204	9.40E-40	-0.020969	0.003481	1.75E-09	-0.029441	0.002557	1.20E-30	2.11E-37	0.049824	F
11	TAGLN	rs2269397	117,203,583	C	T	0.107234	-0.039652	0.003236	1.20E-36	-0.037285	0.005507	1.33E-11	-0.041947	0.004063	5.85E-25	7.90E-34	0.495759	
11	PCSK7	rs201184697	117,206,224	A	G	0.017234	-0.043809	0.007767	3.00E-09	-0.048583	0.013293	0.000259	-0.042043	0.009719	1.54E-05	1.09E-07	0.691275	
11	PCSK7	rs28590104	117,206,318	A	G	0.031492	-0.01473	0.002178	9.40E-12	-0.010184	0.003712	0.006101	-0.01702	0.002732	4.79E-10	8.63E-11	0.138014	
11	PCSK7	rs659955	117,209,663	T	A	0.498881	-0.030664	0.002015	9.20E-55	-0.024084	0.003438	2.55E-12	-0.034252	0.002526	7.44E-42	2.54E-51	0.017166	F
11	PCSK7	rs11216315	117,209,924	G	C	0.10292	-0.041512	0.003294	9.80E-39	-0.038125	0.005608	1.10E-11	-0.04447	0.004134	5.96E-27	6.93E-36	0.362467	
11	PCSK7	rs11216316	117,210,784	A	C	0.496788	-0.030487	0.002011	2.20E-54	-0.023559	0.003431	6.85E-12	-0.034251	0.002521	5.34E-42	4.81E-51	0.012049	F
11	PCSK7	rs171052	117,211,047	C	G	0.355597	-0.01398	0.002098	2.30E-11	-0.00915	0.003578	0.010561	-0.016121	0.002631	9.20E-10	2.67E-10	0.116464	
11	PCSK7	rs236910	117,211,258	A	G	0.355597	-0.01398	0.002098	2.30E-11	-0.00915	0.003578	0.010561	-0.016121	0.002631	9.20E-10	2.67E-10	0.116464	
11	PCSK7	rs12417682	117,211,393	A	G	0.103227	-0.041377	0.00329	1.50E-38	-0.038182	0.005597	9.34E-12	-0.044218	0.00413	1.02E-26	1.01E-35	0.385564	
11	PCSK7	rs76169968	117,212,250	A	G	0.103389	-0.041519	0.003286	6.30E-39	-0.03836	0.005589	7.00E-12	-0.044355	0.004126	6.36E-27	4.75E-36	0.388143	
11	PCSK7	rs67201490	117,212,288	G	T	0.055109	0.045129	0.004392	3.60E-25	0.052052	0.007518	4.56E-12	0.042628	0.005496	9.17E-15	3.36E-24	0.311538	
11	PCSK7	rs4938357	117,213,324	A	G	0.055106	0.045181	0.004392	3.10E-25	0.052044	0.007518	4.60E-12	0.042709	0.005496	8.19E-15	3.03E-24	0.316154	
11	PCSK7	rs12418705	117,213,680	T	C	0.101212	-0.04215	0.003318	4.00E-39	-0.039605	0.005651	2.50E-12	-0.044727	0.004162	6.69E-27	1.81E-36	0.465541	
11	PCSK7	rs77683187	117,214,494	C	A	0.10328	-0.041357	0.003288	1.40E-38	-0.038284	0.005593	7.91E-12	-0.044159	0.004128	1.12E-26	9.40E-36	0.397977	
11	PCSK7	rs236911	117,214,554	A	C	0.496084	-0.030994	0.00201	5.30E-56	-0.023743	0.003429	4.55E-12	-0.034909	0.00252	1.40E-43	8.57E-53	0.008712	F
11	PCSK7	rs56081989	117,214,589	A	G	0.055233	0.044818	0.004389	6.40E-25	0.051808	0.007515	5.64E-12	0.042252	0.00549	1.47E-14	6.60E-24	0.304548	
11	PCSK7	rs56061152	117,216,402	C	G	0.055242	0.045012	0.004389	5.00E-25	0.052197	0.007513	3.87E-12	0.042449	0.005491	1.12E-14	3.48E-24	0.294878	
11	PCSK7	rs2238005	117,217,366	T	C	0.103258	-0.0414	0.003289	1.30E-38	-0.038331	0.005595	7.62E-12	-0.04417	0.004129	1.14E-26	9.20E-36	0.401159	
11	PCSK7	rs236915	117,217,734	A	G	0.298533	-0.026202	0.002196	4.40E-33	-0.02231	0.003738	2.46E-09	-0.028094	0.002757	2.34E-24	5.18E-31	0.212992	
11	PCSK7	rs236916	117,218,912	G	A	0.460334	-0.027961	0.002016	2.30E-45	-0.022583	0.003435	5.03E-11	-0.030805	0.002529	4.39E-34	2.54E-42	0.053926	
11	PCSK7	rs2239009	117,219,006	C	G	0.102983	-0.041292	0.003295	2.20E-38	-0.037709	0.005602	1.74E-11	-0.044326	0.004139	9.79E-27	1.78E-35	0.342027	
11	PCSK7	rs74830	117,219,842	C	T	0.30335	-0.025749	0.002189	3.00E-32	-0.021918	0.003728	4.25E-09	-0.027551	0.002747	1.20E-23	4.48E-30	0.223764	
11	PCSK7	rs236918	117,220,893	G	C	0.498464	-0.03031	0.002006	7.20E-54	-0.023232	0.003423	1.19E-11	-0.034071	0.002515	8.84E-42	1.37E-50	0.010739	F
11	PCSK7	rs7941150	117,221,105	A	G	0.055293	0.044772	0.004386	8.40E-25	0.052077	0.007511	4.28E-12	0.042117	0.005486	1.71E-14	5.83E-24	0.316154	
11	PCSK7	rs78628783	117,221,335	T	C	0.103043	-0.041269	0.003295	2.50E-38	-0.037795	0.005601	1.56E-11	-0.044234	0.004138	1.23E-26	2.00E-35	0.355159	
11	PCSK7	rs80351364	117,221,678	T	C	0.103432	-0.041376	0.003288	1.40E-38	-0.038092	0.005594	1.01E-11	-0.044201	0.004128	1.02E-26	1.09E-35	0.379516	
11	PCSK7	rs6589606	117,222,170	T	A	0.103046	-0.041275	0.003295	2.50E-38	-0.037802	0.005601	1.55E-11	-0.044241	0.004138	1.20E-26	1.09E-35	0.379516	
11	PCSK7	rs17120523	117,223,875	G	A	0.073529	-0.038153	0.003869	1.40E-23	-0.034347	0.006605	2.03E-07	-0.041561	0.004848	1.07E-17	1.48E-22	0.378614	
11	PCSK7	rs236919	117,224,645	C	T	0.308773	-0.020069	0.002192	6.70E-20	-0.016478	0.003733	1.03E-05	-0.022011	0.002751	1.28E-15	7.29E-19	0.232718	
11	PCSK7	rs146871029	117,225,450	T	C	0.011563	0.094664	0.009372	1.80E-23	0.087374	0.016186	6.88E-08	0.09983	0.011671	1.26E-17	6.08E-23	0.532473	
11	PCSK7	rs75519898	117,226,533	A	G	0.025477	0.044723	0.006384	9.50E-13	0.030786	0.010821	0.004454	0.05129	0.00803	1.75E-10	2.42E-11	0.12809	
11	PCSK7	rs2306473	117,227,236	T	C	0.059756	0.038686	0.004228	4.00E-20	0.045889	0.007231	2.28E-10	0.036168	0.005292	8.53E-12	1.29E-09	0.278006	
11	PCSK7	rs111809212	117,228,821	C	T	0.054857	0.037383	0.004433	2.40E-17	0.046465	0.00762	1.11E-09	0.033658	0.005534	1.22E-09	7.83E-17	0.173852	
11	PCSK7	rs4938361	117,229,225	C	G	0.058307	0.038925	0.004293	9.90E-20	0.046976	0.007411	2.40E-10	0.035637	0.005348	2.78E-11	4.32E-09	0.214691	
11	PCSK7	rs4938362	117,229,313	A	G	0.058956	0.039541	0.00427	1.40E-20	0.046187	0.007374	3.89E-10	0.036859	0.005317	4.32E-12	1.12E-19	0.304841	
11	PCSK7	rs11542139	117,229,541	T	C	0.043499	0.039803	0.004967	4.50E-16	0.049726	0.008515	5.38E-09	0.035426	0.00621	1.20E-08	3.38E-15	0.174823	
11	RNF214	rs144580263	117,253,710	T	C	0.048839	-0.035029	0.004658	3.70E-14	-0.044451	0.008022	3.08E-08	-0.030358	0.00581	1.78E-07	2.54E-13	0.154769	
11	RNF214	rs145918995	117,256,488	T	C	0.015272	0.063989	0.008247	2.10E-15	0.066131	0.013902	2.00E-06	0.060696	0.010406	5.60E-09	5.00E-13	0.754309	
11	BACE1, BACE1-AS	rs28989505	117,291,956	G	C	0.029358	0.038476	0.005958	8.00E-11	0.043466	0.010422	3.07E-05	0.036273	0.007372	8.81E-07	9.24E-10	0.5731	
11	BACE1	rs3741288	117,315,499	T	C													

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
11	CEP164	rs610749	117,340,524	T	G	0.153692	0.024933	0.002779	4.20E-19	0.023686	0.004732	5.68E-07	0.024855	0.003487	1.06E-12	3.36E-17	0.842254	
11	CEP164	rs474891	117,341,621	T	G	0.173107	0.019325	0.002682	5.20E-13	0.016771	0.004564	0.00024	0.020119	0.003366	2.33E-09	2.04E-11	0.55489	
11	CEP164	rs561473	117,341,924	C	T	0.150624	0.025681	0.002814	7.90E-20	0.024893	0.004784	2.00E-07	0.025602	0.003534	4.52E-13	5.31E-18	0.905149	
11	CEP164	rs475385	117,342,176	T	C	0.153037	0.024623	0.002789	1.40E-18	0.02362	0.004744	6.52E-07	0.024552	0.003501	2.43E-12	8.67E-17	0.874368	
11	CEP164	rs495473	117,342,192	G	A	0.137103	0.022783	0.002916	6.10E-15	0.021313	0.004953	1.71E-05	0.023071	0.003663	3.11E-10	2.33E-13	0.775279	
11	CEP164	rs493516	117,342,444	A	G	0.153007	0.024647	0.002789	1.30E-18	0.023637	0.004745	6.42E-07	0.024576	0.003501	2.32E-12	8.19E-17	0.873573	
11	CEP164	rs11216360	117,342,473	A	G	0.035601	-0.038933	0.005424	1.90E-13	-0.053583	0.009257	7.29E-09	-0.032016	0.006797	2.52E-06	8.06E-13	0.060399	
11	CEP164	rs10892095	117,343,177	G	A	0.034314	-0.03972	0.005508	1.70E-13	-0.052613	0.0094	2.24E-08	-0.033679	0.006902	1.08E-06	1.07E-12	0.104476	
11	CEP164	rs573827	117,343,375	A	G	0.153164	0.024794	0.002787	8.00E-19	0.023669	0.004743	6.15E-07	0.02478	0.003499	1.47E-12	8.504474	0.850474	
11	CEP164	rs580119	117,345,497	G	T	0.153088	0.024983	0.00279	4.70E-19	0.024092	0.004746	3.93E-07	0.024837	0.003503	1.39E-12	3.07E-17	0.899425	
11	CEP164	rs652346	117,345,883	T	C	0.137152	0.023176	0.002917	2.30E-15	0.021937	0.004956	9.72E-06	0.02331	0.003665	2.08E-10	9.14E-14	0.823762	
11	CEP164	rs494722	117,345,887	T	A	0.137152	0.023176	0.002917	2.30E-15	0.021937	0.004956	9.72E-06	0.02331	0.003665	2.08E-10	9.14E-14	0.823762	
11	CEP164	rs138869088	117,346,455	T	C	0.010843	0.098342	0.00975	5.80E-24	0.087357	0.016906	2.43E-07	0.102254	0.012117	3.37E-17	5.47E-22	0.473888	
11	CEP164	rs1261744	117,347,744	C	T	0.150962	0.024509	0.002807	4.00E-18	0.02411	0.004772	4.45E-07	0.023935	0.003525	1.16E-11	2.79E-16	0.965111	
11	CEP164	rs592828	117,348,589	C	G	0.151788	0.024834	0.0028	1.00E-18	0.024212	0.004763	3.78E-07	0.024475	0.003514	3.43E-12	7.19E-17	0.964558	
11	CEP164	rs508871	117,349,054	A	G	0.150698	0.024104	0.00281	1.30E-17	0.024627	0.004781	2.65E-07	0.023219	0.003528	4.83E-11	6.83E-16	0.8127	
11	CEP164	rs688207	117,351,423	T	C	0.151498	0.025061	0.002803	4.60E-19	0.024283	0.004767	3.59E-07	0.02478	0.003519	1.98E-12	3.99E-17	0.933089	
11	CEP164	rs490262	117,351,876	A	G	0.137943	0.029582	0.002947	6.00E-24	0.02727	0.005012	5.42E-08	0.030124	0.003701	4.17E-16	1.53E-21	0.64694	
11	CEP164	rs514806	117,352,226	T	G	0.151505	0.02501	0.002803	5.40E-19	0.02417	0.004767	4.06E-07	0.02476	0.003519	2.06E-12	4.67E-17	0.920667	
11	CEP164	rs657666	117,353,644	T	G	0.151508	0.025018	0.002803	5.30E-19	0.024191	0.004767	3.97E-07	0.02476	0.003519	2.06E-12	4.57E-17	0.923454	
11	CEP164	rs553303	117,354,102	A	C	0.149586	0.024483	0.002823	4.70E-18	0.025318	0.004802	1.38E-07	0.023423	0.003545	4.03E-11	3.04E-16	0.750934	
11	CEP164	rs655389	117,354,162	A	G	0.151509	0.025017	0.002803	5.40E-19	0.024188	0.004767	3.98E-07	0.02476	0.003519	2.06E-12	4.59E-17	0.923066	
11	CEP164	rs553506	117,354,171	T	C	0.150156	0.024851	0.002816	1.20E-18	0.024358	0.004787	3.69E-07	0.024453	0.003537	4.94E-12	1.00E-16	0.987206	
11	CEP164	rs654479	117,354,418	A	G	0.151509	0.025017	0.002803	5.40E-19	0.024188	0.004767	3.98E-07	0.02476	0.003519	2.06E-12	4.59E-17	0.923066	
11	CEP164	rs542176	117,354,725	T	G	0.151281	0.024969	0.002805	6.30E-19	0.024054	0.004771	4.70E-07	0.024772	0.003522	2.11E-12	5.50E-17	0.903547	
11	CEP164	rs542869	117,354,739	A	T	0.134242	0.023773	0.002948	6.10E-16	0.022291	0.005012	8.79E-06	0.024022	0.003702	8.91E-11	3.63E-14	0.781136	
11	CEP164	rs542900	117,354,751	A	T	0.150206	0.025639	0.002816	8.40E-20	0.024478	0.004794	3.35E-07	0.025608	0.003534	4.47E-13	8.65E-18	0.849526	
11	CEP164	rs535366	117,355,900	C	T	0.151511	0.024988	0.002803	5.80E-19	0.024119	0.004768	4.30E-07	0.024753	0.003519	2.09E-12	5.01E-17	0.914789	
11	CEP164	rs11216364	117,355,903	T	C	0.086277	0.043973	0.003632	1.20E-34	0.042323	0.006193	8.59E-12	0.044335	0.004553	2.25E-22	1.88E-31	0.793561	
11	CEP164	rs537323	117,356,133	T	C	0.151511	0.024988	0.002803	5.80E-19	0.024119	0.004768	4.30E-07	0.024753	0.003519	2.09E-12	5.01E-17	0.914789	
11	CEP164	rs528720	117,356,970	A	G	0.151243	0.025198	0.002806	3.70E-19	0.024014	0.004772	4.94E-07	0.025124	0.003523	1.04E-12	8.51E-16	0.851516	
11	CEP164	rs595367	117,356,978	C	T	0.135292	0.023251	0.002936	2.70E-15	0.021544	0.004986	1.57E-05	0.023576	0.003689	1.71E-10	1.20E-13	0.743221	
11	CEP164	rs534296	117,357,579	G	A	0.151516	0.025053	0.002803	4.90E-19	0.024323	0.004767	3.42E-07	0.024726	0.00352	2.23E-12	4.28E-17	0.945734	
11	CEP164	rs12221818	117,357,803	G	A	0.034695	-0.039769	0.005477	1.10E-13	-0.053478	0.009347	1.08E-08	-0.033241	0.006865	1.31E-06	6.30E-13	0.080892	
11	CEP164	rs558854	117,357,948	A	G	0.151485	0.025103	0.002803	4.10E-19	0.02422	0.004767	3.83E-07	0.024847	0.00352	1.75E-12	3.76E-17	0.915726	
11	CEP164	rs486366	117,357,993	G	A	0.151486	0.025098	0.002803	4.10E-19	0.02422	0.004767	3.83E-07	0.024839	0.00352	1.77E-12	3.81E-17	0.916717	
11	CEP164	rs2508664	117,359,175	T	C	0.135575	0.023196	0.002933	2.60E-15	0.0219	0.004981	1.11E-05	0.023267	0.003686	2.82E-10	1.40E-13	0.825364	
11	CEP164	rs2510450	117,359,186	T	C	0.151507	0.025095	0.002804	4.20E-19	0.024243	0.004768	3.75E-07	0.024827	0.003521	1.83E-12	3.86E-17	0.92147	
11	CEP164	rs512730	117,360,341	A	T	0.153122	0.02424	0.002799	4.40E-18	0.023745	0.004763	6.30E-07	0.023834	0.003513	1.20E-11	4.03E-16	0.988009	
11	CEP164	rs11216366	117,360,895	T	G	0.135915	0.022767	0.002934	7.80E-15	0.021413	0.004984	1.75E-05	0.022885	0.003687	5.57E-10	4.21E-13	0.821348	
11	CEP164	rs12421205	117,361,440	G	C	0.151844	0.024856	0.002805	8.40E-19	0.02415	0.004771	4.23E-07	0.024533	0.003522	3.40E-12	7.96E-17	0.948486	
11	CEP164	rs12421494	117,361,517	A	G	0.151844	0.024856	0.002805	8.40E-19	0.02415	0.004771	4.23E-07	0.024533	0.003522	3.40E-12	7.96E-17	0.948486	
11	CEP164	rs12418678	117,361,544	G	A	0.135899	0.02278	0.002934	7.60E-15	0.021465	0.004984	1.67E-05	0.02288	0.003687	5.61E-10	4.06E-13	0.819412	
11	CEP164	rs17500548	117,361,675	G	A	0.135899	0.02278	0.002934	7.60E-15	0.021465	0.004984	1.67E-05	0.02288	0.003687	5.61E-10	4.06E-13	0.819412	
11	CEP164	rs2305825	117,361,776	T	C	0.151549	0.024884	0.002809	7.90E-19	0.024088	0.004774	4.60E-07	0.024569	0.003527	3.41E-12	8.65E-17	0.935422	
11	CEP164	rs7934067	117,362,238	G	A	0.151844	0.024856	0.002805	8.40E-19	0.02415	0.004771	4.23E-07	0.024533	0.003522	3.40E-12	7.96E-17	0.948486	
11	CEP164	rs11828506	117,362,711	T	C	0.151508	0.025093	0.002804	4.30E-19	0.024238	0.004768	3.77E-07	0.024827	0.003521	1.83E-12	3.88E-17	0.920814	
11	CEP164	rs7945704	117,364,652	A	G	0.108852	-0.026041	0.003224	2.60E-16	-0.029842	0.005469	4.98E-08	-0.024032	0.004054	3.16E-09	8.03E-15	0.3934	
11	CEP164	rs7124084	117,364,696	T	C	0.1515	0.025071	0.002804	4.50E-19	0.024238	0.004768	3.77E-07	0.024794	0.003521	1.97E-12	4.16E-17	0.925144	
11	CEP164	rs10892097	117,365,344	T	C	0.135573	0.02319	0.002933	2.60E-15	0.021895	0.004981	1.12E-05	0.023265	0.003686	2.84E-10	1.42E-13	0.825114	
11	CEP164	rs10790179	117,365,603	T	G	0.135574	0.023189	0.002933	2.60E-15	0.02189	0.004981	1.12E-05	0.023265	0.003686	2.84E-10	1.42E-13	0.824385	
11	CEP164	rs11606575	117,366,491	G	C	0.035241	-0.039913	0.005436	6.30E-14	-0.054473	0.009295	4.74E-09	-0.032921	0.006806	1.34E-06	2.90E-13	0.061398	
11	CEP164	rs7109923	117,366,771	G	A	0.150858	0.024717	0.002812	1.50E-18	0.023607	0.004785	8.21E-07	0.024562	0.00353	3.57E-12	1.58E-16	0.872405	
11	CEP164	rs10892098	117,367,775	T	C	0.150794	0.024564	0.002813	2.60E-18	0.023464	0.004786	9.63E-07	0.024392	0.003531	5.08E-12	2.61E-16	0.876056	
11	CEP164	rs7115177	117,368,457	C	A	0.151432	0.023497	0.002808	6.60E-17	0.022246	0.004776	3.25E-06	0.023427	0.003526	3.17E-11	5.08E-15	0.842337	
11	CEP164	rs7115526	117,368,474	T	G	0.151432	0.023497	0.002808	6.60E-17									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
12	ACACB	rs1013746	109,250,784	C	T	0.251422	-0.011279	0.002349	3.90E-08	-0.007393	0.00398	0.063261	-0.013894	0.002944	2.40E-06	2.59E-06	0.189095	
12	ACACB	rs10744776	109,255,001	A	G	0.251272	-0.011303	0.002345	3.50E-08	-0.007252	0.003973	0.067973	-0.014051	0.002939	1.77E-06	2.05E-06	0.168889	
12	FAM222A *	rs79339138	109,776,127	A	G	0.050004	0.026221	0.004692	3.30E-08	0.016319	0.007995	0.041264	0.031542	0.005863	7.64E-08	6.48E-08	0.124699	
12	ANKRD13A	rs75584653	110,021,680	T	C	0.088524	0.019539	0.003572	4.00E-08	0.013213	0.006078	0.029738	0.023638	0.004466	1.23E-07	7.78E-08	0.166922	
12	IFT81	rs141965372	110,144,533	T	C	0.079391	0.021084	0.003754	2.80E-08	0.018081	0.00635	0.088966	0.028606	0.00471	1.29E-09	2.31E-09	0.024349	F
12	IFT81	rs117624317	110,194,076	T	C	0.096818	0.020198	0.003447	5.60E-09	0.012664	0.005852	0.030494	0.025451	0.004316	3.80E-09	2.70E-09	0.078663	
12	IFT81 *	rs144825998	110,237,558	T	C	0.079989	0.021121	0.00374	2.60E-08	0.010483	0.006322	0.097295	0.028829	0.004694	8.39E-10	1.63E-09	0.019838	F
12	ATP2A2 *	rs117121174	110,259,525	A	G	0.079484	0.021659	0.003751	1.10E-08	0.010235	0.00634	0.106465	0.029768	0.004708	2.64E-10	5.65E-10	0.0134	F
12	CUX2	rs11830764	111,077,216	C	G	0.097669	-0.018561	0.003417	7.70E-09	-0.013819	0.005847	0.018129	-0.021053	0.004426	7.86E-07	3.04E-07	0.317287	
12	CUX2	rs7314285	111,084,222	G	T	0.099949	-0.017818	0.003373	1.30E-08	-0.013662	0.005769	0.017899	-0.020129	0.004207	1.74E-06	6.48E-07	0.365056	
14	C14orf166 *	rs36016197	51,987,660	C	A	0.148088	-0.016557	0.002867	7.60E-09	-0.007715	0.004846	0.11139	-0.02078	0.003596	7.74E-09	1.58E-08	0.030403	F
14	C14orf166	rs56877201	51,992,899	A	G	0.147742	-0.015825	0.002867	2.70E-08	-0.007853	0.004848	0.105217	-0.019726	0.003596	4.21E-08	7.86E-08	0.049191	F
14	C14orf166	rs61971506	51,996,807	A	G	0.14878	-0.015986	0.002865	1.70E-08	-0.007833	0.004844	0.105866	-0.019987	0.003593	2.72E-08	5.17E-08	0.043919	F
14	NID2	rs2029984	52,007,011	G	A	0.159238	-0.015002	0.002783	3.60E-08	-0.005718	0.004703	0.224019	-0.019632	0.003491	1.92E-08	6.49E-08	0.017553	F
14	NID2	rs71422049	52,016,737	G	A	0.156675	-0.014996	0.002783	3.80E-08	-0.006677	0.004716	0.156782	-0.019092	0.003486	4.44E-08	1.13E-07	0.034283	F
14	NID2	rs2645750	52,036,074	C	A	0.153641	-0.015382	0.002819	2.80E-08	-0.002354	0.004765	0.621306	-0.022254	0.003536	3.20E-10	2.22E-09	0.000803	F
14	NID2	rs2645749	52,036,077	C	A	0.153641	-0.015395	0.002819	2.70E-08	-0.002354	0.004765	0.621306	-0.022276	0.003536	3.08E-10	2.13E-09	0.000792	F
14	NID2	rs2516592	52,036,827	T	C	0.154135	-0.015666	0.00281	1.40E-08	-0.002475	0.004751	0.602417	-0.022643	0.003525	1.38E-10	9.61E-10	0.000656	F
14	NID2	rs2749876	52,037,679	T	G	0.154582	-0.015217	0.002804	3.20E-08	-0.002109	0.004742	0.656513	-0.022112	0.003516	3.30E-10	2.34E-09	0.000708	F
14	NID2	rs904061	52,037,906	T	C	0.154627	-0.015238	0.002803	3.10E-08	-0.002148	0.00474	0.650408	-0.022142	0.003515	3.10E-10	2.19E-09	0.000708	F
14	NID2	rs753051	52,038,642	A	G	0.154726	-0.015163	0.002801	3.70E-08	-0.002229	0.004737	0.63804	-0.02196	0.003514	4.23E-10	2.95E-09	0.000826	F
14	NID2	rs753050	52,038,657	A	G	0.154777	-0.01521	0.002802	3.30E-08	-0.002244	0.004737	0.635746	-0.022009	0.003514	3.89E-10	2.71E-09	0.00081	F
14	NID2	rs2029976	52,039,093	C	T	0.154772	-0.015189	0.002801	3.30E-08	-0.002338	0.004737	0.621652	-0.021924	0.003512	4.45E-10	3.06E-09	9.00E-04	F
14	NID2	rs2029975	52,039,352	C	T	0.15484	-0.015218	0.0028	3.10E-08	-0.002383	0.004735	0.614839	-0.021938	0.003511	4.28E-10	2.93E-09	0.000913	F
14	NID2	rs10139288	52,039,768	T	C	0.155032	-0.015227	0.002796	2.80E-08	-0.002584	0.004731	0.584995	-0.021817	0.003506	5.05E-10	3.37E-09	0.001096	F
14	NID2	rs3742536	52,040,711	A	G	0.155123	-0.015317	0.002795	2.40E-08	-0.002774	0.004728	0.557402	-0.021869	0.003505	4.51E-10	2.95E-09	0.001183	F
14	NID2	rs1982963	52,042,383	G	A	0.155257	-0.015578	0.002791	1.30E-08	-0.002272	0.004723	0.63045	-0.022445	0.003499	1.45E-10	1.03E-09	0.000602	F
14	NID2	rs4898729	52,042,765	T	C	0.15489	-0.01549	0.002795	1.70E-08	-0.001994	0.00473	0.673346	-0.022512	0.003503	1.35E-10	9.87E-10	0.000493	F
14	NID2	rs4901186	52,042,766	G	A	0.155261	-0.015601	0.002791	1.30E-08	-0.002356	0.004724	0.618008	-0.022453	0.0035	1.45E-10	1.02E-09	0.000634	F
14	NID2	rs3818187	52,043,070	G	A	0.155125	-0.01565	0.002793	1.20E-08	-0.002454	0.004727	0.60358	-0.022433	0.003501	1.53E-10	1.06E-09	0.000687	F
14	NID2	rs61973203	52,043,849	G	A	0.151574	-0.01635	0.002825	3.50E-09	-0.002983	0.004782	0.532738	-0.023082	0.003542	7.41E-11	4.93E-10	0.000736	F
14	NID2	rs1566132	52,045,118	C	T	0.155079	-0.015949	0.002794	6.20E-09	-0.002638	0.00473	0.577016	-0.022833	0.003503	7.35E-11	5.08E-10	0.000605	F
14	NID2	rs75766425	52,045,193	C	G	0.118712	-0.019996	0.003124	6.30E-11	-0.003895	0.005288	0.461336	-0.028813	0.003916	1.95E-13	1.34E-12	0.000154	F
14	NID2	rs79823890	52,045,251	T	G	0.119045	-0.02013	0.00312	4.80E-11	-0.004451	0.005281	0.399288	-0.028656	0.003912	2.48E-13	1.56E-12	0.000232	F
14	NID2	rs2749880	52,046,151	G	A	0.154596	-0.015949	0.002799	6.30E-09	-0.002228	0.00474	0.630618	-0.023044	0.003508	5.26E-11	3.81E-10	0.000433	F
14	NID2	rs2645738	52,046,484	G	A	0.154574	-0.015878	0.002799	7.40E-09	-0.002192	0.00474	0.643873	-0.022994	0.003508	5.78E-11	4.22E-10	0.000422	F
14	NID2	rs1566131	52,047,966	G	A	0.154574	-0.015919	0.0028	6.40E-09	-0.002082	0.004741	0.660515	-0.023093	0.003509	4.83E-11	3.57E-10	0.00037	F
14	SERPINA5	rs6113	94,587,512	C	T	0.283052	-0.012768	0.002289	2.40E-08	-0.010077	0.003887	0.009547	-0.013218	0.002865	4.02E-06	8.29E-07	0.515446	
14	SERPINA5	rs6118	94,587,526	T	C	0.282586	-0.012799	0.002288	2.20E-08	-0.009893	0.003885	0.0109	-0.01338	0.002863	3.01E-06	7.07E-07	0.46986	
14	SERPINA5	rs6119	94,587,675	G	A	0.265346	-0.012586	0.002317	4.10E-08	-0.008727	0.003928	0.026328	-0.013725	0.002901	2.28E-06	1.17E-06	0.306138	
15	AQP9 *	rs72739147	58,279,202	T	A	0.090947	-0.02106	0.003535	1.90E-10	-0.025402	0.006007	2.38E-05	-0.018568	0.004425	2.74E-05	1.96E-08	0.359703	
15	AQP9 *	rs11854242	58,279,711	T	C	0.186155	-0.014994	0.002633	2.00E-09	-0.018861	0.004459	2.37E-05	-0.012669	0.003302	0.000126	8.31E-08	0.264489	
15	AQP9 *	rs11854318	58,279,783	A	G	0.183166	-0.015973	0.00265	2.20E-10	-0.019458	0.004488	1.47E-05	-0.013827	0.003324	3.22E-05	1.45E-08	0.313285	
15	AQP9 *	rs2869072	58,281,634	G	T	0.102753	-0.021512	0.003326	1.40E-11	-0.025068	0.00564	8.91E-06	-0.019271	0.004169	3.86E-06	1.18E-09	0.40849	
15	AQP9 *	rs71478659	58,281,964	C	C	0.469883	0.011733	0.002051	5.50E-10	0.009529	0.003481	0.006204	0.012967	0.00257	4.62E-07	7.00E-08	0.426888	
15	AQP9 *	rs58038553	58,282,125	G	A	0.101473	-0.020921	0.003349	6.80E-11	-0.025098	0.005677	9.96E-06	-0.018326	0.004199	1.29E-05	4.17E-09	0.337499	
15	AQP9 *	rs56142310	58,282,759	C	T	0.089489	-0.023096	0.003581	7.50E-12	-0.024357	0.006064	5.97E-05	-0.022282	0.004491	7.12E-07	1.42E-09	0.783307	
15	AQP9 *	rs11071371	58,284,027	T	C	0.102428	-0.021938	0.003333	5.40E-12	-0.025406	0.00565	7.00E-06	-0.019862	0.004179	2.03E-06	4.30188		
15	AQP9 *	rs6493996	58,284,097	T	C	0.190189	-0.015515	0.002587	3.90E-10	-0.019059	0.004379	1.37E-05	-0.013276	0.003245	4.34E-05	1.79E-08	0.288687	
15	AQP9 *	rs1711037	58,284,151	T	A	0.468699	0.012015	0.002029	1.30E-10	0.00826	0.003445	0.016525	0.014085	0.002542	3.08E-08	1.22E-08	0.173634	
15	AQP9 *	rs10162642	58,284,964	A	G	0.104444	-0.022544	0.003306	1.20E-12	-0.024862	0.005597	9.05E-06	-0.021054	0.004147	3.91E-07	1.31E-10	0.584619	
15	AQP9 *	rs12903590	58,285,578	T	A	0.466365	0.011925	0.002028	1.90E-10	0.008187	0.003443	0.017426	0.013961	0.00254	3.99E-08	1.64E-08	0.177161	
15	AQP9 *	rs12910051	58,288,326	G	A	0.462021	0.011525	0.002021	6.70E-10	0.007854	0.003432	0.022133	0.0135	0.00253	9.74E-08	4.80E-08	0.185459	
15	AQP9 *	rs1560390	58,288,582	C	T	0.133666	-0.015596	0.002972	3.90E-08	-0.018275	0.005038	0.000289	-0.013225	0.003725	0.000388	2.55E-06	4.020286	
15	AQP9 *	rs7179728	58,289,227	C	G	0.456932	0.01209	0.002028	1.40E-10	0.007875	0.003448	0.022399	0.014388	0.002538	1.47E-08	7.73E-09	0.128161	
15	AQP9 *	rs938507	58,289,835	A	G	0.460268	0.011423	0.002023	8.90E-10	0.007958	0.003435	0.020547	0.013308	0.002533	1.52E-07	6.91E-08	0.209971	
15	AQP9 *	rs16940017</																

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
15	LIPC *	rs11858759	58,384,622	A	G	0.187659	0.023343	0.002585	2.00E-20	0.023758	0.004393	6.50E-08	0.023704	0.002337	2.53E-13	1.01E-18	0.992041	
15	LIPC *	rs10468017	58,386,313	T	C	0.181599	0.022827	0.002619	3.30E-19	0.024453	0.004458	4.22E-08	0.022359	0.003275	9.05E-12	2.23E-17	0.704991	
15	LIPC *	rs261290	58,386,521	T	C	0.322111	0.02468	0.002163	2.40E-31	0.019109	0.003668	1.93E-07	0.028065	0.002711	4.48E-25	6.98E-30	0.049617	F
15	LIPC *	rs7350789	58,387,469	A	G	0.322121	0.024898	0.002163	6.40E-32	0.019758	0.003667	7.26E-08	0.028114	0.002711	3.58E-25	2.16E-30	0.066894	
15	LIPC *	rs261291	58,387,979	C	T	0.414679	0.026795	0.002053	3.30E-40	0.018614	0.003479	8.98E-08	0.031707	0.002574	7.83E-35	6.78E-40	0.002493	F
15	LIPC *	rs7177289	58,387,985	T	C	0.322386	0.024744	0.002162	1.70E-31	0.019782	0.003668	7.06E-08	0.027817	0.00271	1.09E-24	6.38E-30	0.078063	
15	LIPC *	rs261292	58,388,705	A	G	0.465822	-0.016792	0.002033	3.00E-16	-0.013907	0.003459	5.87E-05	-0.018112	0.002543	1.10E-12	2.98E-15	0.327375	
15	LIPC *	rs2043085	58,388,755	T	C	0.441745	0.025766	0.002036	1.20E-37	0.017059	0.003453	7.96E-07	0.030831	0.002551	1.37E-33	9.60E-38	0.001343	F
15	LIPC *	rs80328086	58,388,800	G	A	0.377813	-0.022744	0.002089	2.40E-27	-0.016155	0.003555	5.60E-06	-0.026243	0.002613	1.05E-23	4.08E-27	0.022243	F
15	LIPC *	rs75437656	58,388,929	C	A	0.223939	0.01916	0.002435	5.50E-16	0.019418	0.004137	2.72E-06	0.019492	0.003049	1.67E-10	2.18E-14	0.988395	
15	LIPC *	rs79745310	58,388,956	C	T	0.379515	-0.022738	0.002088	2.80E-27	-0.01598	0.003556	7.11E-06	-0.026283	0.002611	8.40E-24	4.13E-27	0.019555	F
15	LIPC *	rs261293	58,389,573	C	T	0.251535	0.017	0.002345	1.30E-13	0.015939	0.003985	6.42E-05	0.017631	0.002936	1.97E-09	4.97E-12	0.732553	
15	LIPC *	rs2043084	58,390,297	C	G	0.114448	0.022143	0.00321	3.80E-12	0.007176	0.005454	0.18823	0.030992	0.00402	1.32E-14	5.20E-14	0.000442	F
15	LIPC *	rs1825955	58,390,584	A	C	0.247374	0.016742	0.002363	4.70E-13	0.015558	0.004012	0.000104	0.017392	0.002959	4.28E-09	1.68E-11	0.716352	
15	LIPC *	rs12185071	58,391,028	T	C	0.223419	0.019278	0.002438	3.40E-16	0.020066	0.004142	1.29E-06	0.019237	0.003054	3.08E-10	1.93E-14	0.871976	
15	LIPC *	rs1532085	58,391,167	A	G	0.441207	0.026426	0.002036	1.10E-39	0.017463	0.003453	4.34E-07	0.031636	0.002551	2.86E-35	1.15E-39	0.000968	F
15	LIPC *	rs12185072	58,391,211	T	C	0.251275	0.016841	0.002343	1.70E-13	0.015707	0.003981	8.04E-05	0.017463	0.002934	2.72E-09	8.44E-12	0.722658	
15	LIPC *	rs12905732	58,391,343	C	G	0.111892	0.022591	0.003229	2.30E-12	0.007787	0.005488	0.155927	0.031374	0.004042	8.79E-15	3.03E-14	0.000542	F
15	LIPC *	rs28594460	58,391,386	G	A	0.274204	0.014195	0.002287	2.10E-10	0.014257	0.00389	0.00025	0.014295	0.002861	5.97E-07	4.62E-09	0.993784	
15	LIPC *	rs16940167	58,391,498	C	T	0.274095	0.014239	0.002288	1.90E-10	0.014204	0.003891	0.000264	0.014386	0.002862	5.10E-07	4.18E-09	0.969898	
15	LIPC *	rs11853674	58,391,858	G	A	0.111967	0.022669	0.003228	2.00E-12	0.008385	0.005488	0.126497	0.031174	0.00404	1.26E-14	3.68E-14	0.00083	F
15	LIPC *	rs16940168	58,391,955	T	A	0.245453	0.016142	0.002367	2.30E-12	0.017238	0.004024	1.86E-05	0.016059	0.002962	6.06E-08	4.30E-11	0.813501	
15	LIPC *	rs16940170	58,392,083	A	G	0.2448	0.016266	0.002369	1.70E-12	0.017121	0.004027	2.15E-05	0.016301	0.002964	3.91E-08	3.23E-11	0.869763	
15	LIPC *	rs28495863	58,392,182	A	G	0.245585	0.01606	0.002366	2.90E-12	0.01724	0.004023	1.85E-05	0.01587	0.002962	8.58E-08	5.98E-11	0.783974	
15	LIPC *	rs12185093	58,392,477	A	G	0.24403	0.016207	0.002373	2.40E-12	0.016875	0.004036	2.93E-05	0.016347	0.002969	3.78E-08	4.19E-11	0.916019	
15	LIPC *	rs72475921	58,392,838	G	T	0.378524	-0.023272	0.002098	1.30E-28	-0.016549	0.003567	3.55E-06	-0.026798	0.002625	1.93E-24	4.95E-28	0.020689	F
15	LIPC *	rs199962452	58,393,355	A	T	0.37307	-0.023147	0.002115	8.20E-28	-0.015978	0.003596	8.96E-06	-0.026904	0.002648	3.20E-24	1.98E-27	0.014438	F
15	LIPC *	rs28703614	58,393,361	T	C	0.245255	0.016402	0.002368	1.20E-12	0.017372	0.004028	1.63E-05	0.016345	0.002963	3.56E-08	2.66E-11	0.837316	
15	LIPC *	rs7497636	58,393,432	T	C	0.245428	0.016377	0.002367	1.40E-12	0.017307	0.004025	1.73E-05	0.016352	0.002962	3.47E-08	2.34E-11	0.848497	
15	LIPC *	rs1444942	58,393,614	C	G	0.245349	0.016333	0.002368	1.60E-12	0.017127	0.004026	2.13E-05	0.016363	0.002963	3.43E-08	2.81E-11	0.87852	
15	LIPC *	rs8042174	58,393,771	C	T	0.380273	-0.023321	0.002097	9.60E-29	-0.016719	0.003568	2.83E-06	-0.0268	0.002624	1.85E-24	3.81E-28	0.022845	F
15	LIPC *	rs447794	58,394,439	G	C	0.245641	0.016391	0.002368	1.30E-12	0.017208	0.004026	1.94E-05	0.016377	0.002963	3.32E-08	2.50E-11	0.868009	
15	LIPC *	rs76679589	58,394,492	T	C	0.245634	0.016385	0.002368	1.40E-12	0.017103	0.004026	2.18E-05	0.016425	0.002963	3.03E-08	2.56E-11	0.892045	
15	LIPC *	rs7164909	58,394,555	T	C	0.362171	-0.023227	0.002115	1.20E-27	-0.017658	0.003593	9.06E-07	-0.026124	0.002647	6.10E-23	4.06E-27	0.057872	
15	LIPC *	rs7165077	58,394,610	T	C	0.387076	-0.022928	0.002085	4.70E-28	-0.018041	0.003539	3.52E-07	-0.025671	0.002611	8.73E-23	2.32E-27	0.08278	
15	LIPC *	rs261301	58,394,740	T	C	0.245708	0.016437	0.002367	1.10E-12	0.017162	0.004024	2.03E-05	0.016474	0.002962	2.72E-08	1.89E-11	0.89045	
15	LIPC *	rs75663614	58,394,841	C	T	0.363356	-0.023054	0.002111	2.40E-27	-0.017608	0.003587	9.31E-07	-0.025845	0.002643	1.51E-22	1.02E-26	0.064522	
15	LIPC *	rs17240832	58,395,171	G	A	0.245935	0.016537	0.002365	8.70E-13	0.017077	0.004021	2.19E-05	0.016672	0.002959	1.80E-08	1.93E-11	0.935432	
15	LIPC *	rs74019425	58,395,266	T	G	0.245691	0.016539	0.002364	8.40E-13	0.017319	0.00402	1.66E-05	0.016575	0.002958	2.15E-08	1.41E-11	0.881455	
15	LIPC *	rs16940181	58,395,325	C	A	0.245803	0.016504	0.002363	9.30E-13	0.017219	0.004019	1.85E-05	0.016572	0.002956	2.13E-08	1.55E-11	0.896814	
15	LIPC *	rs7171102	58,395,331	A	G	0.109308	0.023512	0.003262	6.00E-13	0.00924	0.005538	0.09521	0.032187	0.004085	3.46E-15	8.22E-15	0.000859	F
15	LIPC *	rs174418	58,395,404	T	C	0.39371	0.022237	0.00208	1.90E-27	0.016994	0.003531	1.51E-06	0.025337	0.002606	2.57E-22	2.76E-26	0.057281	
15	LIPC *	rs1666359	58,395,410	G	T	0.246781	0.016083	0.002362	3.80E-12	0.016934	0.004018	2.53E-05	0.01605	0.002955	5.71E-08	5.44E-11	0.859186	
15	LIPC *	rs495348	58,395,591	C	G	0.246235	0.016636	0.002362	5.40E-13	0.017503	0.004018	1.34E-05	0.016624	0.002956	1.90E-08	1.02E-11	0.860177	
15	LIPC *	rs8032310	58,395,663	A	G	0.247405	0.016563	0.002363	8.00E-13	0.017595	0.004019	1.21E-05	0.016446	0.002956	2.72E-08	1.31E-11	0.817885	
15	LIPC *	rs493987	58,395,707	T	C	0.245812	0.016619	0.002363	6.20E-13	0.017443	0.004019	1.44E-05	0.016625	0.002956	1.91E-08	1.10E-11	0.86974	
15	LIPC *	rs76438892	58,395,733	G	A	0.362257	-0.023119	0.002113	2.40E-27	-0.017331	0.003593	1.44E-06	-0.026078	0.002644	6.48E-23	6.71E-27	0.049909	F
15	LIPC *	rs4238329	58,395,987	C	A	0.359926	-0.023284	0.002116	9.70E-28	-0.016762	0.0036	3.28E-06	-0.026553	0.002648	1.24E-23	2.89E-27	0.028489	F
15	LIPC *	rs920917	58,396,279	C	A	0.24496	0.016414	0.002368	1.20E-12	0.016613	0.004031	3.81E-05	0.016768	0.002961	1.53E-08	2.24E-11	0.975205	
15	LIPC *	rs11855284	58,396,988	C	T	0.111246	0.022781	0.003238	2.00E-12	0.007626	0.005491	0.164878	0.032053	0.004059	3.00E-15	1.09E-14	0.000349	F
15	LIPC *	rs11858481	58,396,998	T	C	0.109086	0.023394	0.003267	9.50E-13	0.009108	0.005542	0.100304	0.032169	0.004094	4.09E-15	1.01E-14	0.000822	F
15	LIPC *	rs17821298	58,398,539	A	C	0.310095	0.01406	0.002209	5.60E-11	0.014563	0.003758	0.000108	0.013515	0.002763	1.02E-06	3.49E-09	0.822245	
15	LIPC *	rs76898656	58,399,003	A	G	0.358042	-0.02282	0.002132	3.20E-26	-0.016135	0.003623	8.57E-06	-0.026271	0.002669	7.71E-23	4.44E-26	0.024312	F
15	LIPC *	rs74019428	58,399,009	T	C	0.358042	-0.022817	0.002132	3.20E-26	-0.016127	0.003623	8.66E-06	-0.026272	0.002669	7.70E-23	4.48E-26	0.024195	F
15	LIPC *	rs490098	58,399,026	C	A	0.252527	0.015812	0.002351	4.40E-12	0.016575	0.003997	3.40E-05	0.015852	0.002942	7.31E-08	9.18E-11	0.884137	
15	LIPC *	rs2082149	58,399,190	A	G	0.258705	0.01625	0.002332	7.60E-13	0.016107	0.003966	4.93E-05	0.016663	0.002919	1.17E-08	2.20E-11	0.910146	
15	LIPC *	rs8024755	58,399,670	A	G	0.416132	-0.022042	0.002079	6.60E-26									

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
15	LIPC	rs8033940	58,432,643	G	A	0.303587	-0.019266	0.002192	1.60E-21	-0.017215	0.003712	3.58E-06	-0.020175	0.002749	2.25E-13	4.31E-17	0.521642	
15	LIPC	rs633695	58,433,640	A	G	0.355986	-0.016136	0.002111	7.90E-17	-0.015457	0.003575	1.56E-05	-0.016198	0.002648	9.88E-10	6.59E-13	0.867678	
15	LIPC	rs261334	58,434,545	G	C	0.342107	0.027608	0.002123	3.10E-42	0.021306	0.003609	3.64E-09	0.030963	0.002658	2.51E-31	9.15E-38	0.031208	F
15	LIPC, LOC101928694	rs261333	58,435,080	C	T	0.238508	-0.016074	0.0024	1.20E-12	-0.012138	0.004072	0.002882	-0.017966	0.003007	2.36E-09	2.08E-10	0.249567	
15	LIPC, LOC101928694	rs17190517	58,436,945	T	C	0.222274	-0.015534	0.002446	3.00E-11	-0.013552	0.004148	0.001091	-0.016278	0.003065	1.12E-07	3.61E-09	0.597241	
15	LIPC, LOC101928694	rs881136	58,438,299	C	T	0.364179	0.024861	0.002101	2.10E-35	0.018226	0.003568	3.32E-07	0.027844	0.002631	3.82E-26	1.03E-30	0.030079	F
15	LIPC, LOC101928694	rs261342	58,438,954	C	G	0.425057	-0.014871	0.00205	1.20E-14	-0.015822	0.003493	5.99E-06	-0.014704	0.002563	9.95E-09	2.51E-12	0.796389	
15	LIPC, LOC101928694	rs17301746	58,439,196	T	C	0.25812	0.018949	0.002339	7.30E-18	0.011837	0.003961	0.002814	0.022011	0.002933	6.46E-14	6.80E-15	0.039011	F
15	LIPC, LOC101928694	rs261341	58,439,368	G	A	0.340337	-0.014038	0.002139	9.70E-13	-0.012666	0.003627	0.000482	-0.01463	0.002681	4.96E-08	7.69E-10	0.663277	
15	LIPC, LOC101928694	rs8043310	58,439,619	A	C	0.232419	0.021419	0.002428	1.40E-20	0.012802	0.004112	0.001858	0.025597	0.003045	4.51E-17	3.59E-18	0.012414	F
15	LIPC, LOC101928694	rs12594375	58,440,269	A	G	0.253583	0.019086	0.002361	7.90E-18	0.011024	0.003987	0.005712	0.022853	0.002966	1.36E-14	2.80E-15	0.017325	F
15	LIPC, LOC101928694	rs6494007	58,442,446	T	C	0.258662	0.020006	0.002348	1.10E-19	0.01248	0.003968	0.001666	0.023654	0.002947	1.06E-15	7.34E-17	0.023791	F
15	LIPC, LOC101928694	rs534933	58,443,023	A	C	0.039407	0.027978	0.005253	4.50E-08	0.043303	0.008805	8.90E-07	0.018498	0.006627	0.005262	1.14E-07	0.024415	M
15	TLE3 *	rs4776482	69,851,564	G	C	0.405895	-0.011944	0.002087	1.10E-09	-0.014311	0.003538	5.29E-05	-0.011544	0.002615	1.03E-05	1.65E-08	0.529361	
15	TLE3 *	rs305006	69,851,871	T	C	0.327456	-0.012207	0.002159	1.20E-09	-0.014267	0.003661	9.85E-05	-0.01194	0.002705	1.03E-05	2.97E-08	0.609169	
15	TLE3 *	rs10468044	69,852,097	C	A	0.405812	-0.012018	0.002086	8.80E-10	-0.014152	0.003536	6.34E-05	-0.011769	0.002615	6.86E-06	1.33E-08	0.587962	
15	TLE3 *	rs305007	69,853,073	G	C	0.362973	-0.011485	0.002109	4.60E-09	-0.014537	0.003572	4.76E-05	-0.010647	0.002645	5.77E-05	7.69E-08	0.381451	
15	TLE3 *	rs305008	69,853,301	A	G	0.362998	-0.01147	0.002109	4.90E-09	-0.014568	0.003571	4.57E-05	-0.010602	0.002645	6.19E-05	7.92E-08	0.372241	
15	TLE3 *	rs305009	69,853,419	A	G	0.327524	-0.012149	0.00215	1.10E-09	-0.014576	0.003645	6.43E-05	-0.011722	0.002695	1.38E-05	2.63E-08	0.528915	
15	TLE3 *	rs305010	69,853,872	G	A	0.362975	-0.01149	0.002109	4.50E-09	-0.014568	0.003572	4.58E-05	-0.01063	0.002645	5.92E-05	7.60E-08	0.375625	
15	TLE3 *	rs480441	69,855,220	C	T	0.327276	-0.012148	0.002152	1.00E-09	-0.014458	0.003648	7.47E-05	-0.011773	0.002697	1.29E-05	2.84E-08	0.553931	
15	TLE3 *	rs442652	69,856,555	C	A	0.327181	-0.012308	0.002154	6.60E-10	-0.014616	0.00365	6.30E-05	-0.01193	0.0027	1.00E-05	1.90E-08	0.554199	
15	TLE3 *	rs428823	69,856,745	C	T	0.327272	-0.012347	0.002153	6.00E-10	-0.014735	0.00365	5.47E-05	-0.011927	0.002699	1.01E-05	1.67E-08	0.536219	
15	TLE3 *	rs28669171	69,857,361	T	G	0.309407	-0.012265	0.002233	3.10E-09	-0.015127	0.003787	6.54E-05	-0.011561	0.002799	3.66E-05	6.75E-08	0.448772	
15	TLE3 *	rs435315	69,857,677	A	T	0.32505	-0.012683	0.002163	2.70E-10	-0.015364	0.003665	2.79E-05	-0.012132	0.002711	7.76E-06	6.84E-09	0.4784	
15	TLE3 *	rs442784	69,857,947	T	C	0.325049	-0.012703	0.002163	2.60E-10	-0.015343	0.003665	2.87E-05	-0.012163	0.002712	7.40E-06	6.73E-09	0.48552	
15	TLE3 *	rs446721	69,858,754	T	C	0.325024	-0.012641	0.002165	3.10E-10	-0.015427	0.003669	2.64E-05	-0.012005	0.002715	9.90E-06	8.19E-09	0.453392	
15	TLE3 *	rs12594366	69,860,568	C	T	0.316652	-0.012299	0.002183	9.10E-10	-0.014897	0.003699	5.70E-05	-0.011626	0.002738	2.20E-05	3.65E-08	0.477285	
15	TLE3 *	rs59650813	69,863,741	C	G	0.31404	-0.012526	0.002196	5.10E-10	-0.015672	0.003724	2.60E-05	-0.011539	0.002753	2.80E-05	2.18E-08	0.372067	
15	TLE3 *	rs13380008	69,867,183	C	T	0.3415	-0.012287	0.002162	1.60E-09	-0.0162	0.003657	9.55E-06	-0.011239	0.002714	3.48E-05	1.03E-08	0.275895	
15	TLE3 *	rs13379513	69,867,218	A	G	0.337617	-0.012705	0.002167	6.30E-10	-0.016903	0.003665	4.04E-06	-0.011526	0.002719	2.27E-05	3.01E-09	0.238715	
15	TLE3 *	rs12593720	69,868,843	T	C	0.237957	-0.017186	0.002388	1.70E-14	-0.022053	0.004044	5.05E-08	-0.015489	0.002995	2.37E-07	5.43E-13	0.192049	
15	TLE3 *	rs304975	69,869,121	G	C	0.347062	-0.012583	0.002143	4.70E-10	-0.016177	0.003622	8.07E-06	-0.011587	0.002691	1.69E-05	4.39E-09	0.309013	
15	TLE3 *	rs304979	69,870,936	C	G	0.346379	-0.01273	0.002144	2.80E-10	-0.016309	0.003624	6.87E-06	-0.011757	0.002693	1.28E-05	2.90E-09	0.313363	
15	TLE3 *	rs4777205	69,872,486	A	C	0.367785	-0.011923	0.002112	3.40E-09	-0.015326	0.003575	1.84E-05	-0.011018	0.00265	3.26E-05	1.81E-08	0.333084	
15	TLE3 *	rs10162636	69,875,502	T	G	0.241729	-0.017418	0.002392	7.90E-15	-0.022425	0.004049	3.12E-08	-0.015836	0.003001	1.34E-07	1.95E-13	0.191062	
15	TLE3 *	rs78943073	69,876,104	A	G	0.238571	-0.017478	0.002397	6.60E-15	-0.023064	0.004057	1.34E-08	-0.015455	0.003006	2.79E-07	1.75E-13	0.131868	
15	TLE3 *	rs78385799	69,878,325	A	G	0.270642	-0.01479	0.002304	5.40E-12	-0.022026	0.003905	1.74E-08	-0.011889	0.002888	3.89E-05	2.58E-11	0.036898	M
15	TLE3 *	rs304959	69,878,607	G	C	0.405038	-0.011301	0.002083	1.70E-08	-0.015816	0.003521	7.17E-06	-0.009754	0.002615	0.000193	3.97E-08	0.16698	
15	TLE3 *	rs6494835	69,879,436	A	T	0.271483	-0.015317	0.002293	7.40E-13	-0.023174	0.003885	2.51E-09	-0.012068	0.002875	2.73E-05	2.80E-12	0.021587	M
15	TLE3 *	rs8035009	69,879,649	G	C	0.271941	-0.015541	0.00229	3.90E-13	-0.023353	0.00388	1.81E-09	-0.012247	0.002871	2.02E-05	1.52E-12	0.021413	M
15	TLE3 *	rs75327024	69,880,728	A	G	0.239865	-0.0175	0.002389	4.00E-15	-0.023658	0.004047	5.17E-09	-0.015192	0.002996	4.03E-07	9.88E-14	0.092698	
15	TLE3 *	rs7166273	69,881,625	C	T	0.239669	-0.017754	0.002383	1.50E-15	-0.023802	0.004037	3.82E-09	-0.015451	0.002989	2.39E-07	4.43E-14	0.096365	
15	TLE3 *	rs304948	69,884,491	A	G	0.348611	-0.014524	0.00213	1.00E-12	-0.017057	0.003599	2.18E-06	-0.014096	0.002675	1.40E-07	1.24E-11	0.509085	
15	TLE3 *	rs1349680	69,886,868	C	T	0.376411	-0.014315	0.002089	2.50E-12	-0.017243	0.003537	1.11E-06	-0.013834	0.00262	1.33E-07	6.13E-12	0.4386	
15	TLE3 *	rs1349679	69,887,061	C	T	0.376077	-0.014415	0.002088	1.60E-12	-0.0172	0.003535	1.16E-06	-0.013974	0.002619	9.73E-08	4.77E-12	0.463444	
15	TLE3 *	rs304941	69,887,624	C	C	0.347007	-0.014704	0.002129	6.10E-13	-0.016964	0.003598	2.45E-06	-0.014408	0.002673	7.24E-08	7.33E-12	0.568404	
15	TLE3 *	rs717568	69,888,636	C	T	0.376131	-0.014336	0.002088	2.20E-12	-0.01709	0.003536	1.36E-06	-0.013927	0.002619	1.08E-07	6.14E-12	0.472316	
15	TLE3 *	rs80287865	69,889,112	T	G	0.230273	-0.019102	0.00241	3.40E-17	-0.023799	0.004081	5.62E-09	-0.017491	0.003022	7.36E-09	2.20E-15	0.214161	
15	TLE3 *	rs77648222	69,890,512	G	A	0.235274	-0.019303	0.002383	1.10E-17	-0.024931	0.004037	6.78E-10	-0.017199	0.002988	8.88E-09	1.23E-09	0.123659	
15	TLE3 *	rs17756181	69,891,852	G	A	0.244714	-0.019359	0.002349	4.90E-18	-0.025195	0.00398	2.51E-10	-0.017272	0.002946	4.69E-09	6.81E-17	0.109602	
15	TLE3 *	rs28521935	69,892,800	C	A	0.239626	-0.018975	0.002375	3.30E-17	-0.024183	0.004021	1.86E-09	-0.017194	0.002979	8.10E-09	8.19E-16	0.162522	
15	TLE3 *	rs881053	69,894,413	A	G	0.374498	-0.014317	0.002091	2.20E-12	-0.016816	0.003538	2.04E-06	-0.014062	0.002624	8.55E-08	7.22E-12	0.531856	
15	TLE3 *	rs1452725	69,895,764	T	C	0.371959	-0.01435	0.002098	1.60E-12	-0.017081	0.003551	1.53E-06	-0.014006	0.002632	1.05E-07	6.67E-12	0.486727	
15	TLE3 *	rs8041139	69,896,404	G	T	0.347326	-0.014844	0.002129	3.30E-13	-0.017292	0.003597	1.55E-06	-0.01447	0.002673	6.31E-08	4.14E-12	0.528885	
15	TLE3 *	rs1155996	69,897,006	C	T	0.34716	-0.014753	0.002127	4.30E-13	-0.016881	0.003593	2.66E-06	-0.014511	0.002671	5.65E-08	6.23E-12	0.596508	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
16	CETP *	rs821840	56,959,974	G	A	0.135714	-0.017111	0.003007	2.60E-09	-0.016388	0.005123	0.001387	-0.017768	0.003757	2.30E-06	8.37E-08	0.828102	
16	CETP *	rs17231506	56,960,616	T	C	0.163661	-0.015979	0.002729	8.40E-10	-0.016979	0.004639	0.000254	-0.016012	0.003415	2.80E-06	2.08E-08	0.866689	
16	CMIP	rs2925979	81,501,185	T	C	0.428822	0.013925	0.002039	3.70E-13	0.007669	0.003465	0.026905	0.018052	0.002551	1.54E-12	1.15E-12	0.015837	F
17	ZNHIT3	rs2306589	36,493,030	T	C	0.335792	0.011238	0.002173	4.30E-08	0.017184	0.003685	3.17E-06	0.007833	0.002722	0.004017	3.02E-07	0.041263	M
17	ZNHIT3	rs7222903	36,494,779	T	G	0.335896	0.012104	0.002172	4.60E-08	0.01713	0.003684	3.38E-06	0.007816	0.002722	0.004094	3.27E-07	0.042049	M
17	MYO19	rs1109442	36,506,381	C	T	0.340559	0.011245	0.00216	3.80E-08	0.017163	0.003666	2.89E-06	0.007809	0.002705	0.003904	2.69E-07	0.040062	M
17	MYO19	rs8070260	36,511,076	A	G	0.340599	0.011196	0.002159	4.20E-08	0.017095	0.003665	3.14E-06	0.007738	0.002703	0.004209	3.13E-07	0.039928	M
17	PIGW	rs11650008	36,536,882	A	C	0.335829	0.011867	0.002166	8.20E-09	0.017959	0.00368	1.08E-06	0.008417	0.002711	0.001915	5.44E-08	0.03686	M
17	PIGW *	rs11263770	36,541,028	A	G	0.337258	0.011499	0.00216	1.90E-08	0.01741	0.003669	2.12E-06	0.008117	0.002704	0.002689	1.43E-07	0.041484	M
17	GGNB2	rs3736166	36,544,987	C	G	0.335881	0.011556	0.002163	1.60E-08	0.017642	0.003674	1.60E-06	0.008113	0.002707	0.002737	1.10E-07	0.036806	M
17	GGNB2	rs9906189	36,549,567	G	A	0.338036	0.011768	0.002155	1.00E-08	0.01715	0.003661	2.85E-06	0.008716	0.002697	0.001235	9.25E-08	0.063631	
17	GGNB2	rs2285642	36,556,904	G	C	0.337792	0.011777	0.002156	1.10E-08	0.016897	0.003661	3.99E-06	0.008807	0.002699	0.001108	1.16E-07	0.07532	
17	GGNB2	rs9903355	36,580,791	T	C	0.337652	0.011841	0.002157	8.60E-09	0.017426	0.003664	2.01E-06	0.008614	0.0027	0.001427	7.55E-08	0.052868	
17	DHRS11	rs2285640	36,594,774	G	A	0.33715	0.011402	0.002165	3.30E-08	0.017913	0.003679	1.14E-06	0.007637	0.00271	0.004851	1.35E-07	0.024549	M
17	CLTC	rs60164173	59,645,912	A	G	0.445368	0.011063	0.002048	2.60E-08	0.008255	0.003469	0.017361	0.013488	0.002567	1.52E-07	5.96E-08	0.225308	
17	CLTC	rs2877975	59,653,444	T	C	0.444761	0.010935	0.002049	3.70E-08	0.008207	0.003471	0.018081	0.013287	0.002568	2.34E-07	9.41E-08	0.239412	
17	CLTC	rs7223899	59,655,224	T	C	0.445403	0.011036	0.002048	2.80E-08	0.008105	0.003469	0.0195	0.013544	0.002567	1.34E-07	5.87E-08	0.207606	
17	CLTC	rs7224631	59,655,553	A	G	0.445402	0.011035	0.002048	2.80E-08	0.008103	0.003469	0.019537	0.013544	0.002567	1.34E-07	5.88E-08	0.207404	
17	CLTC	rs16943748	59,657,329	A	G	0.445404	0.011035	0.002048	2.80E-08	0.008103	0.003469	0.019541	0.013544	0.002567	1.34E-07	5.88E-08	0.207339	
17	CLTC	rs1528493	59,660,002	C	A	0.445402	0.011035	0.002048	2.80E-08	0.00809	0.003469	0.019736	0.013554	0.002567	1.32E-07	5.81E-08	0.205462	
17	CLTC	rs12603541	59,661,283	T	C	0.445396	0.011044	0.002048	2.70E-08	0.008119	0.003469	0.019298	0.013551	0.002567	1.32E-07	5.73E-08	0.208102	
17	CLTC	rs2140001	59,664,425	C	T	0.44555	0.011039	0.002048	2.60E-08	0.008103	0.00347	0.019576	0.013538	0.002567	1.37E-07	6.00E-08	0.207974	
17	CLTC	rs12601863	59,665,475	G	A	0.445435	0.011038	0.002048	2.70E-08	0.00805	0.00347	0.020362	0.013573	0.002567	1.26E-07	5.74E-08	0.200614	
17	CLTC	rs2272411	59,668,746	G	A	0.445424	0.011054	0.002048	2.60E-08	0.008022	0.00347	0.020788	0.013614	0.002567	1.16E-07	5.37E-08	0.195089	
17	CLTC	rs10515171	59,670,178	G	T	0.44545	0.011101	0.002047	2.30E-08	0.008043	0.003469	0.020455	0.013679	0.002566	1.00E-07	4.61E-08	0.19146	
17	CLTC	rs16943773	59,671,161	G	A	0.44548	0.011098	0.002047	2.40E-08	0.00803	0.003469	0.02064	0.013684	0.002566	9.91E-08	4.59E-08	0.190072	
17	CLTC	rs28465103	59,677,230	G	A	0.448932	0.011024	0.00205	3.60E-08	0.008173	0.003474	0.018674	0.013467	0.002569	1.63E-07	6.81E-08	0.220478	
17	CLTC	rs57592560	59,684,662	T	C	0.449702	0.010999	0.002049	3.10E-08	0.008258	0.003471	0.017376	0.013356	0.002568	2.03E-07	7.92E-08	0.237682	
17	CLTC	rs2271303	59,685,510	C	T	0.449128	0.011122	0.002049	2.40E-08	0.008302	0.003471	0.016787	0.013533	0.002568	1.40E-07	5.35E-08	0.225731	
17	CLTC	rs7212825	59,691,837	G	A	0.44896	0.011004	0.002049	3.20E-08	0.00826	0.003472	0.017365	0.013384	0.002569	1.92E-07	7.50E-08	0.235421	
17	PTRH2	rs7226149	59,702,871	C	T	0.435875	0.011091	0.002048	1.40E-08	0.006734	0.003471	0.052421	0.014315	0.002567	2.52E-08	0.07908	0.270E-08	
17	VMP1	rs111723017	59,710,070	C	G	0.435802	0.011223	0.002047	1.00E-08	0.007173	0.00347	0.038711	0.014273	0.002566	2.74E-08	2.27E-08	0.099939	
17	VMP1	rs200302970	59,711,423	T	C	0.40295	-0.010964	0.002076	3.10E-08	-0.008616	0.00352	0.014401	-0.013278	0.002602	3.40E-07	1.10E-07	0.286823	
17	VMP1	rs9903626	59,713,266	G	A	0.436006	0.011299	0.002047	7.80E-09	0.007247	0.003468	0.036648	0.01437	0.002566	2.19E-08	1.74E-08	0.098712	
17	VMP1	rs12947232	59,714,483	G	A	0.406312	-0.011176	0.002066	1.50E-08	-0.009005	0.003503	0.01018	-0.013374	0.002589	2.43E-07	5.88E-08	0.315817	
17	VMP1	rs8065615	59,720,804	T	C	0.461569	-0.011436	0.002033	2.80E-09	-0.009004	0.003449	0.009057	-0.013731	0.002546	7.07E-08	1.60E-08	0.270175	
17	VMP1	rs76856339	59,723,605	A	G	0.434952	0.011448	0.00204	4.80E-09	0.008659	0.003455	0.012223	0.013834	0.002558	6.53E-08	1.93E-08	0.228655	
17	VMP1	rs8080483	59,724,061	C	A	0.435435	0.011444	0.002042	5.00E-09	0.008666	0.003458	0.012229	0.013836	0.00256	6.68E-08	1.97E-08	0.229515	
17	VMP1	rs8081108	59,724,236	T	G	0.400821	-0.010992	0.002064	1.70E-08	-0.009158	0.0035	0.008899	-0.013112	0.002587	4.09E-07	8.61E-08	0.363534	
17	VMP1	rs8081395	59,724,400	A	G	0.40175	-0.010986	0.002062	1.60E-08	-0.00876	0.003495	0.012228	-0.0133	0.002584	2.69E-07	7.63E-08	0.296248	
17	VMP1	rs9900133	59,724,686	G	T	0.461881	-0.011387	0.00203	2.90E-09	-0.009065	0.003445	0.00851	-0.013608	0.002543	8.95E-08	1.90E-08	0.288673	
17	VMP1	rs11870590	59,724,791	A	C	0.462279	-0.011384	0.00203	3.10E-09	-0.008991	0.003444	0.009758	-0.013686	0.002543	7.53E-08	1.82E-08	0.263638	
17	VMP1	rs72840511	59,728,650	T	G	0.435002	0.011427	0.00204	5.20E-09	0.008599	0.003455	0.012832	0.013854	0.002558	6.26E-08	1.94E-08	0.221483	
17	VMP1	rs9901606	59,734,046	C	A	0.434801	0.011461	0.002038	5.00E-09	0.008598	0.003451	0.012737	0.01387	0.002555	5.81E-08	1.79E-08	0.219484	
17	VMP1	rs9910518	59,734,706	C	T	0.434847	0.011487	0.002038	4.60E-09	0.008687	0.003451	0.011834	0.01385	0.002555	6.08E-08	1.75E-08	0.229208	
17	VMP1	rs2271304	59,737,280	G	A	0.434858	0.011455	0.002037	4.60E-09	0.008668	0.00345	0.012006	0.013799	0.002554	6.73E-08	1.96E-08	0.232021	
17	VMP1	rs2777898	59,738,247	C	G	0.402372	-0.010815	0.002061	2.80E-08	-0.008623	0.003493	0.013582	-0.013027	0.002583	4.66E-07	3.10E-07	0.310627	
17	VMP1	rs28516945	59,739,217	C	T	0.426137	0.010736	0.002052	3.80E-08	0.008196	0.003479	0.018503	0.013154	0.002571	3.18E-07	1.29E-07	0.251648	
17	VMP1	rs8067354	59,744,069	G	A	0.462889	-0.010851	0.00203	1.50E-08	-0.008746	0.003442	0.011076	-0.012932	0.002544	3.76E-07	9.66E-08	0.327979	
17	VMP1	rs56236317	59,744,764	T	C	0.434793	0.011401	0.002038	5.70E-09	0.008597	0.003451	0.012746	0.013751	0.002555	7.56E-08	2.31E-08	0.229977	
17	VMP1	rs7215180	59,744,993	G	A	0.434793	0.011401	0.002038	5.70E-09	0.008597	0.003451	0.012746	0.013751	0.002555	7.56E-08	2.31E-08	0.229977	
17	VMP1	rs6503939	59,746,324	G	A	0.462456	-0.011229	0.002028	4.60E-09	-0.008683	0.00344	0.011617	-0.013527	0.00254	1.03E-07	2.87E-08	0.257237	
17	VMP1	rs9907923	59,747,566	T	C	0.433742	0.011264	0.002042	9.20E-09	0.008645	0.003458	0.012443	0.013456	0.00256	1.50E-07	4.39E-08	0.262349	
17	VMP1	rs9896742	59,749,169	T	G	0.464633	-0.010957	0.002035	1.20E-08	-0.008475	0.003452	0.014108	-0.013247	0.002549	2.07E-07	6.72E-08	0.26609	
17	VMP1	rs60451858	59,749,244	G	A	0.435252	0.011453	0.002038	4.50E-09	0.008503	0.003451	0.013778	0.013905	0.002556	5.42E-08	1.79E-08	0.208371	
17	VMP1	rs2665397	59,749,370	A	C	0.401912	-0.01096	0.002061	1.70E-08	-0.008778	0.003493	0.011997	-0.013221	0.002583	3.14E-07	8.69E-08	0.306472	
17	VMP1	rs139779337	59,751,603	A	G													

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
17	VMP1	rs2645467	59,777,422	T	C	0.435273	0.011508	0.002039	4.50E-09	0.008949	0.003452	0.009561	0.013776	0.002556	7.25E-08	1.72E-08	0.261083	
17	VMP1	rs2132715	59,781,013	T	A	0.435065	0.011515	0.00204	4.30E-09	0.008935	0.003454	0.009702	0.013805	0.002558	6.92E-08	1.66E-08	0.257083	
17	VMP1	rs2150879	59,781,849	A	G	0.401291	-0.011016	0.002065	1.50E-08	-0.009333	0.003501	0.007691	-0.013027	0.002587	4.85E-07	8.91E-08	0.396015	
17	VMP1	rs2173119	59,782,344	T	C	0.435073	0.011486	0.00204	4.70E-09	0.008931	0.003454	0.00973	0.013761	0.002558	7.62E-08	1.83E-08	0.261104	
17	VMP1	rs2453913	59,782,789	G	T	0.457371	-0.011159	0.002036	6.90E-09	-0.008868	0.003454	0.010267	-0.013335	0.002551	1.76E-07	4.33E-08	0.298128	
17	VMP1	rs2645474	59,791,240	A	G	0.427832	0.011138	0.002063	1.60E-08	0.007824	0.003494	0.025166	0.013802	0.002587	9.71E-08	5.35E-08	0.169118	
17	VMP1	rs2777900	59,795,133	A	G	0.433133	0.011956	0.002037	1.10E-09	0.009056	0.00345	0.008683	0.014412	0.002555	1.74E-08	3.93E-09	0.212113	
17	VMP1	rs2665405	59,797,931	A	G	0.403831	-0.011419	0.00206	4.10E-09	-0.009127	0.003492	0.008981	-0.013782	0.002581	9.54E-08	2.12E-08	0.28378	
17	VMP1	rs2665404	59,798,035	T	C	0.403732	-0.01142	0.002058	4.10E-09	-0.009007	0.003489	0.00985	-0.013828	0.002579	8.41E-08	0.266448		
17	VMP1	rs2645492	59,798,193	A	G	0.433093	0.011947	0.002037	1.10E-09	0.009016	0.003449	0.008975	0.01443	0.002555	1.66E-08	3.88E-09	0.207151	
17	VMP1	rs2102507	59,798,546	G	A	0.432978	0.01197	0.002037	1.00E-09	0.009119	0.00345	0.008226	0.014387	0.002555	1.84E-08	3.96E-09	0.219746	
17	VMP1	rs2645491	59,799,688	T	C	0.433124	0.011929	0.002037	1.10E-09	0.009032	0.00345	0.008859	0.014394	0.002555	1.81E-08	4.17E-09	0.211634	
17	VMP1	rs2777895	59,802,249	G	A	0.403779	-0.011442	0.002058	3.80E-09	-0.009081	0.003488	0.009256	-0.013822	0.002579	8.54E-08	1.96E-08	0.274476	
17	VMP1	rs2665400	59,802,840	A	G	0.43633	0.012219	0.002038	4.70E-10	0.009378	0.003451	0.006593	0.014705	0.002555	8.86E-09	1.60E-09	0.214722	
17	VMP1	rs2645489	59,806,010	G	T	0.431473	0.012087	0.002043	6.30E-10	0.009044	0.003459	0.008948	0.014667	0.002561	1.05E-08	2.49E-09	0.191437	
17	VMP1	rs12449331	59,806,285	C	T	0.403802	-0.011368	0.002059	4.40E-09	-0.008968	0.003491	0.010228	-0.013783	0.002581	9.45E-08	2.36E-08	0.267312	
17	VMP1	rs4622571	59,807,036	T	A	0.467556	-0.011045	0.002027	6.70E-09	-0.008089	0.003437	0.018632	-0.013571	0.002539	9.23E-08	3.92E-08	0.199492	
17	VMP1	rs2645486	59,808,540	A	T	0.433167	0.011938	0.002037	1.10E-09	0.008975	0.00345	0.009298	0.014444	0.002555	1.61E-08	3.89E-09	0.202691	
17	VMP1	rs2645487	59,808,764	G	T	0.433167	0.011939	0.002037	1.10E-09	0.008975	0.00345	0.009298	0.014446	0.002555	1.61E-08	3.88E-09	0.202534	
17	VMP1	rs11079389	59,810,591	A	G	0.433173	0.011949	0.002037	1.10E-09	0.008983	0.00345	0.00924	0.01446	0.002555	1.55E-08	3.73E-09	0.201929	
17	VMP1	rs2063353	59,811,831	G	T	0.404116	-0.011475	0.002058	3.60E-09	-0.009007	0.003489	0.009853	-0.013917	0.002579	6.99E-08	1.70E-08	0.257723	
17	VMP1	rs2645488	59,812,044	T	G	0.467059	-0.011058	0.002026	6.50E-09	-0.008117	0.003436	0.018164	-0.013572	0.002538	9.13E-08	3.79E-08	0.201577	
17	VMP1	rs2665402	59,812,045	T	A	0.467059	-0.011058	0.002026	6.50E-09	-0.008117	0.003436	0.018164	-0.013572	0.002538	9.13E-08	3.79E-08	0.201577	
17	VMP1	rs2665403	59,812,624	A	G	0.433659	0.011195	0.002036	1.10E-09	0.008949	0.003447	0.009457	0.014468	0.002554	1.50E-08	3.69E-09	0.19828	
17	VMP1	rs2173120	59,815,279	T	A	0.433598	0.011887	0.002036	1.30E-09	0.008861	0.003448	0.01018	0.014399	0.002554	1.76E-08	4.59E-09	0.196756	
17	VMP1	rs115869798	59,815,468	A	T	0.432067	0.012017	0.002042	1.00E-09	0.008615	0.003457	0.012726	0.014785	0.002561	8.00E-09	2.60E-09	0.151603	
17	VMP1	rs4257266	59,817,098	G	A	0.464316	-0.011001	0.00204	1.10E-08	-0.008526	0.003461	0.01378	-0.013408	0.002556	1.58E-07	5.07E-08	0.25641	
17	VMP1	rs11079390	59,818,580	G	C	0.467074	-0.01104	0.002026	6.80E-09	-0.008051	0.003436	0.019136	-0.013583	0.002538	8.93E-08	3.89E-08	0.195264	
17	VMP1	rs7223793	59,818,661	G	T	0.433643	0.011954	0.002036	1.00E-09	0.008946	0.003448	0.00948	0.014474	0.002554	1.48E-08	3.65E-09	0.197569	
17	VMP1	rs2336317	59,818,859	A	T	0.467074	-0.01104	0.002026	6.80E-09	-0.008051	0.003436	0.019136	-0.013583	0.002538	8.93E-08	3.89E-08	0.195264	
17	VMP1	rs7224006	59,818,977	T	C	0.467067	-0.011041	0.002026	6.80E-09	-0.008061	0.003436	0.01898	-0.013582	0.002538	8.95E-08	3.87E-08	0.196205	
17	VMP1	rs12938273	59,824,291	A	G	0.404186	-0.011284	0.00206	6.20E-09	-0.008557	0.003492	0.01427	-0.013841	0.002582	8.48E-08	2.86E-08	0.223658	
17	VMP1	rs2526352	59,827,462	A	G	0.431516	0.011629	0.002042	3.50E-09	0.008697	0.003458	0.011929	0.014034	0.00256	4.30E-08	1.26E-08	0.214883	
17	VMP1	rs1292065	59,828,927	G	C	0.467081	-0.011033	0.002026	7.00E-09	-0.008066	0.003436	0.018919	-0.013565	0.002538	9.30E-08	4.00E-08	0.197942	
17	VMP1	rs1292064	59,828,957	C	A	0.403718	-0.011438	0.002058	3.70E-09	-0.009035	0.003489	0.009625	-0.013857	0.00258	7.99E-08	1.90E-08	0.266313	
17	VMP1	rs1292063	59,830,407	T	A	0.434859	0.011841	0.00204	1.50E-09	0.008788	0.003452	0.010933	0.014435	0.002558	1.72E-08	4.79E-09	0.18876	
17	VMP1	rs1295926	59,832,012	G	A	0.403894	-0.011528	0.002058	2.90E-09	-0.009085	0.003487	0.009202	-0.013957	0.002579	6.37E-08	1.46E-08	0.261266	
17	VMP1	rs1296280	59,832,068	T	A	0.403755	-0.011524	0.002058	3.00E-09	-0.009022	0.003488	0.00971	-0.013984	0.00258	6.06E-08	1.46E-08	0.252767	
17	VMP1	rs1295925	59,832,902	C	T	0.467093	-0.011083	0.002026	6.10E-09	-0.008108	0.003436	0.018296	-0.013612	0.002538	8.37E-08	3.51E-08	0.197523	
17	VMP1	rs1292061	59,833,869	G	A	0.404026	-0.01148	0.002058	3.30E-09	-0.009094	0.003488	0.009146	-0.013886	0.002579	7.48E-08	1.70E-08	0.269362	
17	VMP1	rs1292060	59,836,488	A	G	0.46709	-0.011078	0.002026	6.10E-09	-0.008119	0.003436	0.018146	-0.013599	0.002538	8.61E-08	3.58E-08	0.199502	
17	MIR21 *	rs1292037	59,841,547	C	T	0.433617	0.012	0.002036	9.00E-10	0.008993	0.003447	0.009112	0.014509	0.002554	1.37E-08	3.25E-09	0.198464	
17	MIR21 *	rs13137	59,841,670	T	A	0.433617	0.012	0.002036	9.00E-10	0.008993	0.003447	0.009112	0.014509	0.002554	1.37E-08	3.25E-09	0.198464	
17	MIR21 *	rs2645479	59,843,171	A	G	0.40381	-0.011617	0.002059	2.20E-09	-0.009285	0.00349	0.007818	-0.013965	0.00258	6.35E-08	1.26E-08	0.280798	
17	MIR21 *	rs1292072	59,848,288	G	A	0.433419	0.011827	0.002042	1.70E-09	0.008755	0.003458	0.011371	0.014369	0.002561	2.08E-08	5.96E-09	0.191996	
17	MIR21 *	rs79417738	59,850,363	G	A	0.372738	0.011982	0.002129	2.30E-08	0.010645	0.003602	0.003134	0.013631	0.002671	3.40E-07	2.80E-08	0.505465	
17	TUBD1 *	rs1292067	59,853,285	T	G	0.448238	0.011495	0.002042	1.70E-08	0.010086	0.003453	0.003505	0.013262	0.002562	2.30E-07	2.12E-08	0.460042	
17	TUBD1 *	rs1292066	59,854,953	A	T	0.38686	0.011359	0.002091	4.60E-08	0.00922	0.003537	0.009159	0.013372	0.002624	3.54E-07	7.68E-08	0.345808	
17	TUBD1 *	rs1292043	59,856,808	G	A	0.384122	0.011878	0.002087	1.20E-08	0.009122	0.003528	0.00974	0.014233	0.002619	5.62E-08	1.37E-08	0.244713	
17	TUBD1 *	rs1292042	59,857,634	G	A	0.382678	0.011935	0.002087	9.70E-09	0.00944	0.003529	0.007487	0.014101	0.00262	7.53E-08	1.43E-08	0.288914	
17	TUBD1	rs2526358	59,865,224	G	A	0.380167	0.011793	0.002087	1.50E-08	0.009143	0.003532	0.009662	0.014062	0.002618	7.99E-08	1.91E-08	0.263169	
17	TUBD1	rs2250526	59,874,612	A	G	0.379057	0.0116	0.002083	2.30E-08	0.009197	0.003525	0.009102	0.013784	0.002613	1.35E-07	3.00E-08	0.295834	
17	TUBD1	rs1292049	59,877,544	T	G	0.379056	0.011581	0.002083	2.40E-08	0.009198	0.003525	0.009092	0.01375	0.002612	1.45E-07	3.21E-08	0.299584	
17	TUBD1	rs1292059	59,880,527	A	T	0.379061	0.011604	0.002083	2.20E-08	0.009201	0.003525	0.009071	0.013785	0.002612	1.34E-07	2.98E-08	0.296024	
17	TUBD1	rs1292057	59,880,763	T	C	0.393398	0.011364	0.002071	2.90E-08	0.009745	0.003506	0.005463	0.012967	0.002598	6.09E-07	8.16E-08	0.460301	
17	TUBD1	rs1295923	59,883,075	G	A	0.378523	0.01155	0.002084	2.60E-08	0.008996	0.003527	0.010779	0.013824	0.002614	1.27E-07	3.29E-08	0.271455	
17	TUBD1	rs1292050	59,887,808	C	T	0.379139	0.011643	0.002082</										

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
17	RP5GKB1	rs2645478	59,937,351	A	G	0.379347	0.011485	0.002081	3.10E-08	0.008925	0.003523	0.011305	0.013684	0.00261	1.62E-07	4.34E-08	0.277736	
17	RP5GKB1	rs72840315	59,940,781	C	G	0.379347	0.011485	0.002081	3.10E-08	0.008925	0.003523	0.011305	0.013684	0.00261	1.62E-07	4.34E-08	0.277736	
17	RP5GKB1	rs9789060	59,941,209	G	A	0.378679	0.011493	0.002084	3.30E-08	0.0089	0.003527	0.011648	0.01369	0.002614	1.67E-07	4.60E-08	0.275284	
17	RP5GKB1	rs1051424	59,946,963	G	A	0.379471	0.011432	0.00208	3.80E-08	0.008769	0.003521	0.012783	0.013707	0.002609	1.53E-07	4.59E-08	0.259856	
17	RNF11	rs7219089	59,955,504	T	C	0.379823	0.011657	0.002081	2.00E-08	0.008764	0.003523	0.012888	0.014018	0.002611	8.07E-08	2.49E-08	0.230792	
17	RNF11	rs7221472	59,959,376	T	C	0.379379	0.011538	0.002081	2.70E-08	0.00881	0.003522	0.012383	0.013844	0.00261	1.16E-07	3.40E-08	0.250778	
17	RNF11	rs12600680	59,960,013	C	T	0.378983	0.01144	0.002083	3.80E-08	0.009061	0.003526	0.010201	0.013557	0.002612	2.14E-07	5.21E-08	0.305549	
17	RNF11 *	rs76419616	59,964,765	C	T	0.378291	0.011639	0.002086	2.10E-08	0.008639	0.00353	0.014401	0.014054	0.002616	7.97E-08	2.71E-08	0.217749	
17	BPTF *	rs3936134	67,818,266	C	G	0.374868	-0.011624	0.00213	3.40E-08	-0.005457	0.003616	0.131276	-0.015117	0.002667	1.48E-08	0.031562	F	
17	BPTF *	rs72631329	67,822,258	T	C	0.374318	-0.011785	0.002132	2.30E-08	-0.005758	0.003622	0.111881	-0.015289	0.002669	1.04E-08	0.034146	F	
17	BPTF	rs12603589	67,829,132	T	C	0.343835	-0.013149	0.002163	5.30E-10	-0.004761	0.003681	0.195857	-0.017934	0.002705	3.46E-11	0.003942	F	
17	BPTF	rs12601921	67,829,238	C	T	0.342767	-0.013495	0.002177	2.20E-10	-0.004955	0.003709	0.181533	-0.018399	0.002721	1.42E-11	0.003483	F	
17	BPTF	rs12601919	67,829,258	A	G	0.344266	-0.013287	0.002162	3.90E-10	-0.004919	0.003679	0.18126	-0.017998	0.002703	2.86E-11	0.004184	F	
17	BPTF	rs9915591	67,829,974	C	G	0.344386	-0.013038	0.002162	8.20E-10	-0.004557	0.00368	0.215542	-0.017801	0.002704	4.76E-11	1.80E-10	0.003737	F
17	BPTF	rs12602556	67,830,745	A	G	0.343716	-0.013122	0.00216	5.80E-10	-0.004595	0.003677	0.211387	-0.017896	0.002701	3.56E-11	1.34E-10	0.003561	F
17	BPTF	rs62084208	67,831,327	C	T	0.344143	-0.013225	0.002158	4.50E-10	-0.005161	0.003674	0.160072	-0.017781	0.002698	4.55E-11	1.38E-10	0.005648	F
17	BPTF	rs2080090	67,832,255	T	A	0.347444	-0.013116	0.002174	5.60E-10	-0.004114	0.003701	0.266317	-0.018251	0.002718	1.95E-11	8.73E-11	0.00209	F
17	BPTF	rs62084210	67,832,594	A	G	0.343869	-0.013363	0.002158	2.80E-10	-0.004958	0.003674	0.177071	-0.018075	0.002698	2.15E-11	7.17E-11	0.004015	F
17	BPTF	rs12449312	67,833,242	A	C	0.350329	-0.012676	0.002167	1.70E-09	-0.004776	0.00369	0.195488	-0.017139	0.00271	2.61E-10	8.88E-10	0.006942	F
17	BPTF	rs7223643	67,834,166	A	G	0.344786	-0.013231	0.002145	3.00E-10	-0.005242	0.003653	0.151245	-0.017659	0.002683	4.78E-11	1.39E-10	0.006161	F
17	BPTF	rs1976052	67,834,462	C	T	0.344958	-0.013348	0.002143	2.20E-10	-0.005522	0.003648	0.130033	-0.0177	0.00268	4.11E-11	1.07E-10	0.007151	F
17	BPTF	rs7209675	67,835,142	A	T	0.344758	-0.013259	0.002133	2.20E-10	-0.005594	0.003632	0.123533	-0.017583	0.002666	4.38E-11	1.09E-10	0.007813	F
17	BPTF	rs7218014	67,835,900	T	C	0.343895	-0.013535	0.002134	8.70E-11	-0.005925	0.003634	0.102994	-0.017887	0.002668	2.09E-11	4.59E-11	0.007989	F
17	BPTF	rs7221651	67,836,274	G	A	0.344876	-0.013318	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017645	0.002661	3.46E-11	8.24E-11	0.007913	F
17	BPTF	rs12452511	67,836,460	A	G	0.344876	-0.013318	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017645	0.002661	3.46E-11	8.24E-11	0.007913	F
17	BPTF	rs1976053	67,836,886	C	G	0.337681	-0.01357	0.002145	1.20E-10	-0.006325	0.003649	0.083046	-0.017653	0.002683	4.85E-11	8.80E-11	0.012401	F
17	BPTF	rs1976054	67,837,108	T	G	0.344876	-0.013318	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017645	0.002661	3.46E-11	8.24E-11	0.007913	F
17	BPTF	rs7208909	67,837,430	T	C	0.347887	-0.013138	0.002132	2.50E-10	-0.004811	0.00363	0.185039	-0.017795	0.002667	2.59E-11	8.86E-11	0.003952	F
17	BPTF	rs2052187	67,838,621	T	C	0.344876	-0.013318	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017645	0.002661	3.46E-11	8.24E-11	0.007913	F
17	BPTF	rs11079705	67,839,336	A	T	0.348431	-0.012852	0.002133	6.10E-10	-0.005708	0.003631	0.115861	-0.016948	0.002667	2.15E-10	4.93E-10	0.012612	F
17	BPTF	rs11079706	67,839,354	G	T	0.345168	-0.013259	0.002133	1.90E-10	-0.005747	0.003632	0.113601	-0.017574	0.002667	4.56E-11	1.06E-10	0.00869	F
17	BPTF	rs11079707	67,839,501	G	A	0.345109	-0.0133	0.002129	1.70E-10	-0.005746	0.003624	0.112848	-0.017601	0.002662	3.92E-11	9.13E-11	0.008402	F
17	BPTF	rs80135947	67,839,885	A	C	0.344874	-0.013325	0.002128	1.50E-10	-0.005702	0.003624	0.11561	-0.017655	0.002661	3.37E-11	8.03E-11	0.007859	F
17	BPTF	rs59252707	67,840,471	T	C	0.357273	-0.012712	0.002147	1.40E-09	-0.005364	0.003654	0.142084	-0.01693	0.002686	3.00E-10	8.01E-10	0.010783	F
17	BPTF	rs6504542	67,840,526	T	C	0.344864	-0.013306	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017625	0.002661	3.65E-11	8.68E-11	0.00802	F
17	BPTF	rs8082512	67,840,943	T	C	0.344864	-0.013306	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017625	0.002661	3.65E-11	8.68E-11	0.00802	F
17	BPTF	rs1598959	67,841,077	C	G	0.34471	-0.013228	0.002129	2.10E-10	-0.005556	0.003625	0.125349	-0.017587	0.002662	4.07E-11	1.03E-10	0.007483	F
17	BPTF	rs1966410	67,841,099	T	C	0.34471	-0.013228	0.002129	2.10E-10	-0.005556	0.003625	0.125349	-0.017587	0.002662	4.07E-11	1.03E-10	0.007483	F
17	BPTF	rs58551145	67,841,119	A	G	0.344849	-0.013158	0.002129	2.80E-10	-0.00555	0.003625	0.125775	-0.017487	0.002662	5.26E-11	1.33E-10	0.007967	F
17	BPTF	rs6504543	67,841,543	T	C	0.339096	-0.013601	0.002138	8.10E-11	-0.006487	0.003639	0.074608	-0.017674	0.002674	4.00E-11	6.68E-11	0.013257	F
17	BPTF	rs8067892	67,841,867	A	G	0.344864	-0.013306	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017625	0.002661	3.65E-11	8.68E-11	0.00802	F
17	BPTF	rs8074078	67,842,627	T	G	0.344864	-0.013306	0.002128	1.60E-10	-0.005702	0.003624	0.11561	-0.017625	0.002661	3.65E-11	8.68E-11	0.00802	F
17	BPTF	rs8073510	67,843,094	A	G	0.346046	-0.013167	0.00213	2.70E-10	-0.005246	0.003627	0.148011	-0.017624	0.002662	3.73E-11	1.07E-10	0.005952	F
17	BPTF	rs12450363	67,843,992	T	C	0.345408	-0.012938	0.002132	5.10E-10	-0.005236	0.00363	0.149175	-0.017323	0.002665	8.25E-11	2.35E-10	0.007291	F
17	BPTF	rs62084212	67,844,128	G	A	0.355366	-0.01249	0.002159	2.40E-09	-0.004413	0.003677	0.230066	-0.017052	0.002698	2.69E-10	1.03E-09	0.005601	F
17	BPTF	rs11222385	67,844,408	T	C	0.344279	-0.01331	0.002131	1.50E-10	-0.00585	0.003627	0.106738	-0.017527	0.002665	4.94E-11	1.10E-10	0.009489	F
17	BPTF	rs11871285	67,844,693	G	T	0.346655	-0.013243	0.002128	2.20E-10	-0.005493	0.003623	0.129486	-0.017643	0.002661	3.49E-11	9.06E-11	0.006899	F
17	BPTF	rs11868959	67,844,694	T	C	0.346655	-0.013243	0.002128	2.20E-10	-0.005493	0.003623	0.129486	-0.017643	0.002661	3.49E-11	9.06E-11	0.006899	F
17	BPTF	rs2365466	67,845,013	G	A	0.345307	-0.013279	0.002127	1.70E-10	-0.005551	0.003621	0.125277	-0.017699	0.00266	2.94E-11	7.46E-11	0.006874	F
17	BPTF	rs2365467	67,845,169	A	T	0.340265	-0.013455	0.002139	1.50E-10	-0.006195	0.003639	0.088729	-0.017627	0.002675	4.61E-11	8.83E-11	0.011398	F
17	BPTF	rs2365468	67,845,202	C	T	0.339539	-0.01358	0.002137	8.30E-11	-0.00634	0.003636	0.081243	-0.017748	0.002672	3.21E-11	5.77E-11	0.011488	F
17	BPTF	rs62084213	67,845,900	A	G	0.345307	-0.013279	0.002127	1.70E-10	-0.005551	0.003621	0.125277	-0.017699	0.00266	2.94E-11	7.46E-11	0.006874	F
17	BPTF	rs7223930	67,846,070	G	A	0.345307	-0.013279	0.002127	1.70E-10	-0.005551	0.003621	0.125277	-0.017699	0.00266	2.94E-11	7.46E-11	0.006874	F
17	BPTF	rs7224923	67,846,149	T	G	0.345307	-0.013279	0.002127	1.70E-10	-0.005551	0.003621	0.125277	-0.017699	0.00266	2.94E-11	7.46E-11	0.006874	F
17	BPTF	rs62084214	67,847,209	C	G	0.345307	-0.013279	0.002127	1.70E-10	-0.005551	0.003621	0.125277	-0.017699	0.00266	2.94E-11	7.46E-11	0.006874	F
17	BPTF	rs8081517	67,849,581	A	T	0.345307	-0.013279	0.002127	1.70E-10	-0.005551	0.003621	0.125277	-0.017699	0.00266	2.94E-11	7.46E-11	0.006874	F
17	BPTF	rs8081856	67,849,802	A	G	0.34												

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p_value	gender_heterogeneity_p_value	Male/Female Specific
17	BPTF	rs60432293	67,864,291	T	C	0.345327	-0.013282	0.002127	1.70E-10	-0.005617	0.003621	0.12084	-0.017662	0.00266	3.23E-11	7.97E-11	0.007361	F
17	BPTF	rs59950564	67,864,743	A	G	0.345297	-0.013292	0.002127	1.60E-10	-0.005568	0.003621	0.124128	-0.017706	0.002659	2.88E-11	7.27E-11	0.00692	F
17	BPTF	rs8077872	67,864,943	G	T	0.339528	-0.013581	0.002137	8.20E-11	-0.006357	0.003636	0.080441	-0.017737	0.002672	3.30E-11	5.88E-11	0.011688	F
17	BPTF	rs4790905	67,867,234	C	A	0.345298	-0.013289	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017701	0.002659	2.92E-11	7.36E-11	0.006942	F
17	BPTF	rs34872586	67,867,530	T	C	0.345547	-0.013254	0.002128	1.90E-10	-0.005495	0.003623	0.129296	-0.017678	0.002661	3.15E-11	8.20E-11	0.006739	F
17	BPTF	rs58141639	67,868,786	C	T	0.345321	-0.013272	0.002127	1.70E-10	-0.005563	0.003622	0.124493	-0.017691	0.00266	3.00E-11	7.59E-11	0.006969	F
17	BPTF	rs61067468	67,869,919	G	A	0.349117	-0.013265	0.002135	2.00E-10	-0.005442	0.003634	0.134294	-0.01778	0.002669	2.82E-11	7.57E-11	0.00623	F
17	BPTF	rs62084246	67,871,795	G	C	0.345267	-0.013247	0.002127	1.90E-10	-0.00554	0.003621	0.126065	-0.017661	0.002659	3.23E-11	8.24E-11	0.006997	F
17	BPTF	rs9912084	67,871,919	A	C	0.345294	-0.013283	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017693	0.002659	2.98E-11	7.50E-11	0.006978	F
17	BPTF	rs9912770	67,872,117	C	T	0.345294	-0.013283	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017693	0.002659	2.98E-11	7.50E-11	0.006978	F
17	BPTF	rs11869819	67,872,553	A	C	0.345268	-0.013248	0.002127	1.90E-10	-0.00554	0.003621	0.126065	-0.017662	0.002659	3.22E-11	8.21E-11	0.006991	F
17	BPTF	rs55939964	67,873,181	G	A	0.345864	-0.013396	0.002127	1.30E-10	-0.005571	0.003621	0.123866	-0.017924	0.00266	1.66E-11	4.24E-11	0.005987	F
17	BPTF	rs12602912	67,873,957	C	T	0.345475	-0.013287	0.002126	1.60E-10	-0.00553	0.003619	0.126555	-0.01773	0.002658	2.63E-11	6.75E-11	0.006602	F
17	BPTF	rs12450907	67,874,528	T	G	0.345268	-0.013248	0.002127	1.90E-10	-0.00554	0.003621	0.126065	-0.017662	0.002659	3.22E-11	8.21E-11	0.006991	F
17	BPTF	rs9890629	67,875,443	G	A	0.345268	-0.013248	0.002127	1.90E-10	-0.00554	0.003621	0.126065	-0.017662	0.002659	3.22E-11	8.21E-11	0.006991	F
17	BPTF	rs12451707	67,875,482	G	A	0.345268	-0.013248	0.002127	1.90E-10	-0.00554	0.003621	0.126065	-0.017662	0.002659	3.22E-11	8.21E-11	0.006991	F
17	BPTF	rs4569324	67,876,634	C	T	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs62084247	67,876,787	C	T	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs9915108	67,878,347	T	C	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs9913471	67,878,379	C	T	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs62084248	67,878,425	C	T	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs12451511	67,878,745	T	G	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs62084249	67,878,882	A	G	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs73352808	67,879,041	G	A	0.359412	-0.012071	0.002152	9.00E-09	-0.005355	0.003663	0.143786	-0.015978	0.00269	2.95E-09	7.53E-09	0.019441	F
17	BPTF	rs11867517	67,879,210	C	T	0.34601	-0.013333	0.002131	1.50E-10	-0.005876	0.003628	0.105253	-0.017637	0.002666	3.80E-11	8.39E-11	0.009005	F
17	BPTF	rs11867537	67,879,376	A	G	0.34629	-0.013252	0.002127	2.00E-10	-0.005507	0.003622	0.12841	-0.017704	0.00266	2.92E-11	7.56E-11	0.006665	F
17	BPTF	rs11867618	67,879,471	G	A	0.346614	-0.01313	0.002127	2.90E-10	-0.005367	0.003622	0.138335	-0.017547	0.002659	4.32E-11	1.18E-10	0.006734	F
17	BPTF	rs35243555	67,880,361	G	C	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs58122682	67,880,799	T	C	0.34606	-0.013294	0.002129	1.70E-10	-0.005407	0.003626	0.135934	-0.017795	0.002662	2.39E-11	6.50E-11	0.005901	F
17	BPTF	rs8074644	67,882,101	G	C	0.345367	-0.013271	0.002127	1.70E-10	-0.005475	0.003621	0.130583	-0.017701	0.002659	2.91E-11	7.64E-11	0.00652	F
17	BPTF	rs62084251	67,882,620	G	A	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs9892803	67,883,127	T	G	0.345295	-0.013284	0.002127	1.70E-10	-0.005568	0.003621	0.124128	-0.017694	0.002659	2.97E-11	7.48E-11	0.006973	F
17	BPTF	rs62084252	67,883,462	G	C	0.347103	-0.013186	0.002127	2.70E-10	-0.00583	0.003623	0.107526	-0.017419	0.002661	6.10E-11	1.35E-10	0.009954	F
17	BPTF	rs9897982	67,883,476	G	T	0.340667	-0.013609	0.002138	8.20E-11	-0.006493	0.003639	0.07436	-0.017729	0.002674	3.50E-11	5.83E-11	0.01286	F
17	BPTF	rs6504545	67,884,251	A	G	0.345948	-0.013401	0.00213	1.00E-10	-0.006236	0.003626	0.085446	-0.017593	0.002663	4.06E-11	7.56E-11	0.011607	F
17	BPTF	rs6504546	67,884,269	A	C	0.346146	-0.01354	0.002127	6.90E-11	-0.00604	0.003622	0.09539	-0.017885	0.00266	1.84E-11	3.80E-11	0.008404	F
17	BPTF	rs7213292	67,884,327	A	G	0.345983	-0.013374	0.002127	1.30E-10	-0.006124	0.003622	0.090864	-0.017554	0.00266	4.25E-11	8.32E-11	0.010981	F
17	BPTF	rs115210018	67,884,423	T	C	0.358234	-0.011593	0.002155	2.40E-08	-0.003616	0.00367	0.324563	-0.015879	0.002693	3.84E-09	1.75E-08	0.007086	F
17	BPTF	rs3935969	67,885,843	A	G	0.345283	-0.013302	0.002127	1.60E-10	-0.005568	0.003621	0.124128	-0.017725	0.00266	2.75E-11	6.94E-11	0.006831	F
17	BPTF	rs4318247	67,886,056	A	G	0.345283	-0.013302	0.002127	1.60E-10	-0.005568	0.003621	0.124128	-0.017725	0.00266	2.75E-11	6.94E-11	0.006831	F
17	BPTF	rs8082661	67,888,585	G	A	0.345694	-0.012676	0.002158	2.20E-09	-0.004056	0.003673	0.269513	-0.017433	0.002699	1.09E-10	4.73E-10	0.003346	F
17	BPTF	rs7208663	67,889,055	T	G	0.345283	-0.013302	0.002127	1.60E-10	-0.005568	0.003621	0.124128	-0.017725	0.00266	2.75E-11	6.94E-11	0.006831	F
17	BPTF	rs75231441	67,889,369	A	C	0.345283	-0.013302	0.002127	1.60E-10	-0.005568	0.003621	0.124128	-0.017725	0.00266	2.75E-11	6.94E-11	0.006831	F
17	BPTF	rs12452823	67,889,667	G	A	0.345282	-0.013298	0.002127	1.60E-10	-0.005568	0.003621	0.124128	-0.01772	0.00266	2.78E-11	7.02E-11	0.00683	F
17	BPTF	rs11079710	67,889,795	C	T	0.314619	-0.012058	0.00218	1.10E-08	-0.00514	0.003714	0.166336	-0.015946	0.002726	5.04E-09	1.42E-08	0.019016	F
17	BPTF	rs6504548	67,889,932	T	C	0.339485	-0.01359	0.002137	8.00E-11	-0.006357	0.003636	0.080456	-0.017747	0.002672	3.23E-11	5.76E-11	0.011621	F
17	BPTF	rs8079291	67,891,506	A	G	0.344343	-0.01327	0.002131	1.80E-10	-0.005514	0.003627	0.128479	-0.017693	0.002664	3.21E-11	8.30E-11	0.006822	F
17	BPTF	rs8079754	67,891,780	A	G	0.345266	-0.013283	0.002127	1.70E-10	-0.005565	0.003621	0.124321	-0.0177	0.00266	2.94E-11	7.41E-11	0.006935	F
17	BPTF	rs6504549	67,892,668	A	G	0.339463	-0.013578	0.002137	8.40E-11	-0.006362	0.003636	0.080208	-0.017726	0.002673	3.42E-11	6.07E-11	0.011814	F
17	BPTF	rs61676547	67,896,391	G	C	0.33462	-0.013836	0.002162	8.60E-11	-0.007672	0.003681	0.037175	-0.017431	0.002703	1.17E-10	1.07E-10	0.032619	F
17	BPTF	rs56148300	67,896,636	T	C	0.326956	-0.01434	0.002159	1.40E-11	-0.00757	0.003678	0.039593	-0.018218	0.002698	1.50E-11	1.51E-11	0.019596	F
17	BPTF	rs3206817	67,896,718	A	G	0.332799	-0.014036	0.002148	3.00E-11	-0.006672	0.003662	0.068507	-0.018203	0.002684	1.23E-11	1.95E-11	0.011115	F
17	BPTF	rs56404791	67,896,903	T	G	0.327581	-0.01433	0.002157	1.50E-11	-0.007469	0.003673	0.042046	-0.018279	0.002696	1.25E-11	1.32E-11	0.017691	F
17	BPTF	rs60477798	67,897,174	C	A	0.355808	-0.014259	0.002156	2.60E-11	-0.006379	0.003669	0.082096	-0.018927	0.002697	2.33E-12	4.43E-12	0.005868	F
17	BPTF	rs6504550	67,898,426	A	G	0.294745	-0.013169	0.002222	1.40E-09	-0.006464	0.003785	0.087681	-0.016955	0.002777	1.05E-09	1.86E-09	0.025444	F
17	BPTF	rs7216064	67,902,693	G	A	0.334179	-0.013733	0.002145	8.00E-11	-0.006555	0.003653	0.072767	-0.017819	0.002681	3.09E-11	5.07E-11	0.012945	F
17	B																	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
17	BPTF	rs7223813	67,949,724	A	G	0.332643	-0.013828	0.002147	6.20E-11	-0.006418	0.003659	0.079458	-0.018013	0.002684	1.99E-11	3.54E-11	0.01064	F
17	BPTF	rs12449442	67,951,524	G	A	0.343629	-0.013854	0.002145	6.30E-11	-0.006106	0.003656	0.09488	-0.01819	0.00268	1.19E-11	2.47E-11	0.007704	F
17	BPTF	rs11867401	67,951,854	A	G	0.327014	-0.014211	0.002158	2.30E-11	-0.007067	0.003676	0.054528	-0.018292	0.002698	1.25E-11	1.65E-11	0.013853	F
17	BPTF	rs9907491	67,953,877	A	G	0.326996	-0.014238	0.002158	2.10E-11	-0.007157	0.003675	0.051529	-0.018286	0.002698	1.27E-11	1.59E-11	0.014672	F
17	BPTF	rs4790974	67,954,991	T	A	0.327086	-0.014239	0.002158	2.10E-11	-0.007157	0.003676	0.051584	-0.018295	0.002698	1.24E-11	1.56E-11	0.014612	F
17	BPTF	rs4790973	67,955,017	C	T	0.333034	-0.013921	0.002147	4.40E-11	-0.006521	0.003658	0.074633	-0.018123	0.002683	1.47E-11	2.51E-11	0.010556	F
17	BPTF	rs77706698	67,957,232	G	A	0.346109	-0.013171	0.00213	2.20E-10	-0.005041	0.003627	0.164556	-0.017755	0.002664	2.73E-11	8.56E-11	0.004738	F
17	BPTF	rs12601759	67,959,168	A	G	0.332531	-0.013996	0.002149	3.80E-11	-0.006579	0.003662	0.072415	-0.018237	0.002685	1.14E-11	1.91E-11	0.010259	F
17	BPTF	rs9899520	67,961,452	G	A	0.322888	-0.014359	0.002165	1.90E-11	-0.007235	0.003705	0.050877	-0.018383	0.002719	1.41E-11	1.75E-11	0.015286	F
17	BPTF	rs60626066	67,965,117	G	A	0.352581	-0.014829	0.002146	3.00E-12	-0.006171	0.003651	0.090973	-0.019682	0.002684	2.35E-13	5.06E-13	0.002877	F
17	BPTF	rs10445361	67,966,122	T	G	0.333863	-0.015226	0.002148	6.00E-13	-0.007676	0.00366	0.035998	-0.019643	0.002685	2.68E-13	2.66E-13	0.008403	F
17	BPTF	rs62086042	67,971,327	T	C	0.286656	-0.012742	0.002243	4.90E-09	-0.005473	0.00383	0.153016	-0.017107	0.0028	1.03E-09	2.84E-09	0.014229	F
17	BPTF	rs62086043	67,971,887	A	G	0.328247	-0.014022	0.002166	3.70E-11	-0.006558	0.003695	0.0759	-0.018245	0.002706	1.62E-11	2.78E-11	0.010731	F
17	BPTF	rs62086044	67,974,721	G	T	0.328374	-0.013992	0.002161	3.00E-11	-0.006389	0.003687	0.083102	-0.018305	0.0027	1.24E-11	2.31E-11	0.009131	F
17	BPTF	rs62086045	67,977,615	G	A	0.327275	-0.014196	0.002164	1.90E-11	-0.006789	0.00369	0.065831	-0.018422	0.002703	9.66E-12	1.50E-11	0.011001	F
17	BPTF	rs4791212	67,979,269	C	T	0.339663	-0.013411	0.002147	1.00E-10	-0.004937	0.003661	0.177435	-0.018179	0.002683	1.29E-11	4.34E-11	0.003538	F
17	BPTF	rs7210027	67,980,937	T	C	0.326762	-0.014205	0.002166	1.90E-11	-0.006702	0.003696	0.069746	-0.018471	0.002705	8.98E-12	1.46E-11	0.010205	F
17	BPTF	rs4790941	67,981,016	G	A	0.327167	-0.014208	0.002164	1.80E-11	-0.006813	0.003692	0.064997	-0.018428	0.002703	9.65E-12	1.48E-11	0.011153	F
17	BPTF	rs11656743	67,984,173	A	G	0.325395	-0.014188	0.002169	2.30E-11	-0.007124	0.003701	0.054253	-0.018285	0.002709	1.55E-11	2.02E-11	0.014974	F
17	BPTF *	rs62086046	67,986,827	C	T	0.328042	-0.014163	0.002165	2.10E-11	-0.006624	0.003693	0.072906	-0.018458	0.002703	8.95E-12	1.51E-11	0.009737	F
17	C17orf58 *	rs75772932	67,988,421	G	A	0.343133	-0.012966	0.002145	3.90E-10	-0.004492	0.003656	0.219168	-0.017742	0.00268	3.70E-11	1.43E-10	0.003475	F
17	C17orf58	rs9891146	67,991,933	C	T	0.285256	-0.013291	0.002268	1.50E-09	-0.006457	0.003875	0.095612	-0.017479	0.002831	6.84E-10	1.31E-09	0.021651	F
17	C17orf58 *	rs7502307	67,993,845	C	G	0.343012	-0.013635	0.002176	8.40E-11	-0.005722	0.003709	0.122836	-0.018169	0.002719	2.45E-11	6.15E-11	0.006816	F
17	C17orf58 *	rs113985803	67,993,855	A	G	0.326566	-0.014491	0.002198	1.50E-11	-0.007415	0.00375	0.04801	-0.018634	0.002745	1.18E-11	1.40E-11	0.015787	F
17	C17orf58 *	rs56305452	67,994,384	A	C	0.325001	-0.014329	0.002198	2.50E-11	-0.007026	0.003747	0.060775	-0.018554	0.002746	1.46E-11	2.09E-11	0.013101	F
17	C17orf58 *	rs56315139	67,994,455	G	C	0.28381	-0.013158	0.002283	2.80E-09	-0.006943	0.003897	0.074795	-0.016985	0.00285	2.61E-09	3.98E-09	0.037541	F
17	C17orf58 *	rs62086884	67,998,284	G	C	0.345929	-0.013549	0.002157	7.90E-11	-0.007944	0.003672	0.030522	-0.016825	0.002697	4.54E-10	3.39E-10	0.051281	F
17	C17orf58 *	rs4791295	68,001,201	G	A	0.337558	-0.014425	0.002151	5.30E-12	-0.008452	0.003662	0.021008	-0.017837	0.00269	3.44E-11	1.97E-11	0.038876	F
17	C17orf58 *	rs28855509	68,002,051	T	C	0.33782	-0.014074	0.002149	1.70E-11	-0.007998	0.003659	0.028849	-0.017578	0.002688	6.33E-11	4.71E-11	0.034842	F
17	C17orf58 *	rs74564337	68,003,451	C	T	0.337523	-0.014434	0.002156	6.00E-12	-0.008462	0.003669	0.021117	-0.017842	0.002696	3.75E-11	2.15E-11	0.039411	F
17	C17orf58 *	rs6504568	68,003,532	T	C	0.337175	-0.014423	0.002152	5.70E-12	-0.008372	0.003664	0.02233	-0.017911	0.002692	2.94E-11	1.78E-11	0.035893	F
17	C17orf58 *	rs62086889	68,004,487	C	T	0.338982	-0.014281	0.002155	1.00E-11	-0.008374	0.003667	0.022422	-0.017661	0.002694	5.78E-11	3.46E-11	0.041289	F
17	C17orf58 *	rs8081714	68,005,014	G	A	0.337901	-0.014358	0.002152	7.70E-12	-0.008617	0.003663	0.018667	-0.017666	0.00269	5.34E-11	2.73E-11	0.046473	F
17	C17orf58 *	rs28437386	68,008,555	T	A	0.349708	-0.0139	0.002167	5.50E-11	-0.008254	0.00369	0.02531	-0.017144	0.00271	2.58E-10	1.66E-10	0.052175	F
17	C17orf58 *	rs78186330	68,008,599	G	A	0.342887	-0.01365	0.002161	9.60E-11	-0.008264	0.003678	0.024657	-0.016755	0.002703	5.88E-10	3.64E-10	0.06288	F
17	C17orf58 *	rs62086897	68,011,928	A	C	0.334922	-0.013395	0.002152	2.10E-10	-0.008361	0.003661	0.022423	-0.016288	0.002691	1.48E-09	8.23E-10	0.081091	F
17	C17orf58 *	rs62086898	68,013,004	A	G	0.334922	-0.013395	0.002152	2.10E-10	-0.008361	0.003661	0.022423	-0.016288	0.002691	1.48E-09	8.23E-10	0.081091	F
17	C17orf58 *	rs62086899	68,013,018	C	T	0.334922	-0.013395	0.002152	2.10E-10	-0.008361	0.003661	0.022423	-0.016288	0.002691	1.48E-09	8.23E-10	0.081091	F
17	CPNA2 *	rs7225959	68,018,993	T	C	0.339232	-0.01358	0.002148	9.90E-11	-0.008609	0.003654	0.018498	-0.016377	0.002686	1.12E-09	5.30E-10	0.086794	F
17	CPNA2 *	rs62086903	68,019,890	T	A	0.323031	-0.013523	0.002168	2.20E-10	-0.009565	0.00369	0.009556	-0.015851	0.002711	5.16E-09	1.31E-09	0.169766	F
17	CPNA2 *	rs62086904	68,019,980	C	T	0.337322	-0.013175	0.002144	2.70E-10	-0.008458	0.003648	0.020457	-0.015903	0.002682	3.12E-09	1.58E-09	0.100133	F
17	CPNA2 *	rs8182243	68,022,389	C	T	0.298669	-0.012454	0.002206	5.80E-09	-0.007137	0.003761	0.05775	-0.015752	0.002757	1.14E-08	1.35E-08	0.064687	F
17	CPNA2 *	rs8065296	68,022,446	A	T	0.298724	-0.012398	0.002206	6.80E-09	-0.00712	0.003761	0.058365	-0.015686	0.002757	1.31E-08	1.56E-08	0.066219	F
17	CPNA2 *	rs62086906	68,023,810	T	C	0.336324	-0.013306	0.002145	1.90E-10	-0.008249	0.003651	0.023871	-0.016214	0.002683	1.55E-09	9.10E-10	0.078755	F
17	CPNA2 *	rs145520076	68,024,495	G	A	0.342858	-0.013655	0.002161	1.10E-10	-0.009783	0.003679	0.007858	-0.015922	0.002701	3.87E-09	8.33E-10	0.17864	F
17	CPNA2 *	rs189628481	68,024,502	C	T	0.344026	-0.013471	0.002162	1.70E-10	-0.009646	0.003681	0.008802	-0.015771	0.002703	5.54E-09	1.31E-09	0.179806	F
17	CPNA2 *	rs192988621	68,024,504	C	T	0.342172	-0.013403	0.002156	2.50E-10	-0.009405	0.003671	0.010424	-0.015793	0.002695	4.74E-09	1.31E-09	0.160685	F
17	CPNA2 *	rs183763906	68,024,506	C	T	0.342172	-0.013403	0.002156	2.50E-10	-0.009405	0.003671	0.010424	-0.015793	0.002695	4.74E-09	1.31E-09	0.160685	F
17	CPNA2 *	rs200026262	68,024,507	A	G	0.344026	-0.013471	0.002162	1.70E-10	-0.009646	0.003681	0.008802	-0.015771	0.002703	5.54E-09	1.31E-09	0.179806	F
17	CPNA2 *	rs62086907	68,025,051	A	G	0.334626	-0.012878	0.002175	7.30E-10	-0.008389	0.003701	0.023439	-0.015501	0.002719	1.22E-08	6.73E-09	0.121431	F
17	CPNA2 *	rs62086908	68,025,098	G	C	0.336304	-0.013081	0.002152	4.30E-10	-0.008816	0.003662	0.016078	-0.01559	0.002692	7.16E-09	2.87E-09	0.136069	F
17	CPNA2 *	rs7405987	68,025,278	A	G	0.336858	-0.013418	0.002145	1.30E-10	-0.008424	0.003652	0.021105	-0.016269	0.002683	1.36E-09	7.22E-10	0.08341	F
17	CPNA2 *	rs7406031	68,025,637	T	C	0.298593	-0.012401	0.002206	6.70E-09	-0.007097	0.003761	0.059186	-0.015705	0.002757	1.25E-08	1.52E-08	0.064919	F
17	CPNA2 *	rs7406141	68,025,870	C	T	0.298593	-0.012401	0.002206	6.70E-09	-0.007097	0.003761	0.059186	-0.015705	0.002757	1.25E-08	1.52E-08	0.064919	F
17	CPNA2 *	rs8076753	68,026,725	G	A	0.336588	-0.013329	0.002145	1.90E-10	-0.008353	0.003651	0.022165	-0.016199	0.002682	1.59E-09	8.76E-10	0.083291	F
17	CPNA2 *	rs6504574	68,026,895	A	G	0.298593	-0.012401	0.002206	6.70E-09	-0.007097	0.003761	0						

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
17	KPNA2	rs62084691	68,039,402	C	T	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2	rs62084692	68,039,728	C	T	0.338958	-0.012885	0.002146	1.10E-09	-0.009437	0.003653	0.009794	-0.01484	0.002683	3.27E-08	8.10E-09	0.233206	
17	KPNA2	rs62084693	68,039,994	T	C	0.293697	-0.01223	0.002221	1.60E-08	-0.00754	0.003782	0.04622	-0.015217	0.002777	4.35E-08	4.13E-08	0.101797	
17	KPNA2	rs8078543	68,041,135	T	G	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2	rs62084694	68,041,478	G	T	0.337611	-0.012759	0.002143	1.30E-09	-0.008962	0.003646	0.013988	-0.014945	0.002679	2.50E-08	8.57E-09	0.186117	
17	KPNA2	rs62084696	68,042,065	G	C	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2	rs62084697	68,042,440	G	A	0.337611	-0.012759	0.002143	1.30E-09	-0.008962	0.003646	0.013988	-0.014945	0.002679	2.50E-08	8.57E-09	0.186117	
17	KPNA2	rs4638	68,043,234	G	A	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2	rs35594666	68,043,502	A	G	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2	rs35453056	68,043,552	G	A	0.294699	-0.012282	0.002216	1.40E-08	-0.007625	0.003776	0.043482	-0.015309	0.002769	3.29E-08	2.99E-08	0.100821	
17	KPNA2	rs62084701	68,046,122	T	C	0.29503	-0.012458	0.002214	9.50E-09	-0.007492	0.003773	0.047082	-0.0156	0.002767	1.76E-08	1.74E-08	0.083131	
17	KPNA2 *	rs62084702	68,047,041	T	C	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2 *	rs62084703	68,047,268	C	T	0.337678	-0.012708	0.002142	1.50E-09	-0.008802	0.003645	0.015768	-0.014929	0.002679	2.58E-08	9.80E-09	0.175617	
17	KPNA2 *	rs7405743	68,047,422	T	C	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2 *	rs62084704	68,048,913	A	G	0.295216	-0.012384	0.002214	1.10E-08	-0.007528	0.003773	0.046008	-0.015488	0.002766	2.21E-08	2.13E-08	0.088845	
17	KPNA2 *	rs74354868	68,049,715	G	A	0.337658	-0.012768	0.002143	1.30E-09	-0.008942	0.003646	0.014218	-0.014976	0.002679	2.34E-08	8.14E-09	0.182331	
17	KPNA2 *	rs75885145	68,050,690	G	C	0.295272	-0.012397	0.002214	1.00E-08	-0.007542	0.003773	0.045641	-0.015512	0.002766	2.11E-08	2.02E-08	0.08846	
17	KPNA2 *	rs7214557	68,051,614	T	C	0.295267	-0.012395	0.002215	1.10E-08	-0.007761	0.003775	0.039802	-0.015444	0.002768	2.47E-08	2.10E-08	0.100768	
17	KPNA2 *	rs7503050	68,052,346	G	T	0.337519	-0.012801	0.002143	1.10E-09	-0.008999	0.003647	0.013626	-0.015028	0.00268	2.10E-08	7.05E-09	0.18275	
17	KPNA2 *	rs7503056	68,052,533	C	G	0.295045	-0.01245	0.002214	9.00E-09	-0.007624	0.003774	0.0434	-0.015587	0.002767	1.81E-08	1.67E-08	0.088824	
17	KPNA2 *	rs34503060	68,052,563	G	A	0.295045	-0.01245	0.002214	9.00E-09	-0.007624	0.003774	0.0434	-0.015587	0.002767	1.81E-08	1.67E-08	0.088824	
17	KPNA2 *	rs7503096	68,052,679	C	T	0.295085	-0.012422	0.002214	9.80E-09	-0.007579	0.003773	0.044621	-0.015566	0.002767	1.89E-08	1.78E-08	0.087803	
17	KPNA2 *	rs7503206	68,053,058	G	A	0.29512	-0.012451	0.002214	9.20E-09	-0.007656	0.003774	0.042492	-0.015573	0.002767	1.86E-08	1.69E-08	0.090686	
17	KPNA2 *	rs7503810	68,053,415	G	A	0.333352	-0.013134	0.002149	5.30E-10	-0.00933	0.003657	0.010765	-0.01535	0.002687	1.15E-08	3.18E-09	0.184664	
17	KPNA2 *	rs62084708	68,053,591	G	A	0.333219	-0.013123	0.002149	5.30E-10	-0.009031	0.003657	0.013551	-0.015484	0.002688	8.65E-09	2.96E-09	0.155089	
17	KPNA2 *	rs7209959	68,054,289	T	C	0.29512	-0.012451	0.002214	9.20E-09	-0.007656	0.003774	0.042492	-0.015573	0.002767	1.86E-08	1.69E-08	0.090686	
17	KPNA2 *	rs62084711	68,054,795	T	C	0.29512	-0.012451	0.002214	9.20E-09	-0.007656	0.003774	0.042492	-0.015573	0.002767	1.86E-08	1.69E-08	0.090686	
17	KPNA2 *	rs28592929	68,056,618	C	T	0.295124	-0.012447	0.002214	9.20E-09	-0.007654	0.003774	0.042564	-0.015567	0.002767	1.89E-08	1.71E-08	0.090818	
17	KPNA2 *	rs3890640	68,056,912	T	C	0.295124	-0.012447	0.002214	9.20E-09	-0.007654	0.003774	0.042564	-0.015567	0.002767	1.89E-08	1.71E-08	0.090818	
17	KPNA2 *	rs34843489	68,057,215	T	C	0.294432	-0.012575	0.002217	7.40E-09	-0.007976	0.003781	0.034898	-0.015606	0.00277	1.80E-08	1.38E-08	0.103508	
17	KPNA2 *	rs78429175	68,058,655	G	A	0.294836	-0.012495	0.002215	8.40E-09	-0.007769	0.003776	0.039657	-0.015609	0.002768	1.75E-08	0.940405	0.094045	
17	KPNA2 *	rs76542911	68,059,778	G	A	0.295383	-0.012403	0.002214	9.80E-09	-0.007582	0.003775	0.044608	-0.015532	0.002767	2.03E-08	1.91E-08	0.089449	
17	KPNA2 *	rs62084734	68,060,081	C	T	0.295277	-0.012561	0.002215	6.80E-09	-0.007612	0.003776	0.043817	-0.015762	0.002768	1.27E-08	1.19E-08	0.081734	
17	KPNA2 *	rs35040337	68,060,566	A	G	0.333181	-0.013175	0.00215	4.40E-10	-0.009068	0.003657	0.013185	-0.015549	0.002689	7.51E-09	2.52E-09	0.153342	
17	KPNA2 *	rs8072723	68,060,854	A	T	0.295084	-0.012476	0.002214	8.50E-09	-0.007699	0.003774	0.041391	-0.015588	0.002767	1.81E-08	1.60E-08	0.091868	
17	KPNA2 *	rs6504578	68,061,850	A	G	0.295084	-0.012476	0.002214	8.50E-09	-0.007699	0.003774	0.041391	-0.015588	0.002767	1.81E-08	1.60E-08	0.091868	
17	KPNA2 *	rs62084738	68,063,664	T	C	0.295084	-0.012476	0.002214	8.50E-09	-0.007699	0.003774	0.041391	-0.015588	0.002767	1.81E-08	1.60E-08	0.091868	
17	KPNA2 *	rs74976757	68,064,790	G	T	0.337575	-0.012871	0.002143	9.40E-10	-0.009082	0.003648	0.012811	-0.015094	0.00268	1.83E-08	5.86E-09	0.184181	
17	KPNA2 *	rs62084740	68,065,068	C	T	0.337575	-0.012871	0.002143	9.40E-10	-0.009082	0.003648	0.012811	-0.015094	0.00268	1.83E-08	5.86E-09	0.184181	
17	KPNA2 *	rs77194282	68,065,510	C	T	0.295084	-0.012476	0.002214	8.50E-09	-0.007699	0.003774	0.041391	-0.015588	0.002767	1.81E-08	1.60E-08	0.091868	
17	KPNA2 *	rs7213585	68,066,200	T	A	0.294997	-0.012493	0.002215	8.10E-09	-0.007743	0.003775	0.040271	-0.015596	0.002767	1.79E-08	1.55E-08	0.093434	
17	KPNA2 *	rs62084741	68,066,544	T	C	0.295084	-0.012476	0.002214	8.50E-09	-0.007699	0.003774	0.041391	-0.015588	0.002767	1.81E-08	1.60E-08	0.091868	
17	KPNA2 *	rs74900486	68,066,757	C	T	0.337575	-0.012871	0.002143	9.40E-10	-0.009082	0.003648	0.012811	-0.015094	0.00268	1.83E-08	5.86E-09	0.184181	
17	KPNA2 *	rs8075604	68,066,985	C	T	0.290646	-0.012503	0.002227	9.30E-09	-0.008817	0.003797	0.020255	-0.015009	0.002783	7.06E-08	3.25E-08	0.188431	
17	KPNA2 *	rs28850355	68,068,281	T	C	0.291469	-0.012672	0.002232	7.20E-09	-0.008315	0.003804	0.028849	-0.015537	0.00279	2.62E-08	1.69E-08	0.125755	
17	KPNA2 *	rs75544834	68,070,322	T	C	0.333821	-0.012953	0.002154	1.20E-09	-0.008753	0.003664	0.016916	-0.015427	0.002694	1.05E-08	4.37E-09	0.142151	
17	KPNA2 *	rs79415988	68,070,853	C	T	0.294543	-0.012283	0.002218	1.70E-08	-0.007333	0.00378	0.052415	-0.015497	0.002772	2.32E-08	2.49E-08	0.081577	
17	KPNA2 *	rs9674669	68,071,338	G	A	0.294951	-0.01205	0.00222	3.20E-08	-0.00706	0.003782	0.061955	-0.015332	0.002774	3.35E-08	4.08E-08	0.07711	
17	KPNA2 *	rs184478609	68,071,576	T	C	0.335277	-0.012883	0.002155	7.60E-10	-0.009064	0.003669	0.013523	-0.015272	0.002694	1.47E-08	4.95E-09	0.172559	
17	KPNA2 *	rs190151381	68,071,898	G	A	0.299709	-0.012219	0.002224	2.00E-08	-0.007242	0.00379	0.056011	-0.015595	0.002779	2.05E-08	2.33E-08	0.075449	
17	KPNA2 *	rs9747971	68,073,082	C	G	0.294387	-0.012224	0.002219	1.90E-08	-0.007255	0.003781	0.055056	-0.015472	0.002773	2.47E-08	2.76E-08	0.079689	
17	KPNA2 *	rs9330556	68,073,785	T	G	0.295256	-0.012274	0.002218	1.80E-08	-0.007361	0.00378	0.051527	-0.015512	0.002772	2.26E-08	2.39E-08	0.082094	
17	KPNA2 *	rs62084742	68,079,426	A	G	0.29448	-0.012241	0.002219	1.80E-08	-0.007212	0.003782	0.056531	-0.015516	0.002773	2.27E-08	2.59E-08	0.076642	
17	KPNA2 *	rs34937122	68,079,772	A	G	0.294011	-0.012218	0.002221	2.00E-08	-0.00746	0.003785	0.048707	-0.015362	0.002775	3.18E-08	3.19E-08	0.092263	
17	KPNA2 *	rs78352159	68,082,103	C	G	0.339481	-0.012905	0.002144	1.50E-09	-0.01009	0.003648	0.005696	-0.014569	0.002682	5.67E-08	8.50E-09	0.322513	
17	KPNA2 *	rs75428197	68,082,271	A	G	0.29653	-0.012551	0.002212	8.50E-09	-0.008202	0.003769	0.02958	-0.015487	0.002765	2.18E-08	1.44E-08	0.119103	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
19	ANGPTL4 *	rs11881114	8,356,174	C	T	0.016194	-0.048755	0.008017	3.70E-09	-0.062206	0.013464	3.90E-06	-0.043593	0.010102	1.62E-05	2.10E-09	0.26883	
19	ANGPTL4 *	rs113472294	8,356,384	A	G	0.016198	-0.048646	0.008016	4.00E-09	-0.062206	0.013464	3.90E-06	-0.043415	0.010101	1.74E-05	2.26E-09	0.264231	
19	ANGPTL4 *	rs111651803	8,356,534	G	A	0.016201	-0.048439	0.008015	4.70E-09	-0.062206	0.013464	3.90E-06	-0.043105	0.010099	1.99E-05	2.57E-09	0.256399	
19	ANGPTL4 *	rs62117487	8,359,176	G	A	0.02937	-0.037427	0.006033	2.80E-09	-0.036254	0.01024	0.000402	-0.036965	0.007558	1.54E-07	1.94E-09	0.786859	
19	ANGPTL4 *	rs121090257	8,359,426	A	C	0.016244	-0.048394	0.008005	4.60E-09	-0.061411	0.013448	5.03E-06	-0.043549	0.010085	1.59E-05	2.65E-09	0.287951	
19	ANGPTL4 *	rs112365616	8,360,096	T	C	0.015827	-0.048675	0.00811	7.90E-09	-0.060879	0.013625	7.99E-06	-0.044101	0.010217	1.61E-05	4.16E-09	0.324498	
19	ANGPTL4 *	rs111500536	8,360,674	A	G	0.031865	-0.040301	0.005781	1.20E-11	-0.039299	0.009817	6.31E-05	-0.042656	0.00724	3.93E-09	9.62E-12	0.783107	
19	ANGPTL4 *	rs112634335	8,361,765	C	G	0.016383	-0.049205	0.007968	2.30E-09	-0.062661	0.01342	3.07E-06	-0.044165	0.010024	1.07E-05	1.12E-09	0.269479	
19	ANGPTL4 *	rs12822112	8,363,947	A	G	0.015256	-0.050204	0.008268	2.10E-09	-0.06195	0.013958	9.19E-06	-0.046677	0.010388	7.11E-06	2.18E-09	0.380037	
19	ANGPTL4	rs13446232	8,368,117	T	C	0.016637	-0.048676	0.007907	2.20E-09	-0.062819	0.013322	2.45E-06	-0.043525	0.009947	1.23E-05	1.03E-09	0.245816	
19	ANGPTL4	rs77439987	8,369,178	A	G	0.016917	-0.047762	0.007839	2.60E-09	-0.060819	0.013201	4.14E-06	-0.043031	0.009864	1.30E-05	1.81E-09	0.280374	
19	ANGPTL4	rs35061979	8,371,316	A	G	0.016794	-0.048115	0.007868	2.30E-09	-0.063113	0.013251	1.94E-06	-0.042488	0.009898	1.79E-05	1.18E-09	0.21238	
19	ANGPTL4	rs112625532	8,372,050	A	G	0.016745	-0.048798	0.007877	1.30E-09	-0.063132	0.013255	1.94E-06	-0.043561	0.009916	1.13E-05	7.64E-10	0.23706	
19	RAB11B-AS1	rs111313909	8,374,409	C	T	0.01674	-0.049376	0.007879	8.80E-10	-0.063893	0.013258	1.47E-06	-0.04401	0.009918	9.23E-06	4.80E-10	0.229785	
19	RAB11B-AS1	rs13896502	8,375,087	G	C	0.016739	-0.049371	0.007879	8.90E-10	-0.063893	0.013258	1.47E-06	-0.044003	0.009918	9.25E-06	4.81E-10	0.229638	
19	RAB11B-AS1	rs111910861	8,376,434	A	T	0.016739	-0.049371	0.007879	8.90E-10	-0.063893	0.013258	1.47E-06	-0.044003	0.009918	9.25E-06	4.81E-10	0.229638	
19	RAB11B-AS1	rs13687395	8,377,181	A	C	0.016739	-0.049371	0.007879	8.90E-10	-0.063893	0.013258	1.47E-06	-0.044003	0.009918	9.25E-06	4.81E-10	0.229638	
19	RAB11B-AS1	rs112381844	8,380,361	T	C	0.01674	-0.049361	0.007879	8.90E-10	-0.063874	0.013258	1.48E-06	-0.043993	0.009918	9.30E-06	4.87E-10	0.229832	
19	RAB11B-AS1	rs149784573	8,382,281	A	G	0.016744	-0.049509	0.007878	8.10E-10	-0.063839	0.013258	1.50E-06	-0.044217	0.009916	8.34E-06	4.45E-10	0.235937	
19	RAB11B-AS1	rs13937955	8,385,469	C	T	0.016563	-0.049271	0.007921	1.20E-09	-0.062309	0.013309	2.89E-06	-0.044676	0.009978	7.66E-06	7.71E-10	0.289101	
19	RAB11B	rs112981054	8,390,708	A	G	0.016024	-0.049833	0.008069	1.30E-09	-0.064667	0.013576	1.94E-06	-0.044555	0.010158	1.17E-05	7.86E-10	0.23555	
19	RAB11B	rs13090151	8,390,816	A	G	0.016024	-0.049829	0.008069	1.30E-09	-0.064644	0.013576	1.95E-06	-0.044562	0.010158	1.16E-05	7.90E-10	0.236233	
19	RAB11B	rs10403402	8,401,621	A	G	0.015171	-0.051997	0.008286	7.50E-10	-0.067649	0.013939	1.24E-06	-0.046154	0.010431	9.79E-06	4.31E-10	0.161946	
19	RAB11B *	rs10426486	8,405,069	A	G	0.015212	-0.050781	0.008268	1.50E-09	-0.068982	0.013956	7.84E-07	-0.043979	0.01039	2.33E-05	6.37E-10	0.150698	
19	RAB11B *	rs6603607	8,405,680	C	T	0.015462	-0.052074	0.008198	4.00E-10	-0.068738	0.013826	6.77E-07	-0.045932	0.010306	8.44E-06	2.09E-10	0.185997	
19	MARCHF2 *	rs62117520	8,411,923	A	G	0.015433	-0.052403	0.008207	3.30E-10	-0.067934	0.013822	9.04E-07	-0.047016	0.010325	5.35E-06	1.78E-10	0.225305	
19	MARCHF2 *	rs36868811	8,413,049	T	C	0.015166	-0.050677	0.008282	1.70E-09	-0.067332	0.013961	1.44E-06	-0.044893	0.010414	1.65E-05	8.20E-10	0.197606	
19	MARCHF2	rs62117522	8,416,119	A	G	0.015431	-0.052311	0.008207	3.50E-10	-0.068146	0.013831	8.50E-07	-0.046768	0.010323	5.97E-06	1.87E-10	0.215451	
19	MARCHF2	rs112826244	8,422,486	G	A	0.015179	-0.051176	0.008279	1.20E-09	-0.069292	0.013965	7.11E-07	-0.04455	0.010407	1.88E-05	4.73E-10	0.155418	
19	MARCHF2	rs77968216	8,422,767	C	T	0.014247	-0.051693	0.008545	1.90E-09	-0.068187	0.014412	2.27E-06	-0.045505	0.010741	2.30E-05	1.75E-09	0.206958	
19	MARCHF2	rs61499007	8,428,930	T	C	0.013387	-0.053771	0.008783	1.30E-09	-0.0728	0.014855	9.72E-07	-0.045512	0.011024	3.70E-05	1.21E-09	0.140164	
19	MARCHF2	rs17159300	8,429,250	T	C	0.01336	-0.053282	0.008792	2.00E-09	-0.072575	0.014883	1.10E-06	-0.045006	0.011031	4.55E-05	1.67E-09	0.136684	
19	MARCHF2	rs34344658	8,430,227	C	G	0.013373	-0.052982	0.008788	2.50E-09	-0.072035	0.014867	1.29E-06	-0.044818	0.011029	4.88E-05	2.07E-09	0.141457	
19	MARCHF2	rs34350946	8,430,231	T	C	0.013408	-0.053311	0.008789	1.80E-09	-0.072532	0.014873	1.10E-06	-0.044925	0.011029	4.69E-05	1.71E-09	0.13595	
19	MARCHF2	rs113550925	8,435,655	G	C	0.013396	-0.053108	0.00878	2.20E-09	-0.073132	0.014845	8.52E-07	-0.044293	0.011022	5.92E-05	1.67E-09	0.118805	
19	MARCHF2	rs6603071	8,435,751	T	G	0.013396	-0.053108	0.00878	2.20E-09	-0.073132	0.014845	8.52E-07	-0.044293	0.011022	5.92E-05	1.67E-09	0.118805	
19	MARCHF2	rs112363339	8,437,217	C	T	0.013238	-0.051311	0.008828	1.00E-08	-0.072963	0.014933	1.05E-06	-0.04137	0.011081	0.00019	6.15E-09	0.089322	
19	MARCHF2	rs7408526	8,437,225	A	C	0.013238	-0.051311	0.008828	1.00E-08	-0.072963	0.014933	1.05E-06	-0.04137	0.011081	0.00019	6.15E-09	0.089318	
19	MARCHF2	rs7408547	8,437,349	A	T	0.013238	-0.051318	0.008828	1.00E-08	-0.072963	0.014933	1.05E-06	-0.041379	0.011081	0.00019	6.13E-09	0.089411	
19	MARCHF2	rs12976614	8,437,541	T	C	0.013321	-0.050804	0.008805	1.20E-08	-0.072058	0.014883	1.31E-06	-0.04101	0.011056	0.000209	8.36E-09	0.094016	
19	MARCHF2	rs11259981	8,438,690	A	G	0.013247	-0.05134	0.008825	1.00E-08	-0.072988	0.014927	1.03E-06	-0.041438	0.011076	0.000185	5.88E-09	0.089636	
19	MARCHF2 *	rs7251323	8,440,340	T	C	0.013254	-0.05111	0.008822	1.20E-08	-0.072993	0.014927	1.03E-06	-0.041067	0.011072	0.00021	6.61E-09	0.085832	
19	MARCHF2 *	rs6603074	8,440,448	C	T	0.013529	-0.052293	0.008728	3.50E-09	-0.072518	0.014768	9.24E-07	-0.042995	0.010953	8.74E-05	2.62E-09	0.108321	
19	MARCHF2 *	rs1259982	8,441,103	T	C	0.013282	-0.050601	0.008814	1.50E-08	-0.072242	0.01491	1.29E-06	-0.040781	0.011063	0.000229	8.95E-09	0.090171	
19	HNRNPM *	rs10796330	8,442,955	A	G	0.013289	-0.049986	0.008811	2.40E-08	-0.071567	0.014899	1.59E-06	-0.040204	0.011016	0.00028	1.32E-08	0.09099	
19	HNRNPM	rs11881939	8,445,260	T	C	0.013296	-0.049711	0.008808	2.80E-08	-0.071567	0.014899	1.59E-06	-0.039747	0.011056	0.000326	1.52E-08	0.086337	
19	HNRNPM	rs724537	8,445,529	T	G	0.0133	-0.049347	0.008807	3.60E-08	-0.070598	0.014894	2.17E-06	-0.039747	0.011056	0.000326	2.06E-08	0.096262	
19	HNRNPM	rs6603078	8,446,441	C	G	0.013577	-0.049134	0.008722	3.00E-08	-0.071745	0.014769	1.21E-06	-0.038611	0.010194	0.000419	1.48E-08	0.071427	
19	HNRNPM	rs78136847	8,447,444	T	A	0.013303	-0.049367	0.008806	3.40E-08	-0.0706	0.014894	2.17E-06	-0.039803	0.011053	0.000319	2.02E-08	0.09682	
19	HNRNPM	rs76586439	8,448,918	A	G	0.013303	-0.04938	0.008806	3.40E-08	-0.0706	0.014894	2.17E-06	-0.039821	0.011053	0.000317	2.01E-08	0.097015	
19	HNRNPM	rs11259984	8,450,593	T	G	0.013303	-0.04938	0.008806	3.40E-08	-0.0706	0.014894	2.17E-06	-0.039821	0.011053	0.000317	2.01E-08	0.097015	
19	HNRNPM	rs113420240	8,450,730	A	T	0.010702	-0.056072	0.009832	4.50E-08	-0.0789	0.016516	1.81E-06	-0.045318	0.012389	0.000256	1.38E-08	0.103827	
19	HNRNPM	rs7253907	8,452,130	G	A	0.01331	-0.049178	0.008804	3.70E-08	-0.070603	0.014894	2.17E-06	-0.039459	0.011049	0.000358	2.24E-08	0.093078	
19	HNRNPM	rs6603081	8,454,016	C	T	0.013349	-0.048981	0.008791	4.00E-08	-0.070273	0.014877	2.36E-06	-0.039216	0.011031	0.00038	2.57E-08	0.093557	
19	HNRNPM	rs151032440	8,458,266	C	A	0.013346	-0.048942	0.008792	4.10E-08	-0.070273	0.014877	2.36E-06	-0.03917	0.011033	0.000388	2.62E-08	0.093099	
19	HNRNPM	rs1057253	8,461,561	C	G	0.0136	-0.050683	0.008705	9.40E-09	-0.070332	0.014725	1.81E-06	-0.041649	0.010926	0.000139	7.78E-09	0.117729	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
19	HNRNPM	rs7250951	8,484,576	A	T	0.01337	-0.048908	0.008784	3.90E-08	-0.070492	0.014866	2.15E-06	-0.038997	0.011022	0.000406	2.51E-08	0.088786	
19	HNRNPM	rs10412549	8,485,223	G	C	0.013624	-0.050647	0.008697	8.90E-09	-0.070547	0.014714	1.66E-06	-0.041475	0.010915	0.000146	7.47E-09	0.112549	
19	HNRNPM	rs2230647	8,486,210	T	C	0.01337	-0.048908	0.008784	3.90E-08	-0.070492	0.014866	2.15E-06	-0.038997	0.011022	0.000406	2.51E-08	0.088786	
19	HNRNPM	rs11669139	8,486,968	A	G	0.01337	-0.048908	0.008784	3.90E-08	-0.070492	0.014866	2.15E-06	-0.038997	0.011022	0.000406	2.51E-08	0.088786	
19	HNRNPM	rs12608524	8,487,283	C	T	0.01337	-0.048908	0.008784	3.90E-08	-0.070492	0.014866	2.15E-06	-0.038997	0.011022	0.000406	2.51E-08	0.088786	
19	HNRNPM	rs7507526	8,488,438	C	T	0.013631	-0.050683	0.008695	8.50E-09	-0.070547	0.014714	1.66E-06	-0.041532	0.010911	0.000142	7.28E-09	0.113198	
19	HNRNPM	rs6992	8,488,746	C	T	0.013383	-0.049019	0.008781	3.50E-08	-0.071069	0.014861	1.76E-06	-0.03883	0.011017	0.000427	2.17E-08	0.081388	
19	PRAM1	rs58034536	8,493,082	A	G	0.01336	-0.04923	0.008788	3.20E-08	-0.070753	0.014877	2.01E-06	-0.039333	0.011024	0.000362	2.11E-08	0.08972	
19	NCAN	rs145876852	19,248,021	C	A	0.014551	-0.054875	0.008416	1.70E-10	-0.074158	0.014257	2.02E-07	-0.04558	0.010554	1.59E-05	1.07162	0.107162	
19	HAPLN4 *	rs2074296	19,262,880	G	C	0.317945	-0.013423	0.002178	2.40E-10	-0.016243	0.0037	1.15E-05	-0.012412	0.002727	5.42E-06	2.08E-09	0.404642	
19	HAPLN4 *	rs8105094	19,263,252	T	C	0.298031	-0.012996	0.00222	1.30E-09	-0.015197	0.00377	5.61E-05	-0.012257	0.002779	1.05E-05	1.77E-08	0.530291	
19	HAPLN4 *	rs8105984	19,263,259	C	T	0.298031	-0.012996	0.00222	1.30E-09	-0.015197	0.00377	5.61E-05	-0.012257	0.002779	1.05E-05	1.77E-08	0.530291	
19	TM6SF2	rs10426780	19,265,074	C	T	0.318349	-0.013207	0.00217	4.20E-10	-0.015665	0.003687	2.18E-05	-0.012367	0.002716	5.37E-06	3.80E-09	0.471435	
19	TM6SF2	rs56831097	19,265,416	G	A	0.298846	-0.012984	0.002209	1.50E-09	-0.014578	0.003754	0.000104	-0.012595	0.002766	5.35E-06	1.67E-08	0.67058	
19	TM6SF2	rs2074298	19,266,907	G	C	0.319204	-0.013114	0.002162	4.90E-10	-0.015882	0.003676	1.58E-05	-0.012141	0.002707	7.38E-06	3.78E-09	0.412494	
19	TM6SF2	rs58542926	19,268,740	T	C	0.066469	-0.052502	0.004046	1.40E-39	-0.071797	0.006941	4.75E-25	-0.042625	0.00504	2.87E-17	1.69E-39	0.000675	M
19	TM6SF2	rs2074299	19,269,837	C	T	0.318622	-0.013011	0.002163	6.50E-10	-0.015823	0.003676	1.70E-05	-0.012033	0.002708	8.98E-06	4.90E-09	0.406475	
19	TM6SF2	rs2074300	19,270,187	T	G	0.299528	-0.012917	0.002201	1.50E-09	-0.014958	0.00374	6.41E-05	-0.01233	0.002756	7.78E-06	1.51E-08	0.571521	
19	TM6SF2	rs2074301	19,270,906	A	G	0.299425	-0.012831	0.002201	1.90E-09	-0.014835	0.00374	7.36E-05	-0.012268	0.002756	8.64E-06	1.91E-08	0.58055	
19	TM6SF2	rs2074303	19,270,946	T	C	0.318389	-0.013017	0.002163	6.40E-10	-0.015836	0.003676	1.67E-05	-0.012051	0.002707	8.66E-06	4.66E-09	0.407087	
19	TM6SF2	rs10419245	19,272,946	A	G	0.319923	-0.012423	0.002161	3.60E-09	-0.015567	0.003672	2.27E-05	-0.011272	0.002704	3.11E-05	2.12E-08	0.34624	
19	TM6SF2 *	rs735273	19,274,602	G	T	0.319397	-0.012922	0.002162	8.30E-10	-0.015583	0.003675	2.26E-05	-0.012035	0.002707	8.88E-06	6.38E-09	0.437003	
19	SUGP1 *	rs8103496	19,275,206	C	A	0.318405	-0.01296	0.002162	7.50E-10	-0.015763	0.003674	1.81E-05	-0.012014	0.002706	9.15E-06	5.30E-09	0.411355	
19	SUGP1 *	rs11882123	19,275,530	G	A	0.318404	-0.012965	0.002162	7.40E-10	-0.01577	0.003674	1.79E-05	-0.012014	0.002706	9.15E-06	5.26E-09	0.410458	
19	SUGP1 *	rs2017964	19,276,340	C	T	0.318406	-0.01296	0.002162	7.50E-10	-0.01577	0.003674	1.79E-05	-0.012006	0.002706	9.29E-06	5.33E-09	0.409376	
19	SUGP1	rs2074550	19,276,934	C	A	0.318406	-0.01296	0.002162	7.50E-10	-0.01577	0.003674	1.79E-05	-0.012006	0.002706	9.29E-06	5.33E-09	0.409376	
19	SUGP1	rs2074551	19,277,248	C	G	0.324236	-0.012732	0.002178	1.20E-09	-0.01574	0.003703	2.15E-05	-0.011599	0.002727	2.13E-05	1.40E-08	0.367773	
19	SUGP1	rs8107974	19,277,691	T	A	0.095896	-0.033109	0.003416	2.20E-23	-0.042918	0.005841	2.09E-13	-0.0272	0.004262	1.81E-10	2.71E-21	0.029737	M
19	SUGP1	rs8101938	19,279,688	A	G	0.318411	-0.012961	0.002162	7.50E-10	-0.01577	0.003674	1.79E-05	-0.012003	0.002706	9.33E-06	5.35E-09	0.409079	
19	SUGP1	rs2301784	19,279,940	A	G	0.318566	-0.012876	0.002163	9.90E-10	-0.015815	0.003677	1.72E-05	-0.011874	0.002708	1.18E-05	6.41E-09	0.388106	
19	SUGP1	rs6511026	19,280,593	T	C	0.318413	-0.012957	0.002162	7.60E-10	-0.01577	0.003674	1.79E-05	-0.011997	0.002706	9.44E-06	5.40E-09	0.408259	
19	SUGP1	rs2269873	19,281,592	C	T	0.319064	-0.01318	0.002164	4.20E-10	-0.015671	0.003677	2.05E-05	-0.01242	0.002709	4.61E-06	3.10E-09	0.476557	
19	SUGP1	rs8100204	19,282,905	A	G	0.223054	-0.013396	0.002465	1.50E-08	-0.015981	0.004201	0.000144	-0.012495	0.00308	5.03E-05	1.93E-07	0.503491	
19	SUGP1	rs10407952	19,283,587	T	C	0.316939	-0.012619	0.002171	2.70E-09	-0.015201	0.003688	3.80E-05	-0.01183	0.002718	1.37E-05	1.58E-08	0.461861	
19	SUGP1	rs6511028	19,285,158	C	T	0.317925	-0.012553	0.002165	2.60E-09	-0.015227	0.003679	3.53E-05	-0.011639	0.002711	1.79E-05	1.90E-08	0.432381	
19	SUGP1	rs7254748	19,286,670	C	A	0.317984	-0.012549	0.002163	2.50E-09	-0.015329	0.003677	3.10E-05	-0.011572	0.002708	1.95E-05	1.83E-08	0.410749	
19	SUGP1	rs10418051	19,286,980	T	C	0.317216	-0.012672	0.002166	1.80E-09	-0.015207	0.003681	3.65E-05	-0.011851	0.002711	1.25E-05	1.39E-08	0.462928	
19	SUGP1	rs4808937	19,287,196	G	A	0.318103	-0.012539	0.002163	2.60E-09	-0.015129	0.003676	3.91E-05	-0.011675	0.002708	1.64E-05	1.93E-08	0.449357	
19	SUGP1	rs4808938	19,290,409	A	G	0.318103	-0.012539	0.002163	2.60E-09	-0.015129	0.003676	3.91E-05	-0.011675	0.002708	1.64E-05	1.93E-08	0.449357	
19	SUGP1	rs10409234	19,292,601	G	A	0.318054	-0.012502	0.002163	2.90E-09	-0.015163	0.003677	3.76E-05	-0.011612	0.002708	1.83E-05	2.06E-08	0.449377	
19	SUGP1	rs7254927	19,293,977	G	C	0.318103	-0.012539	0.002163	2.60E-09	-0.015129	0.003676	3.91E-05	-0.011675	0.002708	1.64E-05	1.93E-08	0.449357	
19	SUGP1	rs2023882	19,294,596	C	T	0.318092	-0.012497	0.002163	3.00E-09	-0.015147	0.003677	3.83E-05	-0.011598	0.002708	1.86E-05	2.14E-08	0.437038	
19	SUGP1	rs2023883	19,294,671	A	G	0.29938	-0.012579	0.002202	4.00E-09	-0.014395	0.00374	0.00012	-0.012115	0.002757	1.13E-05	3.89E-08	0.623675	
19	SUGP1	rs12979148	19,296,060	C	T	0.220619	-0.013353	0.002439	2.30E-08	-0.013805	0.004152	0.000889	-0.013473	0.00305	1.01E-05	2.30E-07	0.948505	
19	SUGP1	rs11666553	19,296,362	A	C	0.299301	-0.012547	0.002201	4.40E-09	-0.014386	0.00374	0.000121	-0.012091	0.002756	1.17E-05	4.06E-08	0.621424	
19	SUGP1	rs10401969	19,296,909	C	T	0.096251	-0.032035	0.003413	4.30E-22	-0.043314	0.005834	1.18E-13	-0.025397	0.004259	2.54E-09	2.02E-20	0.013131	M
19	SUGP1	rs4808939	19,299,671	T	C	0.299571	-0.012956	0.002205	1.70E-09	-0.014908	0.003748	7.04E-05	-0.012417	0.002761	6.97E-06	1.49E-08	0.59257	
19	SUGP1	rs4808193	19,299,813	C	T	0.317851	-0.012618	0.002164	2.20E-09	-0.01537	0.003677	2.95E-05	-0.011679	0.002709	1.64E-05	1.48E-08	0.419057	
19	SUGP1	rs4808940	19,300,139	G	C	0.318112	-0.012673	0.002163	1.80E-09	-0.015329	0.003676	3.08E-05	-0.011787	0.002708	1.36E-05	1.29E-08	0.437816	
19	SUGP1	rs4808941	19,300,327	C	T	0.317025	-0.012695	0.002168	1.80E-09	-0.015721	0.003687	2.03E-05	-0.011609	0.002714	1.91E-05	1.20E-08	0.369101	
19	SUGP1	rs2315022	19,302,572	G	A	0.316623	-0.012353	0.002168	4.50E-09	-0.015081	0.003683	4.27E-05	-0.011334	0.002715	3.02E-05	3.76E-08	0.412752	
19	SUGP1	rs2301786	19,303,138	G	A	0.317922	-0.012593	0.002163	2.30E-09	-0.015411	0.003677	2.80E-05	-0.011629	0.002708	1.77E-05	1.51E-08	0.407423	
19	SUGP1	rs1010207	19,305,236	C	T	0.317644	-0.012723	0.002163	1.50E-09	-0.015351	0.003677	3.01E-05	-0.011846	0.002708	1.23E-05	1.15E-08	0.44266	
19	SUGP1	rs2240117	19,308,107	T	C	0.221149	-0.013165	0.002435	3.60E-08	-0.013921	0.004146	0.00079	-0.013125	0.003046	1.66E-05	3.31E-07	0.876976	
19	SUGP1	rs739846	19,308,262	A	G	0.095875	-0.03235	0.003416	2.60E-22	-0.042901	0.005835	2.04E-13	-0.026031	0.004265	1.07E-09	1.49E-20	0.019614	M
19	SUGP1	rs12983137	19,309,001	A	G	0.299355	-0.012529	0.002202	4.80E-09	-0.01461	0.00374	9.46E-05	-0.011985	0.002757	1.39E-05	3.82E-08	0.572134	
19	SUGP1	rs48089																

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p-value	gender_heterogeneity_p-value	Male/Female Specific
19	MAU2	rs111234557	19,325,420	G	C	0.164109	-0.020285	0.002718	1.60E-14	-0.027597	0.00462	2.40E-09	-0.016194	0.003402	1.96E-06	2.15E-13	0.046899	M
19	MAU2	rs62135552	19,326,045	G	A	0.318196	-0.012503	0.002163	2.90E-09	-0.015121	0.003677	3.95E-05	-0.01169	0.002708	1.60E-05	1.90E-08	0.452414	
19	MAU2	rs7247309	19,328,822	A	T	0.317862	-0.012608	0.002163	2.10E-09	-0.015247	0.003676	3.41E-05	-0.011768	0.002708	1.40E-05	1.46E-08	0.446185	
19	MAU2	rs3764567	19,329,257	C	T	0.300037	-0.012669	0.002199	2.90E-09	-0.014929	0.003737	6.53E-05	-0.012023	0.002754	1.28E-05	0.531386		
19	MAU2	rs1009136	19,329,619	A	G	0.318378	-0.012517	0.002164	2.50E-09	-0.015083	0.003679	4.18E-05	-0.011735	0.002709	1.49E-05	1.88E-08	0.463769	
19	MAU2	rs67720221	19,330,055	C	T	0.299017	-0.012333	0.002205	7.50E-09	-0.014152	0.003745	0.000159	-0.011984	0.002761	1.44E-05	6.43E-08	0.641155	
19	MAU2	rs12985655	19,331,625	G	A	0.325112	-0.012638	0.00215	1.20E-09	-0.014653	0.003658	6.26E-05	-0.012031	0.002691	7.89E-06	1.50E-08	0.56372	
19	MAU2	rs8103197	19,332,657	C	T	0.324992	-0.012649	0.00215	1.20E-09	-0.014565	0.003658	6.91E-05	-0.01212	0.00269	6.73E-06	1.41E-08	0.590399	
19	MAU2	rs11085259	19,335,047	T	C	0.299071	-0.012706	0.002201	3.00E-09	-0.014588	0.003739	9.63E-05	-0.012283	0.002756	8.45E-06	0.619757		
19	MAU2	rs769267	19,336,127	G	A	0.325242	-0.012687	0.00215	1.10E-09	-0.014585	0.003657	6.73E-05	-0.012141	0.00269	6.46E-06	1.33E-08	0.590401	
19	MAU2	rs757000	19,337,492	G	A	0.298591	-0.012587	0.002203	4.40E-09	-0.014341	0.003742	0.000128	-0.012244	0.002759	9.21E-06	3.42E-08	0.652054	
19	MAU2	rs757001	19,337,999	A	G	0.299061	-0.012719	0.002201	2.90E-09	-0.014636	0.003739	9.13E-05	-0.012282	0.002756	8.47E-06	2.29E-08	0.612255	
19	MAU2	rs2074090	19,338,877	G	T	0.324961	-0.012619	0.00215	1.40E-09	-0.014676	0.003658	6.07E-05	-0.011997	0.00269	8.33E-06	1.53E-08	0.555077	
19	MAU2	rs2074091	19,339,271	A	G	0.32489	-0.012606	0.002151	1.40E-09	-0.014671	0.003658	6.13E-05	-0.011985	0.002691	8.56E-06	1.59E-08	0.554301	
19	MAU2	rs8111511	19,340,184	T	A	0.327596	-0.012488	0.00216	1.80E-09	-0.01478	0.003674	5.82E-05	-0.011663	0.002703	1.62E-05	2.78E-08	0.494434	
19	MAU2	rs2301668	19,341,440	A	G	0.298909	-0.012675	0.002202	3.40E-09	-0.01465	0.00374	9.04E-05	-0.012197	0.002757	9.84E-06	0.597581		
19	MAU2	rs2965191	19,342,712	T	G	0.324905	-0.012505	0.002151	1.80E-09	-0.014478	0.003659	7.66E-05	-0.011913	0.002691	9.70E-06	2.21E-08	0.572204	
19	MAU2	rs2301669	19,342,751	C	A	0.324807	-0.012565	0.002151	1.60E-09	-0.014612	0.003659	6.57E-05	-0.011944	0.002691	9.18E-06	1.81E-08	0.565692	
19	MAU2	rs2965193	19,344,019	G	A	0.327098	-0.012717	0.002147	1.20E-09	-0.014794	0.003654	5.20E-05	-0.011993	0.002686	8.11E-06	1.29E-08	0.536777	
19	MAU2	rs58489806	19,346,108	T	C	0.16482	-0.020548	0.002714	9.00E-15	-0.028121	0.004616	1.15E-09	-0.016224	0.003396	1.81E-06	9.67E-14	0.03791	M
19	MAU2	rs968525	19,348,406	T	C	0.299082	-0.012834	0.002201	2.20E-09	-0.014743	0.003738	8.09E-05	-0.012399	0.002756	6.96E-06	1.69E-08	0.613696	
19	MAU2	rs10421505	19,348,745	T	C	0.324421	-0.012825	0.002152	7.10E-10	-0.014812	0.003659	5.22E-05	-0.01227	0.002693	5.28E-06	8.58E-09	0.575827	
19	MAU2	rs12982276	19,348,991	C	T	0.323946	-0.012902	0.002153	6.20E-10	-0.014947	0.003661	4.50E-05	-0.012312	0.002694	4.94E-06	6.98E-09	0.562119	
19	MAU2	rs12459854	19,350,628	T	C	0.324646	-0.012842	0.002151	7.10E-10	-0.014751	0.003659	5.59E-05	-0.012322	0.002691	4.75E-06	8.27E-09	0.592847	
19	MAU2	rs11085261	19,351,797	A	G	0.298463	-0.012653	0.002204	3.60E-09	-0.014442	0.003742	0.000115	-0.012266	0.00276	8.93E-06	3.00E-08	0.63987	
19	MAU2	rs11672355	19,351,893	C	G	0.162434	-0.020447	0.002744	2.20E-14	-0.027608	0.004663	3.29E-09	-0.01649	0.003435	1.61E-06	2.42E-13	0.05492	
19	MAU2	rs9304960	19,354,720	A	G	0.299086	-0.012834	0.002201	2.20E-09	-0.0147	0.003738	8.50E-05	-0.01243	0.002756	6.59E-06	1.68E-08	0.625006	
19	MAU2	rs2301671	19,355,460	T	C	0.299086	-0.012834	0.002201	2.20E-09	-0.0147	0.003738	8.50E-05	-0.01243	0.002756	6.59E-06	1.68E-08	0.625006	
19	MAU2	rs2285626	19,356,736	T	C	0.173991	-0.022254	0.00266	5.80E-18	-0.029785	0.004512	4.23E-11	-0.017978	0.003333	7.07E-08	1.67E-16	0.035342	M
19	MAU2	rs2285627	19,357,128	T	C	0.295725	-0.013367	0.002212	5.80E-10	-0.014598	0.003764	0.000106	-0.013206	0.002767	1.85E-06	6.13E-09	0.765624	
19	MAU2	rs2285628	19,357,187	A	T	0.301189	-0.012434	0.002205	8.50E-09	-0.014502	0.00375	0.000111	-0.011864	0.002759	1.73E-05	5.45E-08	0.571065	
19	MAU2	rs117970794	19,357,846	T	C	0.090624	-0.02954	0.003504	4.50E-18	-0.038256	0.005978	1.61E-10	-0.023988	0.004378	4.36E-08	3.87E-16	0.054158	
19	MAU2	rs13964	19,357,901	C	G	0.325462	-0.012545	0.002154	1.90E-09	-0.014437	0.003665	8.26E-05	-0.012047	0.002694	7.87E-06	1.94E-08	0.599364	
19	MAU2	rs15622	19,357,925	G	A	0.3266	-0.012203	0.002152	5.60E-09	-0.014333	0.003662	9.17E-05	-0.011513	0.002692	1.91E-05	5.02E-08	0.535002	
19	MAU2	rs10403731	19,358,487	A	G	0.298699	-0.012681	0.002206	4.10E-09	-0.014316	0.003744	0.000133	-0.01243	0.002764	6.97E-06	2.71E-08	0.685279	
19	MAU2 *	rs2965197	19,360,101	C	T	0.32779	-0.012524	0.002185	3.20E-09	-0.01341	0.003718	0.000313	-0.012524	0.002733	4.68E-06	4.41E-08	0.847654	
19	MAU2 *	rs10419672	19,360,432	C	T	0.323731	-0.012436	0.002157	2.60E-09	-0.014507	0.00367	7.80E-05	-0.011846	0.002698	1.14E-05	2.64E-08	0.559037	
19	MAU2 *	rs6511030	19,360,637	G	A	0.330579	-0.011915	0.002194	1.60E-08	-0.013569	0.003729	0.000277	-0.011541	0.002746	2.66E-05	1.95E-07	0.661496	
19	MAU2 *	rs6511032	19,360,874	C	T	0.323721	-0.012644	0.002156	1.50E-09	-0.014351	0.003668	9.21E-05	-0.012212	0.002698	6.11E-06	1.69E-08	0.638558	
19	MAU2 *	rs2905423	19,360,996	G	A	0.325103	-0.012478	0.002154	2.70E-09	-0.0141	0.003665	0.000121	-0.012082	0.002695	7.43E-06	2.63E-08	0.657347	
19	MAU2 *	rs8101499	19,366,175	A	G	0.301718	-0.012038	0.002199	4.30E-08	-0.012964	0.003746	0.000542	-0.011978	0.002749	1.34E-05	1.90E-07	0.831811	
19	MAU2 *	rs56255430	19,367,068	C	A	0.066193	-0.042068	0.004057	1.70E-25	-0.053525	0.006962	1.56E-14	-0.035632	0.005052	1.81E-12	2.30E-24	0.03753	M
19	MAU2 *	rs2074088	19,367,586	T	C	0.2982	-0.012121	0.002215	3.90E-08	-0.013014	0.003774	0.000568	-0.012162	0.00277	1.14E-05	1.70E-07	0.855622	
19	GATAD2A *	rs59148799	19,373,199	G	A	0.136267	-0.022521	0.002936	7.00E-15	-0.027939	0.005006	2.45E-08	-0.019728	0.00367	7.79E-08	9.15E-14	0.185887	
19	GATAD2A *	rs12052117	19,374,296	T	C	0.136244	-0.022401	0.002937	9.20E-15	-0.028218	0.005006	1.78E-08	-0.019365	0.00367	1.34E-07	1.13E-13	0.153802	
19	GATAD2A *	rs2965180	19,381,164	T	C	0.300596	-0.01206	0.0022	3.80E-08	-0.01319	0.003746	0.000432	-0.011919	0.002751	1.49E-05	1.70E-07	0.784404	
19	GATAD2A *	rs2905435	19,385,145	G	A	0.300157	-0.012069	0.002201	4.00E-08	-0.012983	0.003751	0.00054	-0.012078	0.002752	1.15E-05	1.64E-07	0.84565	
19	GATAD2A	rs10408875	19,392,764	C	T	0.136388	-0.02256	0.002935	4.50E-15	-0.028105	0.005002	1.96E-08	-0.019685	0.003669	8.27E-08	1.74E-14	0.174616	
19	GATAD2A	rs56241616	19,395,283	T	C	0.136362	-0.02256	0.002935	4.40E-15	-0.028105	0.005002	1.96E-08	-0.019686	0.003669	8.26E-08	1.780E-14	0.174692	
19	GATAD2A	rs10424702	19,397,204	G	A	0.220271	-0.013557	0.002438	4.60E-08	-0.013281	0.004147	0.001368	-0.013137	0.003051	1.68E-05	5.58E-07	0.977644	
19	GATAD2A	rs10408596	19,401,848	T	A	0.136344	-0.022571	0.002936	4.20E-15	-0.028216	0.005002	1.73E-08	-0.019655	0.00367	8.70E-08	7.24E-14	0.167583	
19	GATAD2A	rs34324111	19,402,759	G	T	0.140575	-0.021151	0.002941	9.60E-14	-0.028677	0.004998	9.89E-09	-0.017164	0.003682	3.18E-06	1.36E-12	0.063678	
19	GATAD2A	rs113460678	19,402,771	G	T	0.128937	-0.021972	0.003012	1.00E-13	-0.027159	0.005129	1.22E-07	-0.019311	0.003767	3.01E-07	1.60E-12	0.21749	
19	GATAD2A	rs188552254	19,406,360	G	A	0.134033	-0.022448	0.002963	9.60E-15	-0.027429	0.005048	5.63E-08	-0.019903	0.003704	7.93E-08	2.08E-13	0.22931	
19	GATAD2A	rs2965185	19,414,983	C	T	0.160309	-0.024396	0.002746	1.80E-19	-0.03168	0.004674	1.27E-11	-0.020683	0.003436	1.79E-09	1.43E-18	0.058014	
19	GATAD2A	rs11668386	19,421,101	G	A	0.136476	-0.022488	0.002933	5.10E-15	-0.02786	0.004996	2.51E-08	-0.019741	0.003668	7.51E-08	9.04E-14	0.190159	
19	GATAD2A	rs8182472	19,429,															

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differentiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
19	GATAD2A	rs3794991	19,499,787	T	C	0.073207	-0.041344	0.003865	3.60E-27	-0.054267	0.006621	2.60E-16	-0.034637	0.004818	6.79E-13	1.54E-26	0.016537	M
19	GATAD2A	rs3794993	19,500,741	A	C	0.301259	-0.011923	0.002197	4.80E-08	-0.012631	0.003739	0.000735	-0.012014	0.002748	1.25E-05	2.36E-07	0.894208	
19	GATAD2A	rs57009615	19,502,813	G	A	0.147995	-0.025203	0.002836	1.20E-19	-0.032366	0.004818	1.92E-11	-0.021568	0.00355	1.28E-09	1.54E-18	0.071221	
19	GATAD2A	rs148458424	19,507,589	T	G	0.024754	-0.045309	0.006486	3.20E-12	-0.052686	0.011088	2.05E-06	-0.041504	0.008094	2.99E-07	2.44E-11	0.415329	
19	GATAD2A *	rs56273306	19,510,195	C	T	0.138802	-0.022227	0.002914	7.80E-15	-0.028208	0.004964	1.36E-08	-0.019135	0.003643	1.54E-07	9.97E-14	0.140598	
19	GATAD2A *	rs113365218	19,510,388	A	G	0.138238	-0.021736	0.002921	3.90E-14	-0.02801	0.004977	1.87E-08	-0.018572	0.003652	3.74E-07	0.126304		
19	Y1EFN3	rs56397647	19,531,986	T	C	0.136611	-0.022289	0.002937	1.10E-14	-0.027299	0.005006	5.05E-08	-0.019692	0.003672	8.38E-08	1.98E-13	0.220405	
19	CILP2 *	rs10402308	19,546,691	A	G	0.298339	-0.0123	0.002218	2.40E-08	-0.013673	0.003778	0.000297	-0.012074	0.002774	1.36E-05	1.10E-07	0.733047	
19	CILP2 *	rs7245983	19,546,823	C	A	0.299379	-0.012189	0.002214	2.80E-08	-0.01354	0.00377	0.000332	-0.011937	0.00277	1.65E-05	1.46E-07	0.731921	
19	CILP2 *	rs16996148	19,547,663	T	G	0.069331	-0.043469	0.003965	1.40E-28	-0.057151	0.006779	3.62E-17	-0.036341	0.004948	2.15E-13	7.12E-28	0.013173	M
19	CILP2 *	rs17216525	19,551,411	T	C	0.075453	-0.040386	0.003813	7.50E-27	-0.055367	0.006518	2.09E-17	-0.032898	0.004758	4.88E-12	8.87E-27	0.005375	
19	CILP2 *	rs17216588	19,553,268	T	C	0.073819	-0.034748	0.003876	7.20E-20	-0.047985	0.00663	4.75E-13	-0.028333	0.004835	4.76E-09	1.47E-19	0.01664	M
19	PBX4 *	rs143988316	19,556,445	T	C	0.076254	-0.035331	0.003814	2.20E-21	-0.050453	0.006526	1.12E-14	-0.02804	0.004756	3.84E-09	2.98E-21	0.005526	M
19	PBX4 *	rs78916915	19,558,399	A	G	0.075684	-0.032104	0.003817	8.60E-18	-0.046208	0.006531	1.56E-12	-0.025251	0.004761	1.16E-07	1.05E-17	0.009535	M
19	PBX4 *	rs150824230	19,559,801	A	G	0.074789	-0.033363	0.003841	4.50E-19	-0.047272	0.006578	6.90E-13	-0.026716	0.004789	2.49E-08	1.06E-18	0.011543	M
19	PBX4 *	rs73004926	19,560,457	T	C	0.074789	-0.033363	0.003841	4.50E-19	-0.047272	0.006578	6.90E-13	-0.026716	0.004789	2.49E-08	1.06E-18	0.011543	M
19	PBX4	rs73004933	19,564,887	T	C	0.074317	-0.034409	0.00385	5.80E-20	-0.048552	0.006594	1.87E-13	-0.027588	0.004799	9.25E-09	1.12E-19	0.010167	M
19	PBX4	rs73004951	19,584,419	T	C	0.094695	-0.030983	0.003459	9.50E-20	-0.046759	0.005934	3.43E-15	-0.023113	0.004308	8.29E-08	1.85E-20	0.001268	M
19	PBX4	rs374807806	19,584,623	T	G	0.010868	-0.057517	0.009739	3.70E-09	-0.080893	0.016251	6.55E-07	-0.047037	0.012318	0.000135	2.84E-09	0.096854	
19	PBX4	rs12608729	19,589,743	T	C	0.092133	-0.031315	0.00349	1.10E-19	-0.048585	0.00599	5.30E-16	-0.022614	0.004346	2.00E-07	6.89E-21	0.000453	M
19	PBX4	rs73004959	19,600,330	T	C	0.092161	-0.031288	0.003489	1.40E-19	-0.047773	0.005986	1.52E-15	-0.022882	0.004345	1.42E-07	1.40E-20	0.000769	M
19	PBX4	rs73004962	19,602,260	T	A	0.084434	-0.030639	0.003627	8.50E-18	-0.045095	0.006221	4.37E-13	-0.023561	0.004517	1.87E-07	4.82E-18	0.005108	M
19	PBX4	rs73004966	19,605,749	T	C	0.08056	-0.033731	0.003705	2.30E-20	-0.050937	0.006355	1.16E-15	-0.025233	0.004614	4.64E-08	3.61E-21	0.00107	M
19	PBX4	rs57504626	19,609,590	T	C	0.08414	-0.031697	0.003633	5.20E-19	-0.047425	0.006233	2.91E-14	-0.02419	0.004524	9.14E-08	1.67E-19	0.002565	M
19	PBX4	rs16996185	19,609,979	G	T	0.085501	-0.030945	0.003601	2.40E-18	-0.046666	0.00617	4.10E-14	-0.023379	0.004488	1.93E-07	4.84E-19	0.002281	M
19	PBX4	rs12610185	19,610,913	A	G	0.085463	-0.031089	0.003602	1.40E-18	-0.046557	0.006173	4.85E-14	-0.023701	0.004489	1.32E-07	3.96E-19	0.00276	M
19	PBX4	rs12610191	19,611,167	T	C	0.085456	-0.031063	0.003603	1.50E-18	-0.046597	0.006174	4.66E-14	-0.023641	0.00449	1.43E-07	4.09E-19	0.002648	M
19	PBX4	rs10500212	19,612,406	T	C	0.085742	-0.030727	0.0036	3.40E-18	-0.046177	0.006171	7.57E-14	-0.023286	0.004486	2.14E-07	9.75E-19	0.002704	M
19	PBX4	rs58847337	19,615,213	A	G	0.078771	-0.034296	0.003742	1.10E-20	-0.052784	0.006409	1.87E-16	-0.024919	0.004665	9.44E-08	1.19E-21	0.000443	M
19	PBX4	rs73004975	19,616,343	G	A	0.097278	-0.028821	0.003403	6.50E-18	-0.044853	0.005832	1.53E-14	-0.020623	0.004241	1.18E-06	1.05E-18	0.000783	M
19	GMIP	rs2304128	19,635,342	T	G	0.053709	-0.026724	0.004501	5.90E-10	-0.051559	0.007663	1.78E-11	-0.013851	0.00563	0.0139	7.17E-12	7.40E-05	M
19	CEBPA *	rs10403076	33,322,595	T	C	0.159052	0.020031	0.002781	1.30E-12	0.020976	0.004704	8.34E-06	0.019226	0.00349	3.69E-08	1.23E-11	0.765116	
19	CEBPA *	rs10403125	33,322,664	T	C	0.159234	0.019915	0.00278	1.70E-12	0.020889	0.004704	9.07E-06	0.019081	0.003489	4.65E-08	1.67E-14		
19	CEBPA *	rs10402014	33,322,870	A	G	0.170288	0.020648	0.002704	5.50E-14	0.022595	0.004586	8.48E-07	0.019542	0.003389	8.36E-09	3.23E-13	0.592381	
19	CEBPA *	rs10411163	33,323,488	G	A	0.166029	0.020309	0.002729	2.20E-13	0.02175	0.004625	2.61E-06	0.019494	0.003422	1.25E-08	1.41E-12	0.694991	
19	CEBPA *	rs28885440	33,323,563	A	G	0.165905	0.020202	0.002729	2.90E-13	0.021281	0.004623	4.22E-06	0.019581	0.003422	1.08E-08	1.94E-12	0.767533	
19	CEBPA *	rs7254869	33,323,787	C	T	0.159833	0.020155	0.002765	5.90E-13	0.020704	0.004678	9.75E-06	0.019597	0.00347	1.67E-08	6.65E-12	0.849354	
19	CEBPA *	rs7253713	33,324,221	A	G	0.166343	0.020207	0.002722	2.40E-13	0.021522	0.004611	3.10E-06	0.019431	0.003413	1.28E-08	1.70E-12	0.715428	
19	CEBPA *	rs10415737	33,324,300	C	G	0.16635	0.020198	0.002722	2.40E-13	0.021513	0.004611	3.13E-06	0.019424	0.003413	1.29E-08	1.73E-12	0.715826	
19	CEBPA *	rs10415770	33,324,336	A	G	0.166355	0.020213	0.002722	2.30E-13	0.021511	0.004611	3.13E-06	0.019444	0.003413	1.24E-08	1.68E-12	0.718623	
19	CEBPA *	rs60656848	33,325,591	C	T	0.160194	0.020205	0.002761	5.40E-13	0.020482	0.004671	1.18E-05	0.019803	0.003464	1.12E-08	5.37E-12	0.907106	
19	CEBPA *	rs12608723	33,326,227	G	A	0.171552	0.02096	0.002683	1.40E-14	0.02251	0.004549	7.64E-07	0.020133	0.003363	2.20E-09	7.94E-14	0.674293	
19	CEBPA *	rs7251395	33,327,226	C	G	0.165101	0.020815	0.002723	5.10E-14	0.021621	0.004611	2.78E-06	0.020164	0.003416	3.68E-09	4.56E-13	0.799562	
19	CEBPA *	rs7256107	33,327,250	C	T	0.17138	0.020872	0.002684	1.90E-14	0.022197	0.004551	1.09E-06	0.020193	0.003365	2.02E-09	1.03E-13	0.723194	
19	CEBPA *	rs10413354	33,327,308	G	C	0.171582	0.020835	0.002683	2.00E-14	0.022288	0.004548	9.73E-07	0.020077	0.003362	2.42E-09	1.10E-13	0.695818	
19	CEBPA *	rs10414141	33,327,311	T	A	0.165103	0.020804	0.002723	5.30E-14	0.021588	0.004611	2.88E-06	0.020165	0.003416	3.67E-09	4.70E-13	0.804219	
19	CEBPA *	rs7251758	33,327,479	A	G	0.171723	0.020864	0.002682	1.90E-14	0.022245	0.004546	1.01E-06	0.020142	0.003362	2.13E-09	1.01E-13	0.709982	
19	CEBPA *	rs112432604	33,328,149	G	A	0.169619	0.02093	0.002711	4.00E-14	0.022704	0.004595	7.90E-07	0.020129	0.003399	3.26E-09	1.20E-13	0.652314	
19	CEBPA *	rs10421445	33,328,331	G	A	0.171741	0.02068	0.002682	3.10E-14	0.022065	0.004547	1.24E-06	0.019965	0.003362	2.95E-09	1.69E-13	0.710328	
19	CEBPA *	rs10426997	33,328,338	C	T	0.164646	0.020739	0.002727	6.70E-14	0.021422	0.004616	3.53E-06	0.020156	0.00342	3.90E-09	6.06E-13	0.825543	
19	CEBPA *	rs7253865	33,330,342	G	T	0.167084	0.020265	0.002717	2.00E-13	0.021418	0.004607	3.39E-06	0.019624	0.003406	8.52E-09	1.25E-12	0.7541	
19	CEBPA *	rs149222436	33,336,002	T	C	0.159036	0.020327	0.00277	5.20E-13	0.01986	0.004685	2.27E-05	0.020327	0.003477	5.19E-09	4.77E-12	0.936131	
19	CEBPA *	rs141706710	33,336,121	T	C	0.15908	0.020325	0.00277	5.20E-13	0.019829	0.004685	2.34E-05	0.020339	0.003477	5.05E-09	4.77E-12	0.930251	
19	CEBPG *	rs16967971	33,339,692	T	G	0.159714	0.020312	0.002766	3.60E-13	0.019617	0.004676	2.76E-05	0.020486	0.003472	3.71E-09	4.14E-12	0.881343	
19	CEBPG *	rs12610763	33,350,705	A	G	0.159482	0.002367	1.40E-12		0.019461	0.004674	3.16E-05	0.019862	0.003476	1.13E-08	1.40E-11	0.945202	
19	CEBPG *	rs10417389	33,350,819	T	C	0.159465	0.019834	0.002767	1.60E-12	0.01935	0.004674	3.52E-05	0.019848	0.003476	1.16E-08	1.58E-11	0.931782	

CHR	GENE	SNP	Pos (h38)	EA	NEA	EAF	BETA (whole)	SE (whole)	P (whole)	BETA (male)	SE (male)	P (male)	BETA (female)	SE (female)	P (female)	gender_differntiated_p.value	gender_heterogeneity_p.value	Male/Female Specific
20	ZNF335	rs3092073	45,967,010	A	G	0.448103	-0.010976	0.002054	8.00E-09	-0.009392	0.003487	0.00709	-0.011291	0.002572	1.15E-05	1.74E-06	0.66109	
20	ZNF335	rs76907877	45,967,688	T	C	0.066764	0.042214	0.004053	2.30E-27	0.033143	0.006893	1.55E-06	0.047185	0.00507	1.40E-20	1.49E-24	0.100789	
20	ZNF335	rs78558150	45,970,350	T	C	0.052751	0.040097	0.004547	2.40E-20	0.03264	0.007731	2.45E-05	0.04	0.005688	1.08E-14	1.36E-17	0.236537	
20	ZNF335 *	rs16990971	45,972,654	G	A	0.067326	0.040901	0.004045	4.80E-26	0.032696	0.006878	2.03E-06	0.045565	0.00506	2.28E-19	3.04E-23	0.131742	
20	ZNF335 *	rs6017717	45,975,324	C	G	0.378816	-0.01377	0.002112	3.30E-12	-0.009871	0.003591	0.005994	-0.015116	0.002642	1.09E-08	1.79E-09	0.239396	
20	MMP9 *	rs78295912	45,993,859	T	C	0.065687	0.038698	0.004113	3.40E-22	0.032	0.006987	4.72E-06	0.042152	0.005147	2.75E-16	7.59E-20	0.242051	
20	MMP9 *	rs1888235	45,995,328	T	C	0.117195	0.025395	0.003177	3.50E-16	0.016469	0.005374	0.00219	0.030147	0.003985	4.05E-14	3.42E-15	0.040922	F
20	MMP9 *	rs145026700	45,996,044	T	C	0.065172	0.038399	0.004128	7.90E-22	0.03148	0.007015	7.31E-06	0.042064	0.005165	3.99E-16	1.67E-19	0.224328	
20	MMP9 *	rs6073984	46,002,014	G	A	0.115386	0.025275	0.003193	7.50E-16	0.015354	0.005399	0.004472	0.030695	0.004007	1.93E-14	3.16E-15	0.022524	F
20	MMP9 *	rs3918241	46,007,096	A	T	0.12095	0.023305	0.00312	1.90E-14	0.013965	0.005271	0.008086	0.028261	0.003916	5.55E-13	1.47E-13	0.029501	F
20	MMP9 *	rs3918242	46,007,337	T	C	0.120956	0.023295	0.003119	2.00E-14	0.014003	0.005271	0.007914	0.028217	0.003915	5.98E-13	1.55E-13	0.03043	F
20	MMP9	rs2274755	46,011,053	T	G	0.12304	0.023377	0.003084	1.10E-14	0.014178	0.005218	0.006602	0.028053	0.003868	4.23E-13	9.38E-14	0.032685	F
20	MMP9	rs2236416	46,011,936	G	A	0.123716	0.022959	0.003072	2.80E-14	0.013714	0.005201	0.008383	0.027615	0.003852	7.90E-13	2.15E-13	0.031755	F
20	MMP9	rs17577	46,014,472	A	G	0.12589	0.022483	0.003041	3.60E-14	0.013836	0.005151	0.007244	0.026792	0.003813	2.20E-12	5.14E-13	0.043229	F
20	MMP9	rs3918261	46,014,953	G	A	0.125903	0.022485	0.003041	3.60E-14	0.01393	0.00515	0.006854	0.026748	0.003813	2.38E-12	5.29E-13	0.045488	F
20	MMP9	rs13925	46,016,326	A	G	0.125902	0.022482	0.003041	3.50E-14	0.013901	0.00515	0.00697	0.02675	0.003812	2.35E-12	5.32E-13	0.04495	F
20	MMP9 *	rs3918270	46,016,700	A	G	0.122002	0.02176	0.0031	6.00E-13	0.013134	0.005253	0.012428	0.026188	0.003884	1.62E-11	5.92E-12	0.045713	F
20	MMP9 *	rs8184490	46,016,794	G	C	0.071086	0.033155	0.003944	2.80E-18	0.025785	0.006702	0.000121	0.036601	0.004935	1.26E-13	6.98E-16	0.19374	
20	MMP9 *	rs3918271	46,016,954	A	G	0.119407	0.022912	0.003129	7.10E-14	0.014099	0.005301	0.007836	0.02738	0.003921	3.02E-12	7.53E-13	0.043991	F
20	SLC12A5 *	rs10432735	46,021,679	T	A	0.125385	0.022287	0.003044	6.10E-14	0.013459	0.005158	0.009088	0.026658	0.003814	2.88E-12	8.22E-13	0.039649	F
20	SLC12A5	rs62215576	46,023,758	T	C	0.125931	0.022396	0.00304	4.10E-14	0.01383	0.005149	0.007247	0.026674	0.003811	2.69E-12	6.27E-13	0.044988	F
20	SLC12A5	rs6124764	46,027,498	A	T	0.122906	0.022862	0.003091	1.90E-14	0.015097	0.005238	0.003961	0.026631	0.003873	6.42E-12	8.55E-13	0.076667	
20	SLC12A5	rs11908352	46,027,501	A	C	0.122903	0.022868	0.003091	1.90E-14	0.015054	0.005238	0.004068	0.026656	0.003874	6.14E-12	8.38E-13	0.074923	
20	SLC12A5	rs6124765	46,039,572	T	C	0.123908	0.02344	0.003123	2.10E-14	0.014121	0.005277	0.007471	0.027906	0.00392	1.13E-12	2.76E-13	0.036012	F
20	SLC12A5	rs116878061	46,057,452	T	G	0.068687	0.030037	0.004004	1.90E-15	0.02433	0.006814	0.000359	0.03274	0.005006	6.38E-11	8.81E-13	0.319882	
22	MIRLET7BHG	rs8135478	46,086,105	C	T	0.12874	-0.017083	0.003026	6.30E-09	-0.021094	0.005124	3.88E-05	-0.014348	0.003793	0.000157	1.63E-07	0.2899	
22	MIRLET7BHG	rs9626891	46,087,068	C	T	0.124602	-0.016626	0.003053	2.20E-08	-0.019895	0.005162	0.000117	-0.014372	0.003829	0.000176	5.18E-07	0.390039	
22	MIRLET7BHG	rs58280444	46,088,037	A	G	0.115302	-0.017484	0.003194	1.60E-08	-0.020132	0.005404	0.000197	-0.015433	0.004004	0.000117	5.76E-07	0.484816	
22	MIRLET7BHG	rs7290267	46,088,855	G	A	0.119061	-0.017025	0.003153	2.80E-08	-0.020805	0.005316	9.16E-05	-0.014071	0.003962	0.000386	8.60E-07	0.309713	
22	MIRLET7BHG	rs7291040	46,089,093	C	T	0.118368	-0.017007	0.003168	3.20E-08	-0.020847	0.005337	9.45E-05	-0.013961	0.003982	0.000458	1.04E-06	0.301053	
22	PPARA	rs1800234	46,219,983	C	T	0.04395	-0.028196	0.004937	2.70E-09	-0.011421	0.008349	0.171295	-0.036062	0.006193	5.95E-09	1.71E-08	0.017793	F

BETA = Beta coefficients, CHR = chromosome, EA = effect allele, EAF= effect allele frequency, NEA = non-effect allele, P = p-value, Pos = position, SE = standard error

Supplementary Table 21. Summary of female and male-specific genes for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

Sex-specific effect	CHR	Gene	Pos1 (b38)	Pos2 (b38)	IR	TG	HDL-C	T2D	AD	FG	BMI	TG:HDL-C
Female	1	USP1 *	62,436,303	62,451,804		x						
Female	4	RGS12	3,314,146	3,439,913		x					x	
Female	4	HGFAC *	3,441,998	3,449,486		x						
Female	5	FGF10-AS1	44,388,732	44,413,989								
Female	5	TNFAIP8	119,268,691	119,394,604								x
Female	5	HSD17B4 *	119,452,442	119,542,335			x					
Female	6	GSTA1 *	52,791,371	52,803,816								
Female	6	GSTA2	52,750,087	52,763,475		x	x					
Female	6	RGS17	153,004,459	153,131,282								x
Female	7	CAMK2B	44,217,149	44,325,631		x		x		x		
Female	7	FZD9	73,433,778	73,436,120		x	x					
Female	7	BAZ1B	73,440,397	73,522,285		x	x					
Female	7	MLXIPL	73,593,193	73,624,540		x	x				x	x
Female	7	KLF14 *	130,732,553	130,734,033								x
Female	10	REEP3	63,521,362	63,625,123		x	x	x			x	
Female	10	WDR11 *	120,851,362	120,909,524			x	x				
Female	11	GRM5	88,504,642	89,065,982			x				x	
Female	11	APOA5 *	116,789,369	116,792,420		x	x					x
Female	11	APOA4	116,820,701	116,823,295		x	x					x
Female	11	APOA1	116,835,752	116,837,622		x	x				x	
Female	11	PAFAH1B2	117,144,283	117,178,173		x	x				x	
Female	11	SIDT2	117,179,222	117,197,445		x	x					
Female	11	LOC100652768	117,195,613	117,201,914								
Female	11	TAGLN	117,199,323	117,204,792		x	x					
Female	11	PCSK7	117,205,070	117,232,525		x	x				x	x
Female	12	IFT81	110,124,334	110,218,795			x				x	
Female	12	ATP2A2 *	110,281,226	110,351,092			x					
Female	14	RTRAF, C14orf166	51,989,546	52,010,694		x						
Female	14	NID2	52,004,801	52,069,228								x
Female	16	CMIP	81,445,169	81,711,763								x
Female	17	BPTF	67,825,663	67,984,378								x
Female	17	C17orf58	67,991,098	67,993,649		x					x	
Female	19	HPN	35,040,505	35,066,573								x
Female	20	FOXA2 *	22,581,003	22,585,463						x		
Female	20	LNCNEF	22,587,522	22,607,517						x		
Female	20	LINC01747	22,667,293	22,685,344						x		
Female	20	PLTP *	45,898,619	45,912,364		x	x					x
Female	20	MMP9	46,008,907	46,016,561								
Female	20	SLC12A5	46,021,689	46,060,150		x	x					
Female	22	PPARA	46,150,526	46,243,756		x					x	

Sex-specific effect	CHR	Gene	Pos1 (b38)	Pos2 (b38)	IR	TG	HDL-C	T2D	AD	FG	BMI	TG:HDL-C
Male	1	DOCK7	62,454,725	62,688,368		x	x					x
Male	2	MRPL33 *	27,771,716	27,779,741		x				x		
Male	3	SYN2	12,004,388	12,192,032	x	x	x	x				
Male	4	AFF1	86,935,001	87,141,054		x	x				x	x
Male	4	KLHL8 *	87,160,103	87,220,608		x						
Male	6	DDR1	30,880,970	30,900,156								
Male	6	HLA-C *	31,268,749	31,272,092		x	x	x	x		x	x
Male	8	TRIB1 *	125,430,320	125,438,405								x
Male	11	BACE1	117,285,685	117,316,256		x	x					
Male	11	CEP164	117,321,777	117,413,266		x	x				x	x
Male	11	DSCAML1 *	117,427,772	117,797,261		x	x		x			x
Male	15	TLE3 *	70,047,790	70,097,917		x	x				x	
Male	17	ZNHIT3	36,486,681	36,499,312		x		x			x	
Male	17	MYO19	36,495,636	36,544,815				x			x	
Male	17	PIGW	36,534,987	36,539,303								
Male	17	GGNBP2	36,544,919	36,589,848							x	
Male	17	DHRS11	36,591,879	36,600,804							x	
Male	19	TM6SF2	19,264,364	19,273,265		x		x			x	x
Male	19	SUGP1	19,276,512	19,320,512		x		x			x	x
Male	19	MAU2	19,320,820	19,358,754		x					x	x
Male	19	GATAD2A	19,385,832	19,508,932		x		x		x	x	x
Male	19	CILP2 *	19,538,264	19,546,659		x					x	
Male	19	PBX4	19,561,706	19,618,916		x					x	
Male	19	GMIP	19,629,472	19,643,667		x						
Male	19	APOC1P1	44,926,802	44,931,386		x	x	x	x		x	x

AD = Alzheimer's disease; b38 = Genome Research Consortium human build 38; BMI = body mass index; CHR = chromosome; FG = fasting glucose; HDL-C = high-density lipoprotein cholesterol; IR = insulin resistance; NA = not available; Pos = position; T2D = type 2 diabetes; TG = triglycerides; TG:HDL-C = the triglyceride to high-density lipoprotein cholesterol ratio;

x: Previous GWASs reported in the NHGRI-EBI GWAS Catalog have identified various phenotypes that reach genome-wide significance ($P < 5 \times 10^{-8}$).

Supplementary Table 22. Summary of parent-of-origin analysis in the *KLF14* gene in the parent-offspring cohort within the Taiwan Biobank.

CHR	Gene	SNP	Pos (b38)	EA	NEA	EAF	HET	PAT	MAT	P
7	KLF14	rs290796	130730844	T	C	0.1632	642	0	642	< 2.2E-16
7	KLF14	rs290795	130730858	A	T	0.1641	645	0	645	< 2.2E-16
7	KLF14	rs290794	130731566	A	G	0.2239	849	0	849	< 2.2E-16
7	KLF14	rs290793	130731898	C	G	0.2238	849	0	849	< 2.2E-16
7	KLF14	rs62471572	130732297	T	C	0.3742	1,112	0	1,112	< 2.2E-16
7	KLF14	rs76603546	130733698	G	A	0.3793	1,115	0	1,115	< 2.2E-16
7	KLF14	rs111400400	130733862	G	A	0.2211	835	0	835	< 2.2E-16
7	KLF14	rs184537657	130733894	G	T	0.2213	833	0	833	< 2.2E-16
7	KLF14	rs111731678	130733917	A	T	0.2218	835	0	835	< 2.2E-16
7	KLF14 *	rs1364422	130761222	T	C	0.4268	1,173	0	1,173	< 2.2E-16

CHR = chromosome, EA = effect allele, EAF= effect allele frequency, HET = heterozygous offspring, MAT = maternal transmissions, NEA = non-effect allele, P = p-value, PAT = paternal transmissions, Pos = position

Parent-of-origin effects (POE) of genetic variants in family-based cohorts were assessed using a simplified parental asymmetry test.

Supplementary Table 23. Transcriptome-wide association analysis for the TyG index, a marker of insulin resistance, using GTEx tissue expression with p-value < 5.0 x E-8 on chromosome 2 only.

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Pancreas	HS1BP3	2	20,760,208	20,850,849	0.061699	rs6733447	11.4	rs11096689	-6.26E-04	-3.4	8.72	504	1	top1	-0.00063	0.35	-8.72E+00	2.78E-18
Muscle_Skeletal	APOB	2	21,224,301	21,266,945	0.084294	rs6733447	11.4	rs505813	1.18E-03	-3.9	-1.51	425	425	blup	0.036	1.50E-05	5.77E+00	7.85E-09
Thyroid	GCKR	2	27,719,709	27,746,554	0.201367	rs1260326	30.5	rs814295	1.24E-01	7.2	-2.69E+01	290	7	enet	0.13	1.60E-13	-31.90248	2.47E-223
Pituitary	AC074117.10	2	27,579,360	27,590,489	0.068379	rs1260326	30.5	rs2950835	5.88E-03	3.14	28.5	301	1	top1	0.0059	0.17	28.5	1.17E-178
Brain_Cortex	C2orf16	2	27,799,389	27,805,588	0.028402	rs1260326	30.5	rs2950835	5.78E-03	-2.72	28.5	279	1	top1	0.0058	0.18	-28.5	1.17E-178
Thyroid	FNDCA	2	27,714,750	27,718,112	0.465089	rs1260326	30.5	rs814295	2.50E-01	10.05	-2.69E+01	289	29	enet	0.27	2.40E-29	-27.42505	1.38E-165
Pituitary	IFT172	2	27,667,238	27,712,656	0.019327	rs1260326	30.5	rs3817588	-6.22E-03	-2.89	-27.4	287	1	lasso	0.042	0.0057	27.4	2.74E-165
Pituitary	EIF2B4	2	27,587,219	27,593,353	0.104319	rs1260326	30.5	rs6744393	2.21E-02	-3.41	-26.4	303	1	top1	0.022	0.035	26.4	1.37E-153
Thyroid	GPN1	2	27,851,114	27,873,678	0.02207	rs1260326	30.5	rs6744393	3.33E-03	3.17	-2.64E+01	286	1	top1	0.0033	0.13	-26.4	1.37E-153
Thyroid	C2orf16	2	27,799,389	27,805,588	0.05582	rs1260326	30.5	rs6744393	-3.05E-04	3.57	-2.64E+01	280	12	enet	0.0099	0.026	-25.97594	9.26E-149
Thyroid	IFT172	2	27,667,238	27,712,656	0.066227	rs1260326	30.5	rs780092	-1.88E-03	3.27	-2.70E+01	287	22	enet	0.0028	0.15	-23.00013	4.65E-117
Muscle_Skeletal	ZNF513	2	27,600,098	27,603,657	0.018534	rs1260326	30.5	rs4665991	1.94E-02	3.55	22.8	301	1	top1	0.019	0.0012	2.28E+01	4.59E-115
Adipose_Subcutaneous	ABHD1	2	27,346,691	27,353,623	0.000243	rs1260326	30.5	rs4665382	-2.47E-03	-2.67	2.27E+01	316	1	lasso	0.0082	0.042	-22.7	4.48E-114
Thyroid	BRE	2	28,112,808	28,561,768	0.043214	rs1260326	30.5	rs4665382	4.45E-02	4.83	2.27E+01	314	1	top1	0.044	1.30E-05	22.7	4.48E-114
Brain_Hypothalamus	ZNF513	2	27,600,098	27,603,657	0.008958	rs1260326	30.5	rs1919127	-9.39E-03	2.54	22.7	300	1	lasso	0.029	0.043	22.7	4.48E-114
Pancreas	MRPL33	2	27,994,584	28,005,561	0.008903	rs1260326	30.5	rs12478841	3.45E-03	-2.6	22.7	285	1	lasso	0.0049	0.15	-2.25E+01	4.15E-112
Brain_Hypothalamus	SLC4A1AP	2	27,886,677	27,917,836	0.042496	rs1260326	30.5	rs2068834	1.58E-03	-2.94	22.5	298	1	top1	0.0016	0.28	-22.5	4.15E-112
Pancreas	SUPT7L	2	27,874,376	27,886,337	0.05693	rs1260326	30.5	rs2068834	6.26E-03	-3.07	22.5	299	1	top1	0.0063	0.12	-2.25E+01	4.15E-112
Thyroid	ZNF513	2	27,600,098	27,603,657	0.017531	rs1260326	30.5	rs1919127	3.16E-04	3.03	2.27E+01	301	2	lasso	0.01	0.026	21.64888	6.23E-104
Adipose_Visceral_Omentum	C2orf16	2	27,799,389	27,805,588	0.113547	rs1260326	30.5	rs3817588	-2.90E-03	3.23	-2.74E+01	280	280	blup	0.013	0.025	-2.02E+01	1.55E-90
Brain_Hippocampus	GCKR	2	27,719,709	27,746,554	0.066378	rs1260326	30.5	rs13030973	-7.32E-03	-3.04	15.8	289	2	lasso	0.0038	0.24	-19.5988	1.58E-85
Brain_Cortex	GPN1	2	27,851,114	27,873,678	0.07007	rs1260326	30.5	rs1881396	4.43E-03	3.17	-19.4	285	2	lasso	0.0097	0.13	-19.37247	1.32E-83
Brain_Hypothalamus	PPM1G	2	27,604,061	27,632,554	0.008155	rs1260326	30.5	rs2141372	1.39E-02	2.86	-19.3	300	4	lasso	0.053	0.01	-19.32405	3.37E-83
Adipose_Subcutaneous	GTF3C2	2	27,548,716	27,579,868	0.004114	rs1260326	30.5	rs6734059	-9.98E-04	2.82	-1.93E+01	302	1	top1	-0.001	0.43	-19.3	5.37E-83
Muscle_Skeletal	GPN1	2	27,851,114	27,873,678	0.108066	rs1260326	30.5	rs1919128	5.54E-02	5.95	22.7	286	9	enet	0.071	1.20E-09	1.93E+01	1.27E-82
Pituitary	SNX17	2	27,593,389	27,599,995	0.097781	rs1260326	30.5	rs780094	5.50E-02	-3.4	29.5	303	303	blup	0.057	0.0016	-18.11886	2.26E-73
Thyroid	SUPT7L	2	27,874,376	27,886,337	0.027027	rs1260326	30.5	rs2068834	-2.52E-03	-3.11	2.25E+01	299	299	blup	0.0018	0.19	-16.93361	2.54E-64
Brain_Hippocampus	KRTCAP3	2	27,665,233	27,669,348	0.198115	rs1260326	30.5	rs2950835	5.70E-03	-3.35	28.5	298	298	blup	0.057	0.0068	-16.68093	1.80E-62
Pancreas	PPM1G	2	27,604,061	27,632,554	0.021571	rs1260326	30.5	rs8179252	-3.43E-03	-2.79	-4.64	301	2	lasso	-0.0026	0.51	1.56E+01	1.19E-54
Pancreas	C2orf16	2	27,799,389	27,805,588	0.053436	rs1260326	30.5	rs4665382	-4.15E-03	-2.8	22.7	280	280	blup	0.026	0.0094	-1.43E+01	1.16E-46
Adrenal_Gland	AC074091.13	2	27,928,653	27,938,599	0.05385	rs1260326	30.5	rs4666010	2.40E-02	-3.45	-14	298	1	top1	0.024	0.023	14	1.56E-44
Adipose_Subcutaneous	IFT172	2	27,667,238	27,712,656	0.036327	rs1260326	30.5	rs11891554	-2.44E-03	2.81	-2.19E+00	287	287	blup	0.001	0.24	-13.29832	2.37E-40
Adipose_Subcutaneous	EIF2B4	2	27,587,219	27,593,353	0.03205	rs1260326	30.5	rs8179249	1.56E-03	2.92	2.94E+00	303	23	enet	0.0045	0.1	13.27439	3.26E-40
Thyroid	RBKS	2	28,004,231	28,113,965	0.082707	rs1260326	30.5	rs12618742	3.42E-03	4.44	1.26E-01	313	313	blup	0.022	0.0019	12.91555	3.68E-38
Muscle_Skeletal	UCN	2	27,530,308	27,531,313	0.059001	rs1260326	30.5	rs1659689	-8.79E-04	3.3	-4.49	307	307	blup	0.01	0.013	-1.22E+01	2.11E-34
Pituitary	ZNF513	2	27,600,098	27,603,657	0.032474	rs1260326	30.5	rs11127125	-5.64E-03	-2.39	-11.1	301	1	top1	-0.0056	0.72	11.1	1.25E-28
Adipose_Subcutaneous	BRE	2	28,112,808	28,561,768	0.011435	rs1260326	30.5	rs1728918	2.36E-03	2.9	1.10E+01	314	1	top1	0.0024	0.17	11	3.82E-28
Muscle_Skeletal	MRPL33	2	27,994,584	28,005,561	0.01693	rs1260326	30.5	rs4666025	-5.29E-04	-3.29	-8.46	285	285	blup	0.006	0.047	1.09E+01	1.23E-27
Muscle_Skeletal	MPV17	2	27,532,360	27,548,547	0.037295	rs1260326	30.5	rs13017554	7.09E-03	-3.48	4.81	304	304	blup	0.012	0.0086	-9.97E+00	2.02E-23
Adipose_Visceral_Omentum	MRPL33	2	27,994,584	28,005,561	0.082173	rs1260326	30.5	rs13402525	4.11E-04	-4.1	-7.40E+00	285	16	enet	0.035	0.00051	9.93E+00	3.00E-23
Brain_Hippocampus	SUPT7L	2	27,874,376	27,886,337	0.018903	rs1260326	30.5	rs35145802	-9.26E-03	2.62	10.1	298	3	lasso	0.02	0.074	9.59786	8.16E-22
Pituitary	PREB	2	27,353,681	27,357,543	0.011159	rs1260326	30.5	rs4665947	-3.44E-03	-2.9	9.49	320	1	lasso	0.0075	0.14	-9.49	2.31E-21
Muscle_Skeletal	ABHD1	2	27,346,691	27,353,623	0.080515	rs1260326	30.5	rs6741646	2.87E-02	4.41	9.46	316	1	top1	0.029	9.70E-05	9.46E+00	3.08E-21
Adipose_Visceral_Omentum	BRE	2	28,112,808	28,561,768	0.040127	rs1260326	30.5	rs3792252	-2.55E-03	-3.1	-1.28E+01	314	3	enet	-0.0024	0.61	9.42E+00	4.61E-21
Muscle_Skeletal	PPM1G	2	27,604,061	27,632,554	0.077317	rs1260326	30.5	rs4665976	3.99E-02	-5.46	-3.58	301	301	blup	0.042	3.20E-06	9.29E+00	1.58E-20
Muscle_Skeletal	RBKS	2	28,004,231	28,113,965	0.018578	rs1260326	30.5	rs7578052	-1.10E-04	3.08	-7.74	313	11	enet	0.0018	0.17	-9.26E+00	2.01E-20
Brain_Cortex	KRTCAP3	2	27,665,233	27,669,348	0.175948	rs1260326	30.5	rs12475426	3.27E-02	4.58	-3.61	299	299	blup	0.085	0.00035	-9.23697	2.54E-20
Pancreas	AC109829.1	2	27,760,253	27,790,011	0.068591	rs1260326	30.5	rs1866559	6.29E-03	2.9	6.55	285	285	blup	0.011	0.066	9.22E+00	2.90E-20
Liver	KRTCAP3	2	27,665,233	27,669,348	0.083095	rs1260326	30.5	rs2950835	3.72E-03	-3.56	28.5	298	13	enet	0.021	0.043	-9.14444	5.99E-20
Brain_Cortex	FTH1P3	2	27,615,651	27,616,234	0.068839	rs1260326	30.5	rs6743819	7.18E-03	-3.14	-4.48	302	302	blup	0.024	0.04	9.14369	6.04E-20
Brain_Hippocampus	CGREF1	2	27,321,757	27,341,995	0.106859	rs1260326	30.5	rs1275513	-8.88E-03	2.41	8.6	314	314	blup	0.009	0.16	9.02278	1.83E-19
Pancreas	KHK	2	27,309,615	27,323,465	0.117954	rs1260326	30.5	rs1866561	1.21E-01	5.79	9.38	313	3	lasso	0.13	3.70E-08	8.84E+00	9.62E-19
Pituitary	SLC4A1AP	2	27,886,677	27,917,836	0.029601	rs1260326	30.5	rs4666001	-6.41E-03	-2.5	8.66	299	1	lasso	-0.0017	0.39	-8.66	4.72E-18
Adipose_Visceral_Omentum	ABHD1	2	27,346,691	27,353,623	0.035464	rs1260326	30.5	rs1275513	3.30E-02	4.06	8.60E+00	315	1	top1	0.033	0.00074	8.60E+00	7.97E-18
Muscle_Skeletal	AC074091.13	2	27,928,653	27,938,599	0.025579	rs1260326	30.5	rs4666021	3.40E-02	-4.36	-8.43	298	1	top1	0.034	2.40E-05	8.43E+00	3.46E-17
Adipose_Subcutaneous	SUPT7L	2	27,874,376	27,886,337	0.030627	rs1260326	30.5	rs1948922	4.60E-04	3.14	-6.25E+00	299	299	blup	0.0015	0.21	-8.03877	9.07E-16

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Liver	OST4	2	27,293,491	27,294,641	0.193669	rs1260326	30.5	rs10186142	9.16E-03	3.41	-0.824	320	320	blup	0.032	0.016	-7.97717	1.50E-15
Pituitary	ATRAID	2	27,435,155	27,440,046	0.222269	rs1260326	30.5	rs1275501	6.51E-02	4.21	-4.86	315	315	blup	0.081	0.00018	-7.77616	7.48E-15
Pituitary	SUPT7L	2	27,874,376	27,886,337	0.029369	rs1260326	30.5	rs7578052	4.57E-03	-3.09	-7.74	299	1	lasso	0.02	0.041	7.74	9.94E-15
Brain_Hypothalamus	SUPT7L	2	27,874,376	27,886,337	0.036126	rs1260326	30.5	rs7578052	1.34E-01	-3.9	-7.74	298	1	top1	0.13	6.40E-05	7.74	9.94E-15
Adipose_Subcutaneous	C2orf16	2	27,799,389	27,805,588	0.000486	rs1260326	30.5	rs780090	8.85E-03	-2.54	7.61E+00	280	1	top1	0.0088	0.036	-7.61	2.74E-14
Adipose_Visceral_Omentum	EMILIN1	2	27,301,435	27,309,271	0.004948	rs1260326	30.5	rs780090	6.49E-03	3.11	7.61E+00	316	1	lasso	0.015	0.018	7.61E+00	2.74E-14
Adipose_Visceral_Omentum	KHK	2	27,309,615	27,323,465	0.217878	rs1260326	30.5	rs1866559	2.23E-01	8.49	6.55E+00	312	8	lasso	0.23	3.30E-19	7.61E+00	2.85E-14
Brain_Cortex	AC074091.13	2	27,928,653	27,938,599	0.003148	rs1260326	30.5	rs11886375	3.57E-02	-2.21	-7.45	297	1	top1	0.036	0.016	7.45	9.33E-14
Adipose_Subcutaneous	MAPRE3	2	27,193,480	27,250,064	0.047431	rs1728918	11	rs893790	-5.04E-04	3.78	5.04E+00	361	361	blup	0.0022	0.17	7.20004	6.02E-13
Adrenal_Gland	RP11-503P10.1	2	27,276,486	27,277,144	0.029133	rs1260326	30.5	rs780090	-1.01E-03	-3.03	7.61	326	2	enet	0.0012	0.27	-6.90459	5.03E-12
Brain_Cortex	AC013472.4	2	27,173,220	27,232,675	0.0533	rs1260326	30.5	rs509047	-7.01E-03	-3.14	5.13	350	4	lasso	0.00039	0.31	-6.6885	2.25E-11
Adrenal_Gland	MAPRE3	2	27,193,480	27,250,064	0.194262	rs1728918	11	rs13032059	1.02E-01	5.69	5.04	360	360	blup	0.16	2.80E-08	6.36857	1.91E-10
Muscle_Skeletal	KHK	2	27,309,615	27,323,465	0.246989	rs1260326	30.5	rs3769139	3.14E-01	12.6	6.52	313	15	enet	0.32	1.00E-43	6.35E+00	2.20E-10
Muscle_Skeletal	SLC5A6	2	27,422,455	27,435,733	0.087455	rs1260326	30.5	rs4665960	6.72E-03	-4.48	-4.63	315	8	enet	0.017	0.0024	6.15E+00	7.91E-10
Thyroid	KHK	2	27,309,615	27,323,465	0.242268	rs1260326	30.5	rs3769139	2.17E-01	9.83	6.52E+00	313	10	enet	0.23	7.30E-25	6.09512	1.09E-09
Adrenal_Gland	CAD	2	27,440,258	27,466,811	0.097826	rs1260326	30.5	rs2580761	4.01E-02	-4.32	-4.86	312	10	enet	0.06	0.00069	5.90746	3.47E-09
Adipose_Visceral_Omentum	EIF2B4	2	27,587,219	27,593,353	0.023154	rs1260326	30.5	rs12373799	-2.82E-03	-2.83	2.91E+00	302	302	blup	0.0013	0.24	-5.89E+00	3.81E-09
Pituitary	GPN1	2	27,851,114	27,873,678	0.026028	rs1260326	30.5	rs3792252	-6.39E-03	2.8	-12.8	286	286	blup	-0.00071	0.35	-5.8417	5.17E-09
Brain_Hippocampus	NRBP1	2	27,650,657	27,665,126	0.070984	rs1260326	30.5	rs2178198	-8.66E-03	2.93	-1.16	299	299	blup	0.0051	0.21	-5.8375	5.30E-09
Brain_Hippocampus	AGBL5-IT1	2	27,283,906	27,284,683	0.050515	rs1260326	30.5	rs3820823	2.16E-02	-3.05	5.83	324	1	top1	0.022	0.068	-5.83	5.54E-09
Pituitary	KHK	2	27,309,615	27,323,465	0.030497	rs1260326	30.5	rs10865456	-4.11E-03	2.61	5.81	313	1	lasso	0.024	0.031	5.81	6.25E-09
Adipose_Visceral_Omentum	AC074117.10	2	27,579,360	27,590,489	0.151559	rs1260326	30.5	rs6743819	5.44E-02	-5.29	-4.48E+00	300	300	blup	0.064	3.90E-06	5.79E+00	6.87E-09
Thyroid	RP11-503P10.1	2	27,276,486	27,277,144	0.022103	rs1260326	30.5	rs7564363	2.06E-02	-4.01	5.76E+00	327	1	top1	0.021	0.0024	-5.76	8.41E-09
Adipose_Subcutaneous	AGBL5-IT1	2	27,283,906	27,284,683	0.005044	rs1260326	30.5	rs4665381	-8.57E-04	-3.15	5.75E+00	325	1	top1	-0.00086	0.41	-5.75	8.92E-09
Adipose_Visceral_Omentum	PREB	2	27,353,681	27,357,543	0.012151	rs1260326	30.5	rs10181777	1.89E-03	-3.23	5.70E+00	319	1	lasso	0.013	0.027	-5.70E+00	1.20E-08
Pancreas	PREB	2	27,353,681	27,357,543	0.039347	rs1260326	30.5	rs11897800	2.31E-04	-3.47	-2.36	320	320	blup	0.0021	0.23	-5.70E+00	1.23E-08
Brain_Hippocampus	AC074117.10	2	27,579,360	27,590,489	0.172235	rs1260326	30.5	rs4665969	1.99E-02	3.33	-3.98	300	300	blup	0.045	0.014	-5.69113	1.26E-08
Liver	ABHD1	2	27,346,691	27,353,623	0.086371	rs1260326	30.5	rs6759548	2.44E-02	3.31	5.87	315	3	lasso	0.029	0.021	5.54684	2.91E-08
Liver	RP11-503P10.1	2	27,276,486	27,277,144	0.04952	rs1260326	30.5	rs12474099	-5.06E-03	2.79	0.126	326	326	blup	-0.0013	0.37	-5.53282	3.15E-08
Thyroid	ATRAID	2	27,435,155	27,440,046	0.199364	rs1260326	30.5	rs2580759	1.15E-01	7.49	-4.81E+00	315	6	lasso	0.13	5.30E-14	-5.51157	3.56E-08
Muscle_Skeletal	GRB14	2	165,349,326	165,478,358	0.008565	rs6754919	-6.29	rs6754919	-1.81E-03	-2.91	-6.29	344	1	lasso	0.0026	0.13	6.28E+00	3.39E-10
Pancreas	NOSTRIN	2	169,643,049	169,722,024	0.261273	rs16856187	7.48	rs569997	1.38E-01	5.62	-5.91	575	1	top1	0.14	8.60E-09	-5.91E+00	3.42E-09
Pituitary	NOSTRIN	2	169,643,049	169,722,024	0.068999	rs16856187	7.48	rs529002	1.48E-02	-2.97	5.78931	575	1	top1	0.015	0.07	-5.78931	7.07E-09

Supplementary Table 24. Transcriptome-wide association analysis for the TyG index, a marker of insulin resistance, using GTEx tissue expression with p-value < 5.0 x E-8 on chromosome 7 only.

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Liver	UBE2D4	7	43,966,037	43,995,735	0.053882	rs3757840	-10.2	rs9918696	-2.78E-03	3.2	1.34E+00	381	11	enet	0.023	0.033	5.90E+00	3.74E-09
Muscle_Skeletal	SPDYE1	7	44,040,488	44,049,721	0.018144	rs3757840	-10.2	rs2075068	-1.56E-03	-2.93	-6.55	360	1	top1	-0.0016	0.62	6.55	5.75E-11
Brain_Cortex	POLR2J4	7	44,053,161	44,058,769	0.042395	rs3757840	-10.2	rs4236374	-6.25E-03	-2.82	-5.43	352	2	lasso	-0.0057	0.63	5.62E+00	1.90E-08
Brain_Cortex	AEBP1	7	44,143,960	44,154,161	0.078702	rs3757840	-10.2	rs9784990	1.56E-01	4.78	6.24	353	1	top1	0.16	1.30E-06	6.24E+00	4.38E-10
Adipose_Subcutaneous	POLD2	7	44,154,286	44,163,957	0.101564	rs3757840	-10.2	rs17769733	4.21E-02	-4.43	-6.35	357	1	top1	0.042	3.00E-05	6.35E+00	2.15E-10
Adipose_Visceral_Omentum	POLD2	7	44,154,286	44,163,957	0.105161	rs3757840	-10.2	rs17136076	-5.29E-04	-4.25	-6.33	355	36	enet	0.018	0.0097	5.99E+00	2.13E-09
Adrenal_Gland	MYL7	7	44,178,463	44,180,931	0.008761	rs3757840	-10.2	rs2908290	-2.26E-03	2.88	7.49	355	1	lasso	-0.0018	0.41	7.49	6.89E-14
Thyroid	GCK	7	44,183,874	44,237,769	0.210014	rs3757840	-10.2	rs1799884	7.32E-02	6.29	8.54	365	22	enet	0.14	1.10E-14	8.27929	1.24E-16
Adipose_Subcutaneous	YKT6	7	44,240,567	44,253,893	0.02655	rs3757840	-10.2	rs12702070	8.10E-02	-5.7	-6.68	363	1	top1	0.081	8.30E-09	6.68E+00	2.39E-11
Muscle_Skeletal	YKT6	7	44,240,567	44,253,893	0.022539	rs3757840	-10.2	rs12702070	5.68E-02	-5.51	-6.68	363	1	top1	0.057	5.50E-08	6.68	2.39E-11
Brain_Cortex	CAMK2B	7	44,256,749	44,374,176	0.26126	rs3757840	-10.2	rs1990458	1.51E-01	4.63	-5.96	356	1	top1	0.15	1.90E-06	-5.96E+00	2.52E-09
Pituitary	MLXIPL	7	73,007,524	73,038,873	0.118578	rs17145750	-21.1	rs17145750	9.66E-02	4.46	-2.11E+01	250	1	top1	0.097	4.60E-05	-2.11E+01	7.95E-99
Adipose_Subcutaneous	MLXIPL	7	73,007,524	73,038,873	0.153476	rs17145750	-21.1	rs1051921	1.06E-01	6.62	-19.5	251	12	enet	0.11	3.50E-11	-2.01E+01	1.51E-89
Thyroid	MLXIPL	7	73,007,524	73,038,873	0.313561	rs17145750	-21.1	rs13246490	2.32E-01	9.9	-19.5	251	4	lasso	0.24	5.90E-26	-19.45448	2.67E-84
Pancreas	MLXIPL	7	73,007,524	73,038,873	0.350866	rs17145750	-21.1	rs2074755	2.56E-01	7.69	-17.7	251	1	top1	0.26	6.90E-16	-17.7	4.19E-70
Adrenal_Gland	POM121B	7	72,707,497	72,716,496	0.000154	rs17145750	-21.1	rs6951030	-4.48E-03	3.15	3.74	160	160	blup	0.002	0.25	17.337777	2.44E-67
Adipose_Visceral_Omentum	MLXIPL	7	73,007,524	73,038,873	0.226518	rs17145750	-21.1	rs17145813	4.11E-02	5	-9.73	251	251	blup	0.058	9.90E-06	-1.52E+01	4.14E-52
Thyroid	TRIM50	7	72,726,535	72,742,085	0.06619	rs17145750	-21.1	rs13228725	2.76E-04	4.07	-0.569	161	161	blup	0.032	2.00E-04	-15.00511	6.80E-51
Liver	POM121B	7	72,707,497	72,716,496	0.028887	rs17145750	-21.1	rs1178979	-6.48E-03	-2.56	-1.77E+01	159	4	lasso	0.00054	0.3	1.48E+01	1.20E-49
Adipose_Subcutaneous	BAZ1B	7	72,854,728	72,936,608	0.124961	rs17145750	-21.1	rs13246490	3.52E-02	-4.18	-19.5	205	19	enet	0.043	2.70E-05	1.31E+01	3.10E-39
Muscle_Skeletal	CLDN4	7	73,213,872	73,247,014	0.053103	rs17145750	-21.1	rs9647713	-2.02E-03	3.07	0.258	294	294	blup	0.0093	0.018	12.47991	9.61E-36
Liver	TMEM270/WBSCR28	7	73,275,489	73,280,223	0.190036	rs17145750	-21.1	rs11769827	-3.94E-03	2.96	-1.53E+00	285	285	blup	0.008	0.14	-1.15E+01	8.96E-31
Pituitary	ELN	7	73,442,119	73,484,237	0.053923	rs17145750	-21.1	rs17145817	2.00E-02	-3	-1.15E+01	321	1	top1	0.02	0.043	1.15E+01	1.32E-30
Pituitary	POM121B	7	72,707,497	72,716,496	0.080701	rs17145750	-21.1	rs35607697	-5.77E-03	2.52	3.19E+00	159	159	blup	0.0073	0.15	1.12E+01	6.41E-29
Brain_Cortex	TRIM50	7	72,726,535	72,742,085	0.065212	rs17145750	-21.1	rs2237280	-7.48E-03	-2.75	5.33	161	161	blup	-0.006	0.65	-1.10E+01	3.72E-28
Pancreas	POM121B	7	72,707,497	72,716,496	0.247436	rs17145750	-21.1	rs6951030	7.32E-03	3.66	3.74	160	43	enet	0.11	2.10E-07	10.79554	3.61E-27
Brain_Hypothalamus	BAZ1B	7	72,854,728	72,936,608	0.00048	rs17145750	-21.1	rs3793243	-9.52E-03	-2.53	3.16E+00	204	204	blup	-0.0043	0.46	-9.616443	6.81E-22
Adipose_Subcutaneous	POM121B	7	72,707,497	72,716,496	0.21628	rs17145750	-21.1	rs34014814	1.91E-02	-4.07	-6.22922	160	8	lasso	0.074	3.30E-08	8.88E+00	6.91E-19
Muscle_Skeletal	BCL7B	7	72,950,686	72,972,332	0.170918	rs17145750	-21.1	rs2573	7.77E-02	-6.48	-6.103075	224	5	lasso	0.082	6.70E-11	8.7027	3.24E-18
Pancreas	BCL7B	7	72,950,686	72,972,332	0.095106	rs17145750	-21.1	rs35607697	5.59E-03	3.2	4.01065	224	24	enet	0.018	0.025	8.37427	5.56E-17
Thyroid	POM121B	7	72,707,497	72,716,496	0.229045	rs17145750	-21.1	rs35607697	1.09E-02	4.15	3.19133	160	160	blup	0.064	2.00E-07	7.97161	1.57E-15
Muscle_Skeletal	POM121B	7	72,707,497	72,716,496	0.220871	rs17145750	-21.1	rs1178953	1.18E-02	-4.48	-4.438315	160	160	blup	0.087	1.70E-11	7.95875	1.74E-15
Pancreas	STX1A	7	73,113,536	73,133,989	0.001759	rs17145750	-21.1	rs1569061	4.92E-03	-2.58	0.83	278	278	blup	0.0091	0.085	7.53149	5.02E-14
Pancreas	FZD9	7	72,848,109	72,850,450	0.048159	rs17145750	-21.1	rs2108235	3.97E-05	2.85	-8.67224	185	185	blup	0.027	0.0083	-7.27246	3.53E-13
Brain_Hypothalamus	RP11-313P13.5	7	72,394,956	72,395,659	0.079846	rs2240466	-17.8	rs1178953	4.07E-02	-3.05	-5.40E+00	107	107	blup	0.046	0.015	7.196702	6.17E-13
Pituitary	TRIM50	7	72,726,535	72,742,085	0.129111	rs17145750	-21.1	rs13228725	-6.33E-03	2.94	-5.69E-01	160	160	blup	0.029	0.019	-7.07E+00	1.55E-12
Brain_Cortex	BAZ1B	7	72,854,728	72,936,608	0.0866	rs17145750	-21.1	rs7793135	1.60E-03	-2.56	-0.0228	205	205	blup	0.015	0.086	-6.77E+00	1.31E-11
Brain_Hippocampus	ABHD11	7	73,150,424	73,153,197	0.275494	rs17145750	-21.1	rs11979807	1.21E-01	-4.53	0.806	283	283	blup	0.15	2.00E-05	6.497768	8.15E-11
Adipose_Visceral_Omentum	POM121B	7	72,707,497	72,716,496	0.374029	rs17145750	-21.1	rs13224992	1.52E-02	-4.83	-0.361	160	160	blup	0.17	3.20E-14	6.48E+00	9.13E-11
Adipose_Visceral_Omentum	FKBP6	7	72,742,167	72,772,634	0.005729	rs17145750	-21.1	rs2573	4.70E-03	-3.1	-6.1765	161	1	lasso	0.013	0.025	6.18E+00	6.55E-10
Adrenal_Gland	GTF2IRD2P1	7	72,656,902	72,694,143	0.004479	rs17145750	-21.1	rs3763432	6.18E-04	-2.95	5.34	160	160	blup	0.0016	0.26	-6.161166	7.22E-10
Thyroid	BAZ1B	7	72,854,728	72,936,608	0.144308	rs17145750	-21.1	rs799217	2.62E-02	4.66	-5.9511	205	205	blup	0.039	4.50E-05	-6.15771	7.38E-10
Adrenal_Gland	MLXIPL	7	73,007,524	73,038,873	0.051075	rs17145750	-21.1	rs875342	-5.77E-03	-3.3	1.26	251	251	blup	-0.0031	0.5	-6.122977	9.18E-10
Adipose_Visceral_Omentum	BCL7B	7	72,950,686	72,972,332	0.129868	rs17145750	-21.1	rs2573	6.29E-02	-4.75	-6.103075	224	1	top1	0.063	4.30E-06	6.10E+00	1.04E-09
Adipose_Subcutaneous	BCL7B	7	72,950,686	72,972,332	0.202545	rs17145750	-21.1	rs2573	9.25E-02	-6.36	-6.10307	224	3	lasso	0.093	6.90E-10	6.08E+00	1.18E-09
Brain_Cortex	RP11-396K3.1	7	72,569,033	72,619,657	0.070678	rs17145750	-21.1	rs12531884	1.03E-02	3.31	5.61	121	121	blup	0.013	0.095	5.92E+00	3.31E-09
Adipose_Subcutaneous	VPS37D	7	73,082,155	73,086,442	0.131601	rs17145750	-21.1	rs12154779	6.12E-02	4.96	-3.36	263	6	lasso	0.085	3.90E-09	-5.67E+00	1.41E-08
Adipose_Subcutaneous	FKBP6	7	72,742,167	72,772,634	0.028277	rs17145750	-21.1	rs3793243	1.04E-02	-3.49	3.16	161	10	enet	0.04	4.20E-05	-5.66E+00	1.53E-08
Adipose_Subcutaneous	GTF2IRD2P1	7	72,656,902	72,694,143	0.015816	rs17145750	-21.1	rs7780317	-2.47E-03	2.69	-4.94511	160	16	enet	0.0043	0.1	-5.64E+00	1.71E-08
Pituitary	BAZ1B	7	72,854,728	72,936,608	0.052544	rs17145750	-21.1	rs6974424	-4.35E-03	-2.92	-3.15E+00	204	204	blup	-0.0036	0.51	-5.62E+00	1.90E-08
Pituitary	TRIM74	7	72,430,016	72,439,997	0.027385	rs2240466	-17.8	rs6460043	-5.26E-03	-2.49	3.46E-01	100	5	enet	0.006	0.17	-5.52E+00	3.36E-08

Supplementary Table 25. Transcriptome-wide association analysis for the TyG index, a marker of insulin resistance, using GTEx tissue expression with p-value < 5.0 x E-8 on chromosome 11 only.

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Liver	DAK	11	61,101,021	61,120,767	0.024953	rs102275	11.1	rs174566	3.64E-03	2.58	10.9	372	1	top1	0.0036	0.21	10.9	1.15E-27
Thyroid	CPSF7	11	61,170,121	61,197,503	0.008072	rs102275	11.1	rs11603954	2.98E-03	3.33	0.0994	374	374	blup	0.011	0.023	-6.24E+00	4.40E-10
Brain_Hypothalamus	CPSF7	11	61,170,121	61,197,503	0.084986	rs102275	11.1	rs7943167	4.69E-04	2.73	-0.0284	374	374	blup	0.028	0.047	6.19E+00	6.18E-10
Adipose_Subcutaneous	RN7SL23P	11	61,211,602	61,211,899	0.019954	rs102275	11.1	rs3741259	-2.54E-03	-3	4.80E-01	367	367	blup	0.011	0.022	6.00E+00	2.03E-09
Liver	RN7SL23P	11	61,211,602	61,211,899	0.118342	rs102275	11.1	rs11230555	-5.96E-03	2.87	2.05	367	367	blup	-0.0049	0.61	-5.9602	2.52E-09
Adipose_Visceral_Omentum	PPP1R32	11	61,248,592	61,258,403	0.106904	rs102275	11.1	rs2852786	-3.22E-03	3.27	-6	375	375	blup	0.015	0.018	-7.45704	8.85E-14
Pancreas	LRRC10B	11	61,276,272	61,278,482	0.004582	rs102275	11.1	rs628993	-3.95E-03	3.02	-3.35	364	364	blup	0.0059	0.13	-8.61177	7.19E-18
Brain_Hippocampus	RP11-794G24.1	11	61,306,988	61,308,769	0.07753	rs102275	11.1	rs174448	-0.008789	-2.85	5.23	369	369	blup	0.0085	0.17	-6.65243	2.88E-11
Thyroid	RP11-794G24.1	11	61,306,988	61,308,769	0.027032	rs102275	11.1	rs175128	-2.00E-03	3.36	-0.305	370	370	blup	0.0024	0.16	-5.95E+00	2.64E-09
Adipose_Visceral_Omentum	DAGLA	11	61,447,905	61,513,964	0.030332	rs102275	11.1	rs198462	2.66E-02	-3.52	-6.84	377	1	top1	0.027	0.0022	6.84	7.92E-12
Adipose_Subcutaneous	DAGLA	11	61,447,905	61,513,964	0.067902	rs102275	11.1	rs198464	-1.45E-03	-2.77	-6.80E+00	377	1	lasso	0.014	0.013	6.80E+00	1.05E-11
Pancreas	RP11-467L20.10	11	61,514,474	61,525,127	0.226721	rs102275	11.1	rs198462	1.41E-01	5.67	-6.84	412	6	enet	0.14	5.50E-09	-7.20878	5.65E-13
Liver	RP11-467L20.10	11	61,514,474	61,525,127	0.642762	rs102275	11.1	rs198462	2.86E-01	6.81	-6.84	413	1	top1	0.29	7.60E-13	-6.84	7.92E-12
Pancreas	MYRF	11	61,520,121	61,555,990	0.177131	rs102275	11.1	rs2238001	2.92E-02	-4.09	-7.84	412	2	lasso	0.034	0.0035	9.03671	1.61E-19
Liver	MYRF	11	61,520,121	61,555,990	0.620755	rs102275	11.1	rs198476	4.85E-01	-8.61	-6.87	413	1	top1	0.49	1.30E-23	6.87	6.42E-12
Adipose_Subcutaneous	MYRF	11	61,520,121	61,555,990	0.0862	rs102275	11.1	rs198462	5.13E-02	-4.93	-6.84E+00	413	1	top1	0.051	4.40E-06	6.84E+00	7.92E-12
Adipose_Subcutaneous	TMEM258	11	61,535,973	61,560,108	0.051699	rs102275	11.1	rs108499	4.25E-02	4.47	1.10E+01	416	1	top1	0.042	2.80E-05	1.10E+01	3.82E-28
Thyroid	TMEM258	11	61,535,973	61,560,108	0.030073	rs102275	11.1	rs174538	3.99E-02	4.2	10.9	416	1	top1	0.04	3.60E-05	1.09E+01	1.15E-27
Muscle_Skeletal	TMEM258	11	61,535,973	61,560,108	0.05898	rs102275	11.1	rs174535	1.73E-02	4.5	1.09E+01	416	416	blup	0.019	0.0013	7.95E+00	1.82E-15
Brain_Cortex	TMEM258	11	61,535,973	61,560,108	0.087161	rs102275	11.1	rs174570	-6.16E-03	3.45	6.22	415	1	top1	-0.0062	0.67	6.22E+00	4.97E-10
Muscle_Skeletal	FEN1	11	61,560,275	61,564,716	0.059716	rs102275	11.1	rs174577	1.20E-02	-3.92	1.10E+01	416	1	top1	0.012	0.0088	-1.10E+01	3.82E-28
Pituitary	FEN1	11	61,560,275	61,564,716	0.062361	rs102275	11.1	rs174535	2.89E-02	-2.97	10.9	416	1	top1	0.029	0.019	-10.9	1.15E-27
Adipose_Subcutaneous	FEN1	11	61,560,275	61,564,716	0.022749	rs102275	11.1	rs174549	5.99E-03	-3.42	1.02E+01	416	1	lasso	0.022	0.0022	-1.02E+01	1.98E-24
Liver	FEN1	11	61,560,275	61,564,716	0.153675	rs102275	11.1	rs2851682	4.05E-03	-3.29	10	416	3	lasso	0.0055	0.18	-8.86814	7.44E-19
Brain_Hippocampus	FEN1	11	61,560,275	61,564,716	0.20257	rs102275	11.1	rs2903825	0.035614	3.53	-8.38	415	5	lasso	0.058	0.0066	-8.1826	2.78E-16
Adrenal_Gland	FEN1	11	61,560,275	61,564,716	0.139019	rs102275	11.1	rs1692120	-8.63E-04	3.56	0.025	415	415	blup	0.004	0.19	-6.39E+00	1.64E-10
Brain_Hypothalamus	FADS1	11	61,567,099	61,596,790	0.155672	rs102275	11.1	rs174566	3.10E-02	-3.55	10.9	433	1	top1	0.031	0.039	-1.09E+01	1.15E-27
Pancreas	FADS1	11	61,567,099	61,596,790	0.498849	rs102275	11.1	rs174555	3.61E-01	-9.15	10.1	432	10	lasso	0.37	7.40E-24	-10.49096	9.51E-26
Adipose_Subcutaneous	FADS1	11	61,567,099	61,596,790	0.050171	rs102275	11.1	rs174549	4.00E-02	-4.48	1.02E+01	433	1	top1	0.04	4.70E-05	-1.02E+01	1.98E-24
Adipose_Visceral_Omentum	FADS1	11	61,567,099	61,596,790	0.085331	rs102275	11.1	rs174549	5.28E-02	-4.93	10.2	433	1	top1	0.053	2.50E-05	-10.2	1.98E-24
Thyroid	FADS1	11	61,567,099	61,596,790	0.13655	rs102275	11.1	rs174549	1.02E-01	-6.89	10.2	433	1	top1	0.1	4.00E-11	-1.02E+01	1.98E-24
Muscle_Skeletal	FADS1	11	61,567,099	61,596,790	0.121996	rs102275	11.1	rs174555	9.75E-02	-7.19	1.01E+01	433	1	top1	0.097	9.30E-13	-1.01E+01	5.52E-24
Brain_Cortex	FADS1	11	61,567,099	61,596,790	0.126734	rs102275	11.1	rs174555	7.94E-02	-4.79	10.1	433	3	lasso	0.093	2.00E-04	-1.01E+01	6.64E-24
Brain_Hippocampus	FADS1	11	61,567,099	61,596,790	0.2045	rs102275	11.1	rs2845573	0.003064	-3.58	9.63	433	433	blup	0.02	0.075	-7.29805	2.92E-13
Muscle_Skeletal	FADS2	11	61,583,728	61,634,826	0.103516	rs102275	11.1	rs968567	2.49E-02	5.04	7.89E+00	427	6	lasso	0.037	9.60E-06	8.91E+00	4.88E-19
Pancreas	FADS2	11	61,583,728	61,634,826	0.274028	rs102275	11.1	rs968567	1.30E-01	5.54	7.89	426	1	top1	0.13	2.40E-08	7.89	3.02E-15
Adipose_Subcutaneous	FADS2	11	61,583,728	61,634,826	0.08239	rs102275	11.1	rs968567	7.25E-02	5.46	7.89E+00	427	1	top1	0.072	5.10E-08	7.89E+00	3.02E-15
Adipose_Visceral_Omentum	FADS2	11	61,583,728	61,634,826	0.241358	rs102275	11.1	rs968567	8.84E-02	5.38	7.89	427	1	top1	0.088	5.20E-08	7.89	3.02E-15
Thyroid	FADS2	11	61,583,728	61,634,826	0.35178	rs102275	11.1	rs968567	2.68E-01	10.39	7.89	427	1	top1	0.27	7.90E-29	7.89E+00	3.02E-15
Liver	FADS3	11	61,640,991	61,659,523	0.238502	rs102275	11.1	rs174566	1.23E-01	-4.83	10.9	441	1	top1	0.12	5.90E-06	-10.9	1.15E-27
Pancreas	FTH1	11	61,727,190	61,735,132	0.052969	rs102275	11.1	rs2071213	-4.34E-03	3.49	-4.2	462	462	blup	-0.004	0.71	-7.21048	5.58E-13
Adipose_Subcutaneous	FTH1	11	61,727,190	61,735,132	0.076201	rs102275	11.1	rs1160481	-2.54E-03	3.39	1.65E+00	462	23	enet	0.0056	0.077	6.77E+00	1.29E-11
Adipose_Subcutaneous	RP11-867G23.1	11	66,032,248	66,033,125	0.244184	rs11227448	4.57	rs513474	6.27E-02	-6.67	-4.15E+00	325	6	lasso	0.12	6.90E-13	5.47E+00	4.53E-08
Adipose_Subcutaneous	AP006216.10	11	116,644,105	116,644,921	0.006296	rs7350481	38.6	rs623908	2.79E-02	-3.75	-3.28E+01	558	1	top1	0.028	0.00059	3.28E+01	5.89E-236
Pituitary	SIK3	11	116,714,118	116,969,153	0.033542	rs7350481	38.6	rs5072	-6.46E-03	-3.2	28.32171	538	2	lasso	0.022	0.037	-28.32786	1.57E-176
Brain_Hypothalamus	SIDT2	11	117,049,449	117,068,160	0.192903	rs6589567	38.69	rs10750098	-7.77E-03	-3.31	26.1	543	543	blup	0.0079	0.18	-2.52E+01	3.32E-140
Brain_Hippocampus	PAFAH1B2	11	117,014,983	117,047,610	0.02717	rs7350481	38.6	rs2075292	-0.004356	-3.03	18.3	545	3	lasso	0.059	0.006	-23.6267	2.05E-123
Muscle_Skeletal	SIK3	11	116,714,118	116,969,153	0.038028	rs7350481	38.6	rs2298767	-2.04E-03	-3.14	5.39E-01	539	539	blup	0.0013	0.2	-2.34E+01	7.41E-121
Liver	AP006216.11	11	116,645,826	116,646,592	0.136813	rs7350481	38.6	rs672058	-6.51E-03	3.4	16.5	558	558	blup	0.034	0.013	22.78047	7.16E-115
Liver	AP006216.5	11	116,683,920	116,684,719	0.242736	rs7350481	38.6	rs2542063	9.28E-02	-4.83	14.9	550	550	blup	0.1	3.90E-05	-21.02389	3.97E-98
Adipose_Visceral_Omentum	AP006216.11	11	116,645,826	116,646,592	0.119788	rs7350481	38.6	rs180375	2.82E-02	-4.32	-16.4	558	4	lasso	0.032	0.00081	20.10112	7.22E-90
Brain_Hypothalamus	APOA1	11	116,706,467	116,708,666	0.265253	rs7350481	38.6	rs951839	-7.34E-03	2.91	-1.25	538	538	blup	0.046	0.015	1.91E+01	5.83E-81
Thyroid	ZNF259	11	116,648,436	116,658,766	0.005447	rs7350481	38.6	rs481843	3.14E-04	-3.38	17.9	554	1	top1	0.00031	0.29	-1.79E+01	1.18E-71
Thyroid	AP006216.10	11	116,644,105	116,644,921	0.030713	rs7350481	38.6	rs7122363	-3.68E-04	-3.35	-3.630577	558	558	blup	0.002	0.18	1.75E+01	6.87E-69
Liver	APOA1	11	116,706,467	116,708,666	0.018763	rs7350481	38.6	rs11600381	-5.27E-03	-2.5	-9.75	538	538	blup	0.0062	0.17	17.12493	9.67E-66
Thyroid	SIDT2	11	117,049,449	117,068,160	0.123193	rs6589567	38.69	rs90192	4.82E-02	-5.92	14.4	543	20	enet	0.063	2.20E-07	-1.65E+01	3.00E-61
Brain_Cortex	SIDT2	11	117,049,449	117,068,160	0.00953	rs6589567	38.69	rs1242229	-7.04E-03	-2.92	16.2	542	1	lasso	-0.0068	0.75	-1.62E+01	5.04E-59
Pituitary	ZNF259	11	116,648,436	116,658,766	0.046643	rs7350481	38.6	rs1729408	-2.57E-03	3.29	-16.01875	554	1	lasso	0.031	0.016	-16.01875	9.45E-58
Pancreas	A																	

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Pituitary	SIK3-IT1	11	116,756,762	116,761,437	0.203183	rs7350481	38.6	rs1242036:	1.68E-02	-3.76	-15.7	529	1	top1	0.017	0.058	15.7	1.51E-55
Pancreas	SIDT2	11	117,049,449	117,068,160	0.357609	rs6589567	38.69	rs1060211	2.73E-01	-7.81	15	542	1	top1	0.27	5.90E-17	-15	7.34E-51
Adipose_Visceral_Omentum	SIDT2	11	117,049,449	117,068,160	0.035751	rs6589567	38.69	rs1060211	-2.93E-03	-3.21	15	542	1	lasso	0.0033	0.16	-15	7.34E-51
Adrenal_Gland	SIDT2	11	117,049,449	117,068,160	0.362653	rs6589567	38.69	rs1060211	1.83E-01	-5.79	15	542	1	top1	0.18	2.30E-09	-1.50E+01	7.34E-51
Muscle_Skeletal	APOA4	11	116,691,419	116,694,022	0.087664	rs7350481	38.6	rs1271846:	-1.40E-03	3.97	-1.35E+01	544	544	blup	0.0025	0.14	-1.40E+01	1.13E-44
Liver	PCSK7	11	117,075,499	117,103,241	0.170523	rs180326	38.6	rs1121632:	1.42E-02	-4.06	-8.66	536	43	enet	0.049	0.0037	-13.70633	9.31E-43
Pituitary	SIDT2	11	117,049,449	117,068,160	0.00771	rs6589567	38.69	rs563838	-5.73E-03	-2.75	-7.51	542	542	blup	0.006	0.17	-13.60564	3.71E-42
Muscle_Skeletal	BUD13	11	116,618,886	116,643,704	0.017786	rs7350481	38.6	rs1892947	1.17E-02	-3.64	-1.29E+01	558	1	lasso	0.015	0.0042	1.29E+01	4.50E-38
Pituitary	APOA1	11	116,706,467	116,708,666	0.33705	rs7350481	38.6	rs486394	8.63E-04	3.22	18.6	537	6	lasso	0.0078	0.14	12.75873	2.79E-37
Brain_Hippocampus	SIK3-IT1	11	116,756,762	116,761,437	0.73155	rs7350481	38.6	rs549298	-0.004855	3.69	-4.25	529	59	enet	0.19	1.00E-06	12.33123	6.15E-35
Adipose_Visceral_Omentum	SIK3	11	116,714,118	116,969,153	0.132803	rs7350481	38.6	rs518547	2.72E-02	3.94	-0.96094	538	23	enet	0.032	0.00087	-12.03313	2.38E-33
Brain_Hypothalamus	AP006216.10	11	116,644,105	116,644,921	0.033882	rs7350481	38.6	rs1089200:	5.34E-02	3.85	11.7	558	1	top1	0.053	0.0095	1.17E+01	1.27E-31
Adipose_Visceral_Omentum	RP11-109L13.1	11	117,006,244	117,009,298	0.552616	rs7350481	38.6	rs1079017:	4.47E-01	11.8	7.17	541	24	enet	0.48	5.10E-46	10.40323	2.40E-25
Adrenal_Gland	RP11-109L13.1	11	117,006,244	117,009,298	0.49007	rs7350481	38.6	rs585849	3.47E-01	8.01	7.27	541	8	lasso	0.36	9.50E-19	9.61E+00	7.47E-22
Pituitary	CEP164	11	117,185,273	117,283,984	0.387305	rs595049	29	rs1121636:	5.28E-02	4.77	7.77	527	43	enet	0.19	7.90E-09	9.52229	1.69E-21
Thyroid	PCSK7	11	117,075,499	117,103,241	0.04545	rs180326	38.6	rs1121632:	1.75E-02	-3.97	-9.48	536	1	top1	0.018	0.0047	9.48E+00	2.54E-21
Thyroid	AP006216.12	11	116,726,006	116,726,445	0.035174	rs7350481	38.6	rs490592	-2.53E-03	3.31	0.266	532	3	lasso	0.0045	0.096	-9.35E+00	8.88E-21
Thyroid	APOA4	11	116,691,419	116,694,022	0.059981	rs7350481	38.6	rs7935913	-2.47E-03	3.17	-8.38	544	544	blup	0.0058	0.069	-8.63E+00	6.31E-18
Brain_Hypothalamus	RP11-109L13.1	11	117,006,244	117,009,298	0.537619	rs7350481	38.6	rs7107152	3.23E-01	6.71	7.23	542	3	lasso	0.35	1.80E-11	8.23E+00	1.91E-16
Pituitary	AP006216.12	11	116,726,006	116,726,445	0.026997	rs7350481	38.6	rs7946299	-5.99E-03	3.28	-5.57096	531	4	lasso	0.002	0.25	-8.16601	3.19E-16
Pituitary	RP11-109L13.1	11	117,006,244	117,009,298	0.65642	rs7350481	38.6	rs9326248	4.40E-01	8.6	6.6	541	14	lasso	0.47	5.60E-23	8.14522	3.79E-16
Adipose_Visceral_Omentum	PCSK7	11	117,075,499	117,103,241	0.048768	rs180326	38.6	rs4938355	1.19E-02	3.55	10.9	535	3	lasso	0.018	0.0094	7.84222	4.43E-15
Adipose_Visceral_Omentum	APOA1	11	116,706,467	116,708,666	0.064972	rs7350481	38.6	rs6589598	4.23E-04	3.36	7.77	537	1	top1	0.00042	0.29	7.77	7.85E-15
Adipose_Subcutaneous	PCSK7	11	117,075,499	117,103,241	0.050165	rs180326	38.6	rs6589598	7.15E-03	-3.64	7.77E+00	536	1	top1	0.0071	0.053	-7.77E+00	7.85E-15
Liver	RP11-109L13.1	11	117,006,244	117,009,298	0.458445	rs7350481	38.6	rs585849	3.51E-01	8.03	7.27	542	6	lasso	0.39	4.60E-18	7.73076	1.07E-14
Muscle_Skeletal	RP11-109L13.1	11	117,006,244	117,009,298	0.364613	rs7350481	38.6	rs585849	3.94E-01	13.99	7.27E+00	542	9	lasso	0.39	2.10E-55	7.62E+00	2.53E-14
Adipose_Subcutaneous	RP11-109L13.1	11	117,006,244	117,009,298	0.614418	rs7350481	38.6	rs4938354	4.58E-01	14.08	2.26E+00	542	27	enet	0.53	3.90E-64	7.58E+00	3.45E-14
Brain_Hypothalamus	SIK3	11	116,714,118	116,969,153	0.196994	rs7350481	38.6	rs2013131	-9.45E-03	-3.42	0.935	539	539	blup	0.0083	0.17	7.53E+00	5.19E-14
Pancreas	PAFAH1B2	11	117,014,983	117,047,610	0.07926	rs7350481	38.6	rs1712034:	1.01E-02	-3.92	-15.6	545	4	lasso	0.025	0.011	7.28671	3.18E-13
Muscle_Skeletal	TAGLN	11	117,070,037	117,075,052	0.061156	rs6589567	39.06	rs8521	2.46E-02	-4.7	7.23E+00	537	1	top1	0.025	0.00029	-7.23E+00	4.83E-13
Pancreas	TAGLN	11	117,070,037	117,075,052	0.244236	rs6589567	39.05	rs9326248	1.52E-01	-6.52	6.6	536	22	enet	0.17	1.30E-10	-7.12874	1.01E-12
Pancreas	RP11-109L13.1	11	117,006,244	117,009,298	0.454744	rs7350481	38.6	rs9326248	3.89E-01	9.25	6.6	541	3	lasso	0.4	3.10E-26	7.10673	1.19E-12
Brain_Hypothalamus	APOC3	11	116,700,422	116,703,788	0.215339	rs7350481	38.6	rs1236532:	4.58E-02	3.85	6.71	542	1	top1	0.046	0.015	6.71E+00	1.95E-11
Brain_Cortex	RP11-109L13.1	11	117,006,244	117,009,298	0.499942	rs7350481	38.6	rs4938349	3.28E-01	7.33	6.68	541	1	top1	0.33	2.30E-13	6.68E+00	2.39E-11
Adrenal_Gland	AP006216.10	11	116,644,105	116,644,921	0.075295	rs7350481	38.6	rs1121616:	1.83E-02	-3.24	6.63	558	1	top1	0.018	0.041	-6.63E+00	3.36E-11
Brain_Hippocampus	RP11-109L13.1	11	117,006,244	117,009,298	0.4518	rs7350481	38.6	rs9326248	0.353937	6.75	6.6	541	5	lasso	0.39	2.50E-13	6.62992	3.36E-11
Adipose_Subcutaneous	SIK3	11	116,714,118	116,969,153	0.013572	rs7350481	38.6	rs9326248	-2.58E-03	-3.04	6.60E+00	539	2	lasso	0.0017	0.2	-6.60E+00	4.07E-11
Brain_Hippocampus	CEP164	11	117,185,273	117,283,984	0.05809	rs595049	29	rs1121635:	-0.000526	-3.58	-7.62	527	3	lasso	0.0042	0.23	6.5059	7.72E-11
Brain_Cortex	TAGLN	11	117,070,037	117,075,052	0.070166	rs6589567	39.05	rs1089216:	-7.38E-03	3.1	1.57	536	19	enet	-0.0028	0.43	-6.03E+00	1.68E-09
Pituitary	RP11-35P15.1	11	117,539,198	117,539,573	0.159852	rs10892082	16.3	rs3741279	8.22E-03	-3.72	-1.18	663	2	lasso	0.033	0.013	5.9048	3.53E-09
Adipose_Subcutaneous	SIDT2	11	117,049,449	117,068,160	0.044761	rs6589567	38.69	rs1263502	-2.62E-03	-3.6	-1.78E+00	543	20	enet	0.016	0.0075	5.68E+00	1.31E-08
Adipose_Visceral_Omentum	BACE1	11	117,157,162	117,186,975	0.040044	rs595049	29	rs593245	-2.76E-03	3.19	2.78	532	15	enet	0.0037	0.14	5.68238	1.33E-08
Thyroid	RP11-109L13.1	11	117,006,244	117,009,298	0.485254	rs7350481	38.6	rs4938344	4.64E-01	13.6	7.06	542	5	lasso	0.48	8.20E-58	5.48E+00	4.27E-08
Thyroid	NLRX1	11	119,037,277	119,054,725	0.081411	rs10790286	-5.46	rs1079028:	4.39E-02	-4.33	-5.46	387	1	top1	0.044	1.50E-05	5.46E+00	4.76E-08
Adipose_Subcutaneous	PDZD3	11	119,056,184	119,060,346	0.024097	rs10790286	-5.46	rs1079028:	5.92E-03	3.65	-5.46E+00	383	1	top1	0.0059	0.071	-5.46E+00	4.76E-08

Supplementary Table 26. Transcriptome-wide association analysis for the TyG index, a marker of insulin resistance, using GTEx tissue expression with p-value < 5.0 x E-8 on chromosome 19 only.

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Adrenal_Gland	SUGP2	19	19,101,697	19,144,832	0.162715	rs10401969	-9.66	rs10401969	2.37E-03	-3.4	-9.66E+00	330	330 blup		0.011	0.09	6.51E+00	7.69E-11
Brain_Hippocampus	MEF2B	19	19,256,377	19,281,098	0.031323	rs16996148	-11.1	rs16996148	1.32E-02	-3.19	-11.1	328	3 enet		0.075	0.0022	10.41457	2.13E-25
Thyroid	HAPLN4	19	19,366,450	19,373,605	0.122953	rs16996148	-11.1	rs2074296	1.53E-01	8.07	-6.33	355	1 top1		0.15	3.30E-16	-6.33	2.45E-10
Pituitary	HAPLN4	19	19,366,450	19,373,605	0.197107	rs16996148	-11.1	rs2074296	1.57E-01	5.21	-6.33	355	3 lasso		0.16	1.20E-07	-5.81306	6.13E-09
Adipose_Subcutaneous	TM6SF2	19	19,375,175	19,384,200	0.068142	rs16996148	-11.1	rs2074303	8.63E-02	5.92	-6.18	359	1 top1		0.086	2.60E-09	-6.18	6.41E-10
Thyroid	TM6SF2	19	19,375,175	19,384,200	0.134594	rs16996148	-11.1	rs735273	1.30E-01	7.6	-6.14	359	1 top1		0.13	7.50E-14	-6.14	8.25E-10
Adipose_Visceral_Omentum	TM6SF2	19	19,375,175	19,384,200	0.10129	rs16996148	-11.1	rs2074303	5.52E-02	5.63	-6.18	359	3 lasso		0.074	6.50E-07	-6.042467	1.52E-09
Muscle_Skeletal	MAU2	19	19,431,654	19,469,563	0.187367	rs16996148	-11.1	rs3764567	1.72E-01	-9.31	-5.94	366	29 enet		0.19	5.20E-24	5.75224	8.81E-09
Brain_Hippocampus	MAU2	19	19,431,654	19,469,563	0.012636	rs16996148	-11.1	rs2231997	-9.18E-03	-2.68	-1.55	366	365 blup		0.005	0.22	5.7411	9.41E-09
Pancreas	MAU2	19	19,431,654	19,469,563	0.090649	rs16996148	-11.1	rs1859287	7.22E-02	-4.21	-5.69	366	1 top1		0.072	3.30E-05	5.69E+00	1.27E-08
Adipose_Visceral_Omentum	GATAD2A	19	19,496,635	19,619,740	0.040126	rs16996148	-11.1	rs17216588	3.87E-03	2.66	-9.12	346	1 top1		0.0039	0.14	-9.12	7.51E-20
Adipose_Subcutaneous	GATAD2A	19	19,496,635	19,619,740	0.050173	rs16996148	-11.1	rs2231997	5.08E-03	3.41	-1.55	346	346 blup		0.015	0.0092	-6.266669	3.69E-10
Muscle_Skeletal	NDUFA13	19	19,626,839	19,639,863	0.016714	rs16996148	-11.1	rs1036215	-1.55E-03	3.06	-1.12	357	2 enet		0.0016	0.18	5.52258	3.34E-08
Adrenal_Gland	ATP13A1	19	19,756,009	19,774,502	0.130165	rs16996148	-11.1	rs10401969	2.47E-04	4.05	-9.66E+00	334	1 top1		0.00025	0.31	-9.66E+00	4.46E-22
Brain_Hypothalamus	ATP13A1	19	19,756,009	19,774,502	0.018808	rs16996148	-11.1	rs2074296	1.29E-02	3.09	-6.33	334	1 lasso		0.028	0.047	-6.33	2.45E-10
Pituitary	CTC-559E9.9	19	19,861,427	19,863,353	0.033763	rs16996148	-11.1	rs1621688	1.15E-03	-3.06	-0.374	310	310 blup		0.0071	0.15	-5.89403	3.77E-09
Muscle_Skeletal	CEBPG	19	33,864,236	33,873,592	0.038435	rs12608723	7.7	rs12608723	3.09E-02	-4.46	7.7	471	1 top1		0.031	5.30E-05	-7.7	1.36E-14
Liver	LSR	19	35,739,233	35,758,867	0.160326	rs1688030	-7.87	rs1688043	1.40E-04	3.41	-7.45	492	1 top1		0.00014	0.31	-7.45	9.33E-14
Liver	KRTDAP	19	35,978,226	35,986,460	0.00204	rs1688030	-7.87	rs12461158	9.46E-03	-3.13	-7.2	470	1 top1		0.0095	0.12	7.2	6.02E-13
Brain_Cortex	NECTIN2	19	45,349,432	45,392,485	0.103747	rs584007	-21.3	rs445925	-5.70E-03	-3.24	16.8	420	1 top1		-0.0057	0.62	-16.8	2.44E-63
Adrenal_Gland	APOC4	19	45,445,495	45,449,242	0.086339	rs584007	-21.3	rs439401	3.95E-03	3.38	-2.12E+01	402	12 enet		0.016	0.051	-1.43E+01	1.48E-46
Adipose_Subcutaneous	APOE	19	45,409,011	45,412,650	0.043746	rs584007	-21.3	rs4803766	4.13E-02	-4.12	8.85	411	1 top1		0.041	3.60E-05	-8.85	8.75E-19
Muscle_Skeletal	APOC1	19	45,417,504	45,422,606	0.020996	rs584007	-21.3	rs439401	-8.51E-04	-3.52	-21.2	417	417 blup		-4.60E-05	0.32	6.70558	2.01E-11
Pituitary	APOC2	19	45,450,460	45,452,822	0.002463	rs584007	-21.3	rs2288911	7.50E-03	-3.38	6.31	400	1 top1		0.0075	0.14	-6.31	2.79E-10
Thyroid	CEACAM19	19	45,170,227	45,187,631	0.565593	rs584007	-21.3	rs714948	3.29E-01	11.55	3.04	427	52 enet		0.36	6.70E-41	5.79742	6.73E-09
Thyroid	RELB	19	45,504,688	45,541,452	0.001511	rs584007	-21.3	rs405697	1.47E-03	3.15	-20.1	383	1 lasso		0.0029	0.14	-20.1	7.38E-90
Brain_Hypothalamus	PPP1R37	19	45,595,050	45,650,543	0.260897	rs584007	-21.3	rs2288911	5.00E-02	3.9	6.31	373	3 lasso		0.059	0.0067	5.692474	1.25E-08
Thyroid	MARK4	19	45,754,516	45,808,541	0.02297	rs584007	-21.3	rs16979595	-2.15E-03	2.94	-0.0304	359	2 lasso		-0.0015	0.52	7.4042	1.32E-13
Muscle_Skeletal	CKM	19	45,809,672	45,826,235	0.057675	rs584007	-21.3	rs7412	-2.04E-03	3.61	15.9	371	2 lasso		-0.0013	0.54	15.2283	2.29E-52

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Pancreas	FZD9	7	72,848,109	72,850,450	0.048159	rs17145750	-21.1	rs2108235	3.97E-05	2.85	-8.67224	185	185	blup	0.027	0.0083	-7.27246	3.53E-13
Adipose_Subcutaneous	BAZ1B	7	72,854,728	72,936,608	0.124961	rs17145750	-21.1	rs13246490	3.52E-02	-4.18	-19.5	205	19	enet	0.043	2.70E-05	1.31E+01	3.10E-39
Brain_Cortex	BAZ1B	7	72,854,728	72,936,608	0.0866	rs17145750	-21.1	rs7793135	1.60E-03	-2.56	-0.0228	205	205	blup	0.015	0.086	-6.77E+00	1.31E-11
Brain_Hypothalamus	BAZ1B	7	72,854,728	72,936,608	0.00048	rs17145750	-21.1	rs3793243	-9.52E-03	-2.53	3.16E+00	204	204	blup	-0.0043	0.46	-9.616443	6.81E-22
Pituitary	BAZ1B	7	72,854,728	72,936,608	0.052544	rs17145750	-21.1	rs6974424	-4.35E-03	-2.92	-3.15E+00	204	204	blup	-0.0036	0.51	-5.62E+00	1.90E-08
Thyroid	BAZ1B	7	72,854,728	72,936,608	0.144308	rs17145750	-21.1	rs799217	2.62E-02	4.66	-5.9511	205	205	blup	0.039	4.50E-05	-6.15771	7.38E-10
Adipose_Subcutaneous	BCL7B	7	72,950,686	72,972,332	0.202545	rs17145750	-21.1	rs2573	9.25E-02	-6.36	-6.10307	224	3	lasso	0.093	6.90E-10	6.08E+00	1.18E-09
Adipose_Visceral_Omentum	BCL7B	7	72,950,686	72,972,332	0.129868	rs17145750	-21.1	rs2573	6.29E-02	-4.75	-6.103075	224	1	top1	0.063	4.30E-06	6.10E+00	1.04E-09
Muscle_Skeletal	BCL7B	7	72,950,686	72,972,332	0.170918	rs17145750	-21.1	rs2573	7.77E-02	-6.48	-6.103075	224	5	lasso	0.082	6.70E-11	8.7027	3.24E-18
Pancreas	BCL7B	7	72,950,686	72,972,332	0.095106	rs17145750	-21.1	rs35607697	5.59E-03	3.2	4.01065	224	24	enet	0.018	0.025	8.37427	5.56E-17
Adipose_Subcutaneous	MLXIPL	7	73,007,524	73,038,873	0.153476	rs17145750	-21.1	rs1051921	1.06E-01	6.62	-19.5	251	12	enet	0.11	3.50E-11	-2.01E+01	1.51E-89
Adipose_Visceral_Omentum	MLXIPL	7	73,007,524	73,038,873	0.226518	rs17145750	-21.1	rs17145813	4.11E-02	5	-9.73	251	251	blup	0.058	9.90E-06	-1.52E+01	4.14E-52
Adrenal_Gland	MLXIPL	7	73,007,524	73,038,873	0.051075	rs17145750	-21.1	rs875342	-5.77E-03	-3.3	1.26	251	251	blup	-0.0031	0.5	-6.122977	9.18E-10
Pancreas	MLXIPL	7	73,007,524	73,038,873	0.350866	rs17145750	-21.1	rs2074755	2.56E-01	7.69	-17.7	251	1	top1	0.26	6.90E-16	-17.7	4.19E-70
Pituitary	MLXIPL	7	73,007,524	73,038,873	0.118578	rs17145750	-21.1	rs17145750	9.66E-02	4.46	-2.11E+01	250	1	top1	0.097	4.60E-05	-2.11E+01	7.95E-99
Thyroid	MLXIPL	7	73,007,524	73,038,873	0.313561	rs17145750	-21.1	rs13246490	2.32E-01	9.9	-19.5	251	4	lasso	0.24	5.90E-26	-19.45448	2.67E-84
Adipose_Subcutaneous	VPS37D	7	73,082,155	73,086,442	0.131601	rs17145750	-21.1	rs12154779	6.12E-02	4.96	-3.36	263	6	lasso	0.085	3.90E-09	-5.67E+00	1.41E-08
Pancreas	STX1A	7	73,113,536	73,133,989	0.001759	rs17145750	-21.1	rs1569061	4.92E-03	-2.58	0.83	278	278	blup	0.0091	0.085	7.53149	5.02E-14
Brain_Hippocampus	ABHD11	7	73,150,424	73,153,197	0.275494	rs17145750	-21.1	rs1979807	1.21E-01	-4.53	0.806	283	283	blup	0.15	2.00E-05	6.497768	8.15E-11
Muscle_Skeletal	CLDN4	7	73,213,872	73,247,014	0.053103	rs17145750	-21.1	rs9647713	-2.02E-03	3.07	0.258	294	294	blup	0.0093	0.018	12.47991	9.61E-36
Liver	WBSR28	7	73,275,489	73,280,223	0.190036	rs17145750	-21.1	rs11769827	-3.94E-03	2.96	-1.53E+00	285	285	blup	0.008	0.14	-1.15E+01	8.96E-31
Pituitary	ELN	7	73,442,119	73,484,237	0.053923	rs17145750	-21.1	rs17145817	2.00E-02	-3	-1.15E+01	321	1	top1	0.02	0.043	1.15E+01	1.32E-30
Adipose_Subcutaneous	FGL1	8	17,721,889	17,767,874	0.081997	rs1041983	-9.82	rs4646257	2.59E-03	-4.08	9.21	864	4	lasso	0.0087	0.038	-9.21452	3.13E-20
Liver	NAT2	8	18,248,755	18,258,728	0.063891	rs1390357	10.8	rs1112005	9.20E-02	-4.56	-6.02	860	1	top1	0.092	8.60E-05	6.02	1.74E-09
Adipose_Subcutaneous	CSGALNACT1	8	19,261,672	19,615,540	0.269529	rs12679834	-26.4	rs6981898	7.49E-02	6.78	0.824	673	31	enet	0.12	7.40E-13	6.88142	5.93E-12
Adipose_Visceral_Omentum	CSGALNACT1	8	19,261,672	19,615,540	0.217024	rs12679834	-26.4	rs11785649	9.67E-03	4.64	0.454	673	673	blup	0.069	1.60E-06	6.14441	8.03E-10
Adrenal_Gland	CSGALNACT1	8	19,261,672	19,615,540	0.253504	rs12679834	-26.4	rs11985507	-1.22E-03	-3.53	-0.768	673	673	blup	0.039	0.0054	-10.3986	2.52E-25
Liver	CSGALNACT1	8	19,261,672	19,615,540	0.160763	rs12679834	-26.4	rs4379462	-5.49E-03	3.41	1.23	673	673	blup	0.0017	0.27	-5.46004	4.76E-08
Adipose_Subcutaneous	LPL	8	19,759,228	19,824,769	0.065629	rs12679834	-26.4	rs297	3.44E-02	4.32	-23.3	647	1	top1	0.034	0.00015	-23.3	4.43E-120
Adrenal_Gland	LPL	8	19,759,228	19,824,769	0.041453	rs12679834	-26.4	rs7838163	-5.69E-03	-3.03	0.461	647	647	blup	-0.0013	0.38	-7.2931	3.03E-13
Muscle_Skeletal	LPL	8	19,759,228	19,824,769	0.043872	rs12679834	-26.4	rs2410630	-1.74E-03	3.73	-20.4	647	8	enet	-0.00037	0.37	-22.43927	1.63E-111
Pancreas	LPL	8	19,759,228	19,824,769	0.004254	rs12679834	-26.4	rs6586891	-3.85E-03	-3.27	17	647	2	lasso	0.046	0.00079	-16.90289	4.28E-64
Thyroid	LPL	8	19,759,228	19,824,769	0.052488	rs12679834	-26.4	rs297	6.62E-04	3.99	-23.3	647	1	top1	0.00066	0.26	-23.3	4.43E-120
Pancreas	ATP6V1B2	8	20,054,878	20,084,330	0.016831	rs12679834	-26.4	rs7835354	4.05E-04	-2.75	-2.07	623	623	blup	0.011	0.063	-6.48542	8.85E-11
Brain_Cortex	LZTS1	8	20,103,676	20,161,474	0.050423	rs12679834	-26.4	rs4922157	-5.52E-03	3.54	-0.305	604	604	blup	0.007	0.17	-5.98072	2.22E-09
Adrenal_Gland	ZNF572	8	125,985,540	125,991,631	0.09678	rs6982502	15.8	rs10956248	-1.77E-03	2.92	8.7133	512	1	top1	-0.0018	0.41	8.7133	2.95E-18
Brain_Hippocampus	SQLE	8	126,010,739	126,034,525	0.00239	rs6982502	15.8	rs4870938	-6.95E-03	2.93	0.332	518	518	blup	0.0099	0.15	-5.69892	1.21E-08
Liver	RP11-136O12.2	8	126,479,181	126,553,615	0.041123	rs6982502	15.8	rs2980884	2.74E-02	3.65	7.0144	433	1	top1	0.027	0.023	7.01439	2.31E-12
Thyroid	PTPN3	9	112,137,746	112,260,590	0.18302	rs17793873	-8.17	rs10124300	1.42E-01	7.69	6.83	582	13	enet	0.16	1.20E-16	5.596616	2.19E-08
Liver	ADO	10	64,564,516	64,568,238	0.040042	rs4414112	10.7	rs10822008	-6.28E-03	2.73	-0.468	470	470	blup	-0.00036	0.33	-5.5083	6.32E-08
Liver	EGR2	10	64,571,756	64,679,660	0.21218	rs4414112	10.7	rs9415695	-6.47E-03	-3.49	7.854682	451	451	blup	0.0049	0.19	-7.6083	2.78E-14
Brain_Hypothalamus	NRBF2	10	64,893,050	64,914,783	0.13391	rs4414112	10.7	rs7923609	1.33E-01	-4.17	-6.59	383	1	top1	0.13	6.80E-05	6.59	4.40E-11
Liver	NRBF2	10	64,893,050	64,914,783	0.037161	rs4414112	10.7	rs7081275	-4.40E-03	-2.68	10.3	384	1	lasso	0.0033	0.22	-10.3	7.05E-25
Muscle_Skeletal	NRBF2	10	64,893,050	64,914,783	0.01624	rs4414112	10.7	rs4746951	-1.63E-03	-2.65	10.5	384	1	lasso	0.0079	0.027	-10.5	8.64E-26
Muscle_Skeletal	TATDN1P1	10	64,981,915	64,982,805	0.015978	rs4414112	10.7	rs16918575	-9.22E-04	2.91	9.15	374	9	enet	0.00076	0.24	8.16883	3.11E-16
Thyroid	JMJD1C-AS1	10	65,224,989	65,226,323	0.051405	rs4414112	10.7	rs12773283	-2.39E-03	3.53	10.4	362	362	blup	0.013	0.013	7.97405	1.54E-15
Adipose_Subcutaneous	MRPL35P2	10	65,394,077	65,394,587	0.2299	rs10733788	10.7	rs2565186	8.87E-02	6.88	6.61	373	7	lasso	0.17	4.00E-17	6.07538	1.24E-09
Adipose_Visceral_Omentum	MRPL35P2	10	65,394,077	65,394,587	0.308991	rs10733788	10.7	rs2565186	1.07E-01	6.76	6.61	373	28	enet	0.18	4.50E-15	6.457856	1.06E-10
Brain_Cortex	MRPL35P2	10	65,394,077	65,394,587	0.157553	rs10733788	10.7	rs10761741	5.12E-02	-3.56	-6.63	372	1	top1	0.051	0.0048	6.63	3.36E-11
Brain_Hypothalamus	MRPL35P2	10	65,394,077	65,394,587	0.11163	rs10733788	10.7	rs9415695	6.42E-03	2.79	9.71649	371	2	lasso	0.012	0.13	10.079177	6.83E-24
Liver	MRPL35P2	10	65,394,077	65,394,587	0.173111	rs10733788	10.7	rs3847326	8.45E-02	4.7	8.99	373	17	enet	0.11	2.40E-05	7.9591	1.73E-15
Pancreas	MRPL35P2	10	65,394,077	65,394,587	0.106743	rs10733788	10.7	rs16918575	7.62E-02	4.94	9.15	373	1	top1	0.076	2.00E-05	9.15	5.69E-20
Adrenal_Gland	RP11-170M17.2	10	65,662,211	65,663,005	0.000374	rs10822179	9.42	rs16918506	6.80E-03	2.39	-5.05	344	17	enet	0.0088	0.11	-5.73302	9.87E-09
Pituitary	EIF2S2P3	10	94,428,502	94,429,500	0.120422	rs2068888	-8	rs10882099	0.022116	3.41	-5.71	391	1	top1	0.022	0.035	-5.71	1.13E-08
Thyroid	EIF2S2P3	10	94,428,502	94,429,500	0.273199	rs2068888	-8	rs10882099	5.60E-02	6.24	-5.71	392	6	lasso	0.15	1.20E-15	-5.8889	3.89E-09
Liver	DAK	11	61,101,021	61,120,767	0.024953	rs102275	11.1	rs174566	3.64E-03	2.58	10.9	372	1	top1	0.0036	0.21	10.9	1.15E-27
Brain_Hypothalamus	CPSF7	11	61,170,121	61,197,503	0.084986	rs102275	11.1	rs7943167	4.69E-04	2.73	-0.0284	374	374	blup	0.028	0.047	6.19E+00	6.18E-10
Thyroid	CPSF7	11	61,170,121	61,197,503	0.008072	rs102275	11.1	rs11603956	2.98E-03	3.33	0.0994	374	374	blup	0.011	0.023	-6.24E+00	4.40E-10
Adipose_Subcutaneous	RN7SL23P	11	61,211,602	61,211,899	0.019954	rs102275	11.1	rs3741259	-2.54E-03	-3	4.80E-01	367	367	blup	0.01			

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Brain_Hippocampus	RP11-794G24.1	11	61,306,988	61,308,769	0.07753	rs102275	11.1	rs174448	-0.008789	-2.85	5.23	369	369	blup	0.0085	0.17	-6.65243	2.88E-11
Thyroid	RP11-794G24.1	11	61,306,988	61,308,769	0.027032	rs102275	11.1	rs175128	-2.004E-03	3.36	-0.305	370	370	blup	0.0024	0.16	-5.95E+00	2.64E-09
Adipose_Subcutaneous	DAGLA	11	61,447,905	61,513,964	0.067902	rs102275	11.1	rs198464	-1.45E-03	-2.77	-6.80E+00	377	1	lasso	0.014	0.013	6.80E+00	1.05E-11
Adipose_Visceral_Omentum	DAGLA	11	61,447,905	61,513,964	0.030332	rs102275	11.1	rs198462	2.66E-02	-3.52	-6.84	377	1	top1	0.027	0.0022	6.84	7.92E-12
Liver	RP11-467L20.10	11	61,514,474	61,525,127	0.642762	rs102275	11.1	rs198462	2.86E-01	6.81	-6.84	413	1	top1	0.29	7.60E-13	-6.84	7.92E-12
Pancreas	RP11-467L20.10	11	61,514,474	61,525,127	0.226721	rs102275	11.1	rs198462	1.41E-01	5.67	-6.84	412	6	enet	0.14	5.50E-09	-7.20878	5.65E-13
Adipose_Subcutaneous	MYRF	11	61,520,121	61,555,990	0.0862	rs102275	11.1	rs198462	5.13E-02	-4.93	-6.84E+00	413	1	top1	0.051	4.40E-06	6.84E+00	7.92E-12
Liver	MYRF	11	61,520,121	61,555,990	0.620755	rs102275	11.1	rs198476	4.85E-01	-8.61	-6.87	413	1	top1	0.49	1.30E-23	6.87	6.42E-12
Pancreas	MYRF	11	61,520,121	61,555,990	0.177131	rs102275	11.1	rs2238001	2.92E-02	-4.09	-7.84	412	2	lasso	0.034	0.0035	9.03671	1.61E-19
Adipose_Subcutaneous	TMEM258	11	61,535,973	61,560,108	0.051699	rs102275	11.1	rs108499	4.25E-02	4.47	1.10E+01	416	1	top1	0.042	2.80E-05	1.10E+01	3.82E-28
Brain_Cortex	TMEM258	11	61,535,973	61,560,108	0.087161	rs102275	11.1	rs174570	-6.16E-03	3.45	6.22	415	1	top1	-0.0062	0.67	6.22E+00	4.97E-10
Muscle_Skeletal	TMEM258	11	61,535,973	61,560,108	0.05898	rs102275	11.1	rs174535	1.73E-02	4.5	1.09E+01	416	416	blup	0.019	0.0013	7.95E+00	1.82E-15
Thyroid	TMEM258	11	61,535,973	61,560,108	0.030073	rs102275	11.1	rs174538	3.99E-02	4.2	10.9	416	1	top1	0.04	3.60E-05	1.09E+01	1.15E-27
Adipose_Subcutaneous	FEN1	11	61,560,275	61,564,716	0.022749	rs102275	11.1	rs174549	5.99E-03	-3.42	1.02E+01	416	1	lasso	0.022	0.0022	-1.02E+01	1.98E-24
Adrenal_Gland	FEN1	11	61,560,275	61,564,716	0.139019	rs102275	11.1	rs1692120	-8.63E-04	3.56	0.025	415	415	blup	0.004	0.19	-6.39E+00	1.64E-10
Brain_Hippocampus	FEN1	11	61,560,275	61,564,716	0.20257	rs102275	11.1	rs2903825	0.035614	3.53	-8.38	415	5	lasso	0.058	0.0066	-8.1826	2.78E-16
Liver	FEN1	11	61,560,275	61,564,716	0.153675	rs102275	11.1	rs2851682	4.05E-03	-3.29	10	416	3	lasso	0.0055	0.18	-8.86814	7.44E-19
Muscle_Skeletal	FEN1	11	61,560,275	61,564,716	0.059716	rs102275	11.1	rs174577	1.20E-02	-3.92	1.10E+01	416	1	top1	0.012	0.0088	-1.10E+01	3.82E-28
Pituitary	FEN1	11	61,560,275	61,564,716	0.062361	rs102275	11.1	rs174535	2.89E-02	-2.97	10.9	416	1	top1	0.029	0.019	-10.9	1.15E-27
Adipose_Subcutaneous	FADS1	11	61,567,099	61,596,790	0.050171	rs102275	11.1	rs174549	4.00E-02	-4.48	1.02E+01	433	1	top1	0.04	4.70E-05	-1.02E+01	1.98E-24
Adipose_Visceral_Omentum	FADS1	11	61,567,099	61,596,790	0.085331	rs102275	11.1	rs174549	5.28E-02	-4.93	10.2	433	1	top1	0.053	2.50E-05	-10.2	1.98E-24
Brain_Cortex	FADS1	11	61,567,099	61,596,790	0.126734	rs102275	11.1	rs174555	7.94E-02	-4.79	10.1	433	3	lasso	0.093	2.00E-04	-1.01E+01	6.64E-24
Brain_Hippocampus	FADS1	11	61,567,099	61,596,790	0.2045	rs102275	11.1	rs2845573	0.003064	-3.58	9.63	433	433	blup	0.02	0.075	-7.29805	2.92E-13
Brain_Hypothalamus	FADS1	11	61,567,099	61,596,790	0.155672	rs102275	11.1	rs174566	3.10E-02	-3.55	10.9	433	1	top1	0.031	0.039	-1.09E+01	1.15E-27
Muscle_Skeletal	FADS1	11	61,567,099	61,596,790	0.121996	rs102275	11.1	rs174555	9.75E-02	-7.19	1.01E+01	433	1	top1	0.097	9.30E-13	-1.01E+01	5.52E-24
Pancreas	FADS1	11	61,567,099	61,596,790	0.498849	rs102275	11.1	rs174555	3.61E-01	-9.15	10.1	432	10	lasso	0.37	7.40E-24	-10.49096	9.51E-26
Thyroid	FADS1	11	61,567,099	61,596,790	0.13655	rs102275	11.1	rs174549	1.02E-01	-6.89	10.2	433	1	top1	0.1	4.00E-11	-1.02E+01	1.98E-24
Adipose_Subcutaneous	FADS2	11	61,583,728	61,634,826	0.08239	rs102275	11.1	rs968567	7.25E-02	5.46	7.89E+00	427	1	top1	0.072	5.10E-08	7.89E+00	3.02E-15
Adipose_Visceral_Omentum	FADS2	11	61,583,728	61,634,826	0.241358	rs102275	11.1	rs968567	8.84E-02	5.38	7.89	427	1	top1	0.088	5.20E-08	7.89	3.02E-15
Muscle_Skeletal	FADS2	11	61,583,728	61,634,826	0.103516	rs102275	11.1	rs968567	2.49E-02	5.04	7.89E+00	427	6	lasso	0.037	9.60E-06	8.91E+00	4.88E-19
Pancreas	FADS2	11	61,583,728	61,634,826	0.274028	rs102275	11.1	rs968567	1.30E-01	5.54	7.89	426	1	top1	0.13	2.40E-08	7.89	3.02E-15
Thyroid	FADS2	11	61,583,728	61,634,826	0.35178	rs102275	11.1	rs968567	2.68E-01	10.39	7.89	427	1	top1	0.27	7.90E-29	7.89E+00	3.02E-15
Liver	FADS3	11	61,640,991	61,659,523	0.238502	rs102275	11.1	rs174566	1.23E-01	-4.83	10.9	441	1	top1	0.12	5.90E-06	-10.9	1.15E-27
Adipose_Subcutaneous	FTH1	11	61,727,190	61,735,132	0.076201	rs102275	11.1	rs11604814	-2.54E-03	3.39	1.65E+00	462	23	enet	0.0056	0.077	6.77E+00	1.29E-11
Pancreas	FTH1	11	61,727,190	61,735,132	0.052969	rs102275	11.1	rs2071213	-4.34E-03	3.49	-4.2	462	462	blup	-0.004	0.71	-7.21048	5.58E-13
Adipose_Subcutaneous	RP11-867G23.1	11	66,032,248	66,033,125	0.244184	rs11227448	4.57	rs513474	6.27E-02	-6.67	-4.15E+00	325	6	lasso	0.12	6.90E-13	5.47E+00	4.53E-08
Muscle_Skeletal	BUD13	11	116,618,886	116,643,704	0.017786	rs7350481	38.6	rs1892947	1.17E-02	-3.64	-1.29E+01	558	1	lasso	0.015	0.0042	1.29E+01	4.50E-38
Adipose_Subcutaneous	AP006216.10/ZPR1	11	116,644,105	116,644,921	0.006296	rs7350481	38.6	rs623908	2.79E-02	-3.75	-3.28E+01	558	1	top1	0.028	0.00059	3.28E+01	5.89E-236
Adrenal_Gland	AP006216.10/ZPR1	11	116,644,105	116,644,921	0.075295	rs7350481	38.6	rs11216162	1.83E-02	-3.24	6.63	558	1	top1	0.018	0.041	-6.63E+00	3.36E-11
Brain_Hypothalamus	AP006216.10/ZPR1	11	116,644,105	116,644,921	0.033882	rs7350481	38.6	rs10892001	5.34E-02	3.85	11.7	558	1	top1	0.053	0.0095	1.17E+01	1.27E-31
Thyroid	AP006216.10/ZPR1	11	116,644,105	116,644,921	0.030713	rs7350481	38.6	rs7122363	-3.68E-04	-3.35	-3.630577	558	558	blup	0.002	0.18	1.75E+01	6.87E-69
Adipose_Visceral_Omentum	AP006216.11/ZPR1	11	116,645,826	116,646,592	0.119788	rs7350481	38.6	rs180375	2.82E-02	-4.32	-16.4	558	4	lasso	0.032	0.00081	20.10112	7.22E-90
Liver	AP006216.11/ZPR1	11	116,645,826	116,646,592	0.136813	rs7350481	38.6	rs672058	-6.51E-03	3.4	16.5	558	558	blup	0.034	0.013	22.78047	7.16E-115
Pituitary	ZNF259/ZPR1	11	116,648,436	116,658,766	0.046643	rs7350481	38.6	rs1729408	-2.57E-03	3.29	-16.01875	554	1	lasso	0.031	0.016	-16.01875	9.45E-58
Thyroid	ZNF259/ZPR1	11	116,648,436	116,658,766	0.005447	rs7350481	38.6	rs481843	3.14E-04	-3.38	17.9	554	1	top1	0.00031	0.29	-1.79E+01	1.18E-71
Pancreas	APOA5	11	116,660,083	116,663,136	0.114902	rs7350481	38.6	rs12420361	-1.61E-04	3.56	-15.7	552	1	top1	-0.00016	0.33	-15.7	1.51E-55
Liver	AP006216.5/APOA4	11	116,683,920	116,684,719	0.242736	rs7350481	38.6	rs2542063	9.28E-02	-4.83	14.9	550	550	blup	0.1	3.90E-05	-21.02389	3.97E-98
Muscle_Skeletal	APOA4	11	116,691,419	116,694,022	0.087664	rs7350481	38.6	rs12718462	-1.40E-03	3.97	-1.35E+01	544	544	blup	0.0025	0.14	-1.40E+01	1.13E-44
Thyroid	APOA4	11	116,691,419	116,694,022	0.059981	rs7350481	38.6	rs7935913	-2.47E-03	3.17	-8.38	544	544	blup	0.0058	0.069	-8.63E+00	6.31E-18
Brain_Hypothalamus	APOC3	11	116,700,422	116,703,788	0.215339	rs7350481	38.6	rs12365322	4.58E-02	3.85	6.71	542	1	top1	0.046	0.015	6.71E+00	1.95E-11
Adipose_Visceral_Omentum	APOA1	11	116,706,467	116,708,666	0.064972	rs7350481	38.6	rs6589598	4.23E-04	3.36	7.77	537	1	top1	0.00042	0.29	7.77	7.85E-15
Brain_Hypothalamus	APOA1	11	116,706,467	116,708,666	0.265253	rs7350481	38.6	rs951839	-7.34E-03	2.91	-1.25	538	538	blup	0.046	0.015	1.91E+01	5.83E-81
Liver	APOA1	11	116,706,467	116,708,666	0.018763	rs7350481	38.6	rs11600380	-5.27E-03	-2.5	-9.75	538	538	blup	0.0062	0.17	17.12493	9.67E-66
Pituitary	APOA1	11	116,706,467	116,708,666	0.33705	rs7350481	38.6	rs486394	8.63E-04	3.22	18.6	537	6	lasso	0.0078	0.14	12.75873	2.79E-37
Adipose_Subcutaneous	SIK3	11	116,714,118	116,969,153	0.013572	rs7350481	38.6	rs9326248	-2.58E-03	-3.04	6.60E+00	539	2	lasso	0.0017	0.2	-6.60E+00	4.07E-11
Adipose_Visceral_Omentum	SIK3	11	116,714,118	116,969,153	0.132803	rs7350481	38.6	rs518547	2.72E-02	3.94	-0.96094	538	23	enet	0.032	0.00087	-12.03313	2.38E-33
Brain_Hypothalamus	SIK3	11	116,714,118	116,969,153	0.196994	rs7350481	38.6	rs2013131	-9.45E-03	-3.42	0.935	539	539	blup	0.0083	0.17	7.53E+00	5.19E-14
Muscle_Skeletal	SIK3	11	116,714,118	116,969,153	0.038028	rs7350481	38.6	rs2298767	-2.04E-03	-3.14	5.39E-01	539	539	blup	0.0013	0.2	-2.34E+01	7.41E-121
Pituitary	SIK3	11	116,714,118	116,969,153	0.033542	rs73504												

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Pituitary	SIK3-IT1	11	116,756,762	116,761,437	0.203183	rs7350481	38.6	rs12420361	1.68E-02	-3.76	-15.7	529	1	top1	0.017	0.058	15.7	1.51E-55
Adipose_Subcutaneous	RP11-109L13.1	11	117,006,244	117,009,298	0.614418	rs7350481	38.6	rs4938354	4.58E-01	14.08	2.26E+00	542	27	enet	0.53	3.90E-64	7.58E+00	3.45E-14
Adipose_Visceral_Omentum	RP11-109L13.1	11	117,006,244	117,009,298	0.552616	rs7350481	38.6	rs10790175	4.47E-01	11.8	7.17	541	24	enet	0.48	5.10E-46	10.40323	2.40E-25
Adrenal_Gland	RP11-109L13.1	11	117,006,244	117,009,298	0.49007	rs7350481	38.6	rs585849	3.47E-01	8.01	7.27	541	8	lasso	0.36	9.50E-19	9.61E+00	7.47E-22
Brain_Cortex	RP11-109L13.1	11	117,006,244	117,009,298	0.499942	rs7350481	38.6	rs4938349	3.28E-01	7.33	6.68	541	1	top1	0.33	2.30E-13	6.68E+00	2.39E-11
Brain_Hippocampus	RP11-109L13.1	11	117,006,244	117,009,298	0.4518	rs7350481	38.6	rs9326248	0.35937	6.75	6.6	541	5	lasso	0.39	2.50E-13	6.62992	3.36E-11
Brain_Hypothalamus	RP11-109L13.1	11	117,006,244	117,009,298	0.537619	rs7350481	38.6	rs7107152	3.23E-01	6.71	7.23	542	3	lasso	0.35	1.80E-11	8.23E+00	1.91E-16
Liver	RP11-109L13.1	11	117,006,244	117,009,298	0.458445	rs7350481	38.6	rs585849	3.51E-01	8.03	7.27	542	6	lasso	0.39	4.60E-18	7.73076	1.07E-14
Muscle_Skeletal	RP11-109L13.1	11	117,006,244	117,009,298	0.364613	rs7350481	38.6	rs585849	3.94E-01	13.99	7.27E+00	542	9	lasso	0.39	2.10E-55	7.62E+00	2.53E-14
Pancreas	RP11-109L13.1	11	117,006,244	117,009,298	0.454744	rs7350481	38.6	rs9326248	3.89E-01	9.25	6.6	541	3	lasso	0.4	3.10E-26	7.10673	1.19E-12
Pituitary	RP11-109L13.1	11	117,006,244	117,009,298	0.65642	rs7350481	38.6	rs9326248	4.40E-01	8.6	6.6	541	14	lasso	0.47	5.60E-23	8.14522	3.79E-16
Thyroid	RP11-109L13.1	11	117,006,244	117,009,298	0.485254	rs7350481	38.6	rs4938344	4.64E-01	13.6	7.06	542	5	lasso	0.48	8.20E-58	5.48E+00	4.27E-08
Brain_Hippocampus	PAFAH1B2	11	117,014,983	117,047,610	0.02717	rs7350481	38.6	rs2075292	-0.004356	-3.03	18.3	545	3	lasso	0.059	0.006	-23.6267	2.05E-123
Pancreas	PAFAH1B2	11	117,014,983	117,047,610	0.07926	rs7350481	38.6	rs17120344	1.01E-02	-3.92	-15.6	545	4	lasso	0.025	0.011	7.28671	3.18E-13
Adipose_Subcutaneous	SIDT2	11	117,049,449	117,068,160	0.044761	rs6589567	38.69	rs1263502	-2.62E-03	-3.6	-1.78E+00	543	20	enet	0.016	0.0075	5.68E+00	1.31E-08
Adipose_Visceral_Omentum	SIDT2	11	117,049,449	117,068,160	0.035751	rs6589567	38.69	rs1060211	-2.93E-03	-3.21	15	542	1	lasso	0.0033	0.16	-15	7.34E-51
Adrenal_Gland	SIDT2	11	117,049,449	117,068,160	0.362653	rs6589567	38.69	rs1060211	1.83E-01	-5.79	15	542	1	top1	0.18	2.30E-09	-1.50E+01	7.34E-51
Brain_Cortex	SIDT2	11	117,049,449	117,068,160	0.00953	rs6589567	38.69	rs1242229	-7.04E-03	-2.92	16.2	542	1	lasso	-0.0068	0.75	-1.62E+01	5.04E-59
Brain_Hypothalamus	SIDT2	11	117,049,449	117,068,160	0.192903	rs6589567	38.69	rs10750098	-7.77E-03	-3.31	26.1	543	543	blup	0.0079	0.18	-2.52E+01	3.32E-140
Pancreas	SIDT2	11	117,049,449	117,068,160	0.357609	rs6589567	38.69	rs1060211	2.73E-01	-7.81	15	542	1	top1	0.27	5.90E-17	-15	7.34E-51
Pituitary	SIDT2	11	117,049,449	117,068,160	0.00771	rs6589567	38.69	rs563838	-5.73E-03	-2.75	-7.51	542	542	blup	0.006	0.17	-13.60564	3.71E-42
Thyroid	SIDT2	11	117,049,449	117,068,160	0.123193	rs6589567	38.69	rs90192	4.82E-02	-5.92	14.4	543	20	enet	0.063	2.20E-07	-1.65E+01	3.00E-61
Brain_Cortex	TAGLN	11	117,070,037	117,075,052	0.070166	rs6589567	39.05	rs10892162	-7.38E-03	3.1	1.57	536	19	enet	-0.0028	0.43	-6.03E+00	1.68E-09
Muscle_Skeletal	TAGLN	11	117,070,037	117,075,052	0.061156	rs6589567	39.06	rs8521	2.46E-02	-4.7	7.23E+00	537	1	top1	0.025	0.00029	-7.23E+00	4.83E-13
Pancreas	TAGLN	11	117,070,037	117,075,052	0.244236	rs6589567	39.05	rs9326248	1.52E-01	-6.52	6.6	536	22	enet	0.17	1.30E-10	-7.12874	1.01E-12
Adipose_Subcutaneous	PCSK7	11	117,075,499	117,103,241	0.050165	rs180326	38.6	rs6589598	7.15E-03	-3.64	7.77E+00	536	1	top1	0.0071	0.053	-7.77E+00	7.85E-15
Adipose_Visceral_Omentum	PCSK7	11	117,075,499	117,103,241	0.048768	rs180326	38.6	rs4938355	1.19E-02	3.55	10.9	535	3	lasso	0.018	0.0094	7.84224	4.43E-15
Liver	PCSK7	11	117,075,499	117,103,241	0.170523	rs180326	38.6	rs11216322	1.42E-02	-4.06	-8.66	536	43	enet	0.049	0.0037	-13.70633	9.31E-43
Thyroid	PCSK7	11	117,075,499	117,103,241	0.04545	rs180326	38.6	rs11216321	1.75E-02	-3.97	-9.48	536	1	top1	0.018	0.0047	9.48E+00	2.54E-21
Adipose_Visceral_Omentum	BACE1	11	117,157,162	117,186,975	0.040044	rs595049	29	rs593245	-2.76E-03	3.19	2.78	532	15	enet	0.0037	0.14	5.68238	1.33E-08
Brain_Hippocampus	CEP164	11	117,185,273	117,283,984	0.05809	rs595049	29	rs11216357	-0.000526	-3.58	-7.62	527	3	lasso	0.0042	0.23	6.5059	7.72E-11
Pituitary	CEP164	11	117,185,273	117,283,984	0.387305	rs595049	29	rs11216366	5.28E-02	4.77	7.77	527	43	enet	0.19	7.90E-09	9.52229	1.69E-21
Pituitary	RP11-35P15.1	11	117,539,198	117,539,573	0.159852	rs10892082	16.3	rs3741279	8.22E-03	-3.72	-1.18	663	2	lasso	0.033	0.013	5.9048	3.53E-09
Thyroid	NLRX1	11	119,037,277	119,054,725	0.081411	rs10790286	-5.46	rs10790286	4.39E-02	-4.33	-5.46	387	1	top1	0.044	1.50E-05	5.46E+00	4.76E-08
Adipose_Subcutaneous	PDZD3	11	119,056,184	119,060,346	0.024097	rs10790286	-5.46	rs10790286	5.92E-03	3.65	-5.46E+00	383	1	top1	0.0059	0.071	-5.46E+00	4.76E-08
Brain_Cortex	ALDH1A2	15	58,245,622	58,790,065	0.186068	rs1077835	14.9	rs2414544	-5.91E-03	-3.01	-1.15	531	531	blup	-0.00021	0.33	-6.592276	4.33E-11
Brain_Hypothalamus	ALDH1A2	15	58,245,622	58,790,065	0.083587	rs1077835	14.9	rs10162642	1.80E-02	3.16	-7.11	529	1	top1	0.018	0.089	-7.11	1.16E-12
Liver	RP11-925D8.5	15	58,444,805	58,446,606	0.101212	rs1077835	14.9	rs16940204	4.01E-03	-3.31	7.11	665	7	enet	0.01	0.11	-5.95432	2.61E-09
Liver	LIPC	15	58,702,768	58,861,151	0.504977	rs1077835	14.9	rs11635491	7.01E-02	-5.15	10	569	8	lasso	0.24	8.60E-11	-15.08253	2.11E-51
Pancreas	LIPC	15	58,702,768	58,861,151	0.2678	rs1077835	14.9	rs261332	9.34E-02	-5.46	11.7	569	11	enet	0.11	3.40E-07	-10.05737	8.52E-24
Adipose_Subcutaneous	CETP	16	56,995,762	57,017,757	0.118139	rs3764261	-6.14	rs247617	4.11E-02	-4.25	-6.08	531	1	top1	0.041	3.70E-05	6.08	1.20E-09
Muscle_Skeletal	CETP	16	56,995,762	57,017,757	0.041514	rs3764261	-6.14	rs3764261	4.60E-03	-3.62	-6.14	531	2	lasso	0.0054	0.057	6.14604	7.94E-10
Pancreas	CETP	16	56,995,762	57,017,757	0.119145	rs3764261	-6.14	rs247617	7.16E-02	-4.27	-6.08	531	1	top1	0.072	3.60E-05	6.08	1.20E-09
Pituitary	CETP	16	56,995,762	57,017,757	0.202328	rs3764261	-6.14	rs3764261	2.26E-02	-3.93	-6.14	531	1	top1	0.023	0.034	6.14	8.25E-10
Thyroid	CETP	16	56,995,762	57,017,757	0.031857	rs3764261	-6.14	rs3764261	9.82E-03	-3.8	-6.14	531	1	lasso	0.013	0.013	6.14	8.25E-10
Brain_Cortex	DHX40	17	57,642,886	57,685,706	0.053105	rs2645489	6.18	rs1554846	-6.15E-03	3.1	4.99	311	311	blup	0.00029	0.31	5.632	1.78E-08
Liver	VMP1	17	57,784,553	57,918,453	0.000973	rs2645489	6.18	rs180515	-0.002825	2.67	5.43	303	303	blup	0.0028	0.23	5.660445	1.51E-08
Brain_Hypothalamus	RPS6KB1	17	57,970,447	58,027,925	0.062343	rs17580385	-6.3	rs2645467	-0.008428	2.57	5.87	267	1	lasso	0.00082	0.3	5.87	4.36E-09
Muscle_Skeletal	RPS6KB1	17	57,970,447	58,027,925	0.088374	rs17580385	-6.3	rs1292042	1.01E-01	7.25	5.74E+00	267	1	top1	0.1	3.40E-13	5.74	9.47E-09
Pancreas	RPS6KB1	17	57,970,447	58,027,925	0.172006	rs17580385	-6.3	rs2526354	1.44E-01	6.2	5.56	267	1	top1	0.14	4.00E-09	5.56	2.70E-08
Pituitary	RPS6KB1	17	57,970,447	58,027,925	0.178474	rs17580385	-6.3	rs1296279	1.73E-01	5.3	5.62	267	1	top1	0.17	4.10E-08	5.62	1.91E-08
Pancreas	RNF11	17	58,029,601	58,042,122	0.031703	rs17580385	-7.113	rs1295925	3.81E-03	-2.82	5.81	246	1	top1	0.0038	0.18	-5.81	6.25E-09
Adrenal_Gland	RP11-178C3.2	17	58,042,193	58,074,333	0.079901	rs17580385	-7.11	rs2645466	2.36E-02	3.39	5.79E+00	246	246	blup	0.033	0.0098	6.564699	5.21E-11
Brain_Hippocampus	RP11-178C3.2	17	58,042,193	58,074,333	0.036282	rs17580385	-7.113	rs11650106	1.27E-03	2.68	5.62	246	1	lasso	0.0058	0.2	5.62	1.91E-08
Liver	CTD-2319I12.1	17	58,160,927	58,169,246	0.020709	rs17580385	-6.6	rs1292067	-0.005527	2.58	5.64	228	1	top1	-0.0055	0.68	5.64	1.70E-08
Adipose_Visceral_Omentum	CTD-2319I12.4	17	58,203,896	58,212,359	0.004973	rs2645489	6.18	rs17592831	-2.83E-03	-2.53	2.6807	213	213	blup	-0.0025	0.64	-5.708077	1.14E-08
Brain_Hypothalamus	CTD-2319I12.4	17	58,203,896	58,212,359	0.049324	rs2645489	6.18	rs7224006	-0.007566	-2.42	5.8	213	2	lasso	0.024	0.061	-5.79213	6.95E-09
Liver	CTD-2319I12.4	17	58,203,896	58,212,359	0.006481	rs2645489	6.18	rs1051424	-0.000394	2.37	5.5	213	1	lasso	0.016	0.068	5.5	3.80E-08
Adipose_Subcutaneous	C17orf58	17	65,987,217	65,989,765	0													

Tissue	Gene	CHR	P0 (b37)	P1 (b37)	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P
Adipose_Subcutaneous	AC145343.2	17	66,092,187	66,097,615	0.163647	rs10445361	7.2	rs6504574	1.35E-01	7.38	5.8	320	1	top1	0.14	6.10E-14	5.8	6.63E-09
Adipose_Visceral_Omentum	AC145343.2	17	66,092,187	66,097,615	0.18795	rs10445361	7.2	rs7211282	7.13E-02	6.04	5.76	320	3	lasso	0.096	1.50E-08	6.353492	2.10E-10
Thyroid	AC145343.2	17	66,092,187	66,097,615	0.049018	rs10445361	7.2	rs8075604	1.24E-02	3.88	5.74	320	1	top1	0.012	0.015	5.74	9.47E-09
Adipose_Visceral_Omentum	LINC00674	17	66,098,049	66,111,659	0.158484	rs10445361	7.2	rs4791212	9.64E-02	5.75	6.47	320	1	top1	0.096	1.30E-08	6.47	9.80E-11
Adipose_Subcutaneous	LRRC37A16P	17	66,121,918	66,148,609	0.190617	rs10445361	7.2	rs6504574	5.72E-02	5.92	5.8	321	20	enet	0.12	1.50E-12	5.628059	1.82E-08
Adipose_Visceral_Omentum	LRRC37A16P	17	66,121,918	66,148,609	0.042616	rs10445361	7.2	rs8075604	-2.66E-03	3.08	5.74	321	3	lasso	-0.0014	0.45	6.905925	4.99E-12
Adipose_Subcutaneous	SH3GL1P3	17	66,130,816	66,131,745	0.064689	rs10445361	7.2	rs6504574	6.79E-02	5.4	5.8	321	1	top1	0.068	1.30E-07	5.8	6.63E-09
Adipose_Subcutaneous	RP11-147L13.2	17	66,242,770	66,243,714	0.019932	rs10445361	7.2	rs8078543	1.79E-02	2.55	5.71	355	1	top1	0.018	0.005	5.71	1.13E-08
Adrenal_Gland	SUGP2	19	19,101,697	19,144,832	0.162715	rs10401969	-9.66	rs10401969	2.37E-03	-3.4	-9.66E+00	330	330	blup	0.011	0.09	6.51E+00	7.69E-11
Brain_Hippocampus	MEF2B	19	19,256,377	19,281,098	0.031323	rs16996148	-11.1	rs16996148	1.32E-02	-3.19	-11.1	328	3	enet	0.075	0.0022	10.41457	2.13E-25
Pituitary	HAPLN4	19	19,366,450	19,373,605	0.197107	rs16996148	-11.1	rs2074296	1.57E-01	5.21	-6.33	355	3	lasso	0.16	1.20E-07	-5.81306	6.13E-09
Thyroid	HAPLN4	19	19,366,450	19,373,605	0.122953	rs16996148	-11.1	rs2074296	1.53E-01	8.07	-6.33	355	1	top1	0.15	3.30E-16	-6.33	2.45E-10
Adipose_Subcutaneous	TM6SF2	19	19,375,175	19,384,200	0.068142	rs16996148	-11.1	rs2074303	8.63E-02	5.92	-6.18	359	1	top1	0.086	2.60E-09	-6.18	6.41E-10
Adipose_Visceral_Omentum	TM6SF2	19	19,375,175	19,384,200	0.10129	rs16996148	-11.1	rs2074303	5.52E-02	5.63	-6.18	359	3	lasso	0.074	6.50E-07	-6.042467	1.52E-09
Thyroid	TM6SF2	19	19,375,175	19,384,200	0.134594	rs16996148	-11.1	rs735273	1.30E-01	7.6	-6.14	359	1	top1	0.13	7.50E-14	-6.14	8.25E-10
Brain_Hippocampus	MAU2	19	19,431,654	19,469,563	0.012636	rs16996148	-11.1	rs2231997	-9.18E-03	-2.68	-1.55	366	365	blup	0.005	0.22	5.7411	9.41E-09
Muscle_Skeletal	MAU2	19	19,431,654	19,469,563	0.187367	rs16996148	-11.1	rs3764567	1.72E-01	-9.31	-5.94	366	29	enet	0.19	5.20E-24	5.75224	8.81E-09
Pancreas	MAU2	19	19,431,654	19,469,563	0.090649	rs16996148	-11.1	rs1859287	7.22E-02	-4.21	-5.69	366	1	top1	0.072	3.30E-05	5.69E+00	1.27E-08
Adipose_Subcutaneous	GATAD2A	19	19,496,635	19,619,740	0.050173	rs16996148	-11.1	rs2231997	5.08E-03	3.41	-1.55	346	346	blup	0.015	0.0092	-6.266669	3.69E-10
Adipose_Visceral_Omentum	GATAD2A	19	19,496,635	19,619,740	0.040126	rs16996148	-11.1	rs17216588	3.87E-03	2.66	-9.12	346	1	top1	0.0039	0.14	-9.12	7.51E-20
Muscle_Skeletal	NDUFA13	19	19,626,839	19,639,863	0.016714	rs16996148	-11.1	rs1036215	-1.55E-03	3.06	-1.12	357	2	enet	0.0016	0.18	5.52258	3.34E-08
Adrenal_Gland	ATP13A1	19	19,756,009	19,774,502	0.130165	rs16996148	-11.1	rs10401969	2.47E-04	4.05	-9.66E+00	334	1	top1	0.00025	0.31	-9.66E+00	4.46E-22
Brain_Hypothalamus	ATP13A1	19	19,756,009	19,774,502	0.018808	rs16996148	-11.1	rs2074296	1.29E-02	3.09	-6.33	334	1	lasso	0.028	0.047	-6.33	2.45E-10
Pituitary	CTC-559E9.9	19	19,861,427	19,863,353	0.033763	rs16996148	-11.1	rs1621688	1.15E-03	-3.06	-0.374	310	310	blup	0.0071	0.15	-5.89403	3.77E-09
Muscle_Skeletal	CEBPG	19	33,864,236	33,873,592	0.038435	rs12608723	7.7	rs12608723	3.09E-02	-4.46	7.7	471	1	top1	0.031	5.30E-05	-7.7	1.36E-14
Liver	LSR	19	35,739,233	35,758,867	0.160326	rs1688030	-7.87	rs1688043	1.40E-04	3.41	-7.45	492	1	top1	0.00014	0.31	-7.45	9.33E-14
Liver	KRTDAP	19	35,978,226	35,986,460	0.00204	rs1688030	-7.87	rs12461158	9.46E-03	-3.13	-7.2	470	1	top1	0.0095	0.12	7.2	6.02E-13
Thyroid	CEACAM19	19	45,170,227	45,187,631	0.565593	rs584007	-21.3	rs714948	3.29E-01	11.55	3.04	427	52	enet	0.36	6.70E-41	5.79742	6.73E-09
Brain_Cortex	PVRL2	19	45,349,432	45,392,485	0.103747	rs584007	-21.3	rs445925	-5.70E-03	-3.24	16.8	420	1	top1	-0.0057	0.62	-16.8	2.44E-63
Adipose_Subcutaneous	APOE	19	45,409,011	45,412,650	0.043746	rs584007	-21.3	rs4803766	4.13E-02	-4.12	8.85	411	1	top1	0.041	3.60E-05	-8.85	8.75E-19
Muscle_Skeletal	APOC1	19	45,417,504	45,422,606	0.020996	rs584007	-21.3	rs439401	-8.51E-04	-3.52	-21.2	417	417	blup	-4.60E-05	0.32	6.70558	2.01E-11
Adrenal_Gland	APOC4	19	45,445,495	45,449,242	0.086339	rs584007	-21.3	rs439401	3.95E-03	3.38	-2.12E+01	402	12	enet	0.016	0.051	-1.43E+01	1.48E-46
Pituitary	APOC2	19	45,450,460	45,452,822	0.002463	rs584007	-21.3	rs2288911	7.50E-03	-3.38	6.31	400	1	top1	0.0075	0.14	-6.31	2.79E-10
Thyroid	RELB	19	45,504,688	45,541,452	0.001511	rs584007	-21.3	rs405697	1.47E-03	3.15	-20.1	383	1	lasso	0.0029	0.14	-20.1	7.38E-90
Brain_Hypothalamus	PPP1R37	19	45,595,050	45,650,543	0.260897	rs584007	-21.3	rs2288911	5.00E-02	3.9	6.31	373	3	lasso	0.059	0.0067	5.692474	1.25E-08
Thyroid	MARK4	19	45,754,516	45,808,541	0.02297	rs584007	-21.3	rs16979595	-2.15E-03	2.94	-0.0304	359	2	lasso	-0.0015	0.52	7.4042	1.32E-13
Muscle_Skeletal	CKM	19	45,809,672	45,826,235	0.057675	rs584007	-21.3	rs7412	-2.04E-03	3.61	15.9	371	2	lasso	-0.0013	0.54	15.2283	2.29E-52
Thyroid	LINC00261	20	22,528,309	22,559,280	0.16713	rs16984154	-7.15	rs1203943	5.56E-02	-4.85	-6.04	462	1	top1	0.056	1.20E-06	6.04	1.54E-09
Thyroid	FOXA2	20	22,561,643	22,566,093	0.374329	rs16984154	-7.15	rs1203943	1.77E-01	-8.51	-6.04	466	1	top1	0.18	9.00E-19	6.04	1.54E-09
Thyroid	RP4-788L20.3	20	22,568,160	22,588,155	0.26645	rs16984154	-7.15	rs1203923	1.66E-01	-8.4	-6	478	1	top1	0.17	1.30E-17	6	1.97E-09
Pituitary	WFDC2	20	44,098,346	44,110,172	0.052545	rs6065904	8.82	rs435306	-6.18E-03	-3.02	-7.87	495	2	lasso	0.01	0.11	7.36197	1.81E-13
Brain_Cortex	WFDC10A	20	44,258,165	44,259,835	0.104694	rs6065904	8.82	rs6065904	0.010704	3.43	8.82	508	1	top1	0.011	0.12	8.82	1.14E-18
Brain_Hippocampus	SNX21	20	44,462,449	44,471,385	0.054241	rs6065904	8.82	rs394643	-7.95E-03	-2.95	-5.73	524	1	top1	-0.008	0.71	5.73	1.00E-08
Adipose_Subcutaneous	ZSWIM1	20	44,509,866	44,513,905	0.065024	rs6065904	8.82	rs4810479	3.46E-02	-4.05	8.09	516	1	top1	0.035	0.00014	-8.09E+00	5.97E-16
Thyroid	SPATA25	20	44,515,128	44,516,274	0.052309	rs6065904	8.82	rs4810479	6.75E-03	-3.35	8.09	512	1	top1	0.0068	0.055	-8.09	5.97E-16
Liver	NEURL2	20	44,517,264	44,517,526	0.102665	rs6065904	8.82	rs4810479	-2.45E-03	-3.11	8.09	512	1	top1	-0.0025	0.43	-8.09	5.97E-16
Brain_Hypothalamus	CTSA	20	44,518,783	44,527,398	0.003753	rs6065904	8.82	rs394643	-0.003893	-2.87	-5.73	511	1	top1	-0.0039	0.44	5.73	1.00E-08
Adipose_Subcutaneous	PLTP	20	44,527,460	44,540,794	0.275014	rs6065904	8.82	rs4810479	1.28E-01	-7.17	8.09	513	6	lasso	0.14	1.40E-14	-5.84E+00	5.27E-09
Adipose_Visceral_Omentum	PLTP	20	44,527,460	44,540,794	0.328721	rs6065904	8.82	rs6065906	0.101579	-6.73	5.26	513	14	enet	0.11	8.30E-10	-5.7095	1.13E-08
Liver	PLTP	20	44,527,460	44,540,794	0.32081	rs6065904	8.82	rs6065904	9.68E-03	-4.45	8.82	513	12	enet	0.024	0.031	-6.45255	1.10E-10
Muscle_Skeletal	PLTP	20	44,527,460	44,540,794	0.310715	rs6065904	8.82	rs6065904	9.64E-02	-7.28	8.82	513	8	lasso	0.12	1.00E-15	-7.554183	4.21E-14
Pituitary	PLTP	20	44,527,460	44,540,794	0.167754	rs6065904	8.82	rs4810479	3.71E-02	-4.32	8.09	511	6	lasso	0.12	7.50E-06	-5.8351	5.38E-09
Pancreas	MMP9	20	44,637,547	44,645,200	0.035562	rs6065904	8.82	rs2274755	-2.86E-03	-3.08	7.73	496	1	lasso	0.00031	0.3	-7.73	1.08E-14
Adipose_Subcutaneous	SLC12A5	20	44,651,569	44,688,784	0.249535	rs6065904	8.82	rs3918261	1.36E-01	7.3	7.58	497	37	enet	0.14	1.10E-14	5.92E+00	3.29E-09
Adipose_Visceral_Omentum	SLC12A5	20	44,651,569	44,688,784	0.307428	rs6065904	8.82	rs3918261	0.185995	7.81	7.58	497	1	top1	0.19	8.80E-16	7.58	3.46E-14
Thyroid	SLC12A5	20	44,651,569	44,688,784	0.051385	rs6065904	8.82	rs2274755	5.86E-02	5.18	7.73	497	1	top1	0.059	6.10E-07	7.73	1.08E-14

Supplementary Table 28. Summary of pathway analysis using genes exhibiting genome-wide significance for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Benjamini-Hochberg	Gene
WP-4349	16p11.2 proximal deletion syndrome	Wikipedia	1.55E-05	1.30E-02	41.00
WP-4932	Tb12.23 copy number variation syndrome	Wikipedia	2.61E-16	2.33E-13	72.00
R-HSA361904	ABC transporter disorders	Reactome	5.21E-08	4.54E-05	60.00
R-HSA382656	ABC-family of membrane mediated transport	Reactome	1.62E-05	1.36E-02	51.00
R-HSA176814	Activation of APC/C and APC/C-Cdc20 mediated degradation of mitotic proteins	Reactome	7.64E-09	6.37E-06	41.00
R-HSA176187	Activation of ATR in response to replication stress	Reactome	3.45E-05	2.85E-02	23.00
R-HSA4248168	Activation of gene expression by SREBF (SREBF)	Reactome	1.13E-09	9.70E-03	28.00
R-HSA1169991	Activation of NF- κ B in B cells	Reactome	4.79E-12	3.94E-09	41.00
R-HSA447755	Activation of NMDA receptors and postsynaptic events	Reactome	1.11E-07	1.14E-04	52.00
R-HSA172662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	Reactome	4.80E-12	6.07E-09	41.00
KEGG-05021	Acute myeloid leukemia	KEGG	2.50E-02	1.84E-09	47.00
R-HSA1280218	Adaptive Immune System	Reactome	2.50E-02	1.84E-09	41.00
R-HSA4040	Adhesion Junction	KEGG	2.50E-02	1.84E-09	41.00
KEGG-04920	Adipocytokine signaling pathway	KEGG	2.50E-02	1.84E-09	41.00
WP-232	Adipogenesis	Wikipedia	2.50E-02	1.84E-09	41.00
WP-2324	AGE/RAGE pathway	Wikipedia	2.50E-02	1.84E-09	41.00
KEGG-04933	AGE-RAGE signaling pathway in diabetic complications	KEGG	2.50E-02	1.84E-09	41.00
R-HSA3646399	Agglutination	Reactome	2.50E-02	1.84E-09	41.00
KEGG-04936	Alcoholic liver disease	KEGG	2.50E-02	1.84E-09	41.00
WP-244	Alpha 5 beta 4 signaling pathway	Wikipedia	2.50E-02	1.84E-09	41.00
KEGG-05010	Alzheimer disease	KEGG	2.50E-02	1.84E-09	41.00
WP-5124	Alzheimer's disease	Wikipedia	2.50E-02	1.84E-09	41.00
WP-2059	Alzheimer's disease and mRNA effects	Wikipedia	2.50E-02	1.84E-09	41.00
WP-1403	AMP-activated protein kinase (AMPK) signaling	Wikipedia	2.50E-02	1.84E-09	41.00
KEGG-04152	AMPK signaling pathway	KEGG	2.50E-02	1.84E-09	41.00
KEGG-05014	Amnionotic lateral sclerosis	KEGG	2.50E-02	1.84E-09	41.00
R-HSA362012	Anchoring of the basal body to the plasma membrane	Reactome	2.50E-02	1.84E-09	41.00
WP-138	Androgen receptor signaling pathway	Wikipedia	2.50E-02	1.84E-09	41.00
WP-139	Anemias	Wikipedia	2.50E-02	1.84E-09	41.00
WP-3915	Angiotensin-like protein 8 regulatory pathway	Wikipedia	2.50E-02	1.84E-09	41.00
R-HSA363170	Antigen Presentation: Folding, assembly and peptide binding to class I MHC	Reactome	2.50E-02	1.84E-09	41.00
KEGG-04122	Antigen processing and presentation	KEGG	2.50E-02	1.84E-09	41.00
R-HSA363168	Antigen processing: Ubiquitination & Proteasome degradation	Reactome	2.50E-02	1.84E-09	41.00
R-HSA123675	Antigen processing-Cross presentation	Reactome	2.50E-02	1.84E-09	41.00
R-HSA0803197	Antimicrobial peptides	Reactome	2.50E-02	1.84E-09	41.00
R-HSA1168410	Antiviral mechanisms by IFN-stimulated genes	Reactome	2.50E-02	1.84E-09	41.00
R-HSA174154	APC/C-Cdc20 mediated degradation of mitotic proteins	Reactome	2.50E-02	1.84E-09	41.00
R-HSA174154	APC/C-Cdc20 mediated degradation of Securin	Reactome	2.50E-02	1.84E-09	41.00
R-HSA174178	APC/C-Cdh1 mediated degradation of Cdc20 and other APC/C-Cdh1 targeted proteins in late mitosis/early G1	Reactome	2.50E-02	1.84E-09	41.00
R-HSA174143	APC/C-mediated degradation of cell cycle proteins	Reactome	2.50E-02	1.84E-09	41.00
R-HSA179419	APC/Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	Reactome	2.50E-02	1.84E-09	41.00
KEGG-04371	Apelin signaling pathway	KEGG	2.50E-02	1.84E-09	41.00
WP-254	Apoptosis	Wikipedia	2.50E-02	1.84E-09	41.00
WP-2864	Apoptosis-related network due to altered Notch3 in ovarian cancer	Wikipedia	2.50E-02	1.84E-09	41.00
R-HSA111465	Ascorbic cleavage of cellular proteins	Reactome	2.50E-02	1.84E-09	41.00
R-HSA175153	Aspartic execution phase	Reactome	2.50E-02	1.84E-09	41.00
WP-2386	Au1 hydrocarbon receptor pathway	Wikipedia	2.50E-02	1.84E-09	41.00
R-HSA36867	Assembly of the pre-replicative complex	Reactome	2.50E-02	1.84E-09	41.00
R-HSA360471	Association of Tric/DCT with target proteins during biosynthesis	Reactome	2.50E-02	1.84E-09	41.00
R-HSA4608870	Asymmetrical localization of PCP proteins	Reactome	2.50E-02	1.84E-09	41.00
WP-3878	ATM signaling in development and disease	Wikipedia	2.50E-02	1.84E-09	41.00
R-HSA25406	ATM signaling pathway	Reactome	2.50E-02	1.84E-09	41.00
R-HSA40048	AUF1 (hnRNP D0) binds and destabilizes mRNA	Reactome	2.50E-02	1.84E-09	41.00
R-HSA854158	AURKA Activation by TPX2	Reactome	2.50E-02	1.84E-09	41.00
R-HSA174094	Autodegradation of Cdh1 by Cdh1/APC	Reactome	2.50E-02	1.84E-09	41.00
R-HSA349425	Autodegradation of the E3 ubiquitin ligase COP1	Reactome	2.50E-02	1.84E-09	41.00

D	ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni state down (N, Genes)	Associated Genes
						ACB1 ACB1A ACB2 ACB3 ACB4 ACB5 ACB6 ACB7 ACB8 ACB9 ACB10 ACB11 ACB12 ACB13 ACB14 ACB15 ACB16 ACB17 ACB18 ACB19 ACB20 ACB21 ACB22 ACB23 ACB24 ACB25 ACB26 ACB27 ACB28 ACB29 ACB30 ACB31 ACB32 ACB33 ACB34 ACB35 ACB36 ACB37 ACB38 ACB39 ACB40 ACB41 ACB42 ACB43 ACB44 ACB45 ACB46 ACB47 ACB48 ACB49 ACB50 ACB51 ACB52 ACB53 ACB54 ACB55 ACB56 ACB57 ACB58 ACB59 ACB60 ACB61 ACB62 ACB63 ACB64 ACB65 ACB66 ACB67 ACB68 ACB69 ACB70 ACB71 ACB72 ACB73 ACB74 ACB75 ACB76 ACB77 ACB78 ACB79 ACB80 ACB81 ACB82 ACB83 ACB84 ACB85 ACB86 ACB87 ACB88 ACB89 ACB90 ACB91 ACB92 ACB93 ACB94 ACB95 ACB96 ACB97 ACB98 ACB99 ACB100 ACB101 ACB102 ACB103 ACB104 ACB105 ACB106 ACB107 ACB108 ACB109 ACB110 ACB111 ACB112 ACB113 ACB114 ACB115 ACB116 ACB117 ACB118 ACB119 ACB120 ACB121 ACB122 ACB123 ACB124 ACB125 ACB126 ACB127 ACB128 ACB129 ACB130 ACB131 ACB132 ACB133 ACB134 ACB135 ACB136 ACB137 ACB138 ACB139 ACB140 ACB141 ACB142 ACB143 ACB144 ACB145 ACB146 ACB147 ACB148 ACB149 ACB150 ACB151 ACB152 ACB153 ACB154 ACB155 ACB156 ACB157 ACB158 ACB159 ACB160 ACB161 ACB162 ACB163 ACB164 ACB165 ACB166 ACB167 ACB168 ACB169 ACB170 ACB171 ACB172 ACB173 ACB174 ACB175 ACB176 ACB177 ACB178 ACB179 ACB180 ACB181 ACB182 ACB183 ACB184 ACB185 ACB186 ACB187 ACB188 ACB189 ACB190 ACB191 ACB192 ACB193 ACB194 ACB195 ACB196 ACB197 ACB198 ACB199 ACB200 ACB201 ACB202 ACB203 ACB204 ACB205 ACB206 ACB207 ACB208 ACB209 ACB210 ACB211 ACB212 ACB213 ACB214 ACB215 ACB216 ACB217 ACB218 ACB219 ACB220 ACB221 ACB222 ACB223 ACB224 ACB225 ACB226 ACB227 ACB228 ACB229 ACB230 ACB231 ACB232 ACB233 ACB234 ACB235 ACB236 ACB237 ACB238 ACB239 ACB240 ACB241 ACB242 ACB243 ACB244 ACB245 ACB246 ACB247 ACB248 ACB249 ACB250 ACB251 ACB252 ACB253 ACB254 ACB255 ACB256 ACB257 ACB258 ACB259 ACB260 ACB261 ACB262 ACB263 ACB264 ACB265 ACB266 ACB267 ACB268 ACB269 ACB270 ACB271 ACB272 ACB273 ACB274 ACB275 ACB276 ACB277 ACB278 ACB279 ACB280 ACB281 ACB282 ACB283 ACB284 ACB285 ACB286 ACB287 ACB288 ACB289 ACB290 ACB291 ACB292 ACB293 ACB294 ACB295 ACB296 ACB297 ACB298 ACB299 ACB300 ACB301 ACB302 ACB303 ACB304 ACB305 ACB306 ACB307 ACB308 ACB309 ACB310 ACB311 ACB312 ACB313 ACB314 ACB315 ACB316 ACB317 ACB318 ACB319 ACB320 ACB321 ACB322 ACB323 ACB324 ACB325 ACB326 ACB327 ACB328 ACB329 ACB330 ACB331 ACB332 ACB333 ACB334 ACB335 ACB336 ACB337 ACB338 ACB339 ACB340 ACB341 ACB342 ACB343 ACB344 ACB345 ACB346 ACB347 ACB348 ACB349 ACB350 ACB351 ACB352 ACB353 ACB354 ACB355 ACB356 ACB357 ACB358 ACB359 ACB360 ACB361 ACB362 ACB363 ACB364 ACB365 ACB366 ACB367 ACB368 ACB369 ACB370 ACB371 ACB372 ACB373 ACB374 ACB375 ACB376 ACB377 ACB378 ACB379 ACB380 ACB381 ACB382 ACB383 ACB384 ACB385 ACB386 ACB387 ACB388 ACB389 ACB390 ACB391 ACB392 ACB393 ACB394 ACB395 ACB396 ACB397 ACB398 ACB399 ACB400 ACB401 ACB402 ACB403 ACB404 ACB405 ACB406 ACB407 ACB408 ACB409 ACB410 ACB411 ACB412 ACB413 ACB414 ACB415 ACB416 ACB417 ACB418 ACB419 ACB420 ACB421 ACB422 ACB423 ACB424 ACB425 ACB426 ACB427 ACB428 ACB429 ACB430 ACB431 ACB432 ACB433 ACB434 ACB435 ACB436 ACB437 ACB438 ACB439 ACB440 ACB441 ACB442 ACB443 ACB444 ACB445 ACB446 ACB447 ACB448 ACB449 ACB450 ACB451 ACB452 ACB453 ACB454 ACB455 ACB456 ACB457 ACB458 ACB459 ACB460 ACB461 ACB462 ACB463 ACB464 ACB465 ACB466 ACB467 ACB468 ACB469 ACB470 ACB471 ACB472 ACB473 ACB474 ACB475 ACB476 ACB477 ACB478 ACB479 ACB480 ACB481 ACB482 ACB483 ACB484 ACB485 ACB486 ACB487 ACB488 ACB489 ACB490 ACB491 ACB492 ACB493 ACB494 ACB495 ACB496 ACB497 ACB498 ACB499 ACB500 ACB501 ACB502 ACB503 ACB504 ACB505 ACB506 ACB507 ACB508 ACB509 ACB510 ACB511 ACB512 ACB513 ACB514 ACB515 ACB516 ACB517 ACB518 ACB519 ACB520 ACB521 ACB522 ACB523 ACB524 ACB525 ACB526 ACB527 ACB528 ACB529 ACB530 ACB531 ACB532 ACB533 ACB534 ACB535 ACB536 ACB537 ACB538 ACB539 ACB540 ACB541 ACB542 ACB543 ACB544 ACB545 ACB546 ACB547 ACB548 ACB549 ACB550 ACB551 ACB552 ACB553 ACB554 ACB555 ACB556 ACB557 ACB558 ACB559 ACB560 ACB561 ACB562 ACB563 ACB564 ACB565 ACB566 ACB567 ACB568 ACB569 ACB570 ACB571 ACB572 ACB573 ACB574 ACB575 ACB576 ACB577 ACB578 ACB579 ACB580 ACB581 ACB582 ACB583 ACB584 ACB585 ACB586 ACB587 ACB588 ACB589 ACB590 ACB591 ACB592 ACB593 ACB594 ACB595 ACB596 ACB597 ACB598 ACB599 ACB600 ACB601 ACB602 ACB603 ACB604 ACB605 ACB606 ACB607 ACB608 ACB609 ACB610 ACB611 ACB612 ACB613 ACB614 ACB615 ACB616 ACB617 ACB618 ACB619 ACB620 ACB621 ACB622 ACB623 ACB624 ACB625 ACB626 ACB627 ACB628 ACB629 ACB630 ACB631 ACB632 ACB633 ACB634 ACB635 ACB636 ACB637 ACB638 ACB639 ACB640 ACB641 ACB642 ACB643 ACB644 ACB645 ACB646 ACB647 ACB648 ACB649 ACB650 ACB651 ACB652 ACB653 ACB654 ACB655 ACB656 ACB657 ACB658 ACB659 ACB660 ACB661 ACB662 ACB663 ACB664 ACB665 ACB666 ACB667 ACB668 ACB669 ACB670 ACB671 ACB672 ACB673 ACB674 ACB675 ACB676 ACB677 ACB678 ACB679 ACB680 ACB681 ACB682 ACB683 ACB684 ACB685 ACB686 ACB687 ACB688 ACB689 ACB690 ACB691 ACB692 ACB693 ACB694 ACB695 ACB696 ACB697 ACB698 ACB699 ACB700 ACB701 ACB702 ACB703 ACB704 ACB705 ACB706 ACB707 ACB708 ACB709 ACB710 ACB711 ACB712 ACB713 ACB714 ACB715 ACB716 ACB717 ACB718 ACB719 ACB720 ACB721 ACB722 ACB723 ACB724 ACB725 ACB726 ACB727 ACB728 ACB729 ACB730 ACB731 ACB732 ACB733 ACB734 ACB735 ACB736 ACB737 ACB738 ACB739 ACB740 ACB741 ACB742 ACB743 ACB744 ACB745 ACB746 ACB747 ACB748 ACB749 ACB750 ACB751 ACB752 ACB753 ACB754 ACB755 ACB756 ACB757 ACB758 ACB759 ACB760 ACB761 ACB762 ACB763 ACB764 ACB765 ACB766 ACB767 ACB768 ACB769 ACB770 ACB771 ACB772 ACB773 ACB774 ACB775 ACB776 ACB777 ACB778 ACB779 ACB780 ACB781 ACB782 ACB783 ACB784 ACB785 ACB786 ACB787 ACB788 ACB789 ACB790 ACB791 ACB792 ACB793 ACB794 ACB795 ACB796 ACB797 ACB798 ACB799 ACB800 ACB801 ACB802 ACB803 ACB804 ACB805 ACB806 ACB807 ACB808 ACB809 ACB810 ACB811 ACB812 ACB813 ACB814 ACB815 ACB816 ACB817 ACB818 ACB819 ACB820 ACB82

D	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni test (alpha = 0.05)	Nr Genes
KEGG-05926	Gastric cancer	KEGG_20.05.2022	5.59E-08	5.84E-05	73.00
WP-4659	Gastrin signaling pathway	Wikipathways_23.02.2022	6.14E-22	6.72E-19	85.00
R-HSA-21460	Gene expression (Transcription)	REACTOME_Pathways_20.05.2022	2.20E-26	3.16E-23	621.00
R-HSA-212436	Genetic Transcription	REACTOME_Pathways_20.05.2022	1.80E-16	2.44E-13	491.00
WP-4536	Genes related to primary cilium development (based on CRISPRi)	Wikipathways_23.02.2022	4.38E-05	3.50E-02	50.00
R-HSA-107895	GLI3 is processed to GLI3R by the proteasome	REACTOME_Pathways_20.05.2022	1.24E-11	1.52E-08	43.00
WP-2261	Glioblastoma signaling pathways	Wikipathways_23.02.2022	2.94E-15	4.51E-12	59.00
KEGG-00214	Glycine	KEGG_20.05.2022	2.49E-11	3.05E-08	50.00
R-HSA-8696399	Global Genome Nucleotide Excision Repair (GG-NER)	REACTOME_Pathways_20.05.2022	2.01E-09	2.28E-06	51.00
KEGG-00922	Glucagon signaling pathway	KEGG_20.05.2022	5.47E-07	5.25E-04	56.00
R-HSA-10336	Glucose metabolism	REACTOME_Pathways_20.05.2022	3.73E-08	3.95E-05	52.00
KEGG-00964	Glycerophospholipid metabolism	KEGG_20.05.2022	9.47E-06	8.19E-03	60.00
WP-5045	Glycolysis in senescence	REACTOME_Pathways_20.05.2022	2.41E-06	2.11E-03	40.00
R-HSA-01912	GnRH signaling pathway	KEGG_20.05.2022	5.73E-06	5.46E-03	48.00
R-HSA-8656688	Golgi-to-ER retrograde transport	REACTOME_Pathways_20.05.2022	7.06E-07	6.74E-04	66.00
R-HSA-900782	GPCR ligand binding	REACTOME_Pathways_20.05.2022	7.96E-13	1.01E-09	71.00
WP-45	GPRs, class A rhodopsin-like	Wikipathways_23.02.2022	2.58E-07	2.56E-04	40.00
WP-112	GPRs	Wikipathways_23.02.2022	6.14E-08	7.05E-05	70.00
R-HSA-114604	GPVI-mediated activation cascade	REACTOME_Pathways_20.05.2022	1.66E-06	1.54E-03	24.00
KEGG-00935	Growth hormone synthesis, secretion and action	KEGG_20.05.2022	1.81E-11	2.21E-08	70.00
R-HSA-9762114	GSK3R and BTRC-CUL1-mediated-degradation of NF2E2	REACTOME_Pathways_20.05.2022	1.10E-11	1.34E-08	39.00
R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	REACTOME_Pathways_20.05.2022	2.46E-20	3.44E-17	80.00
R-HSA-906990	HCMV Early Events	Wikipathways_23.02.2022	3.29E-08	3.05E-05	70.00
R-HSA-906646	HCMV Infection	Wikipathways_23.02.2022	1.73E-07	1.75E-04	78.00
WP-4674	Had and neck squamous cell carcinoma	Wikipathways_23.02.2022	8.40E-15	1.11E-11	50.00
R-HSA-535346	Hedgehog ligand biosynthesis	REACTOME_Pathways_20.05.2022	1.41E-06	1.32E-03	38.00
R-HSA-10787	Hedgehog 'off' state	REACTOME_Pathways_20.05.2022	6.20E-13	7.88E-10	70.00
R-HSA-6362884	Hedgehog 'on' state	REACTOME_Pathways_20.05.2022	4.55E-09	5.05E-06	50.00
R-HSA-9707616	Heme signaling	REACTOME_Pathways_20.05.2022	1.95E-05	1.35E-02	28.00
R-HSA-109592	Hemostasis	REACTOME_Pathways_20.05.2022	3.01E-07	2.98E-04	240.00
KEGG-00161	Hepatitis B	KEGG_20.05.2022	8.11E-14	1.05E-10	93.00
WP-4660	Hepatitis B infection	Wikipathways_23.02.2022	6.41E-13	8.14E-10	93.00
KEGG-01161	Hepatitis C	KEGG_20.05.2022	2.01E-11	2.45E-08	86.00
WP-3646	Hepatitis C and hepatocellular carcinoma	Wikipathways_23.02.2022	3.83E-07	3.74E-04	32.00
KEGG-00925	Hepatocellular carcinoma	KEGG_20.05.2022	3.71E-14	4.95E-11	96.00
WP-313	Hepatocyte growth factor receptor signaling	Wikipathways_23.02.2022	1.09E-12	1.37E-09	30.00
WP-4206	Hereditary leiomyomatosis and renal cell carcinoma associated	Wikipathways_23.02.2022	3.02E-05	2.45E-02	15.00
R-HSA-3087280	hiL mutants alter ligand secretion	REACTOME_Pathways_20.05.2022	1.27E-07	1.30E-04	37.00
R-HSA-3082768	hiL mutants are degraded by ERAD	REACTOME_Pathways_20.05.2022	1.57E-08	1.69E-05	37.00
KEGG-0066	HIF-1 signaling pathway	KEGG_20.05.2022	3.03E-12	3.77E-09	67.00
KEGG-03930	Hippo signaling pathway	KEGG_20.05.2022	8.85E-07	4.45E-04	70.00
WP-4540	Hippo signaling regulation pathways	Wikipathways_23.02.2022	4.55E-08	4.77E-05	58.00
WP-4541	Hippo-Merlin signaling dysregulation	Wikipathways_23.02.2022	5.77E-05	4.55E-02	57.00
R-HSA-162906	HIV Infection	REACTOME_Pathways_20.05.2022	1.15E-21	1.64E-18	137.00
R-HSA-125687	HIV Life Cycle	REACTOME_Pathways_20.05.2022	4.13E-11	4.91E-08	82.00
R-HSA-167169	HIV Transcription Elongation	REACTOME_Pathways_20.05.2022	1.46E-03	1.78E-03	27.00
R-HSA-9693538	Homologous Recombination	REACTOME_Pathways_20.05.2022	1.92E-05	1.60E-02	64.00
R-HSA-102909	Host Interactions of HIV Factors	REACTOME_Pathways_20.05.2022	3.37E-21	4.75E-18	90.00

D	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni test down	Number Genes
WP-4331	Neovascularisation processes	Wikipedia: 23.02.2022	1.01E-05	8.72E-05	24.00
R-HSA-026533	NEP/N2E interacts with the Cellular Export Machinery	REACTOME: Pathways 25.05.2022	1.44E-05	1.06E-05	27.00
R-HSA-0675108	Nervous system development	REACTOME: Pathways 25.05.2022	1.71E-32	2.45E-29	302.00
WP-4747	Nefrin-UNC5B signaling pathway	Wikipedia: 23.02.2022	2.05E-05	1.73E-02	30.00
KEGG-04080	Neuroactive ligand-receptor interaction	KEGG 25.05.2022	1.38E-06	1.29E-03	66.00
R-HSA-112314	Neurotransmitter receptors and postsynaptic signal transduction	REACTOME: Pathways 25.05.2022	5.17E-05	4.11E-02	87.00
KEGG-04722	Neurotrophin signaling pathway	KEGG 25.05.2022	1.43E-12	1.79E-09	72.00
R-HSA-078895	Neutrophil degranulation	REACTOME: Pathways 25.05.2022	3.57E-09	3.95E-05	201.00
KEGG-04064	NF-kappa B signaling pathway	KEGG 25.05.2022	1.96E-05	1.63E-02	42.00
R-HSA-078590	NF- κ B non-canonical NF- κ B signaling	REACTOME: Pathways 25.05.2022	3.07E-11	3.71E-08	42.00
KEGG-04621	NO-like receptor signalling pathway	KEGG 25.05.2022	9.01E-06	7.82E-03	62.00
WP-4399	Nonalcoholic fatty liver disease	Wikipedia: 23.02.2022	2.38E-18	3.28E-15	100.00
KEGG-04932	Non-alcoholic fatty liver disease	KEGG 25.05.2022	4.60E-19	6.37E-16	99.00
WP-4341	Non-genomic actions of 1,25 dihydroxyvitamin D3	Wikipedia: 23.02.2022	2.34E-07	3.30E-04	42.00
R-HSA-300171	Non-integrin membrane-ECM interactions	REACTOME: Pathways 25.05.2022	1.96E-05	1.83E-02	33.00
R-HSA-078997	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	REACTOME: Pathways 25.05.2022	5.00E-24	7.14E-21	86.00
R-HSA-078996	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	REACTOME: Pathways 25.05.2022	6.52E-21	9.17E-18	72.00
R-HSA-078702	Nonsense-Mediated Decay (NMD)	REACTOME: Pathways 25.05.2022	5.00E-24	7.14E-21	86.00
KEGG-05023	Non-small cell lung cancer	KEGG 25.05.2022	1.84E-12	2.30E-09	66.00
WP-4255	Non-small cell lung cancer	Wikipedia: 23.02.2022	6.44E-11	7.71E-08	48.00
WP-61	Notch signalling pathway	Wikipedia: 23.02.2022	4.47E-06	3.99E-03	36.00
R-HSA-112247	NOTCH1 Intracellular Domain Regulates Transcription	REACTOME: Pathways 25.05.2022	1.45E-07	1.48E-04	32.00
WP-3865	Novel intracellular components of RIG-I-like receptor (RLR) pathway	REACTOME: Pathways 23.02.2022	2.00E-08	2.14E-05	39.00
R-HSA-020958	NR1H2 & NR1H3 regulate gene expression linked to lipogenesis	REACTOME: Pathways 25.05.2022	1.55E-05	1.30E-02	9.00
R-HSA-020446	NR1H2 and NR1H3-mediated signaling	REACTOME: Pathways 25.05.2022	9.77E-07	9.24E-04	30.00
R-HSA-020958	NR1H2 & NR1H3 regulate gene expression linked to cholesterol transport and efflux	REACTOME: Pathways 25.05.2022	1.01E-05	8.72E-03	24.00
WP-4357	NRF2-ARE regulation	Wikipedia: 23.02.2022	1.05E-09	1.05E-09	17.00
WP-514	NRP1-triggered signaling pathways in pancreatic cancer	Wikipedia: 23.02.2022	1.90E-10	2.25E-07	39.00
R-HSA-188276	NS1 Mediated Effects on Host Pathways	REACTOME: Pathways 25.05.2022	6.03E-07	8.80E-04	27.00
R-HSA-078994	Nuclear Envelope (NE) Reassembly	REACTOME: Pathways 25.05.2022	5.88E-10	8.82E-07	47.00
R-HSA-280766	Nuclear Envelope Breakdown	REACTOME: Pathways 25.05.2022	3.25E-07	3.19E-04	32.00
R-HSA-0789194	Nucleic acids mediated by NFYF212	REACTOME: Pathways 25.05.2022	1.18E-10	1.45E-07	51.00
R-HSA-180746	Nuclear import of Rev protein	REACTOME: Pathways 25.05.2022	2.95E-07	2.91E-04	24.00
R-HSA-301054	Nuclear Pore Complex (NPC) Disassembly	REACTOME: Pathways 25.05.2022	1.66E-06	1.54E-03	24.00
KEGG-02013	Nucleocytoplasmic transport	KEGG 25.05.2022	2.89E-11	3.50E-08	65.00
R-HSA-090638	Nucleotide Excision Repair	REACTOME: Pathways 25.05.2022	1.39E-10	1.64E-07	66.00
WP-4793	Nucleotide excision repair	Wikipedia: 23.02.2022	3.97E-05	3.19E-02	26.00
R-HSA-186643	Nucleotide-binding domain, leucine rich repeat containing receptor (NLN) signaling pathways	REACTOME: Pathways 25.05.2022	2.58E-05	2.13E-02	32.00
KEGG-04740	Offspring Signaling Pathway	REACTOME: Pathways 25.05.2022	2.00E-09	2.00E-09	1.00
R-HSA-080957	Oncogenin MAPK signaling pathway	REACTOME: Pathways 25.05.2022	3.91E-08	4.13E-05	46.00
WP-2374	Oncostatin M signaling pathway	Wikipedia: 23.02.2022	1.16E-11	1.43E-08	46.00
KEGG-04114	Oocyte meiosis	KEGG 25.05.2022	2.50E-06	2.27E-03	64.00
R-HSA-08949	Orc1 removal from chromatin	REACTOME: Pathways 25.05.2022	7.84E-13	9.90E-10	50.00
R-HSA-185241	Organole biogenesis and maintenance	REACTOME: Pathways 25.05.2022	1.00E-22	1.42E-19	167.00
KEGG-0380	Osteoclast differentiation	KEGG 25.05.2022	5.12E-06	4.53E-03	62.00
WP-1454	Osteosarcoma signaling	Wikipedia: 23.02.2022	3.66E-03	3.26E-03	12.00
R-HSA-068896	Ovarian tumor domain processes	REACTOME: Pathways 25.05.2022	7.90E-06	6.93E-03	25.00
WP-4879	Overlap between signal transduction pathways contributing to LMNA laminopathies	Wikipedia: 23.02.2022	2.00E-07	2.01E-04	37.00
WP-5695	Overview of proinflammatory and prolifection mediators	Wikipedia: 23.02.2022	4.92E-08	5.16E-05	12.00
KEGG-01916	Oxidative phosphorylation	KEGG 25.05.2022	1.18E-09	1.35E-06	73.00
WP-623	Oxidative phosphorylation	Wikipedia: 23.02.2022	1.64E-07	1.87E-04	38.00
R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	REACTOME: Pathways 25.05.2022	1.64E-09	1.87E-06	38.00
KEGG-04921	Oxytocin signaling pathway	KEGG 25.05.2022	1.00E-05	8.63E-03	71.00
R-HSA-095953	p53-Dependent G1 DNA Damage Response	REACTOME: Pathways 25.05.2022	3.35E-10	5.07E-07	44.00
R-HSA-095952	p53-Dependent G1/S DNA damage checkpoint	REACTOME: Pathways 25.05.2022	4.35E-10	5.07E-07	44.00
R-HSA-09610	p53-Independent DNA Damage Response	REACTOME: Pathways 25.05.2022	2.73E-09	3.05E-06	36.00
R-HSA-096103	p53-Independent G1/S DNA damage checkpoint	REACTOME: Pathways 25.05.2022	2.73E-09	3.05E-06	36.00
WP-4293	Pancreatic adenocarcinoma pathway	Wikipedia: 23.02.2022	2.03E-18	2.80E-15	66.00
KEGG-05012	Pancreatic cancer	KEGG 25.05.2022	1.27E-15	1.70E-12	56.00
R-HSA-020955	Paradoxical activation of RAF signaling by kinase inactive BRAF	REACTOME: Pathways 25.05.2022	1.79E-10	2.10E-07	35.00
R-HSA-066407	Parasite infection	REACTOME: Pathways 25.05.2022	1.27E-07	1.30E-04	37.00
Associated Genes Found					
ACT1, CACNA, EFEB2, HFE1A, KIT, MAPK1, MAPK3, MAPK9, MAPK10, MAPK11, NR2F2, NOTCH1, PDGFR, RPL, RPL18, RSM1, SMOAD, SMOAD2, SMOAD3, SMOAD4, SMOAD5, SMOAD6, SMOAD7, SMOAD8, SMOAD9, SMOAD10, SMOAD11, SMOAD12, SMOAD13, SMOAD14, SMOAD15, SMOAD16, SMOAD17, SMOAD18, SMOAD19, SMOAD20, SMOAD21, SMOAD22, SMOAD23, SMOAD24, SMOAD25, SMOAD26, SMOAD27, SMOAD28, SMOAD29, SMOAD30, SMOAD31, SMOAD32, SMOAD33, SMOAD34, SMOAD35, SMOAD36, SMOAD37, SMOAD38, SMOAD39, SMOAD40, SMOAD41, SMOAD42, SMOAD43, SMOAD44, SMOAD45, SMOAD46, SMOAD47, SMOAD48, SMOAD49, SMOAD50, SMOAD51, SMOAD52, SMOAD53, SMOAD54, SMOAD55, SMOAD56, SMOAD57, SMOAD58, SMOAD59, SMOAD60, SMOAD61, SMOAD62, SMOAD63, SMOAD64, SMOAD65, SMOAD66, SMOAD67, SMOAD68, SMOAD69, SMOAD70, SMOAD71, SMOAD72, SMOAD73, SMOAD74, SMOAD75, SMOAD76, SMOAD77, SMOAD78, SMOAD79, SMOAD80, SMOAD81, SMOAD82, SMOAD83, SMOAD84, SMOAD85, SMOAD86, SMOAD87, SMOAD88, SMOAD89, SMOAD90, SMOAD91, SMOAD92, SMOAD93, SMOAD94, SMOAD95, SMOAD96, SMOAD97, SMOAD98, SMOAD99, SMOAD100, 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D	Term	Ontology Source	Term PValue	Corrected with Bonferroni test down	Nr Genes
KEGG05030	Pathogenic Escherichia coli infection	KEGG 25.05.2022	3.61E-08	3.82E-05	94.00
WP-2272	Pathogenic Escherichia coli infection	Wikipedia 23.02.2022	1.90E-10	2.27E-07	39.00
WP-3651	Pathways affected in adenoid cystic carcinoma	Wikipedia 23.02.2022	1.64E-09	1.87E-06	43.00
KEGG00200	Pathways in cancer	KEGG 25.05.2022	7.06E-20	9.84E-17	253.00
KEGG00022	Pathways of neurodegeneration	KEGG 25.05.2022	1.13E-28	1.91E-25	253.00
R-HSA-048640	PCPCE pathway	REACTOME Pathways 25.05.2022	1.36E-12	1.71E-09	60.00
WP-2426	PDGF pathway	Wikipedia 23.02.2022	5.61E-17	7.63E-14	37.00
WP-2972	PDGF-beta pathway	Wikipedia 23.02.2022	7.05E-13	8.65E-10	27.00
KEGG05035	PD-1 expression and PD-1 checkpoint pathway in cancer	KEGG 25.05.2022	1.28E-13	1.65E-10	60.00
R-HSA-059380	PECAM1 interactions	REACTOME Pathways 25.05.2022	1.16E-05	9.90E-03	11.00
R-HSA-156920	Peptide chain elongation	REACTOME Pathways 25.05.2022	2.81E-19	3.90E-16	67.00
R-HSA-172762	Peptide isoand-binding receptors	REACTOME Pathways 25.05.2022	9.93E-07	3.96E-04	29.00
KEGG04145	Phagosome	KEGG 25.05.2022	9.40E-07	8.91E-04	73.00
WP-3611	Photodynamic therapy-induced AP-1 survival signaling	Wikipedia 23.02.2022	1.15E-06	1.08E-03	32.00
WP-3680	Physico-chemical features and toxicity-associated pathways	Wikipedia 23.02.2022	5.89E-11	7.08E-08	46.00
R-HSA-221928	PI3K/AKT Signaling in Cancer	REACTOME Pathways 25.05.2022	6.05E-09	6.68E-06	59.00
KEGG04151	PI3K-AKT signaling pathway	KEGG 25.05.2022	6.74E-11	8.06E-08	161.00
WP-4172	PI3K-AKT signaling pathway	Wikipedia 23.02.2022	2.05E-09	2.35E-06	153.00
WP-3844	PI3K-AKT-mTOR signaling pathway and therapeutic opportunities	Wikipedia 23.02.2022	7.06E-04	7.06E-04	10.00
R-HSA-0811658	PP2A, PIP2 and ERK3 Regulate PI3K/AKT Signaling	REACTOME Pathways 25.05.2022	1.13E-07	1.36E-04	57.00
R-HSA-126704	PP3 activates AKT signaling	REACTOME Pathways 25.05.2022	9.65E-29	1.39E-25	166.00
R-HSA-0963038	Plasma lipoprotein assembly, remodeling, and clearance	REACTOME Pathways 25.05.2022	1.04E-05	1.02E-05	10.00
R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	REACTOME Pathways 25.05.2022	4.17E-09	4.64E-06	46.00
R-HSA-0963899	Plasma lipoprotein remodeling	REACTOME Pathways 25.05.2022	8.92E-06	1.02E-05	10.00
KEGG04611	Platelet activation	KEGG 25.05.2022	3.49E-06	3.14E-03	61.00
R-HSA-76002	Platelet activation, signaling and aggregation	REACTOME Pathways 25.05.2022	1.94E-05	1.78E-03	113.00
R-HSA-038064	Post NMDA receptor activation events	REACTOME Pathways 25.05.2022	1.68E-07	1.70E-04	46.00
R-HSA-0515933	Postmitotic nuclear pore complex (NPC) reformation	REACTOME Pathways 25.05.2022	2.70E-08	2.88E-05	22.00
KEGG04611	Platelet activation	KEGG 25.05.2022	3.49E-06	3.14E-03	61.00
R-HSA-76002	Platelet activation, signaling and aggregation	REACTOME Pathways 25.05.2022	1.94E-05	1.78E-03	113.00
R-HSA-038064	Post NMDA receptor activation events	REACTOME Pathways 25.05.2022	1.68E-07	1.70E-04	46.00
R-HSA-0515933	Postmitotic nuclear pore complex (NPC) reformation	REACTOME Pathways 25.05.2022	2.70E-08	2.88E-05	22.00
R-HSA-987592	Post-translational protein modification	REACTOME Pathways 25.05.2022	7.11E-20	9.90E-17	573.00
R-HSA-1266071	Potassium Channels	REACTOME Pathways 25.05.2022	3.13E-06	2.83E-03	10.00
R-HSA-0979191	Potential therapeutics for SARS	REACTOME Pathways 25.05.2022	6.80E-12	7.63E-09	57.00
WP-3842	PPAR signaling pathway	Wikipedia 23.02.2022	2.68E-06	2.43E-03	34.00
R-HSA-198781	PPARA activates gene expression	REACTOME Pathways 25.05.2022	8.39E-09	9.18E-06	68.00
WP-2874	PPAR-alpha pathway	Wikipedia 23.02.2022	6.62E-09	7.62E-06	23.00
R-HSA-399597	Protein-mediated transfer of substrate to CcTCT/TC	REACTOME Pathways 25.05.2022	9.94E-09	1.04E-05	29.00
WP-2572	Primary focal segmental glomerulosclerosis (FSGS)	Wikipedia 23.02.2022	2.73E-05	2.25E-02	39.00
KEGG00200	Purin disease	KEGG 25.05.2022	1.03E-22	1.47E-19	167.00
R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	REACTOME Pathways 25.05.2022	8.39E-24	1.20E-20	147.00
R-HSA-069807	Processing of DNA double-strand break ends	REACTOME Pathways 25.05.2022	2.64E-05	2.17E-02	48.00
R-HSA-124414	Processive synthesis on the C-termini of the telomere	Wikipedia 23.02.2022	1.20E-05	1.02E-02	16.00
WP-5103	Prostate-associated lipodystrophy	Wikipedia 23.02.2022	1.19E-07	5.03E-04	54.00
KEGG04914	Progestrone-mediated oocyte maturation	KEGG 25.05.2022	1.19E-07	5.03E-04	54.00
R-HSA-04917	Protein signaling pathway	KEGG 25.05.2022	2.94E-10	3.44E-07	46.00
WP-2037	Protein signaling pathway	Wikipedia 23.02.2022	3.47E-21	4.89E-18	62.00
KEGG05015	Prostate cancer	KEGG 25.05.2022	3.95E-19	5.95E-16	71.00
KEGG03090	Proteasome	KEGG 25.05.2022	1.75E-08	1.87E-05	32.00
WP-183	Protein degradation	Wikipedia 23.02.2022	4.43E-14	5.71E-11	40.00
R-HSA-31261	Protein folding	REACTOME Pathways 25.05.2022	4.78E-06	4.27E-03	50.00
R-HSA-060997	Protein localization	REACTOME Pathways 25.05.2022	5.37E-06	4.74E-03	79.00
ACD2P, ABT1, ABT1, AC1B, AC1B1, AC1B2, AC1B3, AC1B4, AC1B5, AC1B6, AC1B7, AC1B8, AC1B9, AC1B10, AC1B11, AC1B12, AC1B13, AC1B14, AC1B15, AC1B16, AC1B17, AC1B18, AC1B19, AC1B20, AC1B21, AC1B22, AC1B23, AC1B24, AC1B25, AC1B26, AC1B27, AC1B28, AC1B29, AC1B30, AC1B31, AC1B32, AC1B33, AC1B34, AC1B35, AC1B36, AC1B37, AC1B38, AC1B39, AC1B40, AC1B41, AC1B42, AC1B43, AC1B44, AC1B45, AC1B46, AC1B47, AC1B48, AC1B49, AC1B50, AC1B51, AC1B52, AC1B53, AC1B54, AC1B55, AC1B56, AC1B57, AC1B58, AC1B59, AC1B60, AC1B61, AC1B62, AC1B63, AC1B64, AC1B65, AC1B66, AC1B67, AC1B68, AC1B69, AC1B70, AC1B71, AC1B72, AC1B73, AC1B74, AC1B75, AC1B76, AC1B77, AC1B78, AC1B79, AC1B80, AC1B81, AC1B82, AC1B83, AC1B84, AC1B85, AC1B86, AC1B87, AC1B88, AC1B89, AC1B90, AC1B91, AC1B92, AC1B93, AC1B94, AC1B95, AC1B96, AC1B97, AC1B98, AC1B99, AC1B100, AC1B101, AC1B102, AC1B103, AC1B104, AC1B105, AC1B106, AC1B107, AC1B108, AC1B109, AC1B110, AC1B111, AC1B112, AC1B113, AC1B114, AC1B115, AC1B116, AC1B117, AC1B118, AC1B119, AC1B120, 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D	Term	Ontology Source	Term PValue	Term PValue Connected with Bioregion area down, 10, Genes	Associated Genes Found
KEGG04141	Protein processing in endoplasmic reticulum	KEGG 25.05.2022	1.41E-15	1.88E-12	100.00
KEGG05026	Proteoglycans in cancer	KEGG 25.05.2022	1.03E-25	1.45E-22	132.00
R-HSA0807070	PTEN Regulation	REACTOME Pathways 25.05.2022	8.72E-23	1.24E-19	97.00
WP-3303	RAC1/PAK1/p38/MMP2 pathway	Wikipathways 23.02.2022	7.09E-13	1.07E-09	49.00
R-HSA013049	RAC2 GTPase cycle	REACTOME Pathways 25.05.2022	4.74E-05	7.92E-02	44.00
R-HSA067300	RAF activation	REACTOME Pathways 25.05.2022	3.60E-06	3.24E-03	24.00
R-HSA067301	RAF/MAP kinase cascade	REACTOME Pathways 25.05.2022	6.28E-12	7.73E-09	136.00
WP-2299	Raf1 downstream regulated genes	Wikipathways 23.02.2022	3.65E-07	3.76E-04	12.00
WP-2018	RANK/RANK signalling pathway	Wikipathways 23.02.2022	7.41E-14	9.61E-11	43.00
KEGG04015	Rap1 signalling pathway	KEGG 25.05.2022	3.53E-07	3.46E-04	96.00
WP-4223	Ras signalling	Wikipathways 23.02.2022	9.56E-06	8.25E-03	83.00
KEGG04014	Ras signalling pathway	KEGG 25.05.2022	4.95E-05	3.64E-02	98.00
R-HSA069365	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	REACTOME Pathways 25.05.2022	3.58E-06	3.23E-03	52.00
R-HSA030270	Recruitment of mitotic centrosome proteins and complexes	REACTOME Pathways 25.05.2022	8.18E-10	4.44E-07	41.00
R-HSA030320	Recruitment of NuMA to mitotic centrosomes	REACTOME Pathways 25.05.2022	6.53E-11	7.59E-08	58.00
R-HSA043728	Recycling pathway of L1	REACTOME Pathways 25.05.2022	5.45E-06	4.85E-03	29.00
KEGG04810	Regulation of actin cytoskeleton	KEGG 25.05.2022	1.68E-09	1.91E-06	106.00
WP-51	Regulation of actin cytoskeleton	Wikipathways 23.02.2022	2.15E-08	2.36E-05	77.00
R-HSA0202482	Regulation of actin dynamics for phagocytic cup formation	REACTOME Pathways 25.05.2022	5.45E-07	2.58E-04	37.00
R-HSA0211733	Regulation of activated PAK-2alpha by proteasome mediated degradation	REACTOME Pathways 25.05.2022	1.55E-08	1.67E-05	34.00
R-HSA176468	Regulation of APC/C activators between G1/S and early anaphase	REACTOME Pathways 25.05.2022	3.12E-10	3.52E-07	51.00
R-HSA159911	Regulation of Apoptosis	REACTOME Pathways 25.05.2022	4.05E-08	4.31E-05	35.00
R-HSA010953	Regulation of expression of SLTs and ROBOs	REACTOME Pathways 25.05.2022	3.19E-26	4.58E-23	117.00
R-HSA0178827	Regulation of Glucocorticoid by Glucocorticoid Receptor	REACTOME Pathways 25.05.2022	1.48E-06	1.97E-02	22.00
R-HSA1371453	Regulation of HSF1-mediated heat shock response	REACTOME Pathways 25.05.2022	2.65E-11	3.04E-08	34.00
R-HSA010953	Regulation of HSF1-mediated heat shock response	REACTOME Pathways 25.05.2022	2.65E-11	3.04E-08	34.00
R-HSA040206	Regulation of lipid metabolism by PPARalpha	REACTOME Pathways 25.05.2022	2.77E-09	3.10E-06	66.00
R-HSA0202692	Regulation of MECP2 expression and activity	REACTOME Pathways 25.05.2022	1.77E-08	1.63E-05	53.00
R-HSA043578	Regulation of mitotic cell cycle	REACTOME Pathways 25.05.2022	1.27E-10	1.50E-07	55.00
R-HSA050501	Regulation of mRNA stability by proteins that bind AL-rich elements	REACTOME Pathways 25.05.2022	4.10E-14	5.35E-11	60.00
R-HSA030562	Regulation of mRNA decay/biogenesis (ODC)	REACTOME Pathways 25.05.2022	1.15E-06	1.08E-03	32.00
R-HSA0694758	Regulation of pMLK1 activation at G2M Transition	REACTOME Pathways 25.05.2022	4.10E-14	5.35E-11	60.00
R-HSA043724	Regulation of PTEN gene transcription	REACTOME Pathways 25.05.2022	3.02E-11	3.65E-08	43.00
R-HSA0484751	Regulation of PTEN stability and activity	REACTOME Pathways 25.05.2022	2.50E-11	2.94E-08	47.00
R-HSA058442	Regulation of RAS by GAPs	REACTOME Pathways 25.05.2022	2.62E-08	2.79E-05	42.00
R-HSA039902	Regulation of RUNX2 expression and activity	REACTOME Pathways 25.05.2022	3.16E-11	3.62E-08	49.00
R-HSA081808	Regulation of RUNX2 expression and activity	REACTOME Pathways 25.05.2022	4.51E-12	6.05E-09	41.00
R-HSA019311	Regulation of signaling by CBL	REACTOME Pathways 25.05.2022	4.35E-08	4.85E-05	17.00
R-HSA063907	Regulation of TFS3 Activity	REACTOME Pathways 25.05.2022	2.60E-14	3.41E-11	50.00
R-HSA084758	Regulation of TFS3 Activity through Acetylation	REACTOME Pathways 25.05.2022	2.35E-05	2.97E-02	33.00
R-HSA084756	Regulation of TFS3 Activity through Phosphorylation	REACTOME Pathways 25.05.2022	2.18E-08	2.97E-05	33.00
R-HSA084757	Regulation of TFS3 Deacetylation	REACTOME Pathways 25.05.2022	3.60E-06	3.24E-03	25.00
R-HSA080603	Regulation of TFS3 Phosphorylation and Degradation	REACTOME Pathways 25.05.2022	1.54E-06	1.43E-03	24.00
KEGG04026	Retain signaling	KEGG 25.05.2022	2.98E-12	3.72E-09	76.00
R-HSA174437	Removal of the 5' cap intermediate from the C-strand	REACTOME Pathways 25.05.2022	6.87E-07	6.58E-04	49.00
KEGG05011	Renal cell carcinoma	KEGG 25.05.2022	1.67E-10	1.97E-07	46.00
R-HSA1200297	Resolution of Sister Chromatid Cohesion	REACTOME Pathways 25.05.2022	1.72E-07	1.74E-04	65.00
R-HSA011106	Respiratory electron transport	REACTOME Pathways 25.05.2022	1.19E-12	1.49E-09	65.00
R-HSA163200	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins	REACTOME Pathways 25.05.2022	3.75E-10	4.38E-07	71.00
R-HSA033012	Response of EIF2AK4 (GCN2) to amino acid deficiency	REACTOME Pathways 25.05.2022	5.70E-20	7.95E-17	74.00
R-HSA033700	Response of EIF2AK4 to phosphatase	REACTOME Pathways 25.05.2022	1.06E-09	1.28E-06	74.00
WP-2446	Retinoblastoma gene in cancer	Wikipathways 23.02.2022	2.31E-11	2.81E-08	56.00
KEGG03083	Retinol metabolism	KEGG 25.05.2022	1.06E-09	1.06E-06	56.00
KEGG04723	Retrograde endocannabinoid signaling	KEGG 25.05.2022	2.43E-07	2.42E-04	73.00
R-HSA159504	Rev-mediated nuclear export of HIV RNA	REACTOME Pathways 25.05.2022	1.16E-07	1.19E-04	25.00
R-HSA012899	RHO GTPase cycle	REACTOME Pathways 25.05.2022	2.72E-17	3.70E-14	215.00
R-HSA195258	RHO GTPase Effectors	REACTOME Pathways 25.05.2022	3.71E-16	5.00E-13	165.00
R-HSA062900	RHO GTPases activate C17	REACTOME Pathways 25.05.2022	3.76E-06	3.37E-03	16.00
R-HSA066220	RHO GTPases Activate Formins	REACTOME Pathways 25.05.2022	5.53E-09	5.95E-06	17.00
R-HSA0597117	RHO GTPases Activate ROCKs	REACTOME Pathways 25.05.2022	3.03E-07	3.46E-04	17.00
R-HSA088092	RHOA GTPase cycle	REACTOME Pathways 25.05.2022	1.44E-05	1.62E-02	68.00
R-HSA070874	RHOBTB2 GTPase cycle	REACTOME Pathways 25.05.2022	6.00E-09	6.99E-06	17.00
R-HSA010422	RHOBTB2 GTPase cycle	REACTOME Pathways 25.05.2022	1.06E-09	1.28E-06	74.00
R-HSA013418	RHOBTB2 GTPase cycle	REACTOME Pathways 25.05.2022	1.35E-08	1.46E-05	29.00
R-HSA013106	RHOBTB2 GTPase cycle	REACTOME Pathways 25.05.2022	8.29E-06	7.23E-03	40.00

D	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni test down	Nr Genes
R-HSA070206	Signaling by ALK in cancer	REACTOME Pathways 25.05.2022	8.17E-15	1.08E-11	44
R-HSA080262	Signaling by BRAF and RAF1 fusions	REACTOME Pathways 25.05.2022	5.30E-09	9.95E-06	43
R-HSA074565	Signaling by CSF3 (G-CSF)	REACTOME Pathways 25.05.2022	4.52E-06	4.02E-03	21
R-HSA139317	Signaling by cytosolic FGFR1 fusion mutants	REACTOME Pathways 25.05.2022	2.25E-07	2.25E-04	10
R-HSA177929	Signaling by EGFR	REACTOME Pathways 25.05.2022	2.13E-06	1.94E-03	31
R-HSA143713	Signaling by EGFR in C1orf115 Cancer	REACTOME Pathways 25.05.2022	1.20E-05	1.02E-02	18
R-HSA043312	Signaling by EGFR in C1orf115 Cancer	REACTOME Pathways 25.05.2022	9.45E-09	1.04E-05	18
R-HSA127286	Signaling by ERBB2	REACTOME Pathways 25.05.2022	2.85E-09	3.19E-06	26
R-HSA066348	Signaling by ERBB2 ECD mutants	REACTOME Pathways 25.05.2022	2.73E-09	3.12E-06	10
R-HSA122990	Signaling by ERBB2 ECD mutants	REACTOME Pathways 25.05.2022	4.73E-06	4.20E-03	18
R-HSA064591	Signaling by ERBB2 ECD mutants	REACTOME Pathways 25.05.2022	1.04E-05	1.04E-02	18
R-HSA060335	Signaling by Erythropoietin	REACTOME Pathways 25.05.2022	1.20E-05	1.02E-02	18
R-HSA190336	Signaling by FGFR	REACTOME Pathways 25.05.2022	1.60E-08	1.74E-05	44
R-HSA122609	Signaling by FGFR in disease	REACTOME Pathways 25.05.2022	2.92E-11	3.56E-08	51
R-HSA064738	Signaling by FGFR1	REACTOME Pathways 25.05.2022	2.75E-05	2.26E-02	29
R-HSA065302	Signaling by FGFR1 in disease	REACTOME Pathways 25.05.2022	2.54E-09	2.85E-06	29
R-HSA064738	Signaling by FGFR2	REACTOME Pathways 25.05.2022	2.40E-09	2.70E-06	46
R-HSA081708	Signaling by FGFR2 IIIa TM	REACTOME Pathways 25.05.2022	1.04E-05	8.81E-03	44
R-HSA065203	Signaling by FGFR2 in disease	REACTOME Pathways 25.05.2022	5.33E-06	5.71E-03	27
R-HSA064741	Signaling by FGFR3	REACTOME Pathways 25.05.2022	6.03E-07	8.80E-04	27
R-HSA064143	Signaling by FGFR4	REACTOME Pathways 25.05.2022	1.95E-06	1.79E-03	18
R-HSA065521	Signaling by FGFR4 in disease	REACTOME Pathways 25.05.2022	1.32E-06	1.24E-03	11
R-HSA070348	Signaling by FLT3 ITD and TKD mutants	REACTOME Pathways 25.05.2022	2.45E-05	2.02E-02	13
R-HSA038361	Signaling by Hedgehog	REACTOME Pathways 25.05.2022	4.65E-12	5.78E-09	84
R-HSA082948	Signaling by high-kinase activity BRAF mutants	REACTOME Pathways 25.05.2022	2.26E-09	2.55E-06	28
R-HSA14752	Signaling by Insulin receptor	REACTOME Pathways 25.05.2022	2.30E-07	2.30E-04	45
R-HSA49147	Signaling by Interleukins	REACTOME Pathways 25.05.2022	1.17E-17	1.61E-14	221
R-HSA066938	Signaling by KIT in disease	REACTOME Pathways 25.05.2022	2.01E-11	2.45E-08	20
R-HSA063715	Signaling by Ligand-Responsive EGFR Variants in Cancer	REACTOME Pathways 25.05.2022	7.30E-08	7.59E-05	17
R-HSA080834	Signaling by MET	REACTOME Pathways 25.05.2022	6.10E-09	6.73E-06	46
R-HSA082946	Signaling by moderate kinase activity BRAF mutants	REACTOME Pathways 25.05.2022	1.78E-10	2.10E-07	35
R-HSA030627	Signaling by Non-Receptor Tyrosine Kinases	REACTOME Pathways 25.05.2022	6.11E-06	6.37E-03	32
R-HSA157118	Signaling by NOTCH	REACTOME Pathways 25.05.2022	9.05E-13	1.14E-09	121
R-HSA158043	Signaling by NOTCH1	REACTOME Pathways 25.05.2022	9.69E-07	1.47E-04	18
R-HSA151384	Signaling by NOTCH4	REACTOME Pathways 25.05.2022	8.18E-10	1.44E-07	51
R-HSA187037	Signaling by NTRK1 (TRKA)	REACTOME Pathways 25.05.2022	1.34E-09	1.53E-06	66
R-HSA009115	Signaling by NTRK1 (TRKB)	REACTOME Pathways 25.05.2022	1.76E-06	1.83E-03	19
R-HSA156520	Signaling by NTRK6	REACTOME Pathways 25.05.2022	9.44E-11	1.12E-07	75
R-HSA005931	Signaling by Nuclear Receptors	REACTOME Pathways 25.05.2022	6.68E-17	9.07E-14	156
R-HSA196787	Signaling by PDGF	REACTOME Pathways 25.05.2022	5.06E-08	5.30E-05	37
R-HSA071565	Signaling by PDGFR in disease	REACTOME Pathways 25.05.2022	3.02E-05	2.45E-02	10
R-HSA073770	Signaling by PDGFR extracellular domain extrants	REACTOME Pathways 25.05.2022	1.16E-05	9.95E-03	11
R-HSA073787	Signaling by PDGFR transmembrane, judanemembrane and kinase domain	REACTOME Pathways 25.05.2022	1.95E-03	1.85E-01	11
R-HSA074039	Signaling by phosphotyrosine judanemembrane, extracellular and kinase domain KIT mutants	REACTOME Pathways 25.05.2022	2.01E-11	2.45E-08	20
R-HSA048021	Signaling by PTK9	REACTOME Pathways 25.05.2022	6.11E-06	6.37E-03	32
R-HSA065223	Signaling by RAF1 mutants	REACTOME Pathways 25.05.2022	1.51E-10	1.79E-07	13
R-HSA082949	Signaling by RAS mutants	REACTOME Pathways 25.05.2022	1.79E-10	2.10E-07	35
R-HSA006934	Signaling by Receptor Tyrosine Kinases	REACTOME Pathways 25.05.2022	6.22E-30	8.02E-27	274
R-HSA194315	Signaling by Rho GTPases	REACTOME Pathways 25.05.2022	1.12E-29	1.62E-26	346
R-HSA0716542	Signaling by Rho GTPases, Micro GTPases and RHOBTB3	REACTOME Pathways 25.05.2022	2.28E-30	3.31E-27	354
R-HSA376176	Signaling by RHO receptors	REACTOME Pathways 25.05.2022	1.12E-27	1.61E-24	141
R-HSA143357	Signaling by SCF-KIT	REACTOME Pathways 25.05.2022	7.46E-09	8.19E-06	31
R-HSA006336	Signaling by TGF-beta family members	REACTOME Pathways 25.05.2022	1.35E-09	1.54E-06	56
R-HSA170934	Signaling by TGF-beta Receptor Complex	REACTOME Pathways 25.05.2022	1.09E-11	1.34E-08	67
R-HSA083705	Signaling by the T Cell Receptor (BCR)	REACTOME Pathways 25.05.2022	1.40E-16	1.90E-13	75
R-HSA240432	Signaling by Type I Insulin-like Growth Factor 1 Receptor (IGF1R)	REACTOME Pathways 25.05.2022	6.11E-06	6.37E-03	32
R-HSA194138	Signaling by VEGF	REACTOME Pathways 25.05.2022	1.47E-09	1.67E-06	62
R-HSA195741	Signaling by WNT	REACTOME Pathways 25.05.2022	1.05E-12	1.32E-09	158
R-HSA049498	Signaling downstream of RAS mutants	REACTOME Pathways 25.05.2022	1.79E-10	2.10E-07	35
KEGG04550	Signaling pathways regulating pluripotency of stem cells	KEGG 25.05.2022	2.41E-09	2.72E-06	76
R-HSA024047	SL-mediated transmembrane transport	REACTOME Pathways 25.05.2022	1.20E-05	1.02E-02	42
KEGG02022	Small cell lung cancer	KEGG 25.05.2022	3.95E-10	4.61E-07	56

Supplementary Table 29. Summary of pathway analysis using female-specific genes for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort

ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni step down	Nr. Genes	Associated Genes Found
WP-4657	22q11.2 copy number variation syndrome	WikiPathways_ 23.02.2022	3.28E-06	6.44E-03	13(0)	[BCDL2, CDC42, CUL3, EGFR, FGFR, FOXA2, NCOR1, PAKA, POLR2A, PRKN, RBX1, TP53, XPO1]
WP-4932	7q11.23 copy number variation syndrome	WikiPathways_ 23.02.2022	5.11E-12	1.25E-08	18(0)	[BZT1B, BRD4, DEK, DLD, DLST, ELN, FAS, FZD9, GRB2, H2AX, HDAC2, HOXC8, MAPK3, MXL1P, MYC, PCNA, SMCARCS, SSTG1M]
R-HSA-399997	Acetylcholine regulates insulin secretion	REACTOME_ Pathways_ 25.05.2022	6.16E-07	1.68E-03	5(0)	[GNAA1, GNAQ, PLCB1, PLCB3, PKRCA]
R-HSA-902619	Inactivated NTRK3 signals through RAS	REACTOME_ Pathways_ 25.05.2022	2.02E-05	3.65E-02	4(0)	[GRB2, HRAS, KRAS, NRAS]
R-HSA-903484	Activated NTRK3 signals through RAS	REACTOME_ Pathways_ 25.05.2022	1.14E-05	2.12E-02	4(0)	[GRB2, HRAS, KRAS, NRAS]
R-HSA-561742	Activation of anterior HOX genes in hindbrain development	REACTOME_ Pathways_ 25.05.2022	1.22E-06	2.49E-03	13(0)	[EEED, EP300, EZH2, H2AX, HBSC5, HBSC9, HC31, HA-16, JUN, NCOR1, POLR2A, SUZ12, WDR5]
R-HSA-111447	Activation of BAD and translocation to mitochondria	REACTOME_ Pathways_ 25.05.2022	8.93E-06	1.68E-02	5(0)	[BCL2, YYHAB, YYHAE, YYHAG, YYHAZ]
R-HSA-114452	Activation of BH3-only proteins	REACTOME_ Pathways_ 25.05.2022	2.79E-05	4.93E-02	6(0)	[BCL2, TP53, YYHAB, YYHAE, YYHAG, YYHAZ]
WP-5819507	Activation of HOX genes during differentiation	REACTOME_ Pathways_ 25.05.2022	1.22E-06	2.49E-03	13(0)	[EEED, EP300, EZH2, H2AX, HBSC5, HBSC9, HC31, HA-16, JUN, NCOR1, POLR2A, SUZ12, WDR5]
R-HSA-442735	Activation of NMIIA receptors and postsynaptic events	REACTOME_ Pathways_ 25.05.2022	3.15E-06	6.10E-03	11(0)	[CALM1, CAMK2A, CAMK2B, GNAI1, GNAQ, GRB2, GRIN2A, HRAS, KRAS, MAPK3, MAPT, NRAS, RAC1, TUBA1A]
WP-4298	Acute viral myocarditis	WikiPathways_ 23.02.2022	1.14E-05	2.12E-02	10(0)	[BCL2, CASP6, CXCR4, JAK1, MAPK3, MMP9, PARP1, RAC3, STAT1, STAT3]
WP-4298	Acute viral myocarditis	WikiPathways_ 23.02.2022	1.14E-05	2.12E-02	10(0)	[BCL2, CASP6, CXCR4, JAK1, MAPK3, MMP9, PARP1, RAC3, STAT1, STAT3]
R-HSA-1280218	Adaptive Immune System	REACTOME_ Pathways_ 25.05.2022	2.34E-08	5.26E-05	17(0)	[BCAP1, CALM1, CANX, CDCC4, CDCC4, COL1A1, CTSL, CUL1, CUL3, CUL7, DYNLL1F, FBXO2, FBXW7, FZR1, GRB2, HECDW2, HRAS, HUWE1, ITGB1, ITPR3, KIF20A, KIF23, KRAS, NRAS, PPP2CB, PRKRA, PRKCI, RBX1, RHOA, RPL10, RPS19, SHAN1, SHIP2, TRAF6, TRIM37, TRIM63, TUBA1A, UBE2U, UFL1, YYHAB, YYHAZ]
KEGG-04520	Adherens junction	KEGG_ 25.05.2022	1.41E-05	2.59E-02	9(0)	[CDC42, EGFR, EP300, MAPK3, RAC1, RAC3, RHOA, SNAIL, TOFBP2]
KEGG-04261	Adrenergic signaling in cardiomyocytes	KEGG_ 25.05.2022	9.96E-04	1.75E-01	15(0)	[ADRB2, ATP2A2, BCL2, CALM1, CAMK2A, CAMK2B, GNAI1, GNAQ, GNAQ, MAPK3, PLCB1, PLCB3, PLCB4, PP2CA, PRKCA]
KEGG-05143	African trypanosomiasis	KEGG_ 25.05.2022	6.64E-07	1.38E-03	8(0)	[APOA1, F2RL1, FAS, GNAQ, PLCB1, PLCB3, PLCB4, PRKCA]
WP-3234	AGE/RAGE pathway	WikiPathways_ 23.02.2022	8.41E-09	1.92E-05	12(0)	[CDC42, EGFR, JUN, LGALS3, MAPK3, MMP9, PKRCA, PRKCD, RAC1, RHOD, STAT1, STAT3]
KEGG-04383	AGE-RAGE signaling pathway in diabetic complications	KEGG_ 25.05.2022	1.26E-14	3.22E-11	20(0)	[BCL2, CDC42, COL1A1, COL4A1, COL4A3, FN1, HRAS, JUN, KRAS, MAPK3, NRAS, PLCB1, PLCB3, PLCB4, PRKCA, PRKCD, RAC1, STAT1, STAT3, TOFBP2]
GO-000962	aggrease assembly	GO BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_ 25.05.2022_ Ohnho	2.52E-05	5.00E-03	4(0)	[BAG3, PRKN, TRIM37, VCP]
WP-4842	Airway smooth muscle cell contraction	WikiPathways_ 23.02.2022	7.28E-07	1.51E-03	6(0)	[ADRB2, CALM1, GNAQ, ITPR3, PLCB1, RHOD]
KEGG-05034	Alcoholism	KEGG_ 25.05.2022	3.25E-07	6.88E-04	17(0)	[CALM1, GNAI1, GNAI3, GNAQ1, GNSS, GRB2, GRIN2A, H2AX, HBSC5, HBSC9, HC31, HA-16, HDAC2, HRAS, KRAS, MAPK3, NRAS]
KEGG-04925	Alidosterone synthesis and secretion	KEGG_ 25.05.2022	5.28E-06	1.02E-02	11(0)	[CALM1, CAMK2A, CAMK2B, GNAI1, GNAQ, ITPR3, PLCB1, PLCB3, PLCB4, PRKCA, SCARB1]
WP-244	Alpha 6 beta 4 signaling pathway	WikiPathways_ 23.02.2022	5.89E-06	1.13E-02	7(0)	[GRB2, HRAS, MAPK3, PKRCA, PRKCD, RAC1, RHOD]
KEGG-05010	Alzheimer disease	KEGG_ 25.05.2022	1.44E-06	2.91E-03	24(0)	[APOE, APP, ATP2A2, CALM1, DVLF3, FAS, FZD9, GNAQ, GRIN2A, GRMS, HRAS, ITPR3, KRAS, MAPK3, MAPT, NRAS, PLCB1, PLCB3, PLCB4, SDHA, SNCA, TUBA1A]
WP-5124	Alzheimer's disease	WikiPathways_ 23.02.2022	8.26E-07	1.70E-03	20(0)	[APOE, APP, ATP2A2, CALM1, DVLF3, FAS, FZD9, GNAQ, GRIN2A, HRAS, ITPR3, KRAS, MAPK3, MAPT, NRAS, PLCB1, PLCB3, PLCB4, SNCA, TUBA1A]
WP-2059	Alzheimer's disease and mRNA effects	WikiPathways_ 23.02.2022	2.62E-05	4.65E-02	20(0)	[APOE, APP, ATP2A2, CALM1, DVLF3, FAS, FZD9, GNAQ, GRIN2A, HRAS, ITPR3, KRAS, MAPK3, MAPT, NRAS, PLCB1, PLCB3, PLCB4, SNCA, TUBA1A]
GO-0001667	ameboid-type cell migration	GO BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_ 25.05.2022_ Ohnho	3.66E-06	7.15E-03	26(0)	[SPRED1, STAT1, TOFBP2]
KEGG-05146	Anemiasis	KEGG_ 25.05.2022	7.80E-06	1.47E-02	11(0)	[COL1A1, COL4A1, COL4A3, FN1, GNAI1, GNAQ, HSBB1, PLCB1, PLCB3, PLCB4, PRKCA]
R-HSA-977225	Amlyloid fibril formation	REACTOME_ Pathways_ 25.05.2022	2.94E-06	5.80E-03	12(0)	[APOA1, APOA4, APOE, APP, H2AX, HBSC5, HBSC9, HC31, HA-16, PRKN, SNAIL, SNCA]
GO-199000	amyloid fibril formation	GO BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_ 25.05.2				

GO:0010558	negative regulation of macromolecule biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022	00900	4.73E-14	1.20E-10	80.00	[APEX1, BAG3, BMI1, BPTF, CDC73, CDK2, CHD3, CHD4, CTBP2, CUL3, DHX9, EED, EIF3, EP300, ESR1, ESR2, EZH2, FLNA, FKBP, HDAC2, HGF, HNRNP, HNRNP1, HNRNP1A, HNRNP1B, HNRNP1C, HNRNP1D, HNRNP1E, HNRNP1F, HNRNP1G, HNRNP1H, HNRNP1I, HNRNP1J, HNRNP1K, HNRNP1L, HNRNP1M, HNRNP1N, HNRNP1O, HNRNP1P, HNRNP1Q, HNRNP1R, HNRNP1S, HNRNP1T, HNRNP1U, HNRNP1V, HNRNP1W, HNRNP1X, HNRNP1Y, HNRNP1Z, HNRNP2, HNRNP3, HNRNP4, HNRNP5, HNRNP6, HNRNP7, HNRNP8, HNRNP9, HNRNP10, HNRNP11, HNRNP12, HNRNP13, HNRNP14, HNRNP15, HNRNP16, HNRNP17, HNRNP18, HNRNP19, HNRNP20, HNRNP21, HNRNP22, HNRNP23, HNRNP24, HNRNP25, HNRNP26, HNRNP27, HNRNP28, HNRNP29, HNRNP30, HNRNP31, HNRNP32, HNRNP33, HNRNP34, HNRNP35, HNRNP36, HNRNP37, HNRNP38, HNRNP39, HNRNP40, HNRNP41, HNRNP42, HNRNP43, HNRNP44, HNRNP45, HNRNP46, HNRNP47, HNRNP48, HNRNP49, HNRNP50, HNRNP51, HNRNP52, HNRNP53, HNRNP54, HNRNP55, HNRNP56, HNRNP57, HNRNP58, HNRNP59, HNRNP60, HNRNP61, HNRNP62, HNRNP63, HNRNP64, HNRNP65, HNRNP66, HNRNP67, HNRNP68, HNRNP69, HNRNP70, HNRNP71, HNRNP72, HNRNP73, HNRNP74, HNRNP75, HNRNP76, HNRNP77, HNRNP78, HNRNP79, HNRNP80, HNRNP81, HNRNP82, HNRNP83, HNRNP84, HNRNP85, HNRNP86, HNRNP87, HNRNP88, HNRNP89, HNRNP90, HNRNP91, HNRNP92, HNRNP93, HNRNP94, HNRNP95, HNRNP96, HNRNP97, HNRNP98, HNRNP99, HNRNP100]
GO:0010605	negative regulation of macromolecular metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022	00900	1.35E-17	3.53E-14	127.00	[APEX1, APOA1, APOA2, APOE, APP, ADP1, BAG3, BAG6, BIRC3, BMI1, BPTF, CALM1, CDC73, CDK2, CHD3, CHD4, CLU, COL4A3, CORO1C, CTBP2, CUL3, DORGG1, DHX9, EED, EGFR, ERF, ELAV1, EP300, ESR1, ESR2, EZH2, FBLN1, FLNA, FXR2, GNAQ, GRIN2A, HDAC2, HGF, HFN, HNRNP, HNRNP1, HNRNP1A, HNRNP1B, HNRNP1C, HNRNP1D, HNRNP1E, HNRNP1F, HNRNP1G, HNRNP1H, HNRNP1I, HNRNP1J, HNRNP1K, HNRNP1L, HNRNP1M, HNRNP1N, HNRNP1O, HNRNP1P, HNRNP1Q, HNRNP1R, HNRNP1S, HNRNP1T, HNRNP1U, HNRNP1V, HNRNP1W, HNRNP1X, HNRNP1Y, HNRNP1Z, HNRNP2, HNRNP3, HNRNP4, HNRNP5, HNRNP6, HNRNP7, HNRNP8, HNRNP9, HNRNP10, HNRNP11, HNRNP12, HNRNP13, HNRNP14, HNRNP15, HNRNP16, HNRNP17, HNRNP18, HNRNP19, HNRNP20, HNRNP21, HNRNP22, HNRNP23, HNRNP24, HNRNP25, HNRNP26, HNRNP27, HNRNP28, HNRNP29, HNRNP30, HNRNP31, HNRNP32, HNRNP33, HNRNP34, HNRNP35, HNRNP36, HNRNP37, HNRNP38, HNRNP39, HNRNP40, HNRNP41, HNRNP42, HNRNP43, HNRNP44, HNRNP45, HNRNP46, HNRNP47, HNRNP48, HNRNP49, HNRNP50, HNRNP51, HNRNP52, HNRNP53, HNRNP54, HNRNP55, HNRNP56, HNRNP57, HNRNP58, HNRNP59, HNRNP60, HNRNP61, HNRNP62, HNRNP63, HNRNP64, HNRNP65, HNRNP66, HNRNP67, HNRNP68, HNRNP69, HNRNP70, HNRNP71, HNRNP72, HNRNP73, HNRNP74, HNRNP75, HNRNP76, HNRNP77, HNRNP78, HNRNP79, HNRNP80, HNRNP81, HNRNP82, HNRNP83, HNRNP84, HNRNP85, HNRNP86, HNRNP87, HNRNP88, HNRNP89, HNRNP90, HNRNP91, HNRNP92, HNRNP93, HNRNP94, HNRNP95, HNRNP96, HNRNP97, HNRNP98, HNRNP99, HNRNP100]
GO:0008992	negative regulation of metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022	00900	3.11E-17	8.12E-14	133.00	[APEX1, APOA1, APOA2, APOE, APP, ADP1, BAG3, BAG6, BIRC3, BMI1, BPTF, CALM1, CDC73, CDK2, CHD3, CHD4, CLU, COL4A3, CORO1C, CTBP2, CUL3, DORGG1, DHX9, EED, EGFR, ERF, ELAV1, EP300, ESR1, ESR2, EZH2, FBLN1, FLNA, FXR2, GNAQ, GRIN2A, HDAC2, HGF, HFN, HNRNP, HNRNP1, HNRNP1A, HNRNP1B, HNRNP1C, HNRNP1D, HNRNP1E, HNRNP1F, HNRNP1G, HNRNP1H, HNRNP1I, HNRNP1J, HNRNP1K, HNRNP1L, HNRNP1M, HNRNP1N, HNRNP1O, HNRNP1P, HNRNP1Q, HNRNP1R, HNRNP1S, HNRNP1T, HNRNP1U, HNRNP1V, HNRNP1W, HNRNP1X, HNRNP1Y, HNRNP1Z, HNRNP2, HNRNP3, HNRNP4, HNRNP5, HNRNP6, HNRNP7, HNRNP8, HNRNP9, HNRNP10, HNRNP11, HNRNP12, HNRNP13, HNRNP14, HNRNP15, HNRNP16, HNRNP17, HNRNP18, HNRNP19, HNRNP20, HNRNP21, HNRNP22, HNRNP23, HNRNP24, HNRNP25, HNRNP26, HNRNP27, HNRNP28, HNRNP29, HNRNP30, HNRNP31, HNRNP32, HNRNP33, HNRNP34, HNRNP35, HNRNP36, HNRNP37, HNRNP38, HNRNP39, HNRNP40, HNRNP41, HNRNP42, HNRNP43, HNRNP44, HNRNP45, HNRNP46, HNRNP47, HNRNP48, HNRNP49, HNRNP50, HNRNP51, HNRNP52, HNRNP53, HNRNP54, HNRNP55, HNRNP56, HNRNP57, HNRNP58, HNRNP59, HNRNP60, HNRNP61, HNRNP62, HNRNP63, HNRNP64, HNRNP65, HNRNP66, HNRNP67, HNRNP68, HNRNP69, HNRNP70, HNRNP71, HNRNP72, HNRNP73, HNRNP74, HNRNP75, HNRNP76, HNRNP77, HNRNP78, HNRNP79, HNRNP80, HNRNP81, HNRNP82, HNRNP83, HNRNP84, HNRNP85, HNRNP86, HNRNP87, HNRNP88, HNRNP89, HNRNP90, HNRNP91, HNRNP92, HNRNP93, HNRNP94, HNRNP95, HNRNP96, HNRNP97, HNRNP98, HNRNP99, HNRNP100]
GO:0044092	negative regulation of molecular function	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022	00900	4.05E-11	9.76E-08	62.00	[ADRB2, APOA1, APOA2, APOE, APP, ADP1, ATP2A2, AURKAIP1, BIRC3, CALM1, CAMK2A, CT, COL4A3, CORO1C, DISC1, ESR1, ESR2, EZH2, FBXW7, FLNA, FOXA2, GNAI3, GNAQ, HDAC2, HECH2, HGF, HNRNP, HNRNP1, HNRNP1A, HNRNP1B, HNRNP1C, HNRNP1D, HNRNP1E, HNRNP1F, HNRNP1G, HNRNP1H, HNRNP1I, HNRNP1J, HNRNP1K, HNRNP1L, HNRNP1M, HNRNP1N, HNRNP1O, HNRNP1P, HNRNP1Q, HNRNP1R, HNRNP1S, HNRNP1T, HNRNP1U, HNRNP1V, HNRNP1W, HNRNP1X, HNRNP1Y, HNRNP1Z, HNRNP2, HNRNP3, HNRNP4, HNRNP5, HNRNP6, HNRNP7, HNRNP8, HNRNP9, HNRNP10, HNRNP11, HNRNP12, HNRNP13, HNRNP14, HNRNP15, HNRNP16, HNRNP17, HNRNP18, HNRNP19, HNRNP20, HNRNP21, HNRNP22, HNRNP23, HNRNP24, HNRNP25, HNRNP26, HNRNP27, HNRNP28, HNRNP29, HNRNP30, HNRNP31, HNRNP32, HNRNP33, HNRNP34, HNRNP35, HNRNP36, HNRNP37, HNRNP38, HNRNP39, HNRNP40, HNRNP41, HNRNP42, HNRNP43, HNRNP44, HNRNP45, HNRNP46, HNRNP47, HNRNP48, HNRNP49, HNRNP50, HNRNP51, HNRNP52, HNRNP53, HNRNP54, HNRNP55, HNRNP56, HNRNP57, HNRNP58, HNRNP59, HNRNP60, HNRNP61, HNRNP62, HNRNP63, HNRNP64, HNRNP65, HNRNP66, HNRNP67, HNRNP68, HNRNP69, HNRNP70, HNRNP71, HNRNP72, HNRNP73, HNRNP74, HNRNP75, HNRNP76, HNRNP77, HNRNP78, HNRNP79, HNRNP80, HNRNP81, HNRNP82, HNRNP83, HNRNP84, HNRNP85, HNRNP86, HNRNP87, HNRNP88, HNRNP89, HNRNP90, HNRNP91, HNRNP92, HNRNP93, HNRNP94, HNRNP95, HNRNP96, HNRNP97, HNRNP98, HNRNP99, HNRNP100]
GO:0051241	negative regulation of multicellular organismal process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022	00900	2.23E-05	4.01E-02	44.00	[ADRB2, APOA1, APOA2, APOA4, APOE, ATP2A2, BCL2,

GO:001348	protein destabilization	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022_00h00	4.69E-08	1.04E-04	10.00	[CDCT3, CUL3, EP300, FBXW7, MDMP, PRKN, PRNP, SIRT1, SNCA, SUMO1]
GO:000606	protein import into nucleus	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022_00h00	2.15E-05	3.87E-02	14.00	[BAG3, ECT2, ELAVL1, FLNA, FZL1, HSP90AA1, KPN1, LRRK2, NOTCH1, PRKCD, SOSTM1, STAT3, SUMO1, TP53]
GO:0008104	protein localization	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022_00h00	7.03E-14	1.78E-10	109.00	[ABCA1, ADR2, ALG9, APEX1, APOE, AURKAIP1, BAG3, BAG6, BCAP31, BCL2, BCR, BET1, CANX, CDC42, CDK9, CENPA, CFTR, CHAF1B, CHMP4C, CUL1, COL1A1, CORG1C, DOROK1, DHX9, DISC1, DNL3, ECT2, EGFR, ELAVL1, ELP2, ERF, ESR1, ESR2, ESR3, ESR4, ESR5, ESR6, ESR7, ESR8, ESR9, ESR10, ESR11, ESR12, ESR13, ESR14, ESR15, ESR16, ESR17, ESR18, ESR19, ESR20, ESR21, ESR22, ESR23, ESR24, ESR25, ESR26, ESR27, ESR28, ESR29, ESR30, ESR31, ESR32, ESR33, ESR34, ESR35, ESR36, ESR37, ESR38, ESR39, ESR40, ESR41, ESR42, ESR43, ESR44, ESR45, ESR46, ESR47, ESR48, ESR49, ESR50, ESR51, ESR52, ESR53, ESR54, ESR55, ESR56, ESR57, ESR58, ESR59, ESR60, ESR61, ESR62, ESR63, ESR64, ESR65, ESR66, ESR67, ESR68, ESR69, ESR70, ESR71, ESR72, ESR73, ESR74, ESR75, ESR76, ESR77, ESR78, ESR79, ESR80, ESR81, ESR82, ESR83, ESR84, ESR85, ESR86, ESR87, ESR88, ESR89, ESR90, ESR91, ESR92, ESR93, ESR94, ESR95, ESR96, ESR97, ESR98, ESR99, ESR100, ESR101, ESR102, ESR103, ESR104, ESR105, ESR106, ESR107, ESR108, ESR109, ESR110, ESR111, ESR112, ESR113, ESR114, ESR115, ESR116, ESR117, ESR118, ESR119, ESR120, ESR121, ESR122, ESR123, ESR124, ESR125, ESR126, ESR127, ESR128, ESR129, ESR130, ESR131, ESR132, ESR133, ESR134, ESR135, ESR136, ESR137, ESR138, ESR139, ESR140, ESR141, ESR142, ESR143, ESR144, ESR145, ESR146, ESR147, ESR148, ESR149, ESR150, ESR151, ESR152, ESR153, ESR154, ESR155, ESR156, ESR157, ESR158, ESR159, ESR160, ESR161, ESR162, ESR163, ESR164, ESR165, ESR166, ESR167, ESR168, ESR169, ESR170, ESR171, ESR172, ESR173, ESR174, ESR175, ESR176, ESR177, ESR178, ESR179, ESR180, ESR181, ESR182, ESR183, ESR184, ESR185, ESR186, ESR187, ESR188, ESR189, ESR190, ESR191, ESR192, ESR193, ESR194, ESR195, ESR196, ESR197, ESR198, ESR199, ESR200, ESR201, ESR202, ESR203, ESR204, ESR205, ESR206, ESR207, ESR208, ESR209, ESR210, ESR211, ESR212, ESR213, ESR214, ESR215, ESR216, ESR217, ESR218, ESR219, ESR220, ESR221, ESR222, ESR223, ESR224, ESR225, ESR226, ESR227, ESR228, ESR229, ESR230, ESR231, ESR232, ESR233, ESR234, ESR235, ESR236, ESR237, ESR238, ESR239, ESR240, ESR241, ESR242, ESR243, ESR244, ESR245, ESR246, ESR247, ESR248, ESR249, ESR250, ESR251, ESR252, ESR253, ESR254, ESR255, ESR256, ESR257, ESR258, ESR259, ESR260, ESR261, ESR262, ESR263, ESR264, ESR265, ESR266, ESR267, ESR268, ESR269, ESR270, ESR271, ESR272, ESR273, ESR274, ESR275, ESR276, ESR277, ESR278, ESR279, ESR280, ESR281, ESR282, ESR283, ESR284, ESR285, ESR286, ESR287, ESR288, ESR289, ESR290, ESR291, ESR292, ESR293, ESR294, ESR295, ESR296, ESR297, ESR298, ESR299, ESR300, ESR301, ESR302, ESR303, ESR304, ESR305, ESR306, ESR307, ESR308, ESR309, ESR310, ESR311, ESR312, ESR313, ESR314, ESR315, ESR316, ESR317, ESR318, ESR319, ESR320, ESR321, ESR322, ESR323, ESR324, ESR325, ESR326, ESR327, ESR328, ESR329, ESR330, ESR331, ESR332, ESR333, ESR334, ESR335, ESR336, ESR337, ESR338, ESR339, ESR340, ESR341, ESR342, ESR343, ESR344, ESR345, ESR346, ESR347, 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ESR473, ESR474, ESR475, ESR476, ESR477, ESR478, ESR479, ESR480, ESR481, ESR482, ESR483, ESR484, ESR485, ESR486, ESR487, ESR488, ESR489, ESR490, ESR491, ESR492, ESR493, ESR494, ESR495, ESR496, ESR497, ESR498, ESR499, ESR500, ESR501, ESR502, ESR503, ESR504, ESR505, ESR506, ESR507, ESR508, ESR509, ESR510, ESR511, ESR512, ESR513, ESR514, ESR515, ESR516, ESR517, ESR518, ESR519, ESR520, ESR521, ESR522, ESR523, ESR524, ESR525, ESR526, ESR527, ESR528, ESR529, ESR530, ESR531, ESR532, ESR533, ESR534, ESR535, ESR536, ESR537, ESR538, ESR539, ESR540, ESR541, ESR542, ESR543, ESR544, ESR545, ESR546, ESR547, ESR548, ESR549, ESR550, ESR551, ESR552, ESR553, ESR554, ESR555, ESR556, ESR557, ESR558, ESR559, ESR560, ESR561, ESR562, ESR563, ESR564, ESR565, ESR566, ESR567, ESR568, ESR569, ESR570, ESR571, ESR572, ESR573, ESR574, ESR575, ESR576, ESR577, ESR578, ESR579, ESR580, ESR581, ESR582, ESR583, ESR584, ESR585, ESR586, ESR587, ESR588, ESR589, ESR590, ESR591, ESR592, ESR593, ESR594, ESR595, ESR596, ESR597, ESR598, ESR599, ESR600, ESR601, ESR602, ESR603, ESR604, ESR605, ESR606, ESR607, ESR608, ESR609, ESR610, ESR611, ESR61

GO:0050794	regulation of cellular process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP	25.05.2022	00h00	1.21E-12	3.00E-09	302.00	[ABCA1, ADRB2, AGR2, AGRN, ALB, APEX1, APOA1, APOA2, APOA4, APOA5, APOE, APP, AQP1, ATP2A2, AURKAIP1, BAG3, BAG6, BAZ1B, BCAP31, BCL2, BCR, BIRC3, BMI1, BPTF, BRD2, BRD3, BRD4, CALM1, CAMK2A, CAMK2B, CASP8, CDC28, CCND1, CDCA2, CDCA4, CDCA7, CDK2, CDK9, CTRF, CHAF1B, CHD3, CHD4, CHMPV, CTD, CUL1, CMTM5, COL1A1, COL4A1, COL4A3, CPBPS, CTRP2, CTSL, CUL4B, CUL4C, DDX58, DDX59, DDX6, DDX61, DDX62, DDX63, DDX64, DDX65, DDX66, DDX67, DDX68, DDX69, DDX70, DDX71, DDX72, DDX73, DDX74, DDX75, DDX76, DDX77, DDX78, DDX79, DDX80, DDX81, DDX82, DDX83, DDX84, DDX85, DDX86, DDX87, DDX88, DDX89, DDX90, DDX91, DDX92, DDX93, DDX94, DDX95, DDX96, DDX97, DDX98, DDX99, DDX100, DDX101, DDX102, DDX103, DDX104, DDX105, DDX106, DDX107, DDX108, DDX109, DDX110, DDX111, DDX112, DDX113, DDX114, DDX115, DDX116, DDX117, DDX118, DDX119, DDX120, DDX121, DDX122, DDX123, DDX124, DDX125, DDX126, DDX127, DDX128, DDX129, DDX130, DDX131, DDX132, DDX133, DDX134, DDX135, DDX136, DDX137, DDX138, DDX139, DDX140, DDX141, DDX142, DDX143, DDX144, DDX145, DDX146, DDX147, DDX148, DDX149, DDX150, DDX151, DDX152, DDX153, DDX154, DDX155, DDX156, DDX157, DDX158, DDX159, DDX160, DDX161, DDX162, DDX163, DDX164, DDX165, DDX166, DDX167, DDX168, DDX169, DDX170, DDX171, DDX172, DDX173, DDX174, DDX175, DDX176, DDX177, DDX178, DDX179, DDX180, DDX181, DDX182, DDX183, DDX184, DDX185, DDX186, DDX187, DDX188, DDX189, DDX190, DDX191, DDX192, DDX193, DDX194, DDX195, DDX196, DDX197, DDX198, DDX199, DDX200, DDX201, DDX202, DDX203, DDX204, DDX205, DDX206, DDX207, DDX208, DDX209, DDX210, DDX211, DDX212, DDX213, DDX214, DDX215, DDX216, DDX217, DDX218, DDX219, DDX220, DDX221, DDX222, DDX223, DDX224, DDX225, DDX226, DDX227, DDX228, DDX229, DDX230, DDX231, DDX232, DDX233, DDX234, DDX235, DDX236, DDX237, DDX238, DDX239, DDX240, DDX241, DDX242, DDX243, DDX244, DDX245, DDX246, DDX247, DDX248, DDX249, DDX250, 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GO:0032774	RNA biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP 25.05.2022 00h00	2.78E-11	6.73E-08	132.00	[ADRB2, AGRN, APEX1, APOE, APP, AURKA1P, BAG3, BAZ1B, BMI1, BPTF, BRD2, BRD3, BRD4, CAMK2A, CDC73, CDK2, CDK9, CHD3, CHD4, CUL1, COL1A1, COPPS2, CTBP2, CUL3, DORGG1, DDX38, DEK, DDX3, DVL3, EED, EGFR, EP300, ESR1, ESR2, ETS1, EZH2, FZL1, FANCD2, FLNA, FOXA2, FZL1, GRM5, H4-16, HDAC2, HDGF, HGF, HNRNP10, HNRNP11, HNRNP14, HNRNP15, HNRNP16, HNRNP17, HNRNP18, HNRNP19, HNRNP20, HNRNP21, HNRNP22, HNRNP23, HNRNP24, HNRNP25, HNRNP26, HNRNP27, HNRNP28, HNRNP29, HNRNP30, HNRNP31, HNRNP32, HNRNP33, HNRNP34, HNRNP35, HNRNP36, HNRNP37, HNRNP38, HNRNP39, HNRNP40, HNRNP41, HNRNP42, HNRNP43, HNRNP44, HNRNP45, HNRNP46, HNRNP47, HNRNP48, HNRNP49, HNRNP50, HNRNP51, HNRNP52, HNRNP53, HNRNP54, HNRNP55, HNRNP56, HNRNP57, HNRNP58, HNRNP59, HNRNP60, HNRNP61, HNRNP62, HNRNP63, HNRNP64, HNRNP65, HNRNP66, HNRNP67, HNRNP68, HNRNP69, HNRNP70, HNRNP71, HNRNP72, HNRNP73, HNRNP74, HNRNP75, 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Supplementary Table 38. Summary of pathway analysis using meta-specific genes for the TyG index, a marker of insulin resistance, identified within the Taiwan Biobank cohort.

ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni	steo down	Nr. Genes	Associated Genes Found
GO:003036	actin cytoskeleton organization	GO BiologicalProcess-EBI-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.75E-09	3.60E-06	33.00	13	[ACT1, ANLN, ARPC3, CALD1, CALR, CAPZA2, CDC42, CIT, ECT2, EZR, FLNA, GAS2L1, HAX1, KRAS, MYH7, MYH9, MYO19, MYO1C, MYO6, NCCK, NRG1, OBSL1, PALLO, PFN1, PPM1F, RAC1, RAC2, RHOA, RHOB, RHOC, RHOF, TJP1, TMOD3]
GO:005107	actin filament bundle assembly	GO BiologicalProcess-EBI-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.65E-05	2.85E-02	11.00	11	[ICAD1, CDC42, EZR, FLNA, NCCK, PFN1, PPM1F, RAC1, RHOA, RHOD, TJP1]
GO:0081572	actin filament bundle organization	GO BiologicalProcess-EBI-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.93E-05	3.33E-02	11.00	11	[ICAD1, CDC42, EZR, FLNA, NCCK, PFN1, PPM1F, RAC1, RHOA, RHOD, TJP1]
GO:007015	actin filament	GO BiologicalProcess-EBI-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.87E-09	3.75E-05	24.00	24	[ACT1, ARPC3, CALD1, CAPZA2, CDC42, CIT, EZR, FLNA, GAS2L1, HAX1, KRAS, MYH7, MYH9, MYO19, MYO1C, MYO6, NCCK, NRG1, OBSL1, PALLO, PFN1, PPM1F, RAC1, RAC2, RHOA, RHOB, RHOC, RHOF, TJP1, TMOD3]
GO:003029	actin filament-based process	GO BiologicalProcess-EBI-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.30E-09	4.73E-06	35.00	35	[ACT1, ANLN, ARPC3, ARPC2, ARPC1, RAC1, TUBA1A, TUBA1B]
R-HSA-442755	Activation of NMDA receptors and postsynaptic events	REACTOME_Pathways_25.05.2022	2.80E-02	4.75E-02	7.00	7	[ACT1, ANLN, ARPC3, ARPC2, ARPC1, RAC1, TUBA1A, TUBA1B]
GO:001032	actomyosin system organization	GO BiologicalProcess-EBI-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	7.77E-07	1.48E-03	14.00	14	[ACT1, ANLN, CDC42, CIT, ECT2, MYH7, MYH9, OBSL1, PFN1, PPM1F, RAC1, RHOA, TJP1, TMOD3]
R-HSA-126018	Adaptive Immune System	REACTOME_Pathways_25.05.2022	3.89E-10	8.18E-07	34.00	34	[BCAP31, BTNL2, CALM1, CALR, CAPZA2, CDC42, CDH1, CLTC, CTBS, DCTN1, DISC1, DOCK7, FBXO6, FBXW11, FBXW7, FYN, HLA-C, HLA-DQA1, HSPA5, KIF23, KRAS, LYN, NCCK, PKR3, PSM3, PVR, RAC1, RBX1, RNF123, RNF4, TRAF7, TUBA1A, TUBA1B, TUBB1, TUBG1, TUBG2, TUBG3, TUBG4, TUBG5, TUBG6, TUBG7, TUBG8, TUBG9, TUBG10, TUBG11, TUBG12, TUBG13, TUBG14, TUBG15, TUBG16, TUBG17, TUBG18, TUBG19, TUBG20, TUBG21, TUBG22, TUBG23, TUBG24, TUBG25, TUBG26, TUBG27, TUBG28, TUBG29, TUBG30, TUBG31, TUBG32, TUBG33, TUBG34, TUBG35, TUBG36, TUBG37, TUBG38, TUBG39, TUBG40, TUBG41, TUBG42, TUBG43, TUBG44, TUBG45, TUBG46, TUBG47, TUBG48, TUBG49, TUBG50, TUBG51, TUBG52, TUBG53, TUBG54, TUBG55, TUBG56, TUBG57, TUBG58, TUBG59, TUBG60, TUBG61, TUBG62, TUBG63, TUBG64, TUBG65, TUBG66, TUBG67, TUBG68, TUBG69, TUBG70, TUBG71, TUBG72, TUBG73, TUBG74, TUBG75, TUBG76, TUBG77, TUBG78, TUBG79, TUBG80, TUBG81, TUBG82, TUBG83, TUBG84, TUBG85, 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ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni step down	Nr. Genes	Associated Genes Found
R-HSA-264465	FBXW7 Mutants and NOTCH1 in Cancer	REACTOME, Pathways, 25.05.2022	2.11E-09	3.61E-02	3.00	[FBXW7, NOTCH1, RBX1]
KEGG-04964	Tc epsilon RI signaling pathway	KEGG, 25.05.2022	2.86E-06	4.96E-03	8.00	[LYN, KRAS, LYN, MAPK14, MAPK9, PKB3, RAC1, RAC2]
R-HSA-202940	Fcgamma receptor (FCGR) dependent phagocytosis	REACTOME, Pathways, 25.05.2022	1.58E-05	2.74E-02	8.00	[ARPC3, CDCA2, FYN, HSP90AB1, LYN, MYH9, MYO1C, RAC1]
R-HSA-964442	FCGR3A-mediated phagocytosis	REACTOME, Pathways, 25.05.2022	1.08E-05	1.91E-02	7.00	[CREBBP, CDCA2, FYN, LYN, MYH9, MYO1C, RAC1]
R-HSA-201722	Formation of the beta-catenin/TCF transactivating complex	REACTOME, Pathways, 25.05.2022	2.39E-06	4.08E-02	6.00	[CREBBP, H2BC5, H3C1, H4-16, HDAC1, MYC, RUVBL1, TLE3]
R-HSA-981406	FOXO-mediated transcription	REACTOME, Pathways, 25.05.2022	2.07E-05	3.55E-02	7.00	[CREBBP, HDAC1, HDAC2, H3, NR3C1, PINK1, YWHAZ]
WP-524	G1S signaling pathway	WikiPathways, 23.02.2022	1.37E-05	2.40E-02	6.00	[CALM1, CDCA2, CT, PFN1, RAC1, RHOA]
WP-469	Gastrin signaling pathway	WikiPathways, 23.02.2022	2.12E-11	4.53E-08	15.00	[ANXA2, CDCA2, CDH1, ELAVL1, FYN, KRAS, MAPK14, MAPK9, MYC, PKB3, RAC1, RHOA, RHOB, RHOD, TJP1, [ACT1], ADRB2, AFF1, ANXA2, APEX1, APP, AR, ATP1B1, AURKB, BACE1, BASP1, BCAP31, BCOR, BMI1, BRD2, BRD3, BRD4, CALM1, CALR, CBX1, CBX3, CDH1, COPPS, CREBBP, CTBP1, CYCS, DDX20, DDX58, DYRK1A, EBNAP2, EF3F, ELAV1, ERBB2, ESR1, ESR2, EZR, FBXW11, FBXW7, FURIN, FYN, GAD65GPI, GATA2A, GGNBP2, GOLGA2, H3C1, H4-16, HDAC1, HDAC2, HEMX1, HNRNP91, HNRNP1, HSP90AB1, HSPA5, HTRA2, HIF1, H3, KHSRP, KLF3, KRAS, LARP7, LGAL3, LGRA, LINA, LYN, MAPK14, MAPK9, MBD3, MEIS2, MLT1, MOV10, MYH9, MYO1C, MYO6, NABP2, NCX2, NOTCH1, NR3C1, NR61, NTRK1, NTRK2, NRK1, NTRK3, NTRK4, NTRK5, NTRK6, NTRK7, NTRK8, NTRK9, NTRK10, NTRK11, NTRK12, NTRK13, NTRK14, NTRK15, NTRK16, NTRK17, NTRK18, NTRK19, NTRK20, NTRK21, NTRK22, NTRK23, NTRK24, NTRK25, NTRK26, NTRK27, NTRK28, NTRK29, NTRK30, NTRK31, NTRK32, NTRK33, NTRK34, NTRK35, NTRK36, NTRK37, 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ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni step down	Nr. Genes
GO:0006966	organelle organization	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	7.88E-22	1.73E-18	122.00
GO:1901362	organic cyclic compound biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	5.57E-09	1.14E-05	99.00
GO:1901360	organic cyclic compound metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.29E-10	1.72E-06	129.00
GO:1901676	organic substance biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.33E-07	2.60E-04	119.00
GO:1901575	organic substance catabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	5.38E-06	9.73E-03	54.00
GO:0071704	organic substance metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.44E-10	3.13E-07	192.00
GO:1901565	organonitrogen compound catabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	3.09E-07	6.00E-04	43.00
R-HSA689896	Ovarian tumor domain proteases	REACTOME_Pathways_25.05.2022	6.09E-07	1.16E-03	131.00
KEGG:05112	Pancreatic cancer	KEGG_Pathways_23.02.2022	6.24E-09	1.33E-02	11.00
R-HSA6964407	Parasite infection	REACTOME_Pathways_25.05.2022	1.06E-05	1.95E-02	7.00
KEGG:05130	Pathogenic Escherichia coli infection	KEGG_Pathways_25.05.2022	6.36E-09	1.30E-05	16.00
WP:2272	Pathogenic Escherichia coli infection	WinPathways_23.02.2022	2.13E-07	4.49E-04	10.00
WP:3651	Pathways affected in adenoid cystic carcinoma	WinPathways_23.02.2022	2.13E-09	4.49E-04	10.00
KEGG:05200	Pathways in cancer	KEGG_Pathways_25.05.2022	2.91E-08	5.83E-05	25.00
KEGG:05022	Pathways of neurodegeneration	KEGG_Pathways_25.05.2022	4.27E-06	7.79E-03	20.00
GO:0018193	peptidyl-amino acid modification	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	7.72E-07	1.47E-03	41.00
GO:0016310	phosphorylation	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.57E-08	8.31E-05	50.00
R-HSA6811558	PI3P, PIP2A and IER3 Regulate PI3K(AKT) Signaling	REACTOME_Pathways_25.05.2022	9.81E-06	1.95E-02	7.00
R-HSA1126704	PIP3 activates AKT signaling	REACTOME_Pathways_25.05.2022	1.24E-06	2.44E-03	10.00
GO:1903036	platelet membrane bound cell protection organization	REACTOME_Pathways_25.05.2022	1.67E-05	2.90E-02	42.00
R-HSA76002	Pleatema activation, signaling and aggregation	REACTOME_Pathways_25.05.2022	3.56E-07	6.90E-04	16.00
GO:1905209.13	Positive epigenetic regulation of rRNA expression	REACTOME_Pathways_25.05.2022	1.19E-06	2.24E-03	10.00
GO:0043065	positive regulation of apoptotic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.94E-08	8.97E-03	21.00
GO:0048518	positive regulation of biological process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.90E-18	1.95E-14	151.00
GO:0008991	positive regulation of biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.01E-09	1.63E-05	61.00
GO:0008986	positive regulation of catalytic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.52E-06	1.51E-02	21.00
GO:0043986	positive regulation of catalytic activity	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	2.19E-06	4.05E-03	38.00
GO:0045785	positive regulation of cell adhesion	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.72E-07	1.65E-03	22.00
GO:0016047	positive regulation of cell communication	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.21E-08	8.89E-05	52.00
GO:0010942	positive regulation of cell death	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.86E-08	8.96E-05	23.00
GO:0010720	positive regulation of cell development	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.06E-06	2.01E-03	17.00
GO:0045697	positive regulation of cell differentiation	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.11E-07	7.85E-04	32.00
GO:0031328	positive regulation of cellular biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	3.11E-09	6.36E-06	61.00
GO:0031331	positive regulation of cellular catabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.02E-08	7.34E-03	19.00
GO:0040498	positive regulation of cellular component biogenesis	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	5.00E-07	9.62E-04	23.00
GO:0051130	positive regulation of cellular component organization	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	2.99E-10	6.28E-07	42.00
GO:0031325	positive regulation of cellular metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.12E-15	2.45E-12	95.00
GO:0048522	positive regulation of cellular process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	6.39E-15	1.38E-11	135.00
GO:0032467	positive regulation of cytokinesis	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	3.04E-06	5.60E-03	7.00
GO:0051094	positive regulation of developmental process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.97E-09	1.01E-05	14.00
GO:0051091	positive regulation of DNA-binding transcription factor	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.93E-05	3.30E-02	14.00
GO:0010950	positive regulation of endopeptidase activity	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.95E-08	8.89E-03	12.00
GO:1904951	positive regulation of establishment of protein localization	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	4.31E-07	8.31E-04	18.00
GO:0010628	positive regulation of gene expression	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.98E-08	3.98E-05	24.00
GO:0051345	positive regulation of hydrolyase activity	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	2.44E-06	4.55E-03	32.00
GO:0002884	positive regulation of immune system process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	6.64E-06	1.19E-02	36.00
GO:0090316	positive regulation of intracellular protein transport	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.09E-10	1.68E-06	12.00
GO:1901253	positive regulation of intracellular signal transduction	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.69E-06	3.15E-03	34.00
GO:0032388	positive regulation of intracellular transport	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	8.32E-12	1.78E-08	34.00
GO:0010657	positive regulation of macromolecule biosynthetic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	2.22E-09	4.55E-06	59.00
GO:0010604	positive regulation of macromolecule metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	2.77E-16	6.07E-13	104.00
GO:0009893	positive regulation of metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	6.42E-17	1.40E-13	111.00
GO:094093	positive regulation of molecular function	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	5.65E-11	1.20E-07	56.00
GO:0051240	positive regulation of multicellular organismal process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	5.09E-08	9.24E-03	43.00
GO:0051173	positive regulation of nitrogen compound metabolic process	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	3.39E-17	7.36E-14	50.00
GO:1903508	positive regulation of nucleic acid-templated transcript	GO BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	2.37E-07	4.61E-04	50.00

ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni step down	Nr. Genes
GO:000889	regulation of biosynthetic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.54E-11	5.42E-08	104.00
GO:000894	regulation of catabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	4.45E-11	9.48E-08	42.00
GO:005070	regulation of catalytic activity	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.08E-08	2.03E-03	61.00
GO:0030156	regulation of cell adhesion	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	9.85E-08	1.91E-04	31.00
GO:0010646	regulation of cell communication	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	5.11E-10	1.07E-06	87.00
GO:0051726	regulation of cell cycle	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.68E-10	3.55E-07	44.00
GO:0010664	regulation of cell cycle process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.15E-11	2.46E-08	36.00
GO:0010941	regulation of cell death	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	5.02E-10	1.05E-06	55.00
GO:0060284	regulation of cell development	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.57E-07	3.07E-04	24.00
GO:0045596	regulation of cell differentiation	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.82E-08	3.67E-05	50.00
GO:0051302	regulation of cell division	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.42E-05	2.49E-02	12.00
GO:0010450	regulation of cell fate commitment	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.35E-08	4.05E-03	6.00
GO:0042659	regulation of cell fate specification	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.04E-09	3.80E-03	6.00
GO:0030334	regulation of cell migration	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	9.83E-04	1.51E-07	33.00
GO:0032604	regulation of cell morphogenesis	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	7.68E-06	1.37E-02	19.00
GO:2000145	regulation of cell motility	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	6.78E-07	1.29E-03	34.00
GO:0042127	regulation of cell population proliferation	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	7.29E-06	1.31E-02	46.00
GO:0003630	regulation of cell shape	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.12E-05	1.97E-02	11.00
GO:0022407	regulation of cell-cell adhesion	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.53E-08	4.68E-03	21.00
GO:0022407	regulation of cell-cell adhesion	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.53E-08	4.68E-03	21.00
GO:0010810	regulation of cell-substrate adhesion	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.11E-05	1.96E-02	13.00
GO:0031326	regulation of cellular biosynthetic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.21E-11	4.71E-08	103.00
GO:0031328	regulation of cellular catabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.10E-08	2.23E-05	43.00
GO:0044087	regulation of cellular component biogenesis	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.46E-11	5.24E-08	33.00
GO:0051128	regulation of cellular component organization	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	8.85E-19	1.94E-15	35.00
GO:0060341	regulation of cellular localization	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.44E-07	2.83E-04	35.00
GO:0031323	regulation of cellular metabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.09E-13	2.36E-10	133.00
GO:0050574	regulation of cellular process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	3.79E-08	7.95E-05	190.00
GO:0032465	regulation of cytokinesis	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	6.31E-07	1.20E-03	10.00
GO:0051493	regulation of cytoskeleton organization	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.78E-09	3.67E-06	28.00
GO:0050793	regulation of developmental process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	4.53E-13	9.80E-10	78.00
GO:0051096	regulation of DNA-binding transcription factor activity	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.17E-09	4.39E-06	25.00
GO:0052548	regulation of endoplasmic activity	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.00E-08	3.77E-03	20.00
GO:0070201	regulation of establishment of protein localization	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.13E-05	2.09E-02	21.00
GO:0010468	regulation of gene expression	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	7.45E-12	1.60E-08	116.00
GO:0051336	regulation of hydrolase activity	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	6.19E-07	1.19E-03	35.00
GO:0050776	regulation of immune response	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.91E-05	4.93E-02	29.00
GO:0022882	regulation of immune system process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	4.65E-08	9.25E-05	40.00
GO:0033157	regulation of intracellular protein transport	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	3.45E-09	7.12E-06	18.00
GO:1902331	regulation of intracellular signal transduction	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.12E-09	2.32E-06	56.00
GO:0032386	regulation of intracellular transport	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.42E-11	3.04E-08	25.00
GO:0043549	regulation of kinase activity	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.39E-05	2.42E-02	27.00
GO:0032879	regulation of localization	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.24E-07	2.43E-04	58.00
GO:0040012	regulation of locomotion	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.31E-06	4.29E-03	34.00
GO:0010556	regulation of macromolecule biosynthetic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	8.21E-11	1.74E-07	99.00
GO:0060255	regulation of macromolecule metabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	9.41E-16	2.06E-12	146.00
R-HSA-002692	Regulation of MECP2 expression and activity	REACTOME_Pathways_25.05.2022	3.68E-08	6.74E-03	6.00
GO:0019922	regulation of metabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	6.52E-18	1.43E-12	154.00
GO:0060609	regulation of molecular function	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	4.49E-11	9.56E-08	85.00
GO:1903311	regulation of mRNA metabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	1.78E-05	3.07E-02	15.00
GO:2000026	regulation of multicellular organismal development	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	5.82E-06	1.05E-02	40.00
GO:0051239	regulation of multicellular organismal process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.08E-09	4.28E-06	75.00
GO:0051171	regulation of nitrogen compound metabolic process	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	3.92E-15	8.54E-12	137.00
GO:1903598	regulation of nucleic acid-templated transcription	GO BiologicalProcess-EBU-UnProt-GOA-ACAP-ARAP_25.05.2022_0h00	2.15E-10	4.54E-07	89.00

ID	GO Term	Ontology Source	Term PValue	Term PValue Corrected with Bonferroni step down	Nr. Genes	Associated Genes Found
GO:0019129	regulation of nucleobase-containing compound metabolism	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_25.05.2022_00h00	1.52E-11	3.24E-08	102/200	[ADRB2, ANXA2, APEX1, APP, AR, AURKB, BASP1, BCL2, BCL6, BRD4, BRD9, CALR, CBX1, CBX3, CDH1, COP5, CREBBP, CTBP1, DDX58, DYRK1A, E2F1, ERBB2, ESR1, ESR2, EZR, FBXW1, FLNA, FLOT1, FLOT2, GATA2, HAX1, HDAC1, HDAC2, HDXEM1, HNRNP, HSP90A1, HSPA2, HTRA2, HTF, IF16, INM2B, ITK, KIF4, KPN1, KPN2, KPN3, KPN4, KPN5, KPN6, KPN7, KPN8, KPN9, KPN10, KPN11, KPN12, KPN13, KPN14, KPN15, KPN16, KPN17, KPN18, KPN19, KPN20, KPN21, KPN22, KPN23, KPN24, KPN25, KPN26, KPN27, KPN28, KPN29, KPN30, KPN31, KPN32, KPN33, KPN34, KPN35, KPN36, KPN37, KPN38, KPN39, KPN40, KPN41, KPN42, KPN43, KPN44, KPN45, KPN46, KPN47, KPN48, KPN49, KPN50, KPN51, KPN52, KPN53, KPN54, KPN55, KPN56, KPN57, KPN58, KPN59, KPN60, KPN61, KPN62, KPN63, KPN64, KPN65, KPN66, KPN67, KPN68, KPN69, KPN70, KPN71, KPN72, KPN73, KPN74, KPN75, KPN76, KPN77, KPN78, KPN79, KPN80, KPN81, 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ID	Term	Ontology type	Term PValue	Term PValue Corrected with Bonferroni step down	Nr. Genes	Associated Genes
GO:0016760	RNA metabolic process	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	3.80E-10	7.98E-07
R-HSA-73854	RNA Polymerase I Promoter Clearance	REACTOME Pathways	25.05.2022		1.33E-05	2.33E-02
R-HSA-73854	RNA Polymerase I Transcription	REACTOME Pathways	25.05.2022		1.58E-05	2.67E-02
R-HSA-73857	RNA Polymerase II Transcription	REACTOME Pathways	25.05.2022		2.51E-08	5.04E-05
GO:003880	RNA splicing	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	8.01E-07	1.52E-03
GO:000375	RNA splicing, via transesterification reactions	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	8.95E-07	1.69E-03
R-HSA-244692	RNA splicing, via transesterification reactions with bulge	REACTOME Pathways	25.05.2022		1.51E-06	2.75E-03
KEGG:05102	Salmonella infection	KEGG	25.05.2022		6.88E-10	3.39E-06
R-HSA-967590	SARS-CoV Infection	REACTOME Pathways	25.05.2022		1.15E-08	2.33E-05
R-HSA-40068	Sema4d in semaphorin signaling	REACTOME Pathways	25.05.2022		1.56E-05	2.63E-02
R-HSA-40068	Semaphorin interactions	REACTOME Pathways	25.05.2022		2.07E-05	3.55E-02
KEGG:05103	Shigellosis	KEGG	25.05.2022		2.98E-08	1.58E-04
R-HSA-102582	Signal Transduction	REACTOME Pathways	25.05.2022		6.14E-20	3.35E-16
R-HSA-448147	Signaling by Interleukins	REACTOME Pathways	25.05.2022		2.73E-08	5.03E-03
R-HSA-177119	Signaling by NOTCH1	REACTOME Pathways	25.05.2022		5.68E-10	5.67E-07
R-HSA-1980143	Signaling by NOTCH1	REACTOME Pathways	25.05.2022		4.73E-07	9.11E-04
R-HSA-2984858	Signaling by NOTCH1 HD-PEST Domain Mutants in Cancer	REACTOME Pathways	25.05.2022		7.78E-07	1.48E-03
R-HSA-284603	Signaling by NOTCH1 in PEST Domain Mutants in Cancer	REACTOME Pathways	25.05.2022		7.78E-07	1.48E-03
R-HSA-264692	Signaling by NOTCH1 PEST Domain Mutants in Cancer	REACTOME Pathways	25.05.2022		7.78E-07	1.48E-03
R-HSA-900931	Signaling by Nuclear Receptors	REACTOME Pathways	25.05.2022		1.94E-06	3.62E-03
R-HSA-900934	Signaling by Receptor Tyrosine Kinases	REACTOME Pathways	25.05.2022		8.40E-08	1.66E-04
R-HSA-194315	Signaling by Rho GTPases	REACTOME Pathways	25.05.2022		8.01E-20	3.35E-16
R-HSA-9716542	Signaling by Rho GTPases, Micro GTPases and RHOs	REACTOME Pathways	25.05.2022		3.10E-20	6.81E-17
R-HSA-195721	Signaling by WNT	REACTOME Pathways	25.05.2022		1.07E-11	2.26E-08
KEGG:04071	Sphingolipid regulation pathway	KEGG	25.05.2022		2.50E-05	4.26E-02
GO:001146	striated muscle cell differentiation	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	1.49E-06	2.89E-03
R-HSA-102582	SUMO E3 ligase SUMO1/2 target proteins	REACTOME Pathways	25.05.2022		1.68E-09	3.15E-06
R-HSA-269046	Sublytic myelination	REACTOME Pathways	25.05.2022		6.53E-06	1.17E-02
GO:007435	supramolecular fiber organization	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	1.47E-12	3.17E-09
GO:000908	synapse organization	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	3.11E-06	5.71E-03
GO:0043731	system development	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	1.46E-08	2.94E-05
R-HSA-488944	T cell receptor signaling pathway	KEGG	25.05.2022		8.02E-06	1.49E-03
GO:0020181	TGF dependent signaling in response to WNT	REACTOME Pathways	25.05.2022		1.81E-08	3.35E-04
GO:003200	tetrahelomere organization	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	1.29E-05	2.26E-02
WP-366	TGF-beta signaling pathway	WikiPathway	23.02.2022		1.96E-05	3.84E-05
KEGG:04910	Thyroid hormone signalling pathway	KEGG	25.05.2022		5.72E-08	1.14E-04
KEGG:045093	Tight junction	KEGG	25.05.2022		2.17E-09	4.09E-06
GO:000888	tissue development	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	7.98E-06	1.28E-02
GO:000368	transcription by RNA polymerase II	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	1.46E-08	2.94E-05
GO:0003712	transcription coregulatory activity	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	7.61E-06	1.36E-02
GO:000631	transcription, DNA-templated	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	4.06E-10	8.50E-07
R-HSA-889344	Transcriptional Regulation by MECP2	REACTOME Pathways	25.05.2022		1.51E-05	2.75E-02
GO:003043	ubiquitin-dependent ERAD pathway	GO BiologicalProcess-EBIUniProt-GOA-ACAP-ARAP	25.05.2022	0.0000	1.87E-06	3.22E-03
R-HSA-568880	Ub-specific processing proteases	REACTOME Pathways	25.05.2022		6.25E-06	1.13E-02
WP-388						

Supplementary Table 31. Summary of pathway analysis using genes previously associated with insulin-related traits in previous studies

ID	Term	Ontology source	Term PValue	Term PValue Corrected with Bonferroni test	Nr. Genes
WP-4949	16p11.2 proximal deletion syndrome	WikiPathways, 23.02.2022	5.84E-07	5.60E-04	50
WP-3879	4-hydroxyaminofer, deaminotases, and retinoic acids regulation	WikiPathways, 23.02.2022	5.00E-06	4.43E-03	16.00
WP-4932	7q11.23 copy number variation syndrome	WikiPathways, 23.02.2022	5.81E-12	6.87E-09	73.00
R-HSA-5619084	ABC transporter disorders	REACTOME Pathways, 25.05.22	3.08E-09	3.27E-06	54.00
R-HSA-382556	ABC-family proteins mediated transport	REACTOME Pathways, 25.05.22	7.43E-07	7.08E-04	62.00
R-HSA-9687139	Aberrant regulation of mitotic cell cycle due to Rb1 defects	REACTOME Pathways, 25.05.22	6.39E-08	6.73E-06	17.00
R-HSA-9659787	Aberrant regulation of mitotic G1/S transition in cancer due to Rb1	REACTOME Pathways, 25.05.22	2.68E-08	2.73E-05	30.00
R-HSA-178814	Activation of APC/C and APC/C: Cdc20 mediated degradation of Rb1	REACTOME Pathways, 25.05.22	3.60E-13	4.43E-10	59.00
R-HSA-111447	Activation of BAD and translocation to mitochondria	REACTOME Pathways, 25.05.22	2.07E-07	2.05E-04	15.00
R-HSA-114452	Activation of BH3-only proteins	REACTOME Pathways, 25.05.22	2.29E-12	2.74E-09	29.00
R-HSA-1169091	Activation of NF-kappaB in B cells	REACTOME Pathways, 25.05.22	1.15E-16	1.52E-13	57.00
R-HSA-442755	Activation of NMDA receptors and postsynaptic events	REACTOME Pathways, 25.05.22	5.67E-10	6.28E-07	63.00
R-HSA-450341	Activation of the AP-1 family of transcription factors	REACTOME Pathways, 25.05.22	3.51E-05	2.86E-02	10.00
R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex	REACTOME Pathways, 25.05.22	7.25E-18	9.80E-15	53.00
KEGG-05221	Acute myeloid leukemia	KEGG, 25.05.2022	1.09E-15	1.42E-12	56.00
WP-4298	Acute viral myocarditis	WikiPathways, 23.02.2022	6.71E-08	6.78E-05	56.00
R-HSA-1280218	Adaptive Immune System	REACTOME Pathways, 25.05.22	2.70E-33	4.02E-30	435.00
KEGG-04520	Adherens junction	KEGG, 25.05.2022	3.46E-17	4.65E-14	60.00
KEGG-04920	Adipocytokine signaling pathway	KEGG, 25.05.2022	1.07E-09	1.17E-06	50.00
WP-236	Adipogenesis	WikiPathways, 23.02.2022	4.73E-11	5.46E-08	84.00
KEGG-04261	Adrenergic signaling in cardiomyocytes	KEGG, 25.05.2022	6.74E-06	8.85E-03	81.00
WP-2324	AGE/RAGE pathway	WikiPathways, 23.02.2022	1.06E-20	1.47E-17	60.00
KEGG-04933	AGE-RAGE signaling pathway in diabetic complications	KEGG, 25.05.2022	1.49E-15	1.94E-12	75.00
R-HSA-9046399	Agonophagy	REACTOME Pathways, 25.05.22	4.10E-07	3.99E-04	32.00
R-HSA-198323	AKT phosphorylates targets in the cytosol	REACTOME Pathways, 25.05.22	1.51E-05	1.27E-02	13.00
KEGG-04960	Aldosterone-regulated sodium reabsorption	KEGG, 25.05.2022	6.25E-06	5.45E-03	27.00
WP-244	Alpha 6 beta 4 signaling pathway	WikiPathways, 23.02.2022	1.14E-07	1.14E-04	28.00
KEGG-05010	Alzheimer disease	KEGG, 25.05.2022	2.32E-26	3.25E-23	239.00
R-HSA-9046399	Amphophagy	REACTOME Pathways, 25.05.22	4.10E-07	3.99E-04	32.00
R-HSA-198323	AKT phosphorylates targets in the cytosol	REACTOME Pathways, 25.05.22	1.51E-05	1.27E-02	13.00
KEGG-04960	Aldosterone-regulated sodium reabsorption	KEGG, 25.05.2022	6.25E-06	5.45E-03	27.00
WP-244	Alpha 6 beta 4 signaling pathway	WikiPathways, 23.02.2022	1.14E-07	1.14E-04	28.00
KEGG-0501					

R-HSA-400253	Circadian Clock	KEGG04710	Reactome Pathways 25.05.21	3.27E-10	3.66E-07	51.00
R-HSA-400253	Circadian rhythm	KEGG04710	Reactome Pathways 25.05.21	1.68E-05	1.39E-02	23.00
WP-3594	Circadian rhythm genes	WikiPathways 23.02.2022		1.26E-09	1.37E-06	117.00
R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	Reactome Pathways 25.05.21		6.11E-07	5.86E-04	78.00
R-HSA-420499	Class C/3 (Metabotropic glutamate/phormone receptors)	Reactome Pathways 25.05.21		2.17E-05	1.80E-02	2.00
R-HSA-983169	Class I MHC mediated antigen processing & presentation	Reactome Pathways 25.05.21		6.74E-19	9.24E-16	221.00
R-HSA-855628	Clathrin-mediated endocytosis	Reactome Pathways 25.05.21		8.43E-11	9.61E-08	91.00
WP-4018	Clear cell renal cell carcinoma pathways	WikiPathways 23.02.2022		2.60E-06	2.37E-03	53.00
R-HSA-5607784	CLEC7A (Dectin-1) signaling	Reactome Pathways 25.05.21		9.37E-20	1.30E-16	81.00
WP-5117	Cohesin complex - Cornelia de Lange syndrome	WikiPathways 23.02.2022		4.27E-06	3.81E-03	26.00
KEGG-05210	Colorectal cancer	KEGG 25.05.2022		6.84E-20	9.49E-17	72.00
R-HSA-2219530	Constitutive Signaling by Aberrant PI3K in Cancer	Reactome Pathways 25.05.21		4.15E-05	3.35E-02	46.00
R-HSA-5674400	Constitutive Signaling by AKT1 E17K in Cancer	Reactome Pathways 25.05.21		7.24E-09	7.61E-06	23.00
R-HSA-5637810	Constitutive Signaling by EGFRvIII	Reactome Pathways 25.05.21		2.07E-07	2.05E-04	15.00
R-HSA-1236362	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variant	Reactome Pathways 25.05.21		1.20E-07	1.19E-04	16.00
R-HSA-2894862	Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	Reactome Pathways 25.05.21		2.32E-05	1.93E-02	37.00
R-HSA-2644606	Constitutive Signaling by NOTCH1 PEST Domain Mutants	Reactome Pathways 25.05.21		2.32E-05	1.93E-02	37.00
R-HSA-9634285	Constitutive Signaling by Overexpressed ERBB2	Reactome Pathways 25.05.21		1.26E-05	1.07E-02	11.00
R-HSA-389958	Cooperation of Prefoldin and Tric/CCT in actin and tubulin folding	Reactome Pathways 25.05.21		2.16E-09	2.34E-06	28.00
R-HSA-6807878	COPI-mediated anterograde transport	Reactome Pathways 25.05.21		1.43E-05	1.21E-02	58.00
KEGG-05171	Coronavirus disease	KEGG 25.05.2022		1.18E-18	1.60E-15	149.00
WP-2355	Corticotropin-releasing hormone signaling pathway	WikiPathways 23.02.2022		1.50E-12	1.80E-09	67.00
R-HSA-388841	Costimulation by the CD28 family	Reactome Pathways 25.05.21		1.07E-09	1.17E-06	50.00
R-HSA-442472	CREB1 phosphorylation through NMDA receptor-mediated activation	Reactome Pathways 25.05.21		1.56E-05	1.31E-02	22.00
R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	Reactome Pathways 25.05.21		3.28E-09	3.51E-06	38.00
R-HSA-389513	CTLA4 inhibitory signaling	Reactome Pathways 25.05.21		1.69E-08	1.75E-05	20.00
R-HSA-538747	CTNNB1 S331 mutants aren't phosphorylated	Reactome Pathways 25.05.21		5.78E-06	5.05E-03	14.00
R-HSA-538749	CTNNB1 S37 mutants aren't phosphorylated	Reactome Pathways 25.05.21		5.78E-06	5.05E-03	14.00
R-HSA-538751	CTNNB1 S45 mutants aren't phosphorylated	Reactome Pathways 25.05.21		5.78E-06	5.05E-03	14.00
R-HSA-538752	CTNNB1 T141 mutants aren't phosphorylated	Reactome Pathways 25.05.21		5.78E-06	5.05E-03	14.00
KEGG-04625	C-type lectin receptor signaling pathway	KEGG 25.05.2022		3.63E-10	4.05E-07	69.00
R-HSA-5621481	C-type lectin receptors (CLRs)	Reactome Pathways 25.05.21		2.74E-16	3.63E-13	99.00
KEGG-04934	Cushing syndrome	KEGG 25.05.2022		1.78E-06	1.65E-03	85.00
R-HSA-69656	Cyclin A/Cdk2-associated events at S phase entry	Reactome Pathways 25.05.21		1.48E-22	2.10E-19	74.00
R-HSA-69231	Cyclin D associated events in G1	Reactome Pathways 25.05.21		1.02E-16	1.36E-13	44.00
R-HSA-69202	Cyclin E associated events during G1/S transition	Reactome Pathways 25.05.21		7.31E-23	1.04E-19	73.00
WP-477	Cytoplasmic ribosomal proteins	WikiPathways 23.02.2022		6.57E-25	9.52E-22	80.00
R-HSA-9707564	Cytoprotection by HMOX1	Reactome Pathways 25.05.21		5.23E-08	4.63E-03	29.00
R-HSA-379716	Cytosolic RNA aminoacylation	Reactome Pathways 25.05.21		2.45E-06	2.25E-03	20.00
R-HSA-1485950	DAG and IP3 signaling	Reactome Pathways 25.05.21		3.70E-05	3.00E-02	29.00
R-HSA-2424461	DAP12 signaling	Reactome Pathways 25.05.21		1.24E-07	1.24E-04	25.00
R-HSA-180024	DARPP-32 events	Reactome Pathways 25.05.21		3.27E-05	2.67E-02	20.00
R-HSA-168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	Reactome Pathways 25.05.21		3.88E-05	3.14E-02	49.00
R-HSA-3769402	Deactivation of the beta-catenin transactivating complex	Reactome Pathways 25.05.21		5.13E-06	4.54E-03	38.00
R-HSA-429914	Deadenylation-dependent mRNA decay	Reactome Pathways 25.05.21		3.00E-06	2.73E-03	37.00
R-HSA-73887	Death Receptor Signaling	Reactome Pathways 25.05.21		5.49E-08	4.82E-03	50.00
R-HSA-5607781	Dectin-1 mediated noncanonical NF-kB signaling	Reactome Pathways 25.05.21		4.82E-14	6.07E-11	57.00
						51.00
						23.00
						117.00
						78.00
						2.00
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R-HSA-5693532	DNA Double-Strand Break Repair	REACTOME Pathways 25.05.22	1.37E-06	1.28E-03	91.00	[ABL1, APBB1, ATM, ATR, BABAM1, BAP1, BARD1, BAZ1B, BLM, BRCA1, BRIP1, CCNA1, CCNA2, CDK1, CHEK1, CHEK2, ERCC1, EYA1, EYAF1, EYAF2, H2AX, H2BAC1, H2BAC2, H2BAC3, H2BAC4, H3.4, H4, H4.1, H4.2, H4.3, H4.4, H4.5, H4.6, H4.7, H4.8, H4.9, H4.10, H4.11, H4.12, H4.13, H4.14, H4.15, H4.16, H4.17, H4.18, H4.19, H4.20, H4.21, H4.22, H4.23, H4.24, H4.25, H4.26, H4.27, H4.28, H4.29, H4.30, H4.31, H4.32, H4.33, H4.34, H4.35, H4.36, H4.37, H4.38, H4.39, H4.40, H4.41, H4.42, H4.43, H4.44, H4.45, H4.46, H4.47, H4.48, H4.49, H4.50, H4.51, H4.52, H4.53, H4.54, H4.55, H4.56, H4.57, H4.58, H4.59, H4.60, H4.61, H4.62, H4.63, H4.64, H4.65, H4.66, H4.67, H4.68, H4.69, H4.70, H4.71, H4.72, H4.73, H4.74, H4.75, H4.76, H4.77, H4.78, H4.79, H4.80, H4.81, H4.82, H4.83, H4.84, H4.85, H4.86, H4.87, H4.88, H4.89, H4.90, H4.91, H4.92, H4.93, H4.94, H4.95, H4.96, H4.97, H4.98, H4.99, H5.0, H5.1, H5.2, H5.3, H5.4, H5.5, H5.6, H5.7, H5.8, H5.9, H5.10, H5.11, H5.12, H5.13, H5.14, H5.15, H5.16, H5.17, H5.18, H5.19, H5.20, H5.21, H5.22, H5.23, H5.24, H5.25, H5.26, H5.27, H5.28, H5.29, H5.30, H5.31, H5.32, H5.33, H5.34, H5.35, H5.36, H5.37, H5.38, H5.39, H5.40, H5.41, H5.42, H5.43, H5.44, H5.45, H5.46, H5.47, H5.48, H5.49, H5.50, H5.51, H5.52, H5.53, H5.54, H5.55, H5.56, H5.57, H5.58, H5.59, H5.60, H5.61, H5.62, H5.63, H5.64, H5.65, H5.66, H5.67, H5.68, H5.69, H5.70, H5.71, H5.72, H5.73, H5.74, H5.75, H5.76, H5.77, H5.78, H5.79, H5.80, H5.81, H5.82, H5.83, H5.84, H5.85, H5.86, H5.87, H5.88, H5.89, H5.90, H5.91, H5.92, H5.93, H5.94, H5.95, H5.96, H5.97, H5.98, H5.99, H6.0, H6.1, H6.2, H6.3, H6.4, H6.5, H6.6, H6.7, H6.8, H6.9, H6.10, H6.11, H6.12, H6.13, H6.14, H6.15, H6.16, H6.17, H6.18, H6.19, H6.20, H6.21, H6.22, H6.23, H6.24, H6.25, H6.26, H6.27, H6.28, H6.29, H6.30, H6.31, H6.32, H6.33, H6.34, H6.35, H6.36, H6.37, H6.38, H6.39, H6.40, H6.41, H6.42, H6.43, H6.44, H6.45, H6.46, H6.47, H6.48, H6.49, H6.50, H6.51, H6.52, H6.53, H6.54, H6.55, H6.56, H6.57, H6.58, H6.59, H6.60, H6.61, H6.62, H6.63, H6.64, H6.65, H6.66, H6.67, H6.68, H6.69, H6.70, H6.71, H6.72, H6.73, H6.74, H6.75, H6.76, H6.77, H6.78, H6.79, H6.80, H6.81, H6.82, H6.83, H6.84, H6.85, H6.86, H6.87, H6.88, H6.89, H6.90, H6.91, H6.92, H6.93, H6.94, H6.95, H6.96, H6.97, H6.98, H6.99, H7.0, H7.1, H7.2, H7.3, H7.4, H7.5, H7.6, H7.7, H7.8, H7.9, H7.10, H7.11, H7.12, H7.13, H7.14, H7.15, H7.16, H7.17, H7.18, H7.19, H7.20, H7.21, H7.22, H7.23, H7.24, H7.25, H7.26, H7.27, H7.28, H7.29, H7.30, H7.31, H7.32, H7.33, H7.34, H7.35, H7.36, H7.37, H7.38, H7.39, H7.40, H7.41, H7.42, H7.43, H7.44, H7.45, H7.46, H7.47, H7.48, H7.49, H7.50, H7.51, H7.52, H7.53, H7.54, H7.55, H7.56, H7.57, H7.58, H7.59, H7.60, H7.61, H7.62, H7.63, H7.64, H7.65, H7.66, H7.67, H7.68, H7.69, H7.70, H7.71, H7.72, H7.73, H7.74, H7.75, H7.76, H7.77, H7.78, H7.79, H7.80, H7.81, H7.82, H7.83, H7.84, H7.85, H7.86, H7.87, H7.88, H7.89, H7.90, H7.91, H7.92, H7.93, H7.94, H7.95, H7.96, H7.97, H7.98, H7.99, H8.0, H8.1, H8.2, H8.3, H8.4, H8.5, H8.6, H8.7, H8.8, H8.9, H8.10, H8.11, H8.12, H8.13, H8.14, H8.15, H8.16, H8.17, H8.18, H8.19, H8.20, H8.21, H8.22, H8.23, H8.24, H8.25, H8.26, H8.27, H8.28, H8.29, H8.30, H8.31, H8.32, H8.33, H8.34, H8.35, H8.36, H8.37, H8.38, H8.39, H8.40, H8.41, H8.42, H8.43, H8.44, H8.45, H8.46, H8.47, H8.48, H8.49, H8.50, H8.51, H8.52, H8.53, H8.54, H8.55, H8.56, H8.57, H8.58, H8.59, H8.60, H8.61, H8.62, H8.63, H8.64, H8.65, H8.66, H8.67, H8.68, H8.69, H8.70, H8.71, H8.72, H8.73, H8.74, H8.75, H8.76, H8.77, H8.78, H8.79, H8.80, H8.81, H8.82, H8.83, H8.84, H8.85, H8.86, H8.87, H8.88, H8.89, H8.90, H8.91, H8.92, H8.93, H8.94, H8.95, H8.96, H8.97, H8.98, H8.99, H9.0, H9.1, H9.2, H9.3, H9.4, H9.5, H9.6, H9.7, H9.8, H9.9, H10.0, H10.1, H10.2, H10.3, H10.4, H10.5, H10.6, H10.7, H10.8, H10.9, H11.0, H11.1, H11.2, H11.3, H11.4, H11.5, H11.6, H11.7, H11.8, H11.9, H12.0, H12.1, H12.2, H12.3, H12.4, H12.5, H12.6, H12.7, H12.8, H12.9, H13.0, H13.1, H13.2, H13.3, H13.4, H13.5, H13.6, H13.7, H13.8, H13.9, H14.0, H14.1, H14.2, H14.3, H14.4, H14.5, H14.6, H14.7, H14.8, H14.9, H15.0, H15.1, H15.2, H15.3, H15.4, H15.5, H15.6, H15.7, H15.8, H15.9, H16.0, H16.1, H16.2, H16.3, H16.4, H16.5, H16.6, H16.7, H16.8, H16.9, H17.0, H17.1, H17.2, H17.3, H17.4, H17.5, H17.6, H17.7, H17.8, H17.9, H18.0, H18.1, H18.2, H18.3, H18.4, H18.5, H18.6, H18.7, H18.8, H18.9, H19.0, H19.1, H19.2, H19.3, H19.4, H19.5, H19.6, H19.7, H19.8, H19.9, H20.0, H20.1, H20.2, H20.3, H20.4, H20.5, H20.6, H20.7, H20.8, H20.9, H21.0, H21.1, H21.2, H21.3, H21.4, H21.5, H21.6, H21.7, H21.8, H21.9, H22.0, H22.1, H22.2, H22.3, H22.4, H22.5, H22.6, H22.7, H22.8, H22.9, H23.0, H23.1, H23.2, H23.3, H23.4, H23.5, H23.6, H23.7, H23.8, H23.9, H24.0, H24.1, H24.2, H24.3, H24.4, H24.5, H24.6, H24.7, H24.8, H24.9
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R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	REACTOME Pathways 25.05.21	2.60E-25	3.78E-22	135.00
WP-5087	Malignant pleural mesothelioma	WikiPathways 23.02.2022	6.23E-30	9.20E-27	277.00
R-HSA-450294	MAP kinase activation	REACTOME Pathways 25.05.21	1.40E-14	1.78E-11	53.00
R-HSA-5674135	MAP2K and MAPK activation	REACTOME Pathways 25.05.21	1.37E-08	1.43E-05	32.00
R-HSA-5684264	MAP3K8 (TPL2)-dependent MAPK1/3 activation	REACTOME Pathways 25.05.21	3.08E-05	2.52E-02	14.00
WP-3849	MAPK and NFkB signaling pathways inhibited by Yersinia YopJ	WikiPathways 23.02.2022	4.51E-08	4.03E-03	12.00
WP-422	MAPK cascade	WikiPathways 23.02.2022	3.86E-08	3.47E-03	25.00
R-HSA-5683057	MAPK family signaling cascades	REACTOME Pathways 25.05.21	2.45E-22	3.47E-19	20.00
WP-4928	MAPK pathway in congenital thyroid cancer	WikiPathways 23.02.2022	3.08E-05	2.52E-02	14.00
KEGG-04010	MAPK signaling pathway	KEGG 25.05.2022	2.55E-23	3.65E-20	189.00
WP-382	MAPK signaling pathway	WikiPathways 23.02.2022	5.30E-19	7.39E-16	158.00
R-HSA-450282	MAPK targets/ Nuclear events mediated by MAP kinases	REACTOME Pathways 25.05.21	4.13E-10	4.60E-07	28.00
R-HSA-5684996	MAPK1/MAPK3 signaling	REACTOME Pathways 25.05.21	2.16E-19	2.98E-16	177.00
R-HSA-5687128	MAPK6/MAPK4 signaling	REACTOME Pathways 25.05.21	3.05E-13	3.76E-10	66.00
KEGG-05162	Measles	KEGG 25.05.2022	7.71E-15	9.88E-12	95.00
WP-4630	Measles virus infection	WikiPathways 23.02.2022	2.80E-13	3.45E-10	92.00
WP-3584	MECP2 and associated Rett syndrome	WikiPathways 23.02.2022	5.40E-06	4.82E-03	45.00
KEGG-05218	Melanoma	KEGG 25.05.2022	4.17E-13	5.10E-10	56.00
WP-4685	Melanoma	WikiPathways 23.02.2022	4.61E-16	6.06E-13	57.00
R-HSA-199991	Membrane Trafficking	REACTOME Pathways 25.05.21	1.21E-10	1.38E-07	305.00
WP-2857	Mesodermal commitment pathway	WikiPathways 23.02.2022	3.40E-05	2.84E-02	82.00
WP-4205	MET in type 1 papillary renal cell carcinoma	WikiPathways 23.02.2022	1.24E-14	1.58E-11	50.00
R-HSA-71291	Metabolism of amino acids and derivatives	REACTOME Pathways 25.05.21	5.16E-06	4.57E-03	177.00
R-HSA-351202	Metabolism of polyamines	REACTOME Pathways 25.05.21	7.94E-07	7.52E-04	40.00

R-HSA-975966	Nonsense Mediated Decay (NMD) independent of the Exon Junction	REACTOME Pathways 25.05.2022	1.72E-26	2.51E-23	84.00	[EIF4G1, E1F1, GSPT1, NCBP1, NCBP2, PABPC1, RP10, RP10A, RP10L, RP11, RP12, RP12L, RP13, RP13A, RP14, RP15, RP17, RP18, RP18A, RP19, RP21, RP22, RP23, RP23A, RP24, RP26, RP26L1, RP27, RP27A, RP28, RP31, RP31L1, RP31L3, RP32, RP34, RP35, RP35A, RP36A, RP36L, RP37, RP38, RP38A, RP39, RP40, RP41, RP42, RP43, RP44, RP45, RP46, RP47, RP48, RP49, RP50, RP51, RP52, RP53, RP54, RP55, RP56, RP57, RP58, RP59, RP60, RP61, RP62, RP63, RP64, RP65, RP66, RP67, RP68, RP69, RP70, RP71, RP72, RP73, RP74, RP75, RP76, RP77, RP78, RP79, RP80, RP81, RP82, RP83, RP84, RP85, RP86, RP87, RP88, RP89, RP90, RP91, RP92, RP93, RP94, RP95, RP96, RP97, RP98, RP99, RP100, RP101, RP102, RP103, RP104, RP105, RP106, RP107, RP108, RP109, RP110, RP111, RP112, RP113, RP114, RP115, RP116, RP117, RP118, RP119, RP120, RP121, RP122, RP123, RP124, RP125, RP126, RP127, RP128, RP129, RP130, RP131, 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R-HSA-8878159	Transcriptional regulation by RUNX3	REACTOME_Pathways_25.05.21	1.15E+23	1.65E+20	82.00
R-HSA-3709899	Transcriptional Regulation by TP53	REACTOME_Pathways_25.05.21	2.62E+28	3.85E+25	232.00
R-HSA-8853884	Transcriptional Regulation by VENTX	REACTOME_Pathways_25.05.21	1.75E+06	1.62E+03	29.00
R-HSA-452723	Transcriptional regulation of pluripotent stem cells	REACTOME_Pathways_25.05.21	1.83E+05	1.52E+02	19.00
R-HSA-381340	Transcriptional regulation of white adipocyte differentiation	REACTOME_Pathways_25.05.21	2.38E+12	2.84E+09	62.00
R-HSA-199992	trans-Golgi Network Vesicle Budding	REACTOME_Pathways_25.05.21	5.81E+05	4.61E+02	43.00
R-HSA-72766	Translation	REACTOME_Pathways_25.05.21	3.73E+36	5.57E+33	209.00
WP-107	Translation factors	WikiPathways_23.02.2022	1.23E+06	1.15E+03	37.00
WP-4568	Translation inhibitors in chronically activated PDGFRA cells	WikiPathways_23.02.2022	1.29E+14	1.64E+11	43.00
R-HSA-72649	Translation initiation complex formation	REACTOME_Pathways_25.05.21	1.83E+17	2.47E+14	52.00
R-HSA-110320	Translation Synthesis by POLH	REACTOME_Pathways_25.05.21	1.20E+07	1.19E+04	15.00
R-HSA-989121	Translation synthesis by POLI	REACTOME_Pathways_25.05.21	1.20E+08	1.06E+02	14.00
R-HSA-110312	Translation synthesis by REV1	REACTOME_Pathways_25.05.21	3.08E+05	2.52E+02	27.00
R-HSA-110313	Translation synthesis by Y family DNA polymerases bypasses lesions	REACTOME_Pathways_25.05.21	3.03E+05	2.49E+02	27.00
R-HSA-1445148	Translocation of SLC24A4 (GLUT4) to the plasma membrane	REACTOME_Pathways_25.05.21	7.38E+14	9.21E+11	57.00
R-HSA-159236	Transport of Mature mRNA derived from an Intron-Containing Transcription Unit	REACTOME_Pathways_25.05.21	2.68E+06	2.44E+03	47.00
R-HSA-72202	Transport of Mature Transcript to Cytoplasm	REACTOME_Pathways_25.05.21	5.41E+06	4.77E+03	51.00
R-HSA-937061	TRIF(TICAM1)-mediated TLR4 signaling	REACTOME_Pathways_25.05.21	1.91E+17	2.57E+14	77.00
R-HSA-450513	Tristetraprolin (TTP_ZFP636) binds and destabilizes mRNA	REACTOME_Pathways_25.05.21	1.25E+05	1.06E+02	15.00
R-HSA-5467348	Truncations of AMER1 destabilize the destruction complex	REACTOME_Pathways_25.05.21	1.51E+05	1.27E+02	15.00
KEGG-05152	Tuberculosis	KEGG_25.05.2022	3.30E+06	2.99E+03	95.00
WP-4204	Tumor suppressor activity of SMARCB1	WikiPathways_23.02.2022	8.05E+08	8.09E+05	27.00
KEGG-04930	Type II diabetes mellitus	KEGG_25.05.2022	1.95E+07	1.93E+04	34.00
R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	REACTOME_Pathways_25.05.21	4.99E+12	5.91E+09	43.00
KEGG-04120	Ubiquitin mediated proteolysis	KEGG_25.05.2022	2.01E+23	2.88E+20	109.00
R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	REACTOME_Pathways_25.05.21	4.99E+12	5.91E+09	43.00
R-HSA-5869880	Ubi-specific processing proteases	REACTOME_Pathways_25.05.21	1.32E+15	1.73E+12	137.00
R-HSA-5869603	UCH proteinases	REACTOME_Pathways_25.05.21	8.36E+17	1.12E+13	78.00
WP-4925	Unfolded protein response	WikiPathways_23.02.2022	8.11E+06	6.99E+03	20.00
R-HSA-381119	Unfolded Protein Response (UPR)	REACTOME_Pathways_25.05.21	5.31E+08	5.38E+05	60.00
KEGG-04370	VEGF signaling pathway	KEGG_25.05.2022	4.85E+11	5.59E+08	46.00
R-HSA-4420097	VEGFA-VEGFR2 Pathway	REACTOME_Pathways_25.05.21	1.91E+17	2.57E+14	77.00
WP-3888	VEGFA-VEGFR2 signaling pathway	WikiPathways_23.02.2022	0.00E+00	0.00E+00	324.00
R-HSA-5218921	VEGFR2 mediated cell proliferation	REACTOME_Pathways_25.05.21	3.66E+06	3.29E+03	18.00
R-HSA-5218920	VEGFR2 mediated vascular permeability	REACTOME_Pathways_25.05.21	1.58E+09	1.31E+02	22.00
R-HSA-5653656	Vesicle-mediated transport	REACTOME_Pathways_25.05.21	1.43E+11	1.68E+08	325.00
R-HSA-180585	Vif-mediated degradation of APOBEC3G	REACTOME_Pathways_25.05.21	7.54E+12	8.89E+09	44.00
KEGG-05203	Viral carcinogenesis	KEGG_25.05.2022	7.93E+23	1.13E+19	142.00
R-HSA-192823	Viral mRNA Translation	REACTOME_Pathways_25.05.21	3.06E+25	4.45E+22	79.00
KEGG-05416	Viral myocarditis	KEGG_25.05.2022	4.45E+07	4.30E+04	41.00

WP-4482	Vitamin D in inflammatory diseases	WikiPathways_23.02.2022	6.32E-09	6.67E-06	21.00	[CHUK, DUSP1, IKKB, IKKG, MAP2K3, MAP2K6, MAP3K1, MAPK14, MED14, NFATC1, NFKB1, NFKBIA, NR3C1, PPP3CA, PPP3R1, RELA, RXRA, SMAD3, SMAD4, TNF, VDR]
R-HSA:180534	Vpu mediated degradation of CD4	REACTOME_Pathways_25.05.2022	4.90E-12	5.91E-09	43.00	[BTRC, CD4, PSMA1, PSMA2, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB1, PSMB2, PSMB3, PSMB4, PSMB5, PSMB6, PSMB7, PSMC1, PSMC2, PSMC3, PSMC4, PSMC5, PSMC6, PSMD1, PSMD10, PSMD11, PSMD12, PSMD13, PSMD14, PSMD2, PSMD3, PSMD4, PSMD5, PSMD6, PSMD7, PSMD8, PSMD9, PSME2, PSME3, RPS27A, SEM1, SKP1, UBR2, UBR3]
WP-4149	White fat cell differentiation	WikiPathways_23.02.2022	9.91E-07	9.32E-04	26.00	[CEBPA, CEBPB, CEBPD, CREB1, CTNNA1, DDIT3, EBF1, FOXO1, GATA2, GATA3, INS, IRF3, IRF4, KLF15, KLF4, KLF5, MECOM, NR1H3, NR2F2, NR3C1, PPARG, RARA, SREBF1, STAT5A, STAT5B, TLE3]
KEGG:04310	Wnt signaling pathway	KEGG_25.05.2022	5.45E-06	4.80E-03	90.00	[APC, AXIN1, BTRC, CACYBP, CAMK2A, CAMK2B, CAMK2D, CAMK2G, CCND1, CCND2, CCND3, CHD8, CREBBP, CSNK1A1, CSNK1E, CSNK2A1, CSNK2B, CTBP1, CTBP2, CTNNB1, CUL1, DVL2, DVL3, EP300, FBXW11, FOSL1, FZD3, FZD7, GPC4, GSK3B, JUN, LEF1, LGR4, LRP5, LRP6, MAP3K7, MAPK10, MAPK8, MAPK9, MMP7, MYC, NFATC1, NFATC2, NLK, PLCB1, PLCB3, PLCB4, PPARG, PPP3CA, PPP3CC, PPP3R1, PPP3R2, PRKACA, PRKACB, PRKACD, PRKCA, PRKCB, PRKCG, PSEN1, RAC1, RAC2, RAC3, REX1, RHOA, ROCK2, ROCK3, ROR2, RSPD3, RUBE1, RYK, SENP2, SERPINF1, SHH1, SKP1, SMAD3, SMAD4, SOX17, TBL1X, TBL1Y1, TCF7L2, TLE1, TLE3, TLE4, TP53, VANGL2, WIF1, WNT3A, WNT4, WNT5A, WNT8A]
WP-363	Wnt signaling pathway	WikiPathways_23.02.2022	1.73E-11	2.02E-08	43.00	[AKT1, APC, ARRB2, AXIN1, BCL9, CCND1, CKG, CSNK1A1, CSNK1D, CSNK1E, CTBP1, CTNBB1, DVL2, DVL3, GSKR, GJA1, GSK3A, GSK3B, LEF1, LRP5, LRP6, MAP3K7, MAPK1, MAPK8, MAPK9, MTOR, MYC, NFATC2, NLK, PPARG, PRKCA, PRKCB, PRKCG, RAC1, RHOA, ROR2, RYK, TCF3, TCF4, TCF7L2, TEK, TSC1, TSC2]
WP-399	Wnt signaling pathway and pluripotency	WikiPathways_23.02.2022	7.08E-08	7.15E-05	66.00	[APC, AXIN1, CCND1, CCND2, CCND3, CCND4, CREBBP, CSNK1E, CTBP1, CTBP2, CTNBB1, CTNND1, DVL2, DVL3, EP300, FOSL1, FZD3, FZD7, GSK3B, JUN, LDLR, LEF1, LRP5, LRP6, LRRK2, MAP2K4, MAP3K7, MAPK10, MAPK9, MMP7, MYC, NANOG, NYA, NLK, PLAU, POU5F1, PPARG, PPP2CA, PPP2CB, PPP2R1A, PPP2R1B, PPP2R2A, PPP2R2B, PPP2R2C, PPP2R3B, PPP2R5C, PPP2R5C, PRKCA, PRKCB, PRKCD, PRKCE, PRKCG, PRKCH, PRKG1, PRKGD, PRKGD2, PTEN, RAGGAP1, RHOA, SOX2, TCF7L2, TP53, WNT3A, WNT4, WNT5A, ZBTB33]
WP-3658	Wnt/beta-catenin signaling pathway in leukemia	WikiPathways_23.02.2022	3.57E-06	3.21E-03	21.00	[AKT1, APC, BCL9, CCND1, CSNK1A1, CTNBB1, FLT3, GSK3B, JUP, LEF1, LRP5, LRP6, MYC, PML, PPARG, RARA, RUNX1T1, SALL4, TCF3, WIF1, ZBTB16]
KEGG:05135	Yersinia infection	KEGG_25.05.2022	2.00E-19	2.76E-16	101.00	[ACTB, ACTG1, ACTR2, ACTR3, AKT1, AKT2, AKT3, ARF6, ARHGEP7, ARPC1A, ARPC1B, ARPC2, ARPC3, ARPC5, BAAP2, BCAR1, CASP1, CCL2, CD4, CDBA, CDC42, CHUK, CRK, CRKL, FCGR2A, FN1, FOS, FYB1, GIT2, GNAQ, GSK3B, IKKB, IKKG, IRAK1, IRF3, ITGA4, ITGA5, ITGB1, JUN, LAT, LCK, LCP2, LIMK1, MAP2K1, MAP2K2, MAP2K3, MAP2K4, MAP2K6, MAP2K7, MAPK1, MAPK10, MAPK11, MAPK14, MAPK3, MAPK8, MAPK9, MYD88, NFATC1, NFATC2, NFKB1, NFKBIA, PIK3CA, PIK3CB, PIK3CD, PIK3R1, PIK3R2, PIK3R3, PIP5K1A, PIP5K1C, PKN1, PKN2, PLCG1, PTK2, PTK2B, PXN, PYCARD, RAC1, RAC2, RAC3, RELA, RHOA, RHOG, ROCK1, ROCK2, RPS6KA1, RPS6KA2, RPS6KA3, RPS6KA6, SKAP2, SRC, TAB1, TAB2, TBK1, TNF, TRAF2, TRAF6, VAV1, VAV3, WASL, ZAP70]

Supplementary Table 32. The summary of the pathway analysis and gene list results for each PPI network in both the whole cohort, sex-specific cohorts, and genes from previous studies.

Cohort	Whole	Female	Male	Previous
Adherens junction	5.31E-13	2.59E-02	6.39E-04	4.65E-14
Alzheimer's disease	2.24E-26	1.70E-03	2.16E-02	3.25E-23
Cell cycle	1.80E-39	9.35E-06	1.18E-10	3.64E-37
Estrogen signaling pathway	6.79E-10	2.09E-11	-	8.21E-10
Glucose metabolism	3.95E-05	4.39E-02	-	2.31E-03
Insulin resistance	4.76E-10	-	-	8.07E-16
Insulin signaling pathway	8.09E-14	-	-	7.07E-22
Insulin secretion	-	1.92E-02	-	-
Neurodegeneration	1.91E-25	2.64E-06	7.79E-03	3.41E-23
Notch signaling	3.99E-03	9.98E-03	1.91E-02	1.50E-05
Nervous system development	2.49E-29	8.72E-11	7.29E-05	2.41E-43
Plasma lipoprotein assembly, remodeling, and clearance	4.64E-06	3.59E-02	-	1.90E-03
TGF-beta signaling pathway	4.92E-24	8.54E-09	3.84E-05	8.47E-24
Tight junction	2.36E-07	-	4.02E-03	4.78E-11
Wnt signaling pathway	1.30E-06	5.13E-06	6.74E-04	2.02E-08
# of genes	4290	397	248	6087
Gene list	A2M	ABCA1	ACTC1	A2M
	A2ML1	ABHD14A	ADRB2	A2ML1
	AAMDC	ACAA1	AFF1	A4GNT
	AAR2	ACOT7	ANLN	AANAT
	AARS	ADPGK	ANXA2	AAR2
	AARSD1	ADRB2	APEX1	AARS
	AASDHPPT	AGR2	APP	AARSD1
	AATF	AGRN	AQP3	AASDHPPT
	ABCA1	ALB	AR	AATF
	ABCA2	ALDH16A1	ARPC3	AATK
	ABCA6	ALG9	ASF1A	ABCA1
	ABCB11	APEX1	ATG16L1	ABCA2
	ABCB6	APOA1	ATP1B1	ABCA6
	ABCC1	APOA2	ATP2A1	ABCA8
	ABCC2	APOA4	AURKB	ABCB7
	ABCC6	APOA5	B3GNT3	ABCC1
	ABCD3	APOE	BACE1	ABCC2
	ABCE1	APP	BASP1	ABCF3
	ABCF1	AQP1	BCAP31	ABHD11
	ABCF2	ATAD5	BCOR	ABHD15
	ABHD1	ATP2A2	BMI1	ABHD17B
	ABHD11	AURKAIP1	BRD2	ABI1
	ABHD14A	BAG3	BRD3	ABI2
	ABHD17A	BAG6	BRD4	ABL1
	ABHD17B	BAZ1B	BSCL2	ABL2
	ABI1	BCAP31	BTNL2	ABLM1
	ABI2	BCL2	CALD1	ABO
	ABI3	BCR	CALM1	ABT1
	ABL1	BET1	CALR	ACACA
	ABLM1	BIRC3	CANX	ACACB
	ABT1	BMI1	CAPZA2	ACAD10
	ABTB2	BPTF	CBX1	ACAD9
	ACAA1	BRD2	CBX3	ACADM
	ACAA2	BRD3	CDC120	ACAP1
	ACACA	BRD4	CDC8	ACAT1
	ACACB	C2orf49	CDC42	ACAT2
	ACAD8	CALM1	CDH1	ACBD3
	ACAD9	CAMK2A	CEACAM21	ACBD5
	ACADM	CAMK2B	CEP164	ACE2
	ACAT1	CANX	CILP2	ACIN1
	ACBD5	CASP6	CIT	ACKR2
	ACD	CDC8	CKAP5	ACOT7
	ACE2	CCR4	CLTC	ACOX1
	ACLY	CD3EAP	COP1	ACP1
	ACO1	CDC34	COPS5	ACP2
	ACOT7	CDC42	CREBBP	ACPP
	ACOT9	CDC73	CTBP1	ACSF2
	ACOX1	CDK2	CTSB	ACSL1
	ACOX3	CDK9	CYCS	ACSL4
	ACSF2	CENPA	DCAF7	ACSL5
	ACSL1	CFTR	DCTN1	ACSS2
	ACSL3	CHAF1B	DDR1	ACTA1
	ACSL4	CHD3	DDX23	ACTB
	ACTA1	CHD4	DDX58	ACTBL2
	ACTA2	CHMP4C	DHRS11	ACTC1
	ACTB	CIT	DISC1	ACTG1
	ACTBL2	CLU	DOCK7	ACTL6A
	ACTC1	CMIP	DSCAML1	ACTN1
	ACTG1	CMTM5	DYRK1A	ACTN2
	ACTL6A	COL1A1	EBNA1BP2	ACTN4
	ACTN1	COL4A1	ECH1	ACTR1A
	ACTN4	COL4A3	ECT2	ACTR2
	ACTR10	COL6A1	EGLN3	ACTR3
	ACTR1A	COPS5	EIF3F	ACTR5
	ACTR2	CORO1C	ELAVL1	ACTR6
	ACTR3	CTBP2	ERBB2	ACTR8
	ACTR3B	CTSL	ESR1	ACVR1
	ACTRT1	CUL1	ESR2	ACVR1B
	ACVR1B	CUL3	EZR	ACVR1C
	ACVR2A	CUL4A	FBXO2	ACVR2A
	ACVR2B	CUL4B	FBXO6	ACVR2B
	ADAM21	CUL7	FBXW11	ADAM15
	ADAM30	CXCR4	FBXW7	ADAM19
	ADAM33	DDRKG1	FLNA	ADAM21
	ADAMTS1	DDX31	FLOT1	ADAM22

Cohort	Whole	Female	Male	Previous
	ADAR	DDX58	FLOT2	ADAM32
	ADARB1	DEK	FURIN	ADAM33
	ADCK1	DGUOK	FYN	ADAMTS1
	ADCY3	DHFR2	GADD45GIP1	ADAMTS13
	ADCY4	DHX9	GAS2L1	ADAMTS17
	ADCY9	DIPK1A	GATAD2A	ADAMTS2
	ADD3	DISC1	GEM	ADAMTS4
	ADIPOR1	DLD	GGNBP2	ADAMTS7
	ADNP	DLST	GMIP	ADAMTSL4
	ADPGK	DSG1	GOLGA2	ADAR
	ADRB2	DUT	GPR182	ADCK1
	ADRM1	DVL3	HAX1	ADCY2
	AES	DYNC1L12	HDAC1	ADCY4
	AFAP1	ECT2	HDAC2	ADCY5
	AFDN	EED	HEXIM1	ADCY6
	AFF1	EEF2	HIST1H2BG	ADD1
	AFF4	EFTUD2	HIST1H3A	ADD3
	AFG3L2	EGFL8	HIST4H4	ADGRG5
	AGBL4	EGFR	HLA-C	ADGRL1
	AGBL5	EGLN3	HLA-DQA1	ADGRL4
	AGFG1	EIF6	HNRNPH1	ADGRV1
	AGL	ELAVL1	HNRNPL	ADH4
	AGO2	ELN	HSP90AB1	ADIPOR1
	AGO4	EMC2	HSPA5	ADNP
	AGPAT1	EP300	HTRA2	ADNP2
	AGPAT3	EPRS	HTT	ADORA1
	AGPS	ERMP1	IFI16	ADORA2B
	AGR2	ESR1	IMMT	ADPGK
	AGRN	ESR2	INS	ADRB1
	AGTRAP	ETS1	ISLR	ADRB2
	AHCTF1	EVC2	ITM2B	ADRM1
	AHCY	EZH2	ITM2C	ADSL
	AHCYL1	F2RL1	KHSRP	AES
	AHNAK	FAM20C	KIF14	AFDN
	AHNAK2	FAM98B	KIF23	AFF1
	AHSA1	FANCD2	KLF3	AFF4
	AICDA	FAS	KLHL8	AFG1L
	AIFM1	FBLN1	KPNA1	AFG3L2
	AIM2	FBXO2	KPNA2	AFP
	AIMP1	FBXW7	KRAS	AGAP2
	AIMP2	FGD5	LARP7	AGBL4
	AK1	FGF8	LDHD	AGER
	AK2	FLNA	LGALS7	AGGF1
	AK3	FLNC	LGR4	AGO2
	AK4	FN1	LMNA	AGO3
	AKAP1	FOXA2	LYN	AGPAT1
	AKAP10	FUT8	LYPD1	AGPAT3
	AKAP12	FXR2	MAPK14	AGPS
	AKAP2	FZD9	MAPK6	AGR2
	AKAP9	FZR1	MAPK9	AGRN
	AKR1C4	GABARAPL1	MAU2	AGTRAP
	AKR7L	GALNT7	MBD3	AHCTF1
	AKT1	GDPD1	MEIS2	AHCY
	AKT2	GFAP	MFAP4	AHCYL1
	ALAD	GLB1L2	MKI67	AHCYL2
	ALB	GLP1R	MLLT1	AHNAK
	ALDH16A1	GNA11	MOV10	AHNAK2
	ALDH3A2	GNA13	MRPL12	AHR
	ALDH9A1	GNAI1	MRPL33	AHSA1
	ALDOA	GNAI3	MRPL53	AHSG
	ALDOC	GNAO1	MSN	AICDA
	ALG13	GNAQ	MYC	AIF1L
	ALG9	GNG8	MYH7	AIFM1
	ALMS1	GOLM1	MYH8	AIM2
	ALPL	GPC6	MYH9	AIMP1
	ALPP	GPLD1	MYO19	AIMP2
	ALYREF	GPM6A	MYO1C	AIP
	AMBRA1	GRB2	MYO6	AIRE
	AMFR	GRIN2A	NABP2	AK1
	AMOTL1	GRM5	NAP1L1	AK2
	AMPD2	GSTA1	NCK2	AK4
	ANAPC1	GSTA2	NCR3	AKAP1
	ANAPC2	GSTA3	NOTCH1	AKAP2
	ANG	GSTA4	NR3C1	AKAP5
	ANGPTL3	GSTA5	NRG1	AKAP8
	ANGPTL4	H2AFX	NT5E	AKAP8L
	ANGPTL7	HACD3	NTRK1	AKAP9
	ANK2	HDAC2	NXF1	AKNA
	ANK3	HDGF	OBSL1	AKR7A2
	ANKFY1	HECW2	PAK4	AKT1
	ANKLE2	HGF	PALLD	AKT1S1
	ANKRD11	HGFAC	PBX4	AKT2
	ANKRD13A	HIST1H2BG	PCBP1	AKT3
	ANKRD13D	HIST1H2BH	PDCCD11	AKTIP
	ANKRD17	HIST1H3A	PDIA4	ALB
	ANKRD28	HIST4H4	PFN1	ALCAM
	ANKRD36B	HNRNPCL2	PIGW	ALDH18A1
	ANKRD46	HNRNPD	PIK3R3	ALDH1B1
	ANKRD49	HNRNPL	PIN1	ALDH1L1
	ANKRD50	HNRNPU	PINK1	ALDH3A2
	ANKRD55	HOXC8	PLEKHA4	ALDH9A1
	ANLN	HPN	PPIB	ALDOA
	ANO4	HRAS	PPM1F	ALG10
	ANO6	HSD17B4	PPP1CC	ALG13

Cohort	Whole	Female	Male	Previous
	ANOS1	HSD3B7	PPP1R18	ALK
	ANP32A	HSP90AA1	PRNP	ALMS1
	ANP32B	HSPA9	PRPF19	ALOX12
	ANPEP	HSPB1	PRPF31	ALOX15B
	ANTXR1	HSPB8	PRPS2	ALOX5
	ANXA1	HUWE1	PSME3	ALOXE3
	ANXA2	HYOU1	PVR	ALPI
	ANXA7	IFT81	RAB5C	ALPP
	AP1B1	IGHM	RAC1	ALS2CR12
	AP1M1	ISG15	RAC2	ALX4
	AP2A1	ITGB1	RBBP7	ALYREF
	AP2A2	ITPR3	RBM10	AMBRA1
	AP2B1	JAK1	RBMS2	AMD1
	AP2M1	JPH3	RBX1	AMFR
	AP3D1	JUN	RFC2	AMHR2
	AP3M1	KARS	RHOA	AMIGO1
	AP4M1	KIF14	RHOB	AMOT
	APBB1	KIF20A	RHOD	AMOTL1
	APC	KIF23	RHOF	AMPD2
	APEH	KLF16	RIPPLY1	AMPD3
	APEX1	KLF8	RIPPLY2	AMZ1
	API5	KLF9	RNF123	ANAPC1
	APLNR	KLK10	RNF4	ANAPC10
	APLP2	KLKB1	RPN1	ANAPC11
	APMAP	KPNA1	RUVBL1	ANAPC2
	APOA1	KRAS	SEC16A	ANAPC4
	APOA2	KRR1	SF1	ANAPC5
	APOA4	KRTAP10-3	SGCA	ANG
	APOA5	KRTAP6-2	SLAIN2	ANGPTL3
	APOB	LAMP2	SMARCD1	ANGPTL4
	APOBEC1	LCE1A	SNRNP70	ANK1
	APOC1	LGALS3	SNRPA1	ANKFY1
	APOC2	LGALS7	SNRPB2	ANKHD1-EIF4
	APOC3	LGALS9	SNU13	ANKLE2
	APOD	LLCFC1	SNW1	ANKRD11
	APOE	LMAN1	SORT1	ANKRD13D
	APOL2	LRRCS9	SOX2	ANKRD17
	APOO	LRRK2	SOX6	ANKRD26
	APP	LSM12	SP7	ANKRD28
	APBP2	MAD2L2	SPANXN2	ANKRD46
	APPL1	MANEA	SSSCA1	ANKRD55
	AQP1	MAPK3	STOM	ANKRD9
	AQP3	MAPT	STX7	ANKS1A
	AQP6	MATN2	SUGP1	ANKS3
	AQP9	MBD3	SYN2	ANLN
	AR	MBNL1	SYNE3	ANO3
	ARAF	MDM2	TERF2IP	ANO6
	ARCN1	MECOM	TFIP11	ANO9
	ARF1	MED4	THY1	ANP32B
	ARF4	MGARP	TJP1	ANP32E
	ARF6	MLXIPL	TLE3	ANPEP
	ARFGAP1	MMP9	TM6SF2	ANTXR1
	ARHGEF2	MRPL50	TMOD3	ANTXR2
	ARFIP1	MTNR1A	TNIP2	ANXA1
	ARFIP2	MYC	TOP2B	ANXA2
	ARG1	NAA40	TP53	ANXA2P2
	ARHGAP11A	NCOA1	TRIB1	ANXA5
	ARHGAP21	NCOR1	TRIM25	ANXA6
	ARHGAP22	NDRG1	TRIM37	ANXA7
	ARHGAP25	NDUFV2	TSPAN15	AOC1
	ARHGAP29	NFX1	TUBA1A	AP1G1
	ARHGAP36	NHLRC2	TUBA1B	AP1M1
	ARHGAP39	NID2	UBD	AP1M2
	ARHGAP9	NIN	UBXN6	AP2A1
	ARHGDIA	NINL	UPK2	AP2B1
	ARHGEF10	NKX2-1	USP7	AP2M1
	ARHGEF12	NME2	VCP	AP3D1
	ARHGEF25	NMRAL1	VDAC1	AP3M1
	ARHGEF3	NOTCH1	VDAC2	AP3S1
	ARHGEF39	NR2C2	VDAC3	AP4M1
	ARHGEF4	NR3C1	VIRMA	AP5Z1
	ARHGEF5	NRAS	VSIG4	APAF1
	ARID1A	NSD2	WWOX	APBB1
	ARID1B	NTRK1	XPO1	APBB2
	ARID2	NUFIP1	XRCC6	APBB3
	ARID4B	NUFIP2	YBX1	APC
	ARID5A	OBSL1	YWHAZ	APEX1
	ARIH2	OGT	ZNF330	API5
	ARL1	PAFAH1B2	ZNHIT3	APLNR
	ARL13B	PAFAH1B3		APLP1
	ARL16	PAK4		APLP2
	ARL6IP1	PARP1		APOA1
	ARMC1	PCNA		APOA2
	ARMC12	PCSK7		APOA4
	ARMC6	PDHA1		APOA5
	ARMC7	PEX3		APOB
	ARMC8	PHB		APOC1
	ARMCX3	PHF11		APOC2
	ARNT	PICALM		APOD
	ARNTL	PLAT		APOE
	ARPC1B	PLCB1		APOH
	ARPC2	PLCB3		APOL2
	ARPC3	PLCB4		APOL6
	ARPC4	PLEKHA4		APOO
	ARPC5	PLTP		APP
	ARR3	POLR2A		APPBP2

Cohort	Whole	Female	Male	Previous
	ARRB1	PPARA		APPL1
	ARRB2	PPARGC1B		AQP1
	ARRDC1	PPIB		AQP2
	ARSA	PPP2CB		AQP3
	ARSG	PPT1		AQP6
	ARV1	PRC1		AQR
	ARX	PRDM16		AR
	ASB14	PRKCA		ARAF
	ASB3	PRKCD		ARF1
	ASB7	PRKN		ARF4
	ASF1A	PRNP		ARF5
	ASGR2	PSMG1		ARF6
	ASH2L	PTPRK		ARFGAP1
	ASIC4	RAC1		ARFGAP2
	ASNSD1	RAC3		ARFGEF1
	ASPH	RACGAP1		ARFGEF2
	ASS1	RAD18		ARFIP1
	ASXL1	RBM39		ARG1
	ATAD3A	RBX1		ARHGAP1
	ATAD3B	RC3H2		ARHGAP17
	ATAD5	RCHY1		ARHGAP21
	ATAT1	RECQL4		ARHGAP26
	ATE1	REEP3		ARHGAP29
	ATF2	RFC4		ARHGAP32
	ATF3	RGS12		ARHGAP35
	ATF4	RGS17		ARHGAP40
	ATF5	RHBDD1		ARHGDIA
	ATF6	RHOA		ARHGEF10
	ATF7IP	RHOC		ARHGEF11
	ATG14	RHOF		ARHGEF15
	ATG16L1	RIN3		ARHGEF19
	ATG2A	RNF2		ARHGEF7
	ATG4C	RNF4		ARHGEF9
	ATL3	RPA3		ARID1A
	ATM	RPL10		ARID1B
	ATN1	RPS4X		ARID2
	ATOH1	RRP1B		ARID3A
	ATP11C	RTCB		ARID3B
	ATP13A1	RTRAF		ARID4B
	ATP1A1	RXRG		ARID5A
	ATP1A2	RYBP		ARIH1
	ATP1A3	SARAF		ARIH2
	ATP1B1	SCARB1		ARL1
	ATP1B3	SCARNA22		ARL10
	ATP2A1	SCGB1D1		ARL13B
	ATP2A2	SDCBP		ARL15
	ATP2A3	SDHA		ARL4D
	ATP2B1	SH3GLB1		ARL6IP1
	ATP2B4	SHMT2		ARL8B
	ATP4A	SHPRH		ARMC1
	ATP5F1A	SIAH1		ARMC2
	ATP5F1B	SIDT2		ARMC8
	ATP5F1C	SIN3A		ARMCX3
	ATP5ME	SIRT1		ARNT
	ATP5PF	SIRT7		ARNT2
	ATP5PO	SKP2		ARNTL
	ATP6AP2	SLC12A5		ARPC1A
	ATP6VOA1	SLC25A13		ARPC1B
	ATP6VOA2	SMARCA1		ARPC2
	ATP6VOD1	SMARCA5		ARPC3
	ATP6V1A	SMARCD1		ARPC5
	ATP6V1B1	SMARCD2		ARR3
	ATP6V1B2	SNAI1		ARRB1
	ATP6V1C1	SNCA		ARRB2
	ATP6V1D	SNX27		ARSA
	ATP6V1E1	SORT1		ARSG
	ATP6V1F	SOX2		ARSK
	ATP6V1H	SPOP		ASB13
	ATR	SPP1		ASB14
	ATXN1	SPRED1		ASB6
	ATXN10	SOSTM1		ASB9
	ATXN2	ST6GALNAC6		ASCC2
	ATXN2L	STAT1		ASCC3
	ATXN3	STAT3		ASF1A
	ATXN3L	STAU1		ASGR2
	ATXN7	SUMO1		ASH2L
	ATXN7L3	SUMO2		ASIC1
	AUP1	SUZ12		ASIC4
	AURKA	SYNCRIP		ASNA1
	AURKAIP1	SYVN1		ASPH
	AURKB	TAGLN		ASPM
	AUTS2	TAGLN2		ASS1
	AVPR2	TAZ		ASXL1
	AXIN1	TCF3		ASXL2
	B2M	TEX101		ATAD3A
	B3GAT1	TGFBR2		ATAD3B
	B3GNT2	TGOLN2		ATE1
	B3GNT3	TIMP3		ATF2
	B4GALT2	TMEM43		ATF3
	B4GAT1	TMEM63B		ATF4
	BABAM1	TMPO		ATF6
	BABAM2	TMX1		ATF7
	BACE1	TNC		ATF7IP
	BACE2	TNFAIP8		ATG16L1
	BACH2	TNIP2		ATG3
	BAG1	TP53		ATG4A

Cohort	Whole	Female	Male	Previous
	BAG2	TRAF6		ATG7
	BAG3	TRIM14		ATG9A
	BAG5	TRIM25		ATG9B
	BAG6	TRIM33		ATL3
	BAK1	TRIM37		ATM
	BANF1	TRIM54		ATOH1
	BANP	TRIM55		ATP12A
	BAP1	TRIM63		ATP13A2
	BARD1	TUBA1A		ATP13A3
	BASP1	TUSC3		ATP1A1
	BATF	UBE2U		ATP1A3
	BATF2	UFL1		ATP1B1
	BATF3	UGT8		ATP1B3
	BAZ1B	UNC93B1		ATP1B4
	BBS1	UQCRCQ		ATP2A1
	BBS2	USP1		ATP2A2
	BBS7	USP15		ATP2A3
	BBX	VAR5		ATP2B1
	BCAP31	VCP		ATP2B2
	BCAR1	VIRMA		ATP2B4
	BCKDHA	WDR11		ATP2C1
	BCL11A	WDR5		ATP4A
	BCL11B	WDR76		ATP5F1A
	BCL2	XPO1		ATP5F1B
	BCL2L1	XRCC6		ATP5F1C
	BCL2L12	YIF1A		ATP5IF1
	BCL2L13	YWHAB		ATP5MD
	BCL2L14	YWHAE		ATP5ME
	BCL2L2	YWHAG		ATP5MF
	BCL7A	YWHAZ		ATP5MG
	BCL7B	ZBTB2		ATP5PB
	BCL7C	ZBTB21		ATP5PD
	BCOR	ZDHHC18		ATP5PF
	BCR	ZDHHC5		ATP5PO
	BCS1L	ZNF330		ATP6AP1
	BECN1	ZNF397		ATP6AP2
	BEND3			ATP6V0A2
	BEND7			ATP6V1A
	BET1			ATP6V1B2
	BEX2			ATP6V1C1
	BGN			ATP6V1G1
	BHLHE40			ATP6V1H
	BICD1			ATPAF1
	BICD2			ATPAF2
	BICRA			ATR
	BIN1			ATRN
	BIRC3			ATRN1
	BLK			ATRX
	BLM			ATXN1
	BMI1			ATXN10
	BMP1			ATXN1L
	BMP2K			ATXN2
	BMP4			ATXN2L
	BMP8A			ATXN3
	BMPR1A			ATXN7L1
	BMX			ATXN7L2
	BNIP3			AURKA
	BOLA1			AURKAIP1
	BOLA2			AURKB
	BORCS6			AVPR2
	BPTF			AXIN1
	BRCA1			AXL
	BRD1			AZGP1
	BRD2			B2M
	BRD3			B3GAT1
	BRD4			B3GNT2
	BRD7			B4GALNT4
	BRDT			B4GALT2
	BRICD5			B4GALT3
	BRINP1			B4GALT5
	BRINP2			B4GALT7
	BRIX1			B4GAT1
	BRMS1L			BAAT
	BSCL2			BABAM1
	BSG			BACE1
	BSND			BACE2
	BSPRY			BACH1
	BTAFA1			BACH2
	BTBD1			BAD
	BTF3			BAG1
	BTB			BAG2
	BTN3A3			BAG3
	BTNL2			BAG4
	BTNL9			BAG5
	BTRC			BAG6
	BUB1			BAGE2
	BUD13			BAHD1
	BYSL			BAIAP2
	C10orf88			BAIAP2L1
	C11orf52			BAK1
	C11orf54			BANF1
	C12orf43			BANK1
	C12orf49			BANP
	C12orf65			BAP1
	C14orf119			BARD1
	C15orf48			BASP1

Cohort	Whole	Female	Male	Previous
	C16orf58			BATF2
	C17orf49			BAZ
	C17orf53			BAZ1B
	C17orf75			BAZ2A
	C17orf80			BBC3
	C18orf25			BBOX1
	C19orf38			BBS7
	C1orf109			BBX
	C1orf216			BCAP31
	C1orf35			BCAR1
	C1orf54			BCAR3
	C1QA			BCAS2
	C1QB			BCCIP
	C1QBP			BCHE
	C1QTNF7			BCKDHA
	C20orf197			BCKDHB
	C2CD2L			BCKDK
	C2CD6			BCL10
	C2orf49			BCL11A
	C2orf73			BCL11B
	C3orf18			BCL2
	C3orf52			BCL2A1
	C4A			BCL2L1
	C6orf106			BCL2L10
	C6orf141			BCL2L11
	C6orf15			BCL2L12
	C6orf203			BCL2L13
	C8A			BCL2L2
	C8orf74			BCL3
	C8orf82			BCL6
	CA14			BCL6B
	CA9			BCL7A
	CABP5			BCL7C
	CACNA2D1			BCL9
	CACNG6			BCLAF1
	CACYBP			BCOR
	CAD			BCORL1
	CALCOCO2			BCR
	CALD1			BCS1L
	CALHM4			BDNF
	CALM1			BECN1
	CALML3			BEND3
	CALR			BEND7
	CALR3			BET1
	CALU			BEX1
	CAMK2A			BFAR
	CAMK2B			BFSP1
	CAMK2D			BGN
	CAMK2G			BHLHB9
	CAMKV			BHLHE40
	CAMLG			BICD1
	CAMSAP1			BICRA
	CAMSAP2			BID
	CAMSAP3			BIK
	CAND1			BIN1
	CANX			BIRC2
	CAPN1			BIRC3
	CAPN10			BIRC6
	CAPN2			BIRC7
	CAPZA1			BLK
	CAPZA2			BLM
	CAPZB			BLNK
	CARD10			BLOC1S2
	CARM1			BLOC1S6
	CARS			BLZF1
	CASK			BMF
	CASP6			BMi1
	CAV1			BMP4
	CAVIN1			BMP7
	CBARP			BMP8B
	CBFA2T3			BMPR1A
	CBL			BMPR1B
	CBLC			BMPR2
	CBLN4			BMS1
	CBR1			BNIP2
	CBS			BNIP3
	CBWD1			BOLA1
	CBX1			BOLA2
	CBX3			BOP1
	CBX4			BORCS6
	CBX5			BPGM
	CBX6			BPIFA1
	CBX8			BPIFB1
	CBY1			BPTF
	CCAR2			BRAF
	CCDC102B			BRCA1
	CCDC106			BRD1
	CCDC107			BRD2
	CCDC115			BRD3
	CCDC120			BRD4
	CCDC137			BRD7
	CCDC138			BRD8
	CCDC140			BRD9
	CCDC155			BRF1
	CCDC167			BRF2
	CCDC183			BRICD5

Cohort	Whole	Female	Male	Previous
	CCDC198			BRINP2
	CCDC22			BRIP1
	CCDC26			BRIX1
	CCDC36			BRK1
	CCDC47			BRMS1
	CCDC57			BRMS1L
	CCDC71			BRPF3
	CCDC8			BRWD1
	CCDC85C			BSCL2
	CCDC87			BSG
	CCDC88A			BTAF1
	CCDC90B			BTBD1
	CCDC92			BTB
	CCDC93			BTB3
	CCDC96			BTB3L4
	CCHCR1			BTG3
	CCL3			BTB
	CCL3L3			BTB2A1
	CCL4L1			BTB2
	CCM2L			BTB3
	CCN2			BTB8
	CCNA2			BTB9
	CCNB1			BTB
	CCNC			BUB1
	CCND1			BYSL
	CCND2			C10orf88
	CCNF			C11orf52
	CCNH			C12orf49
	CCNT1			C12orf65
	CCNT2			C12orf74
	CCPG1			C15orf48
	CCR1			C16orf58
	CCR4			C16orf71
	CCT2			C16orf87
	CCT3			C17orf49
	CCT4			C17orf80
	CCT5			C19orf25
	CCT6A			C1D
	CCT6B			C1GALT1C1
	CCT7			C1orf109
	CCT8			C1orf112
	CCT8L2			C1orf131
	CD177			C1orf220
	CD1A			C1orf35
	CD1B			C1orf43
	CD247			C1orf54
	CD274			C1orf94
	CD2AP			C1QB
	CD2BP2			C1QBP
	CD36			C1QC
	CD3D			C1QTNF2
	CD3EAP			C1QTNF7
	CD44			C1QTNF9B
	CD55			C2CD2L
	CD6			C2CD4A
	CD63			C2CD4B
	CD70			C2CD4C
	CD79A			C2CD6
	CD79B			C3
	CD80			C3orf18
	CD81			C3orf36
	CD83			C3orf52
	CD8A			C3orf62
	CD9			C4A
	CD99L2			C4BPB
	CDA			C4orf45
	CDC14B			C5AR1
	CDC16			C5AR2
	CDC20			C6orf106
	CDC20B			C6orf203
	CDC23			C7orf50
	CDC25A			C8A
	CDC27			C8orf82
	CDC34			CA10
	CDC37			CA14
	CDC42			CA6
	CDC45			CA8
	CDC5L			CA9
	CDC73			CABIN1
	CDCA3			CABP2
	CDCA5			CABP5
	CDH1			CACNA1A
	CDH13			CACNA1D
	CDH5			CACNB3
	CDIPT			CACNB4
	CDK1			CACNG4
	CDK11A			CACYBP
	CDK13			CAD
	CDK17			CALCA
	CDK18			CALCOCO1
	CDK19			CALCOCO2
	CDK2			CALCR
	CDK20			CALD1
	CDK2AP1			CALHM4
	CDK4			CALM1
	CDK5			CALML3

Cohort	Whole	Female	Male	Previous
	CDK5R1			CALR
	CDK5RAP2			CALR3
	CDK5RAP3			CALU
	CDK6			CAMK1
	CDK7			CAMK2A
	CDK8			CAMK2B
	CDK9			CAMK2D
	CDKAL1			CAMK2G
	CDKL3			CAMKK1
	CDKL5			CAMKMT
	CDKN1A			CAMKV
	CDKN1B			CAMSAP1
	CDKN1C			CAND1
	CDKN2A			CANX
	CDKN2C			CAPN1
	CDKN2D			CAPN2
	CDS2			CAPNS2
	CDT1			CAPRIN1
	CDV3			CAPZA1
	CDX1			CAPZA2
	CEACAM21			CAPZB
	CEACAM8			CARD10
	CEBPA			CARM1
	CEBPB			CARS
	CEBPD			CARTPT
	CEBPE			CASK
	CEBPG			CASP1
	CEBPZ			CASP3
	CELF1			CASP6
	CENPA			CASP7
	CENPO			CASP8
	CEP126			CASP9
	CEP128			CASQ2
	CEP131			CASZ1
	CEP135			CAT
	CEP152			CATSPER1
	CEP162			CAV1
	CEP164			CAV2
	CEP170			CAV3
	CEP250			CAVIN1
	CEP295			CBARP
	CEP350			CBFA2T2
	CEP44			CBFA2T3
	CEP55			CBFB
	CEP63			CBL
	CEP76			CBLB
	CEP85			CBLC
	CEP89			CBLN4
	CEP97			CBR1
	CETN2			CBR3
	CETP			CBWD3
	CFAP206			CBX1
	CFC1			CBX3
	CFL1			CBX4
	CFTR			CBX5
	CGAS			CBX6
	CGGBP1			CBX8
	CGREF1			CC2D1A
	CGRRF1			CC2D1B
	CHAF1A			CCAR1
	CHAF1B			CCAR2
	CHAMP1			CCDC102B
	CHCHD1			CCDC107
	CHCHD10			CCDC120
	CHCHD2			CCDC124
	CHCHD3			CCDC125
	CHD1			CCDC136
	CHD3			CCDC137
	CHD4			CCDC14
	CHD5			CCDC141
	CHD7			CCDC18
	CHEK2			CCDC183
	CHERP			CCDC22
	CHFR			CCDC26
	CHIC2			CCDC33
	CHMP1A			CCDC36
	CHMP4B			CCDC47
	CHMP4C			CCDC57
	CHRD			CCDC59
	CHRM4			CCDC62
	CHRM5			CCDC69
	CHRNA1			CCDC71
	CHRNA4			CCDC8
	CHRNA9			CCDC85B
	CHRNA1			CCDC85C
	CHRNA2			CCDC86
	CHRNA4			CCDC88A
	CHST14			CCDC88B
	CHST8			CCDC9
	CHUK			CCDC90B
	CIAO1			CCDC92
	CIAO2A			CCDC93
	CIC			CCDC96
	CILP2			CCHCR1
	CIPC			CCL2
	CIR1			CCL3

Cohort	Whole	Female	Male	Previous
	CISD1			CCL3L3
	CISD2			CCL4L1
	CISD3			CCN2
	CIT			CCN3
	CKAP4			CCNA1
	CKAP5			CCNA2
	CKB			CCNB1
	CKM			CCND1
	CKMT1B			CCND2
	CLASP1			CCND3
	CLASP2			CCNE1
	CLCC1			CCNE2
	CLDN3			CCNF
	CLDND1			CCNK
	CLEC12B			CCNL2
	CLEC2B			CCNO
	CLEC2D			CCNT1
	CLEC3A			CCPG1
	CLEC4A			CCR1
	CLEC4D			CCR6
	CLEC4E			CCT2
	CLGN			CCT3
	CLIC1			CCT4
	CLINT1			CCT5
	CLIP2			CCT6A
	CLK2			CCT6B
	CLK3			CCT7
	CLN3			CCT8
	CLN6			CCT8L2
	CLNS1A			CD109
	CLOCK			CD151
	CLPB			CD160
	CLPP			CD177
	CLPTM1L			CD1A
	CLSTN3			CD1B
	CLTA			CD22
	CLTB			CD244
	CLTC			CD247
	CLTCL1			CD274
	CLU			CD2AP
	CLUAP1			CD2BP2
	CLUH			CD300LG
	CMIP			CD302
	CMKLR1			CD36
	CMPK1			CD3D
	CMTM5			CD3EAP
	CMTM7			CD4
	CMTR1			CD40
	CNBP			CD44
	CNGA3			CD5
	CNN3			CD6
	CNNM1			CD63
	CNNM3			CD7
	CNOT1			CD70
	CNOT11			CD74
	CNOT2			CD79A
	CNOT7			CD79B
	CNOT9			CD80
	CNR2			CD81
	CNTRL			CD83
	COBL			CD8A
	COBLL1			CD9
	COG6			CD93
	COIL			CD99
	COL12A1			CDA
	COL13A1			CDC123
	COL14A1			CDC14B
	COL1A1			CDC16
	COL1A2			CDC20
	COL2A1			CDC20B
	COL4A1			CDC25A
	COL4A3			CDC25C
	COL4A4			CDC27
	COL4A5			CDC34
	COL6A1			CDC37
	COMT			CDC42
	COMTD1			CDC45
	COP1			CDC5L
	COPA			CDC6
	COPB1			CDC7
	COPB2			CDC73
	COPE			CDCA2
	COPG1			CDCA5
	COPS2			CDH1
	COPS3			CDH16
	COPS5			CDH23
	COPS6			CDH3
	COPS7A			CDH5
	COPZ1			CDIPT
	COQ8A			CDK1
	COQ9			CDK11B
	CORO1B			CDK17
	CORO1C			CDK18
	CORO2A			CDK19
	COX14			CDK2
	COX15			CDK2AP1

Cohort	Whole	Female	Male	Previous
	COX2			CDK3
	COX4I1			CDK4
	COX5A			CDK5
	COX5B			CDK5RAP2
	COX6B1			CDK6
	COX8A			CDK7
	CPEB1			CDK8
	CPEB4			CDK9
	CPLX4			CDKAL1
	CPNE7			CDKL3
	CPSF1			CDKN1A
	CPSF6			CDKN18
	CPSF7			CDKN1C
	CPT1A			CDKN2A
	CPT2			CDKN2AIP
	CPVL			CDKN2B
	CRBN			CDKN2B-AS1
	CREB3			CDKN2C
	CREB3L1			CDKN2D
	CREB3L3			CDS2
	CREB5			CDSN
	CREBBP			CDV3
	CRELD1			CDX1
	CRK			CEACAM1
	CRKL			CEACAM21
	CRLF1			CEACAM8
	CRNN			CEBPA
	CRTAP			CEBPB
	CRTC2			CEBPD
	CRY1			CEBPZ
	CRY2			CELA1
	CRYAA			CELF1
	CRYAB			CELSR1
	CRYZ			CELSR2
	CS			CENPA
	CSAG1			CENPB
	CSAG3			CENPJ
	CSDE1			CENPQ
	CSE1L			CENPV
	CSK			CEP126
	CSNK1A1			CEP128
	CSNK1D			CEP135
	CSNK1E			CEP164
	CSNK1G2			CEP170
	CSNK1G3			CEP170P1
	CSNK2A1			CEP19
	CSNK2A2			CEP250
	CSNK2B			CEP55
	CSPP1			CEP57L1
	CSRP2			CEP63
	CST1			CEP68
	CST11			CEP70
	CSTF2			CEP76
	CT45A5			CEP85
	CTBP1			CERCAM
	CTBP2			CERK
	CTCF			CERS2
	CTDSP1			CERS4
	CTDSP2			CERS6
	CTDSPL			CETP
	CTDSPL2			CFAP161
	CTLA4			CFAP206
	CTNNA1			CFAP410
	CTNNA3			CFAP97
	CTNNB1			CFL1
	CTNND1			CFL2
	CTPS1			CFP
	CTR9			CFTR
	CTSB			CGAS
	CTSL			CGB3
	CTSS			CGGBP1
	CTTN			CGN
	CTTNBP2			CGREF1
	CUL1			CGRRF1
	CUL2			CHAC2
	CUL3			CHAF1A
	CUL4A			CHAF1B
	CUL4B			CHCHD1
	CUL5			CHCHD10
	CUL7			CHCHD2
	CUL9			CHCHD3
	CUX1			CHCHD4
	CUX2			CHD1
	CWF19L2			CHD1L
	CXADR			CHD3
	CXCL16			CHD4
	CXCL8			CHD5
	CXCR2			CHD7
	CXCR4			CHD8
	CYB5B			CHEK1
	CYB5R1			CHEK2
	CYB5R3			CHERP
	CYC1			CHFR
	CYCS			CHGB
	CYHR1			CHIC2
	CYLD			CHID1

Cohort	Whole	Female	Male	Previous
	CYP26A1			CHM
	CYP27A1			CHMP4B
	CYP2C8			CHMP4C
	CYP2C9			CHPF
	CYP51A1			CHPT1
	CYP7A1			CHRD
	CYSRT1			CHRD2
	D2HGDH			CHRM3
	DAB2			CHRM4
	DAD1			CHST12
	DAGLA			CHST14
	DAP3			CHSY1
	DAPK3			CHSY3
	DARS			CHTOP
	DARS2			CHUK
	DAXX			CIAO1
	DAZAP2			CIAO2A
	DAZL			CIAO2B
	DBI			CIB1
	DBN1			CIB2
	DBP			CIB3
	DCAF13			CIC
	DCAF15			CIDEB
	DCAF16			CINP
	DCAF4			CIP2A
	DCAF7			CIR1
	DCAF8			CIRBP
	DCD			CISD2
	DCLK1			CISH
	DCLRE1B			CIT
	DCN			CKAP4
	DCP1A			CKAP5
	DCP1B			CKB
	DCPS			CKMT1B
	DCTN1			CLASP1
	DCTN2			CLASRP
	DCTPP1			CLDN7
	DCUN1D1			CLEC11A
	DCX			CLEC12B
	DDA1			CLEC2B
	DDHD1			CLEC2D
	DDHD2			CLEC4A
	DDIT3			CLEC4D
	DDIT4L			CLEC4E
	DDOST			CLGN
	DDR1			CLIC1
	DDR2			CLIP1
	DDRGK1			CLK1
	DDX1			CLK2
	DDX11			CLMN
	DDX17			CLN3
	DDX18			CLN6
	DDX19B			CLNK
	DDX20			CLOCK
	DDX21			CLP1
	DDX23			CLPB
	DDX24			CLPP
	DDX31			CLPTM1
	DDX39A			CLSTN1
	DDX39B			CLSTN3
	DDX3X			CLTA
	DDX3Y			CLTC
	DDX41			CLTCL1
	DDX42			CLU
	DDX5			CLUAP1
	DDX51			CMIP
	DDX56			CMKLR1
	DDX58			CMSS1
	DDX6			CMTM4
	DECR1			CMTM5
	DEF6			CMTR1
	DEFA1			CNBP
	DEFA5			CNDP2
	DEK			CNKSR1
	DERL1			CNKSR3
	DES			CNNM1
	DGCR2			CNNM3
	DGCR8			CNNM4
	DGKZ			CNOT1
	DGUOK			CNOT10
	DHCR7			CNOT11
	DH0H			CNOT2
	DHFR2			CNOT3
	DHRS11			CNOT6
	<i>DHRS7B</i>			CNOT6L
	DHRSX			CNOT7
	DHX15			CNOT9
	DHX16			CNP
	DHX37			CNTN1
	DHX38			CNTN2
	DHX40			CNTNAP3
	DHX8			CNTNAP3B
	DHX9			CNTRL
	DIABLO			CNTR0B
	DIAPH3			COBLL1
	DICER1			COG3

Cohort	Whole	Female	Male	Previous
	DIP2A			COG6
	DIP2B			COIL
	DIPK1A			COL10A1
	DIPK2A			COL13A1
	DIRAS3			COL14A1
	DISC1			COL1A1
	DKK3			COL4A1
	DKKL1			COL4A2
	DLAT			COL4A5
	DLD			COL6A1
	DLG1			COL6A2
	DLG3			COLEC11
	DLG5			COLGALT2
	DLK1			COMMD1
	DLK2			COMMD2
	DLST			COMMD3
	DMRT2			COMMD4
	DNA2			COMMD5
	DNAAF2			COMMD8
	DNAJA1			COMT
	DNAJA2			COP1
	DNAJA3			COPA
	DNAJA4			COPB1
	DNAJB1			COPB2
	DNAJB11			COPG1
	DNAJB12			COPS2
	DNAJB14			COPS3
	DNAJB4			COPS4
	DNAJB6			COPS5
	DNAJB9			COPS6
	DNAJC1			COPS8
	DNAJC10			COQ8A
	DNAJC11			COQ9
	DNAJC12			CORO1A
	DNAJC16			CORO1B
	DNAJC18			CORO1C
	DNAJC19			CORO6
	DNAJC2			COX14
	DNAJC25			COX15
	DNAJC30			COX2
	DNAJC5			COX4I1
	DNAJC6			COX5A
	DNAJC7			COX6A1
	DNAJC8			COX6B1
	DNAJC9			COX7A2
	DNAL4			COX7C
	DNASE1L1			COX8A
	DNM1L			CPA2
	DNM2			CPD
	DNMT1			CPE
	DOCK5			CPEB1
	DOCK7			CPEB4
	DOCK8			CPNE2
	DOK4			CPNE4
	DOK7			CPNE5
	DOT1L			CPS1
	DPEP1			CPSF1
	DPF1			CPSF6
	DPF2			CPSF7
	DPP4			CPT1A
	DPPA4			CPT2
	DPY30			CPVL
	DPYSL3			CRACR2B
	DPYSL4			CRCP
	DPYSL5			CREB1
	DR1			CREB3
	DRD2			CREB5
	DRG1			CREBBP
	DRG2			CRELD1
	DSC1			CRELD2
	DSCAML1			CRIP2
	DSE			CRK
	DSG1			CRKL
	DSG2			CRLF3
	DSG4			CRMP1
	DSN1			CRNKL1
	DSP			CRP
	DST			CRTAC1
	DTL			CRTAP
	DTNB			CRTC2
	DTNBP1			CRX
	DTX2			CRY1
	DTX3			CRY2
	DUSP1			CRYAB
	DUSP14			CRYBB3
	DUSP16			CS
	DUSP19			CSDE1
	DUSP22			CSE1L
	DUSP23			CSF1
	DUSP4			CSF1R
	DUSP6			CSF2RA
	DUT			CSF2RB
	DUX4			CSGALNACT2
	DUX4L1			CSK
	DUX4L9			CSN1S1
	DVL1			CSNK1A1

Cohort	Whole	Female	Male	Previous
	DVL2			CSNK1D
	DVL3			CSNK1E
	DYNC1H1			CSNK1G2
	DYNC1I2			CSNK1G3
	DYNC1LI1			CSNK2A1
	DYNC1LI2			CSNK2A2
	DYNLL1			CSNK2B
	DYNLL2			CSPG5
	DYNLRB1			CST11
	DYNLT1			CST5
	DYRK1A			CSTB
	DYRK2			CTAG1B
	E2F3			CTAGE1
	EAF1			CTBP1
	EBAG9			CTBP2
	EBNA1BP2			CTCF
	EBP			CTDNBP1
	ECEL1			CTDP1
	ECH1			CTDSP1
	ECPAS			CTDSP2
	ECSIT			CTHRC1
	ECT2			CTLA4
	ECT2L			CTNNA1
	EDAR			CTNNA2
	EDC3			CTNNB1
	EDC4			CTNND1
	EDEM1			CTPS1
	EDF1			CTR9
	EDN3			CTSA
	EED			CTSB
	EEF1A1			CTSL
	EEF1A2			CTSS
	EEF1AKMT3			CTSZ
	EEF1D			CTTN
	EEF1E1			CTTNBP2
	EEF1G			CTTNBP2NL
	EEF2			CTU1
	EEF2K			CTU2
	EFEMP2			CUEDC1
	EFNA2			CUL1
	EFNA4			CUL2
	EFNB1			CUL3
	EFNB2			CUL4A
	EFR3A			CUL4B
	EFTUD2			CUL5
	EGF			CUL7
	EGFL7			CUL9
	EGFL8			CUTC
	EGFR			CUX1
	EGLN3			CWC15
	EHBP1			CWC22
	EHD2			CWC27
	EHHADH			CWF19L2
	EHMT1			CXADR
	EHMT2			CXCL16
	EID3			CXCR3
	EIF1AD			CXCR4
	EIF1AX			CXorf56
	EIF2AK2			CXXC1
	EIF2AK3			CYB5B
	EIF2B2			CYB5R3
	EIF2B3			CYC1
	EIF2S3			CYCS
	EIF3A			CYFIP2
	EIF3B			CYHR1
	EIF3C			CYLD
	EIF3D			CYP19A1
	EIF3E			CYP1A1
	EIF3F			CYP26A1
	EIF3H			CYP27A1
	EIF3I			CYP2C9
	EIF4A1			CYP2S1
	EIF4A3			CYP51A1
	EIF4B			CYP7A1
	EIF4E			CYSRT1
	EIF4E2			CYTH1
	EIF4EBP1			CYTH2
	EIF4ENIF1			CYTH3
	EIF4G1			CYTOR
	EIF4H			D2HGDH
	EIF5A			DAB2
	EIF6			DAB2IP
	EIPR1			DACH1
	ELAC2			DAG1
	ELANE			DAP3
	ELAVL1			DAPK1
	ELF1			DAPK3
	ELF2			DAPP1
	ELF4			DARS
	ELK1			DARS2
	ELK3			DAXX
	ELK4			DAZAP2
	ELN			DBN1
	ELOA			DBT
	ELOC			DCAF1
	ELOVL4			DCAF10

Cohort	Whole	Female	Male	Previous
	ELOVL5			DCAF11
	ELP2			DCAF13
	ELP3			DCAF15
	ELSPBP1			DCAF5
	EMC1			DCAF7
	EMC2			DCANP1
	EMC4			DCBLD2
	EMC7			DCC
	EMC8			DCD
	EMD			DCLK1
	EMILIN1			DCP1B
	EMSY			DCP2
	EN1			DCPS
	ENG			DCTN1
	ENKD1			DCTN2
	ENO1			DCTN3
	ENO2			DCTN4
	ENY2			DCUN1D1
	EP300			DDA1
	EPB41			DDB2
	EPB41L1			DDIT3
	EPB41L2			DDIT4
	EPB41L3			DDIT4L
	EPB41L4A			DDOST
	EPB41L5			DDR1
	EPDR1			DDRKG1
	EPHA2			DDT
	EPHA7			DDX1
	EPHB2			DDX10
	EPN1			DDX11L8
	EPN2			DDX17
	EPRS			DDX18
	EPS15			DDX19B
	EPS15L1			DDX20
	ERAP1			DDX21
	ERBB2			DDX23
	ERBB3			DDX24
	ERBIN			DDX27
	ERCC3			DDX31
	ERCC6			DDX39A
	ERCC8			DDX39B
	ERG			DDX3X
	ERGIC1			DDX41
	ERGIC3			DDX42
	ERLEC1			DDX46
	ERLIN2			DDX47
	ERMP1			DDX5
	ERP29			DDX50
	ERRF1			DDX52
	ESR1			DDX54
	ESR2			DDX55
	ESRRA			DDX56
	ESYT1			DDX58
	ETFA			DDX6
	ETFRF1			DEFA1
	ETS1			DEFA5
	ETV3			DEFB109B
	ETV6			DEGS1
	EVA1B			DEK
	EVA1C			DENND6A
	EVC2			DEPDC1B
	EVI5			DERL1
	EVI5L			DERL2
	EWSR1			DET1
	EXD2			DEUP1
	EXOC1			DGCR2
	EXOC2			DGKQ
	EXOC3			DGKZ
	EXOC4			DGUOK
	EXOC5			DHCR7
	EXOC6			DHFR
	EXOC7			DHFR2
	EXOC8			DHRS2
	EXOSC1			DHRS4
	EXOSC4			DHRS9
	EXOSC5			DHX15
	EXOSC6			DHX30
	EXPH5			DHX36
	EXT2			DHX37
	EYA1			DHX40
	EYA2			DHX57
	EZH1			DHX8
	EZH2			DHX9
	EZR			DIABLO
	F10			DIAPH1
	F2			DICER1
	F2RL1			DIDO1
	FABP1			DIMT1
	FABP4			DIP2B
	FABP5			DIPK1A
	FADD			DIRAS3
	FADS1			DIS3
	FADS2			DISC1
	FADS3			DKC1
	FAF1			DKK3
	FAF2			DKKL1

Cohort	Whole	Female	Male	Previous
	FAM110A			DLAT
	FAM118B			DLC1
	FAM120C			DLD
	FAM161A			DLEU1
	FAM161B			DLEU2
	FAM163B			DLG1
	FAM168A			DLG2
	FAM170A			DLG3
	FAM171A2			DLG4
	FAM171B			DLG5
	FAM174A			DLGAP2
	FAM177A1			DLGAP3
	FAM184B			DLGAP4
	FAM189A2			DLK1
	FAM189B			DLK2
	FAM192A			DLST
	FAM209A			DMAP1
	FAM20C			DMD
	FAM217B			DMRTA1
	FAM222A			DMRTB1
	FAM230I			DNAAF2
	FAM234A			DNAAF5
	FAM241A			DNAH10
	FAM3C			DNAI2
	FAM76B			DNAJA1
	FAM83A			DNAJA2
	FAM83B			DNAJA3
	FAM83H			DNAJA4
	FAM8A1			DNAJB1
	FAM90A1			DNAJB11
	FAM91A1			DNAJB12
	FAM98A			DNAJB14
	FAM98B			DNAJB2
	FAM9A			DNAJB4
	FAM9B			DNAJB5
	FANCA			DNAJB6
	FANCD2			DNAJB8
	FANCI			DNAJB9
	FANCL			DNAJC1
	FANCM			DNAJC10
	FARP1			DNAJC11
	FARS2			DNAJC12
	FARSA			DNAJC13
	FAS			DNAJC14
	FASN			DNAJC16
	FASTKD1			DNAJC18
	FASTKD5			DNAJC2
	FATE1			DNAJC25
	FAXC			DNAJC3
	FBF1			DNAJC30
	FBL			DNAJC5
	FBLN1			DNAJC6
	FBLN5			DNAJC7
	FBP1			DNAJC8
	FBR5			DNAJC9
	FBXL13			DNASE1L1
	FBXL17			DNASE1L2
	FBXL19			DNM1
	FBXO2			DNM1L
	FBXO25			DNM2
	FBXO28			DNM3
	FBXO38			DNMBP
	FBXO45			DNMT1
	FBXO46			DNMT3A
	FBXO6			DNMT3B
	FBXO7			DNMT3L
	FBXW11			DNTTIP2
	FBXW5			DOCK3
	FBXW7			DOCK5
	FBXW8			DOCK6
	FCER1G			DOCK7
	FCGRT			DOCK8
	FCHO2			DOK1
	FDFT1			DOK7
	FDPS			DOLK
	FEM1A			DOP1B
	FEN1			DOT1L
	FERMT2			DPEP1
	FEV			DPEP2
	FFAR1			DPF1
	FGA			DPF2
	FGB			DPF3
	FGD5			DPH6
	FGF1			DPM1
	FGF11			DPP3
	FGF12			DPP4
	FGF13			DPPA4
	FGF2			DPY30
	FGF4			DPYD
	FGF8			DPYSL2
	FGFBP1			DPYSL3
	FGFR1			DPYSL5
	FGFR1OP			DRD2
	FGFR2			DRG1
	FGFR3			DROSHA
	FGFR4			DSC2

Cohort	Whole	Female	Male	Previous
	FGL1			DSCAML1
	FGR			DSG1
	FHL1			DSG2
	FHL2			DSG4
	FHL3			DSN1
	FHL5			DSP
	FIBIN			DST
	FIP1L1			DSTN
	FIS1			DTL
	FITM2			DTNA
	FKBP10			DTNB
	FKBP1A			DTNBP1
	FKBP3			DTX2
	FKBP4			DUSP1
	FKBP5			DUSP14
	FKBP6			DUSP15
	FKBP8			DUSP16
	FLG			DUSP19
	FLII			DUSP22
	FLNA			DUSP3
	FLNB			DUSP4
	FLNC			DUSP6
	FLOT1			DUT
	FLOT2			DUX4
	FLT3			DUX4L1
	FMN2			DVL2
	FMNL1			DVL3
	FMR1			DYM
	FN1			DYNC1H1
	FNDC11			DYNC1I1
	FNDC3A			DYNLL1
	FNDC4			DYNLL2
	FNTA			DYNLRB1
	FOS			DYNLT1
	FOSL1			DYRK1A
	FOSL2			DYRK1B
	FOXA1			DYRK2
	FOXA2			DZIP3
	FOXA3			E2F1
	FOXB1			E2F2
	FOXD4L6			E2F3
	FOXE1			E2F4
	FOXG1			E2F5
	FOXI1			E2F6
	FOXJ2			EEF1
	FOXJ1			EAPP
	FOXN2			EBAG9
	FOXO3			EBF1
	FOXP2			EBNA1BP2
	FOXQ1			EBP
	FOXRED2			ECD
	FPR1			ECEL1
	FPR2			ECH1
	FRS2			ECHS1
	FRS3			ECI2
	FSCN1			ECM2
	FTH1			ECPAS
	FTL			ECSIT
	FUBP3			ECT2
	FURIN			EDA
	FUS			EDAR
	FUT1			EDC4
	FUT8			EDDM3B
	FXR1			EDEM1
	FXR2			EDEM2
	FXVD3			EDEM3
	FYN			EDN3
	FZD3			EDNRA
	FZD7			EDNRB
	FZD8			EDRF1
	FZD9			EEA1
	FZR1			EED
	G3BP1			EEF1A1
	G3BP2			EEF1A2
	G6PC2			EEF1AKMT3
	GAB1			EEF1B2
	GABARAP			EEF1D
	GABARAPL1			EEF1E1
	GABARAPL2			EEF1G
	GABBR1			EEF2
	GABRA3			EEF2K
	GABRD			EFEMP1
	GABRE			EFEMP2
	GADD45A			EFHD1
	GADD45B			EFNA4
	GADD45G			EFNB1
	GADD45GIP1			EFNB2
	GAGE4			EFS
	GAK			EFTUD2
	GAL3ST1			EGF
	GALNT2			EGFL7
	GALNT7			EGFL8
	GALT			EGFR
	GAN			EGLN1
	GANAB			EGLN3
	GAPDH			EHD4

Cohort	Whole	Female	Male	Previous
	GARS			EHHADH
	GART			EHMT1
	GAS2L1			EHMT2
	GAS2L2			EIF1AD
	GAS2L3			EIF1B
	GATA2			EIF2A
	GATA3			EIF2AK2
	GATA6			EIF2AK3
	GATAD1			EIF2B2
	GATAD2A			EIF2B3
	GATAD2B			EIF2B4
	GBA			EIF2B5
	GBAP1			EIF2S1
	GBE1			EIF2S2
	GBF1			EIF3A
	GCC2			EIF3B
	GCDH			EIF3C
	GCK			EIF3D
	GCKR			EIF3E
	GCM1			EIF3F
	GCN1			EIF3G
	GCNT1			EIF3H
	GCOM1			EIF3I
	GDI1			EIF3K
	GDI2			EIF3L
	GDPD1			EIF3M
	GEM			EIF4A1
	GEMIN4			EIF4A2
	GFAP			EIF4A3
	GF11B			EIF4B
	GFPT1			EIF4E
	GGA1			EIF4E2
	GGA2			EIF4E3
	GGA3			EIF4EBP1
	GGH			EIF4ENIF1
	GNB2P2			EIF4G1
	GIGYF1			EIF4H
	GIGYF2			EIF5
	GIN53			EIF5A
	GJA1			EIF5B
	GJD3			EIF6
	GLB1L2			EIPR1
	GLE1			ELAVL1
	GLG1			ELF1
	GLI1			ELF2
	GLI4			ELF4
	GLP1R			ELK1
	GLUD1			ELK3
	GLUL			ELL2
	GMCL1			ELMSAN1
	GMIP			ELOA
	GMNN			ELOB
	GMPS			ELOC
	GNAI1			ELOVL5
	GNAI2			ELP3
	GNAI3			ELSPBP1
	GNAO1			EMC1
	GNAQ			EMC2
	GNAS			EMC3
	GNAT3			EMC4
	GNAZ			EMC8
	GNB1			EMD
	GNB2			EMILIN1
	GNB4			EML2
	GNE			EML3
	GNG13			EMSY
	GNG8			EN1
	GNL2			ENDOG
	GNL3L			ENG
	GOLGA1			ENKD1
	GOLGA2			ENO1
	GOLGA3			ENTPD2
	GOLGA5			ENTPD7
	GOLGA8A			ENTR1
	GOLM1			EOGT
	GOLT1B			EP300
	GON4L			EP400
	GOPC			EPAS1
	GORASP2			EPB41
	GOT1			EPB41L1
	GOT2			EPB41L2
	GPANK1			EPB41L3
	GPATCH4			EPB41L4A
	GPC1			EPB41L5
	GPC4			EPC1
	GPC6			EPC2
	GPIHBP1			EPHA1
	GPKOW			EPHA2
	GPLD1			EPHA4
	GPM6A			EPHB1
	GPN1			EPHB2
	GPN3			EPHB4
	GPR17			EPHB6
	GPR173			EPHX1
	GPR182			EPN1
	GPR21			EPN2

Cohort	Whole	Female	Male	Previous
	GPR37			EPOR
	GPR45			EPPK1
	GPR50			EPRS
	GPRC5A			EPS15
	GPRC5B			EPS8
	GPS1			EPST11
	GPX1			ERAL1
	GPX8			ERBB2
	GRB10			ERBB3
	GRB14			ERBB4
	GRB2			ERBIN
	GRB7			ERC1
	GRDX			ERCC4
	GREM2			ERCC6
	GRIA1			ERG
	GRIA2			ERGIC1
	GRIA3			ERGIC2
	GRIA4			ERGIC3
	GRIN2C			ERH
	GRK2			ERICH2
	GRK5			ERLEC1
	GRM2			ERLIN1
	GRM4			ERLIN2
	GRM7			ERMP1
	GRN			ERN1
	GRPEL1			ERO1A
	GRPR			ERP29
	GRSF1			ERP44
	GRWD1			ERRF1
	GSC2			ESM1
	GSDMA			ESPL1
	GSK3A			ESR1
	GSK3B			ESR2
	GSN			ESRRA
	GSPT1			ESRRG
	GSPT2			ESS2
	GSTA1			ESYT1
	GSTA2			ETF1
	GSTA3			ETFA
	GSTA4			ETFB
	GSTA5			ETS1
	GSTP1			ETV4
	GSX1			ETV6
	GTF2B			EVA1B
	GTF2E1			EVA1C
	GTF2E2			EVC2
	GTF2F1			EVI5
	GTF2F2			EVI5L
	GTF2H1			EWSR1
	GTF2H2			EXD2
	GTF2H3			EXOC1
	GTF2H4			EXOC2
	GTF2I			EXOC3
	GTF2IRD1			EXOC5
	GTF2IRD2			EXOC6
	GTF2IRD2B			EXOC7
	GTF3C1			EXOC8
	GTF3C2			EXOSC1
	GTF3C3			EXOSC10
	GTF3C4			EXOSC2
	GTPBP4			EXOSC3
	GTSE1			EXOSC4
	GYP A			EXOSC5
	H1FNT			EXOSC7
	H2AFB2			EXOSC8
	H2AFJ			EXOSC9
	H2AFX			EXT1
	H2AFY			EXT2
	H2AFY2			EXTL3
	H2AFZ			EYA1
	H2BFS			EYA2
	H3F3A			EYA4
	HABP4			EZH1
	HACD3			EZH2
	HADH			EZR
	HADHA			F11R
	HADHB			F12
	HAP1			F2
	HAPLN4			FABP4
	HARS			FABP5
	HARS2			FADD
	HAT1			FADS1
	HAUS1			FADS2
	HAUS3			FAF1
	HAUS6			FAF2
	HAUS8			FAM117B
	HAVCR1			FAM120A
	HAX1			FAM120C
	HBA1			FAM136A
	HBB			FAM13A
	HBP1			FAM161A
	HCFC1			FAM167A
	HCFC2			FAM171B
	HCG18			FAM173A
	HCG27			FAM174A
	HCK			FAM184A

Cohort	Whole	Female	Male	Previous
	HCRTR2			FAM189B
	HDAC1			FAM209A
	HDAC11			FAM20C
	HDAC2			FAM214B
	HDAC3			FAM217B
	HDAC4			FAM227A
	HDAC5			FAM234A
	HDAC6			FAM241A
	HDCC3			FAM3C
	HDGF			FAM50B
	HDGFL2			FAM76B
	HEATR1			FAM81A
	HEATR6			FAM8A1
	HECTD1			FAM90A1
	HECW2			FAM91A1
	HELZ			FAM98A
	HELZ2			FAM9A
	HEPHL1			FANCA
	HERC1			FANCC
	HERC2			FANCD2
	HEXIM1			FANCI
	HEYL			FAP
	HFE			FARP2
	HGF			FARS2
	HGFAC			FARSA
	HGS			FARSB
	HHEX			FAS
	HIF1A			FASN
	HIF1AN			FASTKD1
	HINT1			FASTKD3
	HIP1			FASTKD5
	HIP1R			FAT1
	HIST1H1A			FAT3
	HIST1H1B			FAT4
	HIST1H1C			FAU
	HIST1H1D			FBF1
	HIST1H1E			FBL
	HIST1H2AE			FBLN1
	HIST1H2AH			FBLN2
	HIST1H2AI			FBLN5
	HIST1H2BB			FBP1
	HIST1H2BD			FBRS
	HIST1H2BG			FBXL2
	HIST1H2BH			FBXL5
	HIST1H2BK			FBXO10
	HIST1H2BL			FBXO11
	HIST1H3A			FBXO2
	HIST2H2AB			FBXO22
	HIST2H2AC			FBXO25
	HIST2H2BE			FBXO28
	HIST2H2BF			FBXO32
	HIST2H3C			FBXO38
	HIST2H3PS2			FBXO42
	HIST3H3			FBXO44
	HIST4H4			FBXO45
	HIVEP1			FBXO6
	HJURP			FBXO7
	HK1			FBXW11
	HLA-A			FBXW5
	HLA-B			FBXW7
	HLA-C			FBXW8
	HLA-DPA1			FCER1G
	HLA-DPB1			FCGR2A
	HLA-DQA1			FCGR2B
	HLA-DQB1			FCGRT
	HLA-DRA			FDFT1
	HLA-DRB1			FEN1
	HLA-DRB3			FER
	HLA-E			FES
	HLA-F			FEV
	HLA-G			FEZ1
	HLA-H			FFAR1
	HLF			FGB
	HMBOX1			FGD5
	HMG20A			FGF1
	HMGA1			FGF11
	HMGB1			FGF12
	HMGB3			FGF13
	HMGXB4			FGF2
	HMMR			FGF21
	HMOX2			FGF4
	HNF1A			FGF7
	HNF1B			FGF9
	HNF4A			FGFBP1
	HNRNPA0			FGFR1
	HNRNPA1			FGFR1OP
	HNRNPA2B1			FGFR1OP2
	HNRNPA3			FGFR2
	HNRNPC			FGFR3
	HNRNPCL2			FGFR4
	HNRNPD			FGG
	HNRNPDL			FGL1
	HNRNPF			FGR
	HNRNPH1			FHL1
	HNRNPH2			FHL2
	HNRNPK			FHL3

Cohort	Whole	Female	Male	Previous
	HNRNPL			FHL5
	HNRNPLL			FHOD1
	HNRNPM			FIBIN
	HNRNPR			FIP1L1
	HNRNPU			FIS1
	HNRNPUL1			FIZ1
	HOGA1			FKBP10
	HOMER3			FKBP14
	HOMEZ			FKBP1A
	HOOK3			FKBP3
	HOXA1			FKBP4
	HOXA5			FKBP5
	HOXB5			FKBP6
	HOXC5			FKBP8
	HOXC8			FKBP9
	HP			FKBPL
	HPN			FLCN
	HPRT1			FLG2
	HPX			FLII
	HR			FLNA
	HRAS			FLNB
	HSCB			FLNC
	HSD11B1			FLOT1
	HSD17B10			FLOT2
	HSD17B11			FLRT1
	HSD17B12			FLT1
	HSD17B4			FLT3
	HSD3B7			FLT4
	HSF1			FLYWCH2
	HSF2			FMC1
	HSF2BP			FMR1
	HSP90AA1			FN1
	HSP90AA5P			FNBP1
	HSP90AB1			FNBP4
	HSP90B1			FNDC11
	HSPA1A			FNIP1
	HSPA2			FOS
	HSPA4			FOSL1
	HSPA5			FOSL2
	HSPA6			FOXA1
	HSPA8			FOXB1
	HSPA9			FOXE1
	HSPB1			FOXH1
	HSPB11			FOXI1
	HSPB2			FOXJ2
	HSPB8			FOXK1
	HSPBP1			FOXK2
	HSPD1			FOXL1
	HSPE1			FOXM1
	HTR2C			FOXN1
	HTR3A			FOXN3
	HTR6			FOXO1
	HTR7			FOXO3
	HTRA2			FOXO6
	HTRA4			FOXP1
	HTT			FOXP2
	HULC			FOXP3
	HUS1			FOXP4
	HUWE1			FOXQ1
	HYOU1			FOXR1
	HYPK			FOXR2
	HYPM			FPR1
	IAPP			FPR2
	IARS			FRA10AC1
	IARS2			FRAS1
	ID2			FREM2
	IDE			FRMD6
	IDH2			FRS2
	IDH3G			FRS3
	IDS			FSCN1
	IER2			FST
	IER3			FTH1
	IER5			FTL
	IFFO1			FTO
	IFI16			FTSJ1
	IFI27			FTSJ3
	IFI27L1			FUBP3
	IFIH1			FURIN
	IFIT1			FUS
	IFIT2			FUT8
	IFIT3			FXR1
	IFITM1			FXR2
	IFITM3			FXYD3
	IFNGR1			FXYD6
	IFT172			FYB1
	IFT20			FYN
	IFT22			FZD3
	IFT27			FZD7
	IFT46			FZR1
	IFT52			G3BP1
	IFT57			G3BP2
	IFT74			GAB1
	IFT80			GAB2
	IFT81			GAB3
	IFT88			GABARAP
	IGBP1			GABARAPL1

Cohort	Whole	Female	Male	Previous
	IGF1			GABARAPL2
	IGF1R			GABBR1
	IGF2			GABPB1
	IGF2BP1			GABRA3
	IGF2BP2			GABRE
	IGF2BP3			GADD45A
	IGFBP3			GADD45B
	IGFBP5			GADD45G
	IGFBP7			GADD45GIP1
	IGFL3			GAGE4
	IGHA1			GAK
	IGHD			GAL
	IGHG1			GALNS
	IGHM			GALNT1
	IGKC			GALNT12
	IGSF8			GALNT18
	IK			GALNT2
	IKBIP			GALNT7
	IKBKB			GALT
	IKBKE			GAN
	IKBKG			GANAB
	IKZF1			GAPDH
	IL12RB1			GAPDHS
	IL17B			GAR1
	IL17RB			GARS
	IL1R2			GAS2L2
	IL27RA			GAS6
	IL32			GATA1
	IL5RA			GATA2
	ILF2			GATA3
	ILF3			GATA4
	ILK			GATA6
	ILVBL			GATAD1
	IMMP1L			GATAD2A
	IMMP2L			GATAD2B
	IMMT			GBA
	IMPA2			GBF1
	IMPDH2			GC
	INAVA			GCDH
	ING3			GCG
	INHBB			GCGR
	INHBE			GCHFR
	INO80E			GCK
	INPP5D			GCKR
	INPP5J			GCM1
	INPPL1			GCN1
	INS			GCNT1
	INSL5			GDA
	INSR			GDAP1
	INSRR			GDF9
	INSYN1			GDI1
	INTS1			GDI2
	INTS10			GDPD1
	INTS12			GEM
	INTS2			GEMIN4
	INTS4			GET4
	INTS5			GFAP
	INTS8			GFM1
	INTS9			GFPT1
	IP6K1			GGA1
	IPO13			GGA2
	IPO4			GGA3
	IPO5			GGH
	IPO9			GHITM
	IQCB1			GHR
	IQGAP1			GIGYF1
	IQUB			GIGYF2
	IRAK1			GIMAP1
	IRF1			GIMAP2
	IRF3			GIMAP5
	IRF5			GIMAP7
	IRF7			GINM1
	IRS1			GINS2
	IRS2			GIP
	IRS4			GIPC1
	ISCA1			GIPR
	ISG15			GIT1
	ISLR			GIT2
	ISM2			GJA1
	ISOC2			GJB1
	ITCH			GJD3
	ITFG1			GKAP1
	ITGA4			GLB1
	ITGA5			GLB1L
	ITGA6			GLB1L2
	ITGB1			GLCE
	ITGB3			GLE1
	ITGB3BP			GLG1
	ITGB4			GLI1
	ITGB5			GLI2
	ITIH2			GLIS2
	ITK			GLIS3
	ITM2B			GLMN
	ITM2C			GLP1R
	ITPR3			GLRB
	ITPRID2			GLRX

Cohort	Whole	Female	Male	Previous
	ITSN1			GLRX3
	IVNS1ABP			GLRX5
	IZUMO1			GLS
	JAK1			GLUD1
	JAK2			GLUL
	JAK3			GLYR1
	JMD1C			GMCL1
	JMD4			GMCL2
	JMD6			GMPPB
	JMD7			GMPS
	JOSD1			GNA11
	JPH3			GNA12
	JPH4			GNA13
	JPT1			GNA14
	JUN			GNAI1
	JUNB			GNAI2
	JUND			GNAI3
	JUP			GNAL
	KANK2			GNAO1
	KANSL1			GNAQ
	KARS			GNAS
	KAT14			GNAZ
	KAT2A			GNB1
	KAT2B			GNB2
	KAT5			GNB4
	KATNA1			GNB5
	KBTBD7			GNE
	KBTBD8			GNG12
	KCMF1			GNG2
	KCNA2			GNG8
	KCNC4			GNGT1
	KCNE3			GNL2
	KCNJ2			GNL3
	KCNJ6			GNL3L
	KCNU1			GNPAT
	KCTD13			GNPDA1
	KCTD17			GNS
	KCTD3			GOLGA1
	KCTD9			GOLGA2
	KDEL2			GOLGA3
	KDF1			GOLGA5
	KDM1A			GOLGA6A
	KDM5C			GOLGA6L2
	KDM6A			GOLGA6L9
	KEAP1			GOLM1
	KHDRBS1			GOLPH3
	KHDRBS2			GOLT1B
	KHK			GOPC
	KHSRP			GORASP1
	KIAA0355			GORASP2
	KIAA0556			GOT1
	KIAA0754			GOT2
	KIAA1107			GP5
	KIAA1211			GP9
	KIAA1217			GPAM
	KIAA1549			GPANK1
	KIAA1671			GPAT4
	KIDINS220			GPATCH8
	KIF11			GPBP1L1
	KIF14			GPC1
	KIF18B			GPC3
	KIF1A			GPC4
	KIF1B			GPC6
	KIF1BP			GPD2
	KIF20A			GPHN
	KIF21A			GPIHBP1
	KIF23			GPKOW
	KIF2C			GPM6A
	KIF5A			GPR12
	KIF9			GPR146
	KIFAP3			GPR151
	KIFC3			GPR152
	KIR2DL1			GPR156
	KIR2DL2			GPR17
	KIR2DL3			GPR173
	KIR2DS4			GPR180
	KIR3DL1			GPR182
	KIR3DL2			GPR183
	KIR3DL3			GPR35
	KIR3DS1			GPR37
	KISS1			GPR45
	KIT			GPR50
	KLC2			GPRASP1
	KLC3			GPRASP2
	KLC4			GPRC5B
	KLF11			GPRIN3
	KLF12			GPS1
	KLF15			GPS2
	KLF16			GPSM3
	KLF3			GPX8
	KLF4			GRAMD4
	KLF5			GRB10
	KLF6			GRB14
	KLF8			GRB2
	KLF9			GRB7
	KLHDC2			GRIN2A

Cohort	Whole	Female	Male	Previous
	KLHL22			GRIP1
	KLHL38			GRIPAP1
	KLHL8			GRK2
	KLK1			GRK5
	KLK10			GRK7
	KLK15			GRM1
	KLK2			GRN
	KLK6			GRPEL1
	KLKB1			GRSF1
	KLRC1			GRWD1
	KLRC3			GSDMA
	KLRC4			GSE1
	KLRD1			GSK3A
	KLRG2			GSK3B
	KMT2A			GSN
	KMT2C			GSPT1
	KNOP1			GSTA2
	KPNA1			GSTK1
	KPNA2			GSTM3
	KPNA3			GSTO1
	KPNA4			GSTP1
	KPNA6			GTF2B
	KPNB1			GTF2E2
	KPRP			GTF2F1
	KRAS			GTF2F2
	KRBA1			GTF2H1
	KRR1			GTF2H3
	KRT1			GTF2H5
	KRT14			GTF2I
	KRT16			GTF2IRD1
	KRT17			GTF2IRD2B
	KRT18			GTF3C1
	KRT19			GTF3C2
	KRT2			GTF3C3
	KRT3			GTF3C5
	KRT31			GTPBP2
	KRT34			GTPBP4
	KRT38			GTSE1
	KRT4			GUSBP5
	KRT40			GXYLT1
	KRT6B			GYP A
	KRT75			GYS2
	KRT76			H1FO
	KRT78			H1FNT
	KRT8			H1FX
	KRTAP10-1			H2AFB2
	KRTAP10-3			H2AFX
	KRTAP10-5			H2AFY
	KRTAP10-7			H2AFZ
	KRTAP10-8			H2BFS
	KRTAP1-1			H3F3A
	KRTAP1-3			HABP4
	KRTAP13-2			HACD2
	KRTAP5-9			HACD3
	KRTAP6-2			HADH
	KRTAP6-3			HADHA
	KSR1			HADHB
	KSR2			HAGH
	KXD1			HAL
	KYNU			HAND2
	L1TD1			HAP1
	L3MBTL2			HAPLN2
	LACC1			HARS2
	LACTB2			HAT1
	LAGE3			HAUS1
	LAMA1			HAUS6
	LAMB1			HAUS8
	LAMB2			HAVCR2
	LAMC1			HAX1
	LAMP1			HBA1
	LAMP2			HBB
	LAMP3			HBP1
	LAMTOR1			HBS1L
	LAMTOR2			HCAR1
	LAMTOR3			HCCS
	LAMTOR5			HCFC1
	LPTM5			HCK
	LARP1			HCLS1
	LARP4B			HCRT
	LARP7			HCST
	LARS			HDAC1
	LASP1			HDAC11
	LATS2			HDAC2
	LCA5			HDAC3
	LCA7			HDAC4
	LCE1A			HDAC5
	LCE2B			HDAC6
	LCE2C			HDAC7
	LCE5A			HDAC9
	LCK			HDGF
	LCN1			HDGFL2
	LCN2			HDHD3
	LCOR			HDLBP
	LCORL			HEATR1
	LCP1			HEATR6
	LDAH			HECTD1

Cohort	Whole	Female	Male	Previous
	LDHA			HECW2
	LDHB			HELLS
	LDHD			HELZ
	LDLR			HELZ2
	LDLRAD1			HEPHL1
	LDLRAD4			HERC1
	LDLRAP1			HERC2
	LENG1			HERPUD1
	LENG8			HES1
	LETM1			HES6
	LETMD1			HEXIM1
	LGALS1			HEXIM2
	LGALS3			HEY1
	LGALS3BP			HFE
	LGALS7			HGF
	LGALS8			HGFAC
	LGALS9			HGS
	LGR4			HHEX
	LHFPL5			HHIP
	LHX1			HIBADH
	LHX2			HIC1
	LHX3			HIF1A
	LHX4			HIF1AN
	LIG3			HIINT1
	LILRB1			HINT2
	LILRB2			HIP1
	LIMA1			HIP1R
	LIMCH1			HIPK2
	LIMK1			HIRA
	LIMK2			HIST1H1A
	LIN28A			HIST1H1B
	LIN37			HIST1H1C
	LIN52			HIST1H1D
	LIN7C			HIST1H1E
	LIN9			HIST1H1T
	LINC01554			HIST1H2AE
	LIPC			HIST1H2AH
	LIPH			HIST1H2AI
	LITAF			HIST1H2BA
	LLCFC1			HIST1H2BB
	LLGL1			HIST1H2BG
	LLGL2			HIST1H2BH
	LMAN1			HIST1H3A
	LMBR1L			HIST2H2AB
	LMF1			HIST2H2AC
	LMNA			HIST2H2BC
	LMNB1			HIST2H2BE
	LMNB2			HIST2H2BF
	LMO1			HIST2H3C
	LMO2			HIST2H3PS2
	LMO3			HIST3H2BB
	LMO4			HIST3H3
	LMO7			HIST4H4
	LNPEP			HIVEP1
	LNPK			HJURP
	LNK1			HK1
	LNK2			HK2
	LOC100290337			HLA-A
	LOC100290651			HLA-B
	LONP1			HLA-C
	LOXL4			HLA-DMB
	LPAR2			HLA-DPA1
	LPAR6			HLA-DPB1
	LPIN1			HLA-DQA1
	LPL			HLA-DQA1
	LPP			HLA-DQB1
	LPXN			HLA-DQB1
	LRFN4			HLA-DRA
	LRIF1			HLA-DRB1
	LRP1			HLA-DRB3
	LRP2			HLA-DRB5
	LRP3			HLA-E
	LRP8			HLA-F
	LRPAP1			HLA-G
	LRPPRC			HLA-H
	LRRC15			HLF
	LRRC17			HLTF
	LRRC25			HMBX1
	LRRC31			HMG20A
	LRRC59			HMG20B
	LRRC8A			HMGA1
	LRRC8E			HMGA2
	LRRFIP1			HMGB1
	LRRFIP2			HMGB2
	LRRIQ1			HMGCL
	LRRK1			HMGCR
	LRRK2			HMGN2
	LSG1			HMGN4
	LSM1			HMGXB4
	LSM12			HMMR
	LSM14A			HMOX1
	LSM2			HMOX2
	LSM5			HNF1A
	LSM6			HNF1B
	LSR			HNF4A
	LTA4H			HNRNPA0

Cohort	Whole	Female	Male	Previous
	LTBR			HNRNPA1
	LTN1			HNRNPA1L2
	LUC7L			HNRNPA2B1
	LUC7L2			HNRNPA3
	LUZP1			HNRNPAB
	LY6H			HNRNPC
	LY86			HNRNPCL1
	LYAR			HNRNPCL2
	LYG2			HNRNPD
	LYN			HNRNPD
	LYPD1			HNRNPF
	LYPD3			HNRNPH1
	LYPD4			HNRNPH2
	LYPD6			HNRNPH3
	LYPD6B			HNRNPK
	LYRM4			HNRNPL
	LYZ			HNRNPLL
	LYZL1			HNRNPM
	LZTS2			HNRNPR
	MAB21L2			HNRNPU
	MACF1			HNRNPUL1
	MAD2L1			HNRNPUL2
	MAD2L2			HOGA1
	MAEA			HOMER1
	MAFB			HOMER3
	MAFF			HOMER3
	MAGEA1			HOOK1
	MAGEA3			HOOK3
	MAGEA6			HOPX
	MAGEA8			HOXA1
	MAGEA9			HOXB2
	MAGEB2			HOXB9
	MAGED1			HOXC13
	MAGED4			HOXC4
	MAGEF1			HOXC5
	MAGEH1			HOXC8
	MAGOHB			HOXD12
	MAGT1			HOXD13
	MAIP1			HP
	MALL			HP1BP3
	MAMDC4			HPN
	MANEA			HPRT1
	MANSC1			HPX
	MAP1LC3A			HRAS
	MAP1LC3B			HRNR
	MAP1S			HS2ST1
	MAP2			HSBP1
	MAP2K1			HSCB
	MAP2K2			HSD17B10
	MAP2K3			HSD17B11
	MAP2K5			HSD17B12
	MAP2K7			HSD17B4
	MAP3K1			HSD3B7
	MAP3K14			HSF1
	MAP3K3			HSF2
	MAP3K5			HSF2BP
	MAP3K7			HSFY2
	MAP4			HSP90AA1
	MAP4K1			HSP90AB1
	MAP4K4			HSP90AB3P
	MAP7			HSP90B1
	MAP7D1			HSPA13
	MAP7D2			HSPA1A
	MAP7D3			HSPA1L
	MAPK1			HSPA2
	MAPK13			HSPA4
	MAPK14			HSPA4L
	MAPK3			HSPA5
	MAPK6			HSPA6
	MAPK7			HSPA8
	MAPK8			HSPA9
	MAPK8IP2			HSPB1
	MAPK9			HSPB2
	MAPRE1			HSPB8
	MAPRE3			HSPBP1
	MAPT			HSPD1
	MARCKS			HSPE1
	MARF1			HSPH1
	MARK2			HTR1B
	MARK3			HTR2C
	MARS			HTR3C
	MAS1			HTR6
	MAS1L			HTR7
	MAST1			HTRA1
	MAST3			HTRA2
	MATN2			HTRA4
	MATN4			HTT
	MATR3			HULC
	MAU2			HUWE1
	MAVS			HYAL2
	MAX			HYOU1
	MBD2			HYPK
	MBD3			HYPK
	MBD3L1			IARS
	MBD4			IARS2
	MBIP			IBTK

Cohort	Whole	Female	Male	Previous
	MBNL1			ICAM1
	MBOAT7			ICK
	MCC			ID1
	MCL1			ID2
	MCM10			ID3
	MCM2			IDE
	MCM3			IDH1
	MCM4			IDH2
	MCM5			IDI2
	MCM6			IDS
	MCM7			IDUA
	MCOLN3			IER2
	MCUR1			IFI16
	MDC1			IFI27L1
	MDFI			IFIH1
	MDH2			IFIT18
	MDK			IFITM1
	MDM2			IFITM3
	MDN1			IFNAR1
	MECOM			IFNLR1
	MECP2			IFT57
	MED1			IGBP1
	MED12			IGF1
	MED14			IGF1R
	MED17			IGF2
	MED19			IGF2BP1
	MED21			IGF2BP2
	MED23			IGF2BP3
	MED24			IGF2R
	MED26			IGFBP1
	MED29			IGFBP3
	MED4			IGFBP4
	MED9			IGFBP5
	MEIS1			IGFBP7
	MEIS2			IGFL3
	MEMO1			IGHA1
	MEOX2			IGHD
	MEP1B			IGHG1
	MEPCE			IGHG2
	MET			IGHM
	METAP2			IGKC
	METTL14			IGLL5
	METTL15			IGSF3
	METTL17			IGSF8
	METTL3			IK
	METTL7A			IKBIP
	MEX3B			IKKB8
	MFAP1			IKBKE
	MFAP4			IKBKG
	MFF			IKZF1
	MFHAS1			IKZF3
	MFN2			IKZF4
	MFSD4A			IL12RB1
	MFSD6			IL13RA2
	MGARP			IL16
	MGAT5B			IL17RA
	MGST3			IL17RC
	MIA2			IL1A
	MIA2			IL1R1
	MIA3			IL1R2
	MIB1			IL1RAP
	MIB2			IL20RA
	MICA			IL24
	MICAL3			IL27RA
	MICOS10			IL2RB
	MICOS13			IL2RG
	MICU1			IL32
	MID1P1			IL3RA
	MID2			IL4R
	MIF			IL5RA
	MIF4GD			IL6ST
	MINDY4			IL7R
	MINK1			IL9R
	MIP			ILF2
	MIPOL1			ILF3
	MIR106A			ILK
	MIR106B			ILKAP
	MIR107			ILVBL
	MIR10B			IMMP1L
	MIR1-1			IMMP2L
	MIR1-2			IMMT
	MIR122			IMPA2
	MIR128-1			IMPDH1
	MIR128-2			IMPDH2
	MIR138-1			INAVA
	MIR138-2			INF2
	MIR140			ING1
	MIR141			ING3
	MIR143			INHBA
	MIR145			INHBB
	MIR155			INHBC
	MIR15A			INHBE
	MIR15B			INO80
	MIR16-1			INO80B
	MIR16-2			INO80C
	MIR17			INO80E

Cohort	Whole	Female	Male	Previous
	MIR18A			INPP5A
	<i>MIR18B</i>			INPP5D
	MIR199A1			INPP5E
	MIR199A2			INPP5K
	MIR19A			INPPL1
	MIR19B1			INS
	MIR19B2			INSIG1
	MIR200A			INSIG2
	MIR200B			INSL5
	MIR200C			INSR
	MIR205			INSRR
	MIR206			INSYN1
	MIR20A			INTS1
	MIR20B			INTS12
	MIR21			INTS3
	<i>MIR214</i>			INTS4
	MIR221			INTS5
	MIR222			INTS6
	MIR25			INTS8
	MIR29A			IPO4
	MIR29B1			IPO5
	<i>MIR29B2</i>			IPO7
	MIR29C			IPO8
	MIR31			IPO9
	MIR34A			IPPK
	MIR34B			IQCB1
	MIR34C			IQCF2
	MIR363			IQGAP1
	MIR429			IRAK1
	MIR451A			IRF1
	MIR7-1			IRF2
	MIR7-2			IRF2BP1
	MIR7-3			IRF2BP2
	<i>MIR9-1</i>			IRF3
	MIR9-2			IRF4
	MIR92A1			IRF7
	MIR92A2			IRS1
	<i>MIR93</i>			IRS2
	MIR9-3			IRS4
	MIR98			ISCA1
	MIRLET7A1			ISCU
	MIRLET7A2			ISG15
	MIRLET7A3			ISL1
	MIRLET7B			ISLR
	MIRLET7BHG			ISM2
	MIRLET7C			ISX
	MIRLET7D			ISY1
	MIRLET7E			ITCH
	MIRLET7F1			ITFG1
	MIRLET7F2			ITGA2
	MIRLET7G			ITGA4
	MIRLET7I			ITGA5
	MIS12			ITGA6
	MKI67			ITGA7
	MKRN1			ITGAM
	MKRN2			ITGAV
	MKRN3			ITGB1
	MKS1			ITGB2
	MLEC			ITGB3
	MLF1			ITGB3BP
	MLH1			ITGB5
	MLLT1			ITGB8
	MLLT3			ITIH2
	MLLT6			ITIH3
	MLST8			ITLN1
	MLXIPL			ITLN2
	MMAB			ITM2B
	MMGT1			ITM2C
	MMP10			ITPKA
	MMP14			ITPKB
	MMP2			ITPR1
	MMP26			ITPR2
	MMP7			ITPR3
	MMP9			ITPRIP
	MMS19			ITSN1
	MNAT1			IVNS1ABP
	MNDA			IWS1
	MOG			JADE1
	MOGS			JAK1
	MON2			JAK2
	MORC3			JAK3
	MORF4L1			JAM3
	MORF4L2			JAZF1
	MOS			JMJD1C
	MOV10			JMJD6
	MPDZ			JMY
	MPG			JPH1
	MPP5			JPH3
	MPP6			JUN
	MPPE1			JUNB
	MPV17			JUND
	MR1			JUP
	MRAP2			KANK2
	MRE11			KANSL1
	MRFAP1L1			KANSL2
	MRGBP			KANSL3

Cohort	Whole	Female	Male	Previous
	MRM1			KARS
	MRM3			KAT14
	MROH1			KAT2A
	MRPL11			KAT2B
	MRPL12			KAT5
	MRPL13			KAT6A
	MRPL18			KAT7
	MRPL22			KAT8
	MRPL23			KBTBD7
	MRPL27			KCMF1
	MRPL33			KCNA2
	MRPL37			KCNB2
	MRPL38			KCND3
	MRPL40			KCNE1
	MRPL42			KCNE2
	MRPL50			KCNE3
	MRPL51			KCNE4
	MRPL53			KCNH2
	MRPL55			KCNJ2
	MRPL58			KCNJ6
	MRPS10			KCNJ8
	MRPS22			KCNK1
	MRPS27			KCNK3
	MRPS30			KCNMB3
	MRPS31			KCNQ1
	MRPS5			KCNS3
	MRPS7			KCTD10
	MRPS9			KCTD12
	MRRF			KCTD13
	MS4A13			KCTD17
	MS4A15			KCTD6
	MSH2			KCTD9
	MSH6			KDELC2
	MSI2			KDELR2
	MSMO1			KDM1A
	MSN			KDM1B
	MSX2			KDM2A
	MT2A			KDM2B
	MTA1			KDM4B
	MTA2			KDM5B
	MTA3			KDM6A
	MTCH1			KDR
	MTCH2			KEAP1
	MTDH			KHDRBS1
	MTERF3			KHDRBS2
	MTF1			KHSRP
	MTF2			KIAA0232
	MTG2			KIAA0355
	MTHFD1			KIAA1522
	MTMR1			KIAA1671
	MTMR12			KIDINS220
	MTMR6			KIF11
	MTMR9			KIF13A
	MTNR1A			KIF13B
	MTNR1B			KIF14
	MTOR			KIF17
	MTPAP			KIF1B
	MTPN			KIF20A
	MTR			KIF21B
	MTUS1			KIF22
	MTUS2			KIF23
	MTX1			KIF2C
	MTX2			KIF5A
	MTX3			KIF5B
	MUC1			KIF7
	MVP			KIFAP3
	MXD1			KIFC3
	MYB			KIR2DL1
	MYBBP1A			KIR2DL2
	MYBL2			KIR2DL3
	MYC			KIR2DS4
	MYEF2			KIR3DL3
	MYH1			KIR3DS1
	MYH10			KIT
	MYH4			KLB
	MYH7			KLC4
	MYH8			KLF11
	MYH9			KLF12
	MYL1			KLF13
	MYL12A			KLF15
	MYL12B			KLF16
	MYL6			KLF3
	MYL6B			KLF4
	MYL7			KLF5
	MYLK2			KLF6
	MYO15B			KLF8
	MYO18A			KLF9
	MYO19			KLHDC10
	MYO1B			KLHDC3
	MYO1C			KLHDC4
	MYO5A			KLHL12
	MYO5B			KLHL20
	MYO6			KLHL34
	MYO9B			KLHL36
	MYOD1			CLK1
	MYRF			CLK10

Cohort	Whole	Female	Male	Previous
	MZF1			KLK15
	NAA11			KLK5
	NAA15			KLK6
	NAA40			KLK8
	NAAA			KLKB1
	NABP2			KLRB1
	NAE1			KLRC1
	NANOG			KLRC4
	NAP1L1			KLRD1
	NAPA			KLRG2
	NAPRT			KMT2A
	NAT10			KMT2B
	NAT2			KMT2C
	NAT9			KMT2D
	NBEA			KMT2E
	NBEAL2			KMT5A
	NBN			KNG1
	NBR1			KNOP1
	NCAM1			KNTC1
	NCAN			KPNA1
	NCAPD2			KPNA2
	NCAPD3			KPNA3
	NCAPG			KPNA4
	NCAPH2			KPNA5
	NCBP1			KPNA6
	NCBP2			KPNB1
	NCBP3			KPRP
	NCK1			KRAS
	NCK2			KRBOX4
	NCKAP5			KRI1
	NCKAP5L			KRR1
	NCL			KRT1
	NCOA1			KRT10
	NCOA2			KRT14
	NCOA3			KRT18
	NCOA6			KRT19
	NCOR1			KRT2
	NCOR2			KRT27
	NCR3			KRT3
	NCSTN			KRT31
	ND1			KRT32
	ND4			KRT34
	NDC80			KRT37
	NDEL1			KRT38
	NDN			KRT40
	NDRG1			KRT78
	NDUFA1			KRT8
	NDUFA10			KRT9
	NDUFA12			KRTAP10-1
	NDUFA13			KRTAP10-3
	NDUFA2			KRTAP10-5
	NDUFA3			KRTAP10-7
	NDUFA4			KRTAP10-8
	NDUFA5			KRTAP10-9
	NDUFA6			KRTAP1-1
	NDUFA7			KRTAP12-2
	NDUFA8			KRTAP12-3
	NDUFA9			KRTAP1-3
	NDUFAB1			KRTAP13-1
	NDUFAF1			KRTAP13-2
	NDUFAF3			KRTAP13-3
	NDUFAF4			KRTAP19-1
	NDUFAF8			KRTAP19-5
	NDUFB1			KRTAP2-3
	NDUFB10			KRTAP3-1
	NDUFB11			KRTAP4-2
	NDUFB3			KRTAP5-6
	NDUFB4			KRTAP5-7
	NDUFB5			KRTAP5-9
	NDUFB6			KRTAP6-1
	NDUFB7			KRTAP6-2
	NDUFB8			KRTAP6-3
	NDUFB9			KRTAP8-1
	NDUFC2			KRTAP9-8
	NDUFS1			KRTCAP2
	NDUFS2			KSR1
	NDUFS3			KTN1
	NDUFS4			KXD1
	NDUFS5			L1CAM
	NDUFS6			L3MBTL2
	NDUFS7			L3MBTL3
	NDUFS8			L3MBTL4
	NDUFV1			LACRT
	NDUFV2			LACTB
	NDUFV3			LAMA3
	NECAB2			LAMA5
	NECTIN1			LAMB1
	NECTIN2			LAMB2
	NECTIN3			LAMC1
	NEDD1			LAMC3
	NEDD4			LAMP1
	NEDD4L			LAMP2
	NEDD8			LAMP3
	NEDD9			LAMTOR1
	NEFL			LAMTOR2
	NEFM			LAMTOR5

Cohort	Whole	Female	Male	Previous
	NEIL1			LANCL1
	NEK4			LANCL2
	NEK6			LAPTM4B
	NEK7			LARGE1
	NELFB			LARGE2
	NEPRO			LARP1
	NEU2			LARP1B
	NEURL4			LARP4
	NEUROG3			LARP4B
	NEXN			LARP7
	NF2			LARS
	NFATC1			LARS2
	NFATC2			LASP1
	NFATC3			LAT
	NFE2L2			LATS1
	NFE2L3			LATS2
	NFIA			LBR
	NFIB			LBX1
	NFIC			LCE1A
	NFIX			LCE1D
	NFKB1			LCK
	NFKB2			LCN1
	NFKBIA			LCN2
	NFKBIB			LCN6
	NFKBIE			LCOR
	NFU1			LCORL
	NFX1			LCP1
	NFYA			LCP2
	NGB			LDB2
	NGEF			LDHA
	NHLH1			LDHB
	NHLRC2			LDLR
	NID2			LDLRAP1
	NIF3L1			LEF1
	NIFK			LEMD2
	NIN			LENG1
	NINL			LEP
	NIPAL1			LETM1
	NIPBL			LGALS1
	NIPSNAP1			LGALS3
	NIT1			LGALS3BP
	NKX2-1			LGALS4
	NKX2-5			LGALS7
	NLK			LGALS8
	NLRP1			LGALS9
	NLRP12			LGR4
	NLRX1			LHB
	NMD3			LHCGR
	NME2			LHFPL5
	NME3			LHX1
	NME4			LHX2
	NME7			LHX3
	NMNAT1			LHX4
	NMRAL1			LHX5
	NMS			LHX6
	NMT1			LHX8
	NNT			LIFR
	NOD2			LIG1
	NOL10			LIG3
	NOL11			LILRA3
	NOL12			LILRB1
	NOL6			LILRB2
	NOLC1			LILRB5
	NOMO1			LIMA1
	NONO			LIMK1
	NOP14			LIN28A
	NOP2			LIN28B
	NOP53			LIN37
	NOP56			LIN52
	NOP58			LIN54
	NOS1AP			LIN7A
	NOS2			LIN7C
	NOS3			LIN9
	NOSTRIN			LINC00452
	NOTCH1			LINC00839
	NOTCH2			LINC00910
	NOTCH2NLA			LINC01554
	NPAS1			LIPC
	NPC1			LIPG
	NPEPPS			LITAF
	NPHP1			LLCFC1
	NPIP86			LLGL2
	NPLOC4			LMAN1
	NPM1			LMAN2L
	NPM3			LMBR1
	NPTN			LMBR1L
	NPY2R			LMF1
	NR1H2			LMNA
	NR1H3			LMNB1
	NR1H2			LMNB2
	NR2C1			LMO1
	NR2C2			LMO2
	NR3C1			LMO3
	NR4A1			LMO4
	NR4A2			LMO7
	NR4A3			LMX1B

Cohort	Whole	Female	Male	Previous
	NRAS			LNPEP
	NRBF2			LNPK
	NRBP1			LNK1
	NRBP2			LNK2
	NRG1			LOC10029030
	NRIP1			LOC10029060
	NRP1			LOC10029310
	NRP2			LOC254896
	NRXN2			LONP1
	NSA2			LONRF2
	NSD1			LOXL2
	NSD2			LPA
	NSD3			LPAR1
	NSF			LPAR2
	NSMAF			LPAR5
	NSRP1			LPAR6
	NSUN2			LPCAT1
	NSUN5			LPCAT3
	NSUN5P1			LPGAT1
	NT5DC2			LPL
	NT5E			LPP
	NTRK1			LPXN
	NTSR1			LRCH2
	NUCB1			LRFN3
	NUCB2			LRFN4
	NUDC			LRIF1
	NUDCD1			LRIG3
	NUDCD2			LRP1
	NUDT21			LRP1B
	NUDT3			LRP2
	NUDT5			LRP4
	NUF2			LRP5
	NUFIP1			LRP6
	NUFIP2			LRP8
	NUMA1			LRPAP1
	NUMB			LRPPRC
	NUP107			LRRC1
	NUP153			LRRC15
	NUP155			LRRC25
	NUP160			LRRC29
	NUP188			LRRC31
	NUP205			LRRC42
	NUP210			LRRC59
	NUP35			LRRIQ1
	NUP43			LRK1
	NUP50			LRK2
	NUP54			LRRTM1
	NUP58			LRRTM4
	NUP62			LRTM2
	NUP98			LRWD1
	NUPR1			LSG1
	NUSAP1			LSM12
	NUTF2			LSM5
	NVL			LSR
	NXF1			LTA4H
	NXPH3			LTB4R2
	OAS3			LTBP2
	OASL			LTBR
	OAT			LTF
	OBSL1			LTN1
	OCIAD1			LTV1
	OCIAD2			LUC7L
	OCLN			LUC7L2
	OCRL			LUC7L3
	ODF2			LURAP1
	ODR4			LUZP1
	OFCC1			LXN
	OFD1			LY6H
	OGDH			LY86
	OGFOD3			LYAR
	OGT			LYG2
	OIP5			LYN
	OLFM2			LYPD3
	OLFM4			LYPD4
	OPA1			LYPD6
	OPA3			LYPLAL1
	OPALIN			LYRM1
	OPRL1			LYZ
	OPTN			LYZL1
	OR10H2			LYZL2
	ORC1			LYZL6
	ORC2			LZTR1
	ORC5			LZTS1
	ORC6			LZTS2
	ORMDL1			M6PR
	ORMDL2			MAB21L2
	ORMDL3			MACF1
	OSBPL8			MACROD1
	OST4			MAD1L1
	OSTF1			MAD2L1
	OSTM1			MAD2L2
	OTUB1			MAF
	OTUB2			MAF1
	OTUD4			MAFB
	OTULINL			MAFF
	OTX1			MAGEA10

Cohort	Whole	Female	Male	Previous
	OXSRI			MAGEA3
	P2RY10			MAGEA6
	P2RY6			MAGEA9
	P2RY8			MAGEB2
	P3H1			MAGEB4
	P4HA1			MAGED1
	P4HA2			MAGED2
	P4HB			MAGEF1
	PA2G4			MAGEH1
	PAAF1			MAGI1
	PABPC1			MAGI2
	PABPC4			MAGI3
	PACSIN2			MAGOH
	PADI3			MAIP1
	PAEP			MAL
	PAFAH1B2			MALL
	PAFAH1B3			MALSU1
	PAGE4			MALT1
	PAICS			MAML1
	PAIP1			MAML3
	PAIP2			MAN1A1
	PAK1			MAN1B1
	PAK4			MAN2A1
	PAK6			MAN2A2
	PALLD			MANBA
	PALM			MANEA
	PALM2			MANF
	PAN2			MANSC1
	PANX1			MAP1A
	PARD3			MAP1B
	PARK7			MAP1LC3A
	PARL			MAP1LC3B
	PARN			MAP1LC3C
	PARP1			MAP1S
	PARP2			MAP2K1
	PARS2			MAP2K2
	PATE1			MAP2K3
	PATJ			MAP2K4
	PATL1			MAP2K5
	PAWR			MAP2K6
	PAX2			MAP2K7
	PAX6			MAP3K1
	PAX7			MAP3K10
	PAX8			MAP3K11
	PAX9			MAP3K14
	PAXBP1			MAP3K19
	PAXIP1			MAP3K3
	PBRM1			MAP3K4
	PBX2			MAP3K5
	PBX3			MAP3K7
	PBX4			MAP4
	PC			MAP4K1
	PCBP1			MAP4K4
	PCBP2			MAP7
	PCDH10			MAP7D1
	PCDH20			MAP7D3
	PCDHB3			MAPK1
	PCDHGB1			MAPK10
	PCDHGB4			MAPK11
	PCDHGC4			MAPK14
	PCGF1			MAPK3
	PCGF3			MAPK6
	PCGF5			MAPK7
	PCGF6			MAPK8
	PCIF1			MAPK8IP1
	PKC1			MAPK8IP2
	PCLAF			MAPK8IP3
	PCLO			MAPK9
	PCM1			MAPKAP1
	PCMT1			MAPKAPK2
	PCNA			MAPRE1
	PCSK6			MAPRE2
	PCSK7			MAPRE3
	PCYOX1			MAPT
	PCYT1A			MARCKS
	PDCD11			MARCKSL1
	PDCD5			MARF1
	PDCD6IP			MARK2
	PDCL3			MARK3
	PDE2A			MARS
	PDE4A			MARS2
	PDE4DIP			MAS1
	PDE8A			MAST1
	PDE9A			MAST3
	PDGFB			MAT2A
	PDGFRA			MATK
	PDGFRB			MATN2
	PDHA1			MATR3
	PDHB			MAU2
	PDIA3			MAX
	PDIA4			MAZ
	PDIA5			MB
	PDIA6			MB21D2
	PK1			MBD2
	PK3			MBD3
	PK4			MBD3L1

Cohort	Whole	Female	Male	Previous
	PDLIM4			MBD3L2
	PDLIM7			MBD4
	PDPK1			MBD6
	PDXDC1			MBIP
	PDZK1			MBNL1
	PDZK1IP1			MBOAT7
	PEAK1			MBP
	PEBP1			M8TD1
	PECAM1			M8TPS1
	PEG10			MC1R
	PER2			MC4R
	PES1			MCAM
	PEX14			MCAT
	PEX3			MCC
	PEX5			MCCC1
	PEX6			MCCC2
	PEX7			MCL1
	PFAS			MCM2
	PFDN2			MCM3
	PFDN4			MCM4
	PFDN5			MCM5
	PFKM			MCM6
	PFN1			MCM7
	PGAM1			MCOLN3
	PGAM5			MCPH1
	PGD			MCRS1
	PGK1			MCTS1
	PGLS			MCUB
	PGM1			MDC1
	PGR			MDFI
	PGRMC1			MDH1
	PGRMC2			MDH2
	PHACTR4			MDM2
	PHB			MDM4
	PHB2			MDN1
	PHF1			MEAF6
	PHF10			MECOM
	PHF11			MECP2
	PHF12			MED1
	PHF5A			MED10
	PHF7			MED12
	PHF8			MED13
	PHGDH			MED13L
	PHKG2			MED14
	PHLDA3			MED15
	PHLDB2			MED16
	PHLPP1			MED17
	PHLPP2			MED19
	PHPT1			MED20
	PI15			MED23
	PI4K2A			MED24
	PI4KA			MED25
	PIAS1			MED26
	PIAS2			MED27
	PIAS3			MED31
	PIAS4			MED4
	PIBF1			MEF2C
	PICALM			MEGF10
	PICK1			MEGF8
	PIGH			MELTF
	PIGV			MEN1
	PIH1D1			MEOX1
	PIH1D2			MEOX2
	PIK3C2A			MEPCE
	PIK3C3			MESD
	PIK3CA			MET
	PIK3CD			METAP1
	PIK3R1			METAP2
	PIK3R2			METTL15
	PIK3R3			METTL17
	PIK3R4			METTL3
	PIN1			METTL7A
	PINK1			METTL9
	PINX1			MEX3B
	PIP			MEX3C
	PIP4K2A			MEX3D
	PIP4K2C			MFAP1
	PIPSL			MFAP4
	PITX1			MFF
	PITX2			MFHAS1
	PKM			MFN1
	PKN1			MFSD4A
	PKN2			MFSD8
	PKN3			MGA
	PKP1			MGARP
	PKP2			MGAT1
	PKP3			MGAT4B
	PKP4			MGAT5
	PLAG1			MGAT5B
	PLAT			MGRN1
	PLAU			MGST3
	PLCB1			MIA2
	PLCB3			MIA2
	PLCB4			MIA3
	PLCD3			MIB1
	PLCG1			MICAL1

Cohort	Whole	Female	Male	Previous
	PLEC			MICB
	PLEKHA4			MICOS10
	PLEKHA5			MICOS13
	PLEKHA7			MICU1
	PLEKHB2			MID1IP1
	PLEKHF2			MID2
	PLEKHG3			MIER3
	PLGRKT			MIF
	PLK1			MIF4GD
	PLK4			MINK1
	PLN			MIOS
	PLOD1			MIP
	PLOD3			MIR100HG
	PLRG1			MIR122
	PLS3			MIS12
	PLTP			MKI67
	PLXDC2			MKLN1
	PM20D2			MKRN2
	PMAIP1			MKRN3
	PMCH			MLF1
	PMF1			MLF2
	PML			MLH1
	PMPCB			MLLT1
	PMS1			MLLT3
	PMS2			MLLT6
	PNKP			MLST8
	PNMA2			MLX
	PNMA5			MLXIP
	PNMA8A			MLXIPL
	PNP			MMA8
	POC1B			MME
	POC5			MMGT1
	POF1B			MMP12
	POGZ			MMP14
	POLA2			MMP2
	POLD1			MMP7
	POLD2			MMP9
	POLDIP2			MMS19
	POLDIP3			MNAT1
	POLH			MNDA
	POLR1A			MOAP1
	POLR1B			MOB1A
	POLR1C			MOB1B
	POLR1E			MOB3C
	POLR2A			MOB4
	POLR2B			MOCOS
	POLR2C			MOGS
	POLR2D			MOK
	POLR2E			MON2
	POLR2H			MORC1
	POLR2I			MORC2
	POLR2J			MORF4L1
	POLR2M			MORF4L2
	POLR3C			MORN3
	POLR3K			MORN4
	POM121			MOV10
	POMK			MPC2
	POMT1			MPDZ
	POMT2			MPHOSPH8
	PON2			MPP1
	POP1			MPP5
	POP5			MPP6
	POR			MPP7
	POT1			MPPE1
	POU1F1			MPRIIP
	POU5F1			MPZL1
	PPA1			MR1
	PPAN			MRAP
	PPARA			MRAP2
	PPARD			MRC2
	PPARG			MRE11
	PPARGC1A			MRGBP
	PPARGC1B			MRM2
	PPEF1			MRM3
	PPEF2			MROH1
	PPFIA3			MRPL11
	PPIA			MRPL12
	PPIB			MRPL15
	PPIE			MRPL22
	PPIL4			MRPL27
	PPL			MRPL28
	PPM1A			MRPL3
	PPM1B			MRPL38
	PPM1D			MRPL39
	PPM1F			MRPL41
	PPM1G			MRPL42
	PPM1H			MRPL43
	PPME1			MRPL44
	PPP1CA			MRPL45
	PPP1CB			MRPL46
	PPP1CC			MRPL47
	PPP1R10			MRPL49
	PPP1R12A			MRPL58
	PPP1R12B			MRPS10
	PPP1R13B			MRPS11
	PPP1R13L			MRPS14

Cohort	Whole	Female	Male	Previous
	PPP1R15A			MRPS15
	PPP1R18			MRPS16
	PPP1R21			MRPS17
	PPP1R32			MRPS18B
	PPP1R7			MRPS18C
	PPP1R9A			MRPS2
	PPP1R9B			MRPS21
	PPP2CA			MRPS22
	PPP2CB			MRPS23
	PPP2R1A			MRPS24
	PPP2R2A			MRPS25
	PPP2R2B			MRPS26
	PPP2R2D			MRPS27
	PPP2R5C			MRPS28
	PPP3CA			MRPS31
	PPP3CC			MRPS33
	PPP4R2			MRPS34
	PPP4R3A			MRPS35
	PPP5C			MRPS5
	PPP6C			MRPS6
	PPT1			MRPS7
	PRAM1			MRPS9
	PRAME			MRRF
	PRC1			MRTFA
	PRDM1			MRT04
	PRDM16			MRV1
	PRDX2			MS4A1
	PRDX3			MS4A2
	PRDX5			MSH2
	PRDX6			MSH3
	PREB			MSH6
	PREP			MSI2
	PRG2			MSN
	PRKAA1			MST1R
	PRKAA2			MSX2
	PRKAB1			MTA1
	PRKAB2			MTA2
	PRKACA			MTA3
	PRKACB			MTCH1
	PRKACG			MTCH2
	PRKAG2			MTDH
	PRKAG3			MTERF3
	PRKAR1A			MTF2
	PRKCA			MTFR1L
	PRKCD			MTHFD1
	PRKCI			MTHFD1L
	PRKCSH			MTHFD2
	PRKCZ			MTHFR
	PRKD2			MTIF2
	PRKD3			MTMR1
	PRKDC			MTMR14
	PRKG1			MTMR3
	PRKN			MTMR6
	PRKRA			MTNR1A
	PRKY			MTNR1B
	PRMT1			MTOR
	PRMT2			MTPN
	PRMT3			MTREX
	PRMT5			MTSS2
	PRMT6			MTUS2
	PRMT8			MTX1
	PRNP			MTX2
	PROP1			MUC1
	PROSER2			MVD
	PRPF18			MVP
	PRPF19			MXD1
	PRPF3			MYB
	PRPF31			MYBBP1A
	PRPF38A			MYBL2
	PRPF40A			MYC
	PRPF4B			MYCBP2
	PRPF6			MYCL
	PRPF8			MYD88
	PRPS1			MYH10
	PRPS2			MYH14
	PRR11			MYH2
	PRR13			MYH7
	PRR30			MYH9
	PRR35			MYL12A
	PRRC1			MYL12B
	PRRC2A			MYL6
	PRRC2C			MYL9
	PRRG4			MYLK2
	PRTN3			MYO18A
	PRXL2A			MYO18B
	PSCA			MYO19
	PSEN1			MYO1B
	PSIP1			MYO1C
	PSMA1			MYO1D
	PSMA2			MYO1E
	PSMA3			MYO5A
	PSMA4			MYO5B
	PSMA6			MYO6
	PSMB1			MYO9B
	PSMB3			MYOC
	PSMB4			MYOD1

Cohort	Whole	Female	Male	Previous
	PSMB8			MYOF
	PSMC1			MYPOP
	PSMC2			NAA10
	PSMC3			NAA15
	PSMC4			NAA40
	PSMC5			NAA50
	PSMC6			NAAA
	PSMD1			NAB2
	PSMD10			NACA
	PSMD11			NACC1
	PSMD12			NADK2
	PSMD13			NAF1
	PSMD14			NAGK
	PSMD2			NAMPT
	PSMD3			NANOG
	PSMD4			NANOS2
	PSMD6			NAP1L1
	PSMD7			NAPA
	PSMD8			NAPRT
	PSMD9			NARS
	PSME1			NAT10
	PSME2			NAT2
	PSME3			NAXD
	PSMG1			NBEAL2
	PSMG2			NBN
	PSMG3			NBR1
	PSMG4			NCAPD2
	PSORS1C2			NCAPD3
	PSPC1			NCAPG2
	PSTPIP1			NCAPH2
	PTAFR			NCBP1
	PTBP1			NCBP2
	PTBP3			NCBP3
	PTCD3			NCEH1
	PTCH1			NCF1
	PTCHD3			NCF1C
	PTEN			NCF2
	PTGER3			NCK1
	PTGES2			NCK2
	PTGES3			NCKAP5L
	PTH1R			NCL
	PTK2			NCLN
	PTK2B			NCOA1
	PTK6			NCOA2
	PTMA			NCOA3
	PTN			NCOA4
	PTP4A2			NCOA5
	PTP4A3			NCOA6
	PTPA			NCOR1
	PTPMT1			NCOR2
	PTPN1			NCR3
	PTPN11			NCSTN
	PTPN12			NDC80
	PTPN2			NDEL1
	PTPN23			NDFIP1
	PTPN3			NDN
	PTPN4			NDRG1
	PTPN5			NDST1
	PTPN6			NDUFA11
	PTPRB			NDUFA12
	PTPRF			NDUFA2
	PTPRG			NDUFA3
	PTPRJ			NDUFA4
	PTPRK			NDUFA5
	PTPRN			NDUFA6
	PTPRO			NDUFA7
	PTPRR			NDUFA8
	PTRH2			NDUFA9
	PUDP			NDUFAB1
	PUF60			NDUFAB3
	PUM1			NDUFAB4
	PURA			NDUFAB7
	PURG			NDUFB10
	PUS1			NDUFB8
	PUS7			NDUFB9
	PVR			NDUFS1
	PWWP2A			NDUFS2
	PXMP2			NDUFS3
	PXN			NDUFS4
	PYCR3			NDUFS5
	PYGM			NDUFS6
	PYHIN1			NDUFS7
	QARS			NDUFS8
	QDPR			NDUFV1
	QPR1			NDUFV2
	QSOX1			NDUFV3
	RAB11A			NEBL
	RAB11B			NECAB2
	RAB11FIP1			NECTIN2
	RAB11FIP2			NEDD1
	RAB11FIP5			NEDD4
	RAB14			NEDD4L
	RAB1A			NEDD8
	RAB1B			NEFL
	RAB21			NEFM
	RAB27A			NEGR1

Cohort	Whole	Female	Male	Previous
	RAB29			NEK10
	RAB2A			NEK4
	RAB31			NEK6
	RAB35			NEK7
	RAB3B			NEK8
	RAB3IL1			NEK9
	RAB3IP			NELFB
	RAB4A			NELFE
	RAB5A			NES
	RAB5B			NEU1
	RAB5C			NEURL4
	RAB5IF			NEUROD1
	RAB6A			NEUROG3
	RAB7A			NF1
	RAB8A			NF2
	RAB9A			NFAT5
	RABEP1			NFATC1
	RABGEF1			NFATC2
	RABGGTA			NFE2L1
	RAC1			NFE2L2
	RAC2			NFE2L3
	RAC3			NFIA
	RACGAP1			NFIB
	RACK1			NFIC
	RAD1			NFIX
	RAD18			NFKB1
	RAD21			NFKB2
	RAD23A			NFKBIA
	RAD50			NFKBIB
	RAD51			NFKBID
	RAD51AP1			NFKBIE
	RAD9A			NFKBIL1
	RAE1			NFRKB
	RAF1			NFU1
	RAI14			NFX1
	RALA			NFYA
	RALBP1			NGB
	RALY			NGFR
	RAMP3			NGRN
	RAN			NHLH1
	RANBP1			NHLRC1
	RANBP2			NHLRC2
	RANBP3			NID2
	RANBP9			NIF3L1
	RANGAP1			NIFK
	RAP1A			NIN
	RAPSN			NINL
	RARA			NIP7
	RARS			NIPAL1
	RASA1			NIPBL
	RASSF1			NIPSNAP1
	RASSF10			NIPSNAP2
	RASSF8			NIPSNAP3A
	RB1			NISCH
	RB1CC1			NKRF
	RBBP4			NKX2-1
	RBBP5			NKX2-5
	RBBP7			NKX2-6
	RBBP8			NLGN2
	RBFOX2			NLGN3
	RBKS			NLK
	RBL1			NLRC5
	RBM10			NLRP12
	RBM14			NMB
	RBM15B			NMD3
	RBM17			NME1
	RBM23			NME2
	RBM25			NME3
	RBM27			NME4
	RBM28			NMNAT1
	RBM39			NMRAL1
	RBM4			NMS
	RBM41			NMT1
	RBM42			NMT2
	RBM45			NMU
	RBM47			NNT
	RBM4B			NOC2L
	RBM8A			NOC4L
	RBMS1			NOCT
	RBMS2			NOD2
	RBMX			NOL10
	RBMX2			NOL4
	RBMXL1			NOL6
	RBPI			NOLC1
	RBPMS			NOM1
	RBX1			NOMO1
	RC3H1			NONO
	RC3H2			NOP14
	RCC1			NOP16
	RCC2			NOP2
	RCHY1			NOP56
	RCN1			NOP58
	RCN2			NOP9
	RCOR1			NOS1
	RCOR3			NOS1AP
	RDH8			NOS2

Cohort	Whole	Female	Male	Previous
	RDX			NOS3
	RECK			NOTCH1
	RECQL			NOTCH2
	RECQL4			NOTCH2NLA
	REEP3			NOTCH3
	REEP4			NPAS1
	REEP5			NPC1
	REEP6			NPDC1
	REL			NPEPP5
	RELA			NPHP1
	RELB			NPHP4
	RELL2			NPLOC4
	RELT			NPM1
	REPIN1			NPM3
	REST			NPRL2
	REXO4			NPSR1
	RFC1			NPTN
	RFC2			NPTX1
	RFC4			NPY2R
	RFTN1			NQO1
	RFXANK			NR0B1
	RGP1			NR0B2
	RGPD6			NR1D1
	RGS12			NR1H2
	RGS17			NR1H3
	RGS20			NR1I2
	RHBDD1			NR1I3
	RHBDF2			NR2C1
	RHEB			NR2C2
	RHOA			NR2F1
	RHOB			NR2F2
	RHOBTB1			NR3C1
	RHOBTB2			NR3C2
	RHOC			NR4A1
	RHOD			NR4A2
	RHOF			NR5A1
	RHOG			NR5A2
	RHOH			NRAS
	RHOJ			NRBP2
	RHOQ			NRCAM
	<i>RHOT2</i>			NRDC
	RHOU			NRF1
	RHOV			NRIP1
	RHPN1			NRIP2
	RIBC1			NRM
	RICTOR			NRN1L
	RIDA			NRP1
	RIF1			NRP2
	RILP			NRSN1
	RIN1			NSA2
	RIN3			NSD1
	RING1			NSD2
	RIOK1			NSD3
	RIOK2			NSF
	RIPK1			NSFL1C
	RIPK3			NSRP1
	RIPK4			NSUN2
	RIPPLY1			NT5C2
	RIPPLY2			NT5E
	RMC1			NTAN1
	RMDN3			NTF3
	RMND1			NTNG1
	RNASEL			NTPCR
	RND1			NTRK1
	RND2			NTRK2
	RND3			NTRK3
	RNF10			NTSR1
	RNF11			NUB1
	RNF111			NUBP2
	RNF123			NUCB2
	RNF126			NUDC
	RNF139			NUDCD1
	RNF144A			NUDCD3
	RNF149			NUDT16L1
	RNF166			NUDT21
	RNF168			NUDT3
	RNF181			NUDT5
	RNF185			NUDT9
	RNF19B			NUF2
	RNF2			NUFIP1
	RNF213			NUFIP2
	RNF214			NUMA1
	RNF219			NUMB
	RNF31			NUMBL
	RNF32			NUP107
	RNF4			NUP153
	RNF40			NUP155
	RNF41			NUP160
	RNF6			NUP188
	RNFT1			NUP205
	<i>RNPEP</i>			NUP35
	RNPS1			NUP50
	ROCK1			NUP62
	ROCK2			NUP62CL
	ROR2			NUP93
	RPA1			NUP98

Cohort	Whole	Female	Male	Previous
	RPA2			NUPR1
	RPA3			NUS1
	RPAP1			NUSAP1
	RPAP2			NUTF2
	RPE			NXF1
	RPGRIP1			NXPH3
	RPGRIP1L			NYAP2
	RPL10			OASL
	RPL10A			OAT
	RPL11			OBSCN
	RPL12			OBSL1
	RPL13			OCIAD1
	RPL13A			OCIAD2
	RPL14			OCLN
	RPL15			OCRL
	RPL17			ODF2
	RPL18			ODR4
	RPL18A			OFD1
	RPL19			OGDH
	RPL22			OGFOD2
	RPL23			OGFOD3
	RPL23A			OGT
	RPL26			OIP5
	RPL26L1			OLA1
	RPL27			OLFM2
	RPL27A			OLFM4
	RPL28			OMA1
	RPL3			OPA1
	RPL30			OPA3
	RPL31			OPRL1
	RPL32			OPTC
	RPL35			OPTN
	RPL35A			ORC5
	RPL36			ORC6
	RPL36AL			ORMDL2
	RPL37A			OS9
	RPL39			OSBPL1A
	RPL4			OSBPL3
	RPL5			OSBPL5
	RPL6			OSBPL8
	RPL7			OSGEP
	RPL7A			OSGIN1
	RPL8			OTUB1
	RPL9			OTUD4
	RPLP0			OTULIN
	RPLP0P6			OTULINL
	RPN1			OTX1
	RPN2			OXA1L
	RPP14			OXCT1
	RPP21			OXSR1
	RPP38			P2RX2
	RPRD1A			P2RX3
	RPRD1B			P2RY1
	RPRD2			P2RY10
	RPRM			P2RY12
	RPS10			P2RY2
	RPS13			P2RY6
	RPS14			P2RY8
	RPS15			P3H1
	RPS15A			P3H3
	RPS16			P3H4
	RPS18			P4HA1
	RPS19			P4HA3
	RPS2			P4HB
	RPS20			PA2G4
	RPS21			PAAF1
	RPS23			PABPC1
	RPS24			PABPC4
	RPS25			PABPC5
	RPS26			PABPN1
	RPS28			PACSLN1
	RPS3			PADI3
	RPS3A			PAF1
	RPS4X			PAICS
	RPS4Y1			PAK1
	RPS5			PAK4
	RPS6			PAK5
	RPS6KA1			PAK6
	RPS6KA2			PALLD
	RPS6KA3			PAM16
	RPS6KB1			PAN2
	RPS6KB2			PANX1
	RPS7			PANX2
	RPS8			PAQR9
	RPS9			PARD6B
	RPSA			PARK7
	RPSAP58			PARL
	RPTOR			PARN
	RPUSD3			PARP1
	RRBP1			PARP12
	RREB1			PARP2
	RRM2			PARVB
	RRP1B			PASK
	RRP7A			PATE1
	RRP8			PATJ
	RRS1			PATZ1

Cohort	Whole	Female	Male	Previous
	RSAD2			PAWR
	RSBN1			PAX2
	RSL1D1			PAX5
	RSPH14			PAX6
	RSPRY1			PAX7
	RTCA			PAX8
	RTCB			PAX9
	RTEL1			PAXBp1
	RTN1			PAXIP1
	RTN3			PBK
	RTN4			PBRM1
	RTRAF			PBX1
	RUNX1			PBX4
	RUNX1T1			PBXIP1
	RUVBL1			PC
	RUVBL2			PCBD1
	RXRA			PCBP1
	RXRB			PCBP2
	RXRG			PCBP4
	RYBP			PCCA
	RYK			PCCB
	S100A2			PCDH20
	S100A3			PCDH7
	S100A6			PCDH9
	S100A9			PCDHB16
	S100B			PCDHB3
	S100P			PCDHGC4
	SAAL1			PCDHGC5
	SAFB2			PCGF1
	SALL1			PCGF2
	SAMD1			PCGF3
	SAMHD1			PCGF5
	SAMM50			PCGF6
	SAP130			PCK1
	SAP30			PCLAF
	SAR1A			PCL0
	SARAF			PCM1
	SARM1			PCMT1
	SARNP			PCNA
	SARS			PCNT
	SART1			PCOLCE2
	SART3			PCSK5
	SASS6			PCSK7
	SATB2			PCYOX1
	SBDS			PCYT1A
	SCAMP1			PDCD10
	SCAMP2			PDCD11
	SCAP			PDCD2
	SCARB1			PDCD4
	SCARB2			PDCD5
	SCARNA22			PDCD6
	SCCPDH			PDCD6IP
	SCD			PDE2A
	SCFD1			PDE3A
	SCGB1D1			PDE3B
	SCGB2A1			PDE4A
	SCGB2A2			PDE4D
	SCLT1			PDE4DIP
	SCML1			PDE6D
	SCN3B			PDGFB
	SCN4A			PDGFC
	SCNM1			PDGFRA
	SCP2			PDGFRB
	SDAD1			PDHA1
	SDC1			PDHB
	SDC2			PDIA2
	SDC4			PDIA3
	SDCBP			PDIA4
	SDCCAG8			PDIA5
	SDF2L1			PDIA6
	SDHA			PDK1
	SDHB			PDK2
	SEC13			PDPK1
	SEC16A			PDRG1
	SEC22B			PDSSA
	SEC23A			PDSSB
	SEC61A1			PDXDC1
	SEC61B			PDZK1
	SEC62			PDZK1IP1
	SEC63			PDZK1P1
	SECISBP2			PEA15
	SEH1L			PEAK1
	SELENBP1			PEBP1
	SELENOK			PECAM1
	SELENOS			PEF1
	SELENOT			PEG10
	SEM1			PELI1
	SEMA3C			PELO
	SEMA3D			PELP1
	SEMA3F			PEMT
	SEMA4C			PEPD
	SEMG1			PER1
	SEMG2			PER2
	SENP2			PES1
	SENP3			PEX14
	SERBP1			PEX16

Cohort	Whole	Female	Male	Previous
	SERF2			PEX19
	SERPINA3			PEX3
	SERPINA5			PEX5
	SERPINB3			PF4
	SERPINB4			PFAS
	SERPINF1			PFDN1
	SERPINH1			PFDN2
	SERTAD1			PFDN4
	SERTAD3			PFDN5
	SET			PFDN6
	SETDB1			PFKFB1
	SETDB2			PFKFB2
	SETX			PFKL
	SF1			PFKP
	SF3A1			PFN1
	SF3A2			PFN2
	SF3A3			PGAM1
	SF3B1			PGAM5
	SF3B2			PGAP1
	SF3B3			PGD
	SF3B4			PGF
	SFN			PGK1
	SFPQ			PGR
	SFT2D1			PGRMC1
	SFTA2			PGS1
	SFTPC			PHACTR2
	SFXN1			PHACTR3
	SFXN5			PHB
	SGCA			PHB2
	SGK1			PHC2
	SGPL1			PHF1
	SGTA			PHF10
	SGTB			PHF11
	SH2D3C			PHF12
	SH2D4A			PHF14
	SH3BGRL			PHF20L1
	SH3GL3			PHF21A
	SH3GLB1			PHF5A
	SH3KBP1			PHGDH
	SH3RF1			PHIP
	SHANK3			PHKB
	SHARPIN			PHKG2
	SHC1			PHLDA3
	SHISA3			PHLDB3
	SHISAL1			PHLPP1
	SHMT1			PHLPP2
	SHMT2			PHTF2
	SHPRH			PI4K2B
	SIAE			PI4KA
	SIAH1			PI4KB
	SIDT2			PIAS1
	SIGLECL1			PIAS2
	SIK3			PIAS3
	SIN3A			PIAS4
	SIN3B			PIBF1
	SIPA1L1			PICK1
	SIPA1L3			PID1
	SIRPD			PIDD1
	SIRT1			PIGH
	SIRT2			PIGP
	SIRT4			PIGT
	SIRT6			PIH1D1
	SIRT7			PIH1D3
	SIX1			PIK3C3
	SIX3			PIK3CA
	SIX6			PIK3CB
	SKA3			PIK3CD
	SKAP1			PIK3CG
	SKI			PIK3R1
	SKIL			PIK3R2
	SKP2			PIK3R3
	SLAIN2			PIK3R4
	SLAMF1			PIKFYVE
	SLC12A2			PILRA
	SLC12A4			PIM1
	SLC12A5			PIN1
	SLC12A7			PINK1
	SLC12A9			PIP
	SLC14A1			PIP4K2A
	SLC15A3			PIP4K2B
	SLC15A4			PIP4K2C
	SLC16A1			PIP4P2
	SLC16A11			PIP5K1A
	SLC18A1			PIP5K1C
	SLC18A2			PIPSL
	SLC19A1			PISD
	SLC1A1			PITRM1
	SLC1A5			PITX2
	SLC22A4			PKLR
	SLC22A9			PKM
	SLC25A1			PKMYT1
	SLC25A10			PKN1
	SLC25A11			PKN2
	SLC25A12			PKN3
	SLC25A13			PKP1
	SLC25A20			PKP2

Cohort	Whole	Female	Male	Previous
	SLC25A24			PKP4
	SLC25A3			PLA2G12B
	SLC25A4			PLA2G4A
	SLC25A46			PLAC1
	SLC25A5			PLAGL2
	SLC25A6			PLAT
	SLC29A1			PLAU
	SLC2A2			PLAUR
	SLC2A7			PLCB1
	SLC30A1			PLCB3
	SLC30A2			PLCB4
	SLC30A8			PLCD1
	SLC30A9			PLCD3
	SLC31A1			PLCD4
	SLC33A1			PLCE1
	SLC35C2			PLCG1
	SLC38A1			PLCG2
	SLC38A7			PLD1
	SLC39A10			PLD2
	SLC39A12			PLD3
	SLC39A2			PLEC
	SLC39A3			PLEKHA4
	SLC39A4			PLEKHA5
	SLC39A6			PLEKHA7
	SLC3A2			PLEKHB1
	SLC4A1			PLEKHF1
	SLC4A1AP			PLEKHF2
	SLC4A7			PLEKHG4
	SLC5A6			PLEKHH1
	SLC6A15			PLEKHH3
	SLC7A5			PLG
	SLC9A6			PLGRKT
	SLFN11			PLK1
	SLIRP			PLLP
	SLN			PLOD1
	SLTM			PLOD3
	SLURP1			PLP1
	SMAD1			PLP2
	SMAD2			PLPP3
	SMAD3			PLRG1
	SMAD5			PLS1
	SMAD7			PLS3
	SMAD9			PLSCR1
	SMAP2			PLSCR4
	SMARCA1			PLTP
	SMARCA2			PLXNA1
	SMARCA4			PLXNA2
	SMARCA5			PLXNA3
	SMARCAD1			PLXNB1
	SMARCB1			PLXNB2
	SMARCC1			PM20D2
	SMARCC2			PMAIIP1
	SMARCD1			PMEL
	SMARCD2			PMEPA1
	SMARCD3			PMF1
	SMARCE1			PML
	SMC1A			PMPCB
	SMC2			PNKP
	SMC3			PNLIPRP1
	SMC4			PNMA1
	SMG1			PNMA2
	SMG5			PNN
	SMG7			PNOC
	SMG9			PNP
	SMIM29			PNPLA2
	SMN1			PNPLA6
	SMPDL3B			PNRC2
	SMURF1			POC1A
	SMURF2			POF1B
	SNAI1			POGLUT1
	SNAP23			POGZ
	SNAP29			POLA1
	SNAP47			POLD3
	SNAPC4			POLDIP2
	SNAPC5			POLDIP3
	SNAPIN			POLH
	SNCA			POLI
	SND1			POLR1A
	SNIP1			POLR1B
	SNRNP200			POLR1C
	SNRNP27			POLR1E
	SNRNP40			POLR2A
	SNRNP70			POLR2C
	SNRPA			POLR2L
	SNRPA1			POLRMT
	SNRPB			POM121
	SNRPB2			POMGNT2
	SNRPC			POMK
	SNRPD3			PON2
	SNRPE			POP1
	SNRPF			POR
	SNRPG			POT1
	SNTA1			POTEI
	SNTB2			POTEKP
	SNU13			POU2F1
	SNUPN			POU2F2

Cohort	Whole	Female	Male	Previous
	SNW1			POUSF1
	SNX1			POU6F2
	SNX12			PPA1
	SNX17			PPAN
	SNX2			PPARA
	SNX27			PPARD
	SNX3			PPARG
	SNX5			PPARGC1A
	SNX6			PPARGC1B
	SNX9			PPCS
	SOAT1			PPFIA1
	SOCs1			PPFIBP1
	SOCs2			PPIA
	SOCs6			PPIB
	SOCs7			PPID
	SOD1			PPIF
	SOD2			PPIL4
	SON			PPL
	SORBS1			PPM1A
	SORBS2			PPM1B
	SORBS3			PPM1D
	SORL1			PPM1F
	SORT1			PPM1G
	SOS1			PPM1H
	SOX10			PPM1M
	SOX15			PPP1CA
	SOX17			PPP1CB
	SOX2			PPP1CC
	SOX4			PPP1R10
	SOX5			PPP1R12A
	SOX6			PPP1R12B
	SOX7			PPP1R15B
	SOX8			PPP1R16A
	SP1			PPP1R3A
	SP100			PPP1R3B
	SP110			PPP1R9B
	SP3			PPP2CA
	SP7			PPP2CB
	SP8			PPP2R1A
	SPAG5			PPP2R1B
	SPAG6			PPP2R2A
	SPAG9			PPP2R2B
	SPANXN2			PPP2R2C
	SPANXN3			PPP2R2D
	SPANXN4			PPP2R3B
	SPATA20			PPP2R5A
	SPATA5L1			PPP2R5B
	SPC24			PPP2R5C
	SPC25			PPP2R5D
	SPCS1			PPP2R5E
	SPDL1			PPP3CA
	SPECC1			PPP3CC
	SPECC1L			PPP3R1
	SPERT			PPP3R2
	SPG21			PPP4C
	SPHK1			PPP4R1L
	SPINK14			PPP5C
	SPINT2			PPP6R1
	SPNS1			PPT1
	SPON2			PPTC7
	SPOP			PRAF2
	SPOUT1			PRC1
	SPP1			PRDM1
	SPPL2B			PRDM14
	SPPL3			PRDM16
	SPR			PRDM6
	SPRED1			PRDX1
	SPRR1B			PRDX2
	SPTN			PRDX3
	SPTAN1			PRDX4
	SPTBN1			PREP
	SPTBN2			PREX1
	SPTLC1			PREX2
	SQLE			PRG2
	SQSTM1			PRG3
	SRC			PRKAA1
	SRCAP			PRKAA2
	SREBF1			PRKAB1
	SREBF2			PRKAB2
	SREK1			PRKACA
	SREK1P1			PRKACB
	SRF			PRKACG
	SRGN			PRKAG2
	SRMS			PRKAG3
	SRP14			PRKAR1A
	SRP68			PRKAR1B
	SRP72			PRKAR2A
	SRP9P1			PRKAR2B
	SRPK1			PRKCA
	SRPK2			PRKCB
	SRPK3			PRKCD
	SRPRB			PRKCE
	SRRM1			PRKCG
	SRRM2			PRKCH
	SRSF1			PRKCI
	SRSF11			PRKCQ

Cohort	Whole	Female	Male	Previous
	SRSF2			PRKCSH
	SRSF3			PRKCZ
	SRSF4			PRKD2
	SRSF5			PRKD3
	SRSF6			PRKDC
	SRSF7			PRKG1
	SRXN1			PRKN
	SS18L2			PRKRA
	SSB			PRKY
	SSBP1			PRMT1
	SSH1			PRMT2
	SSMEM1			PRMT3
	SSR1			PRMT5
	SSR3			PRMT6
	SSSCA1			PRMT8
	SSX2IP			PRNP
	ST14			PROM1
	ST3GAL3			PROSER2
	ST6GAL1			PROX1
	ST6GALNAC3			PROZ
	ST6GALNAC6			PRPF19
	ST7			PRPF3
	ST8SIA4			PRPF31
	STAG2			PRPF38A
	STAM			PRPF39
	STAMBP			PRPF4
	STAMBPL1			PRPF40A
	STARD3			PRPF4B
	STARD7			PRPF6
	STAT1			PRPF8
	STAT3			PRPS2
	STAT5A			PRR12
	STAT5B			PRR20A
	STAT6			PRR20E
	STAU1			PRR3
	STIM1			PRR4
	STIM2			PRR5L
	STIP1			PRRC2B
	STK11			PRRC2C
	STK24			PRRG4
	STK25			PRSS23
	STK26			PRTN3
	STK3			PRUNE2
	STK32C			PRXL2A
	STK4			PSAP
	STMN1			PSCA
	STMN2			PSEN1
	STMN4			PSEN2
	STOM			PSG11
	STOML2			PSG8
	STON2			PSIP1
	STRAP			PSMA1
	STRN			PSMA2
	STRN3			PSMA3
	STRN4			PSMA4
	STS			PSMA5
	STT3A			PSMA6
	STT3B			PSMA7
	STUB1			PSMB1
	STX11			PSMB2
	STX12			PSMB3
	STX1A			PSMB4
	STX2			PSMB5
	STX3			PSMB6
	STX4			PSMB7
	STX6			PSMC1
	STX7			PSMC2
	STX8			PSMC3
	STXBP4			PSMC4
	SUB1			PSMC5
	SUDS3			PSMC6
	SUFU			PSMD1
	SUGP1			PSMD10
	SUGP2			PSMD11
	SULT1A1			PSMD12
	SULT1C4			PSMD13
	SUMF2			PSMD14
	SUMO1			PSMD2
	SUMO2			PSMD3
	SUMO3			PSMD4
	SUN2			PSMD5
	SUPT16H			PSMD6
	SUPT5H			PSMD7
	SUPT6H			PSMD8
	SUPT7L			PSMD9
	SURF1			PSME2
	SURF2			PSME3
	SURF6			PSORS1C2
	SUV39H1			PSTPIP1
	SUZ12			PTBP1
	SV2A			PTBP3
	SVIL			PTCD3
	SYCE1			PTCH1
	SYCE3			PTEN
	SYDE2			PTF1A
	SYK			PTGER3

Cohort	Whole	Female	Male	Previous
	SYN1			PTGER4
	SYN2			PTGES2
	SYNCRIP			PTGES3
	SYNE3			PTGIR
	SYNGR1			PTH1R
	SYNJ2BP			PTH2R
	SYNPO			PTK2
	SYS1			PTK2B
	SYT1			PTK6
	SYT16			PTK7
	SYT2			PTN
	SYT6			PTP4A1
	SYVN1			PTP4A3
	TAB1			PTPA
	TAB2			PTPDC1
	TAB3			PTPMT1
	TACC1			PTPN1
	TACO1			PTPN11
	TACR1			PTPN12
	TACSTD2			PTPN3
	TADA2A			PTPN4
	TADA3			PTPN6
	TAF10			PTPN9
	TAF15			PTPRA
	TAF2			PTPRB
	TAF8			PTPRC
	TAF9			PTPRD
	TAF9B			PTPRF
	TAF3			PTPRJ
	TAGLN			PTPRK
	TAGLN2			PTPRO
	TAGLN3			PTPRR
	TAL1			PTPRS
	TANC1			PTPRU
	TANGO6			PTRH2
	TANK			PTTG1
	TAP1			PUF60
	TAP2			PUM1
	TAPBP			PURA
	TARDBP			PURB
	TARS			PURG
	TARS2			PUS1
	TATDN1			PUS7
	TAX1BP1			PUSL1
	TAZ			PVR
	TBC1D15			PWWP2A
	TBC1D22B			PXMP2
	TBC1D4			PXN
	TBCA			PYCARD
	TBCE			PYCR1
	TBK1			PYCR2
	TBKBP1			PYGM
	TBL1X			PYHIN1
	TBL1XR1			PYM1
	TBL2			QARS
	TBL3			QKI
	TBP			QPCTL
	TBR1			QPRT
	TBXT			QSER1
	TCEA2			RAB10
	TCEANC			RAB11A
	TCEANC2			RAB11B
	TCERG1			RAB11FIP1
	TCF20			RAB11FIP2
	TCF23			RAB11FIP5
	TCF3			RAB13
	TCF4			RAB14
	TCF7L2			RAB17
	TCHP			RAB18
	TCIRG1			RAB1A
	TCOF1			RAB1B
	TCP1			RAB29
	TCTN1			RAB2A
	TCTN2			RAB32
	TCTN3			RAB35
	TDP1			RAB3B
	TDRD3			RAB3IP
	TEAD1			RAB4A
	TEAD2			RAB5A
	TEAD4			RAB5B
	TECTB			RAB5C
	TEKT4			RAB5IF
	TELO2			RAB6A
	TEPSIN			RAB7A
	TERF1			RAB8A
	TERF2			RAB9A
	TERF2IP			RABEP1
	TERT			RABEP2
	TES			RABGAP1L
	TET2			RABGEF1
	TEX101			RABL3
	TEX264			RABL6
	TF			RAC1
	TFAM			RAC2
	TFAP2A			RAC3
	TFAP4			RACGAP1

Cohort	Whole	Female	Male	Previous
	TFCP2			RACK1
	TFDP1			RAD18
	TFG			RAD21
	TFIP11			RAD23A
	TFPI2			RAD50
	TFPT			RAD51
	TFRC			RAD52
	TGFA			RAD54L2
	TGFB1			RAE1
	TGFBR1			RAF1
	TGFBR2			RAI1
	TGIF2LY			RAI14
	TGM1			RALA
	TGOLN2			RALBP1
	THAP11			RALY
	THAP4			RAMP2
	THAP7			RAMP3
	THBD			RAN
	THBS1			RANBP2
	THOC1			RANBP6
	THOP1			RANBP9
	THRAP3			RANGAP1
	THRB			RAP1A
	THRSP			RAP1B
	THY1			RAP1GDS1
	TIAM1			RAP2C
	TIFA			RAPGEF2
	TIGIT			RAPGEF3
	TIMD4			RAPGEF5
	TIMM10			RAPH1
	TIMM13			RARA
	TIMM23B			RARB
	TIMM44			RARG
	TIMM50			RARS
	TIMM8A			RASA1
	TIMM9			RASD2
	TIMMDC1			RASEF
	TIMP1			RASL10B
	TIMP3			RASSF1
	TIMP4			RASSF8
	TINF2			RB1
	TJP1			RB1CC1
	TJP2			RBBP4
	TK1			RBBP5
	TKT			RBBP6
	TLE1			RBBP7
	TLE2			RBBP8
	TLE3			RBCK1
	TLL1			RBFox2
	TLN1			RBL1
	TLR10			RBL2
	TLX1			RBM10
	TLX2			RBM11
	TLX3			RBM14
	TM6SF2			RBM15
	TM9SF2			RBM15B
	TMBIM6			RBM17
	TMED2			RBM19
	TMED6			RBM20
	TMED7			RBM23
	TMEM106A			RBM25
	TMEM106B			RBM26
	TMEM109			RBM27
	TMEM120B			RBM28
	TMEM126A			RBM3
	TMEM126B			RBM34
	TMEM128			RBM39
	TMEM130			RBM4
	TMEM131			RBM42
	TMEM131L			RBM45
	TMEM14A			RBM47
	TMEM14B			RBM48
	TMEM169			RBM4B
	TMEM17			RBM5
	TMEM179B			RBM7
	TMEM189-UBE2V1			RBM8A
	TMEM192			RBMS1
	TMEM205			RBMS2
	TMEM206			RBMX
	TMEM208			RBPJ
	TMEM214			RBPMS
	TMEM216			RBPMS2
	TMEM218			RBX1
	TMEM223			RC3H1
	TMEM231			RC3H2
	TMEM237			RCC1
	TMEM239			RCC1L
	TMEM246			RCC2
	TMEM25			RGY1
	TMEM258			RCL1
	TMEM270			RCN1
	TMEM30A			RCN2
	TMEM30B			RCOR1
	TMEM31			RCOR3
	TMEM41B			RDH13
	TMEM43			RDX

Cohort	Whole	Female	Male	Previous
	TMEM52B			RECK
	TMEM59			RECQL4
	TMEM63B			REEP4
	TMEM63C			REEP5
	TMEM67			REL
	TMEM86A			RELA
	TMEM87A			RELB
	TMEM9			RELL1
	<i>TMEM9B</i>			REST
	TMOD1			RET
	TMOD3			RETREG3
	TMPO			RETSAT
	TMPRSS11B			REV1
	TMPRSS13			REXO4
	TMPRSS2			RFC1
	TMPRSS4			RFC2
	TMPRSS5			RFC3
	TMX1			RFC4
	TNC			RFC5
	TNF			RFFL
	TNFAIP1			RFLNA
	TNFAIP8			RFX2
	TNFRSF10A			RFXANK
	TNFRSF10B			RGMA
	TNFRSF10C			RGPD1
	TNFRSF10D			RGPD6
	TNFRSF1A			RGS17
	TNFRSF1B			RGS2
	TNFSF8			RGS20
	TNFSF9			RGS3
	TNIK			RHBDD1
	TNIP2			RHBDD2
	TNK2			RHBDF2
	TNKS			RHEB
	TNKS1BP1			RHEBL1
	TNKS2			RHOA
	TNP1			RHOB
	TNP2			RHOBTB1
	TNPO1			RHOBTB2
	TNPO2			RHOBTB3
	TNPO3			RHOC
	TNR			RHOD
	TNRC6A			RHOF
	TNRC6B			RHOG
	TNS2			RHOH
	TOLLIP			RHOJ
	TOM1			RHOQ
	TOM1L1			RHOT1
	TOMM20			RHOT2
	TOMM22			RHOU
	TOMM40			RHOV
	TOMM70			RHPN2
	TOP1			RIC8B
	TOP2B			RICTOR
	TOP3B			RIF1
	TOPORS			RILP
	TOR1A			RIMS3
	TOR1AIP1			RIN1
	TOR1AIP2			RIN3
	TOX4			RING1
	TP53			RINT1
	TP53BP1			RIOK1
	TP53BP2			RIOK2
	TP53RK			RIOK3
	TPCN2			RIPK1
	TPD52L2			RIPK4
	TPI1			RIPPLY1
	TPM1			RITA1
	<i>TPM2</i>			RLN1
	TPM3			RMC1
	TPM4			RMDN3
	TPP1			RM11
	TPP2			RMND1
	TPR			RNASE3
	TPRG1			RND1
	TPT1			RND2
	TPTE			RND3
	TPX2			RNF103
	TRA			RNF11
	TRA2A			RNF114
	TRA2B			RNF123
	TRADD			RNF126
	TRAF1			RNF138
	TRAF2			RNF139
	TRAF3			RNF144A
	TRAF3IP1			RNF146
	TRAF4			RNF149
	TRAF5			RNF157
	TRAF6			RNF166
	TRAF7			RNF168
	TRAIIP			RNF170
	TRAK1			RNF183
	TRAK2			RNF185
	TRAP1			RNF2
	TRAPPC2L			RNF20
	TRAPPC3			RNF213

Cohort	Whole	Female	Male	Previous
	TRARG1			RNF214
	TREM2			RNF219
	TRGV3			RNF31
	TRIB1			RNF32
	TRIB2			RNF4
	TRIB3			RNF40
	TRIM13			RNF41
	TRIM14			RNF5
	TRIM15			RNF7
	TRIM21			RNF8
	TRIM23			RNPEP
	TRIM24			RNPS1
	TRIM25			RO60
	TRIM26			ROBO1
	TRIM27			ROCK1
	TRIM28			ROCK2
	TRIM29			ROR2
	TRIM3			RORC
	TRIM31			RP2
	TRIM32			RPA1
	TRIM33			RPA2
	TRIM37			RPA3
	TRIM40			RPAIN
	TRIM41			RPE
	TRIM46			RPF2
	TRIM52			RPL10
	TRIM54			RPL10A
	TRIM55			RPL10L
	TRIM6			RPL11
	TRIM63			RPL12
	TRIM66			RPL13
	TRIM68			RPL13A
	TRIM8			RPL14
	TRIM9			RPL15
	TRIO			RPL17
	TRIP13			RPL18
	TRIP4			RPL18A
	TRIP6			RPL19
	TRMT112			RPL21
	TRMT61A			RPL22
	TRMT61B			RPL23
	TROAP			RPL23A
	TRPS1			RPL24
	TSACC			RPL26
	TSC1			RPL26L1
	TSC22D1			RPL27
	TSC22D2			RPL27A
	TSC22D4			RPL28
	TSEN15			RPL3
	TSFM			RPL30
	TSG101			RPL31
	TSGA10			RPL32
	TSHR			RPL34
	TSHZ3			RPL35
	TSN			RPL35A
	TSNAX			RPL36
	TSPAN15			RPL36A
	TSPAN17			RPL36AL
	TSPAN3			RPL37A
	TSPAN33			RPL38
	TSSK3			RPL4
	TSSK6			RPL5
	TTBK2			RPL6
	TTC26			RPL7
	TTC27			RPL7A
	TTC28			RPL7L1
	TTC29			RPL8
	TTC30A			RPL9
	TTC30B			RPLP0
	TTC33			RPLP1
	TTC9C			RPLP2
	TTF2			RPN1
	TTK			RPN2
	TTN			RPP38
	TTPA			RPRD1A
	TTR			RPRD2
	TTYH1			RPRM
	TUBA1A			RPS10
	TUBA1B			RPS11
	TUBA1C			RPS12
	TUBA4A			RPS13
	TUBB			RPS14
	TUBB2A			RPS15
	TUBB2B			RPS15A
	TUBB3			RPS16
	TUBB4A			RPS17
	TUBB4B			RPS18
	TUBB6			RPS19
	TUBB8			RPS2
	TUBD1			RPS20
	TUBG1			RPS21
	TUBGCP4			RPS23
	TUFM			RPS24
	TUFT1			RPS25
	TULP3			RPS26
	TUSC3			RPS27

Cohort	Whole	Female	Male	Previous
	TUT7			RPS27A
	TXLNA			RPS27L
	TXN			RPS28
	TXNDC9			RPS3
	TXNIP			RPS3A
	TXNL1			RPS4X
	TYSDN1			RPS5
	U2AF1			RPS6
	U2AF2			RPS6KA1
	U2SURP			RPS6KA2
	UBA1			RPS6KA3
	UBA2			RPS6KA5
	UBA5			RPS6KA6
	UBA52			RPS6KB1
	UBAC2			RPS6KB2
	UBAP2			RPS7
	UBAP2L			RPS8
	UBASH3B			RPS9
	UBB			RPSA
	UBD			RPTOR
	UBE2A			RRAGB
	UBE2D1			RRAS
	UBE2D2			RRAS2
	UBE2D3			RRBP1
	UBE2D4			RREB1
	UBE2E1			RRM1
	UBE2E2			RRM2
	UBE2E3			RRP1
	UBE2I			RRP12
	UBE2K			RRP15
	UBE2L3			RRP1B
	UBE2M			RRP7A
	UBE2N			RRP8
	UBE2O			RRP9
	UBE2U			RSBN1
	UBE2V2			RSBN1L
	UBE2W			RSL1D1
	UBE2Z			RSP03
	UBE3A			RSRC2
	UBE3C			RTCA
	UBL4A			RTCB
	UBQLN1			RTKL1
	UBQLN2			RTRAF
	UBQLN4			RUNX1
	UBR4			RUNX1T1
	UBR5			RUNX2
	UBXN1			RUNX3
	UBXN4			RUVBL1
	UBXN6			RUVBL2
	UBXN7			RXRA
	UCHL1			RXR8
	UCHL3			RXRG
	UCHL5			RYBP
	UFC1			RYK
	UFL1			S100A10
	UFSP2			S100A11
	UGGT1			S100A14
	UGP2			S100A2
	UGT2B15			S100A3
	UGT8			S100A6
	UHRF2			S100A7
	ULK1			S100A8
	ULK3			S100A9
	UNC45A			S100B
	UNC5CL			S100P
	UNC93B1			S1PR1
	UNG			S1PR4
	UNK			SAAL1
	UNKL			SAC3D1
	UPF1			SAE1
	UPF3A			SAFB
	UPF3B			SAFB2
	UPK1A			SALL1
	UPK2			SALL4
	UQCC1			SAMD1
	UQCRC1			SAMHD1
	UQCRC2			SAMM50
	UQCRFS1			SAP130
	UQCRH			SAP18
	UQCRQ			SAP30
	URI1			SAP30BP
	USE1			SAR1A
	USF1			SARAF
	USHBP1			SARM1
	USO1			SART1
	USP1			SART3
	USP10			SASS6
	USP11			SAT1
	USP14			SATB1
	USP15			SATB2
	USP18			SBD5
	USP19			SBSN
	USP2			SCAF1
	USP20			SCAF11
	USP30			SCAMP2
	USP34			SCAMP3

Cohort	Whole	Female	Male	Previous
	USP36			SCAP
	USP4			SCARB1
	USP49			SCARB2
	USP5			SCARNA22
	USP51			SCCPDH
	USP54			SCD
	USP7			SCEL
	USP8			SCFD1
	USP9X			SCGB1A1
	UTP14A			SCGB1D1
	UTP14C			SCGB2A1
	UTP20			SCGB2A2
	UTP23			SCGN
	UTP4			SCHIP1
	UTRN			SCIN
	UXS1			SCLT1
	UXT			SCN10A
	VAC14			SCN2B
	VAMP2			SCN3B
	VAMP3			SCNN1A
	VAMP5			SCO1
	VANGL1			SCRIB
	VANGL2			SDAD1
	VAPA			SDC1
	VAPB			SDC2
	VARS			SDC4
	VARS2			SDCBP
	VASP			SDF2L1
	VAV1			SDHA
	VAV2			SDHB
	VAV3			SEC11A
	VBP1			SEC13
	VCAM1			SEC16A
	VCL			SEC22B
	VCP			SEC23A
	VCP1P1			SEC23B
	VDAC1			SEC24B
	VDAC2			SEC31A
	VDAC3			SEC61A1
	VDR			SEC61B
	VEGFA			SEC62
	VENTX			SEC63
	VGf			SECISBP2
	VHL			SEL1L
	VHLL			SEL1L3
	VIM			SELENBP1
	VIRMA			SELENOF
	VKORC1			SELENOS
	VLDLR			SEPLG
	VMA21			SEM1
	VMP1			SEMA3C
	VPS26A			SEMA3F
	VPS28			SEMA4C
	VPS29			SEMA4F
	VPS33A			SEMG1
	VPS35			SENP1
	VPS37D			SENP2
	VPS51			SENP3
	VPS53			SERBP1
	VPS9D1			SERP1
	VRK1			SERP2
	VRK3			SERPINA1
	VSIG1			SERPINA3
	VSIG4			SERPINA5
	Vsx1			SERPINB13
	VTN			SERPINB2
	VWA2			SERPINB3
	VWA8			SERPINB4
	WVCE			SERPINB5
	WAPL			SERPINC1
	WARS			SERPINE1
	WASL			SERPINF1
	WBP11			SERPINH1
	WBP2			SERTAD1
	WDCP			SERTAD2
	WDR1			SERTAD4
	WDR11			SET
	WDR3			SETD1A
	WDR34			SETD2
	WDR37			SETDB1
	WDR4			SETX
	WDR44			SF1
	WDR46			SF3A1
	WDR48			SF3A3
	WDR5			SF3B1
	WDR5B			SF3B2
	WDR6			SF3B3
	WDR70			SF3B4
	WDR74			SFMBT1
	WDR76			SFN
	WDR77			SFPQ
	WDR82			SFSWAP
	WDR89			SFTPC
	WDR92			SFXN1
	WDTc1			SFXN4
	WDYHV1			SFXN5

Cohort	Whole	Female	Male	Previous
	WFS1			SGCA
	WIF1			SGCB
	WLS			SGF29
	WNT3A			SGK1
	WNT4			SGK3
	WRAP53			SGPL1
	WRN			SGPP1
	WWOX			SGTA
	WWP1			SGTB
	WWP2			SH2B1
	XPA			SH2B2
	XPC			SH2B3
	XPNPEP1			SH2D1B
	XPNPEP3			SH2D2A
	XPO1			SH2D3C
	XPO7			SH2D4A
	XPOT			SH3BGRL
	XPR1			SH3BGRL3
	XRCC1			SH3BP2
	XRCC3			SH3BP5
	XRCC5			SH3BP5L
	XRCC6			SH3GL1
	XRN1			SH3GL2
	YAF2			SH3GL3
	YAP1			SH3GLB1
	YARS2			SH3GLB2
	YBX1			SH3KBP1
	YBX3			SH3RF1
	YEATS4			SHANK2
	YES1			SHANK3
	YIF1A			SHARPIN
	YIPF3			SHB
	YIPF4			SHC1
	YIPF6			SHC3
	YJEFN3			SHMT1
	YJU2			SHMT2
	YKT6			SHOC2
	YME1L1			SHPRH
	YOD1			SHROOM3
	YTHDF1			SHTN1
	YTHDF2			SIAE
	YTHDF3			SIAH1
	YWHAB			SIAH2
	YWHAE			SIGLECL1
	YWHAG			SIK2
	YWHAH			SIK3
	YWHAQ			SIKE1
	YWHAZ			SIN3A
	YY1			SIN3B
	YY1AP1			SINHCAF
	ZACN			SIPA1L1
	ZBTB10			SIRPA
	ZBTB16			SIRPD
	ZBTB2			SIRT1
	ZBTB20			SIRT2
	ZBTB21			SIRT3
	ZBTB24			SIRT4
	ZBTB38			SIRT5
	ZBTB7A			SIRT6
	ZC2HC1C			SIRT7
	ZC3H10			SIVA1
	ZC3H18			SIX1
	ZC3H3			SIX2
	ZC3H7A			SIX4
	ZC3HAV1			SKAP1
	ZC4H2			SKAP2
	ZCCHC10			SKI
	ZCCHC17			SKIL
	ZDHHHC11			SKP1
	ZDHHHC12			SKP2
	ZDHHHC17			SLA2
	ZDHHHC18			SLAIN2
	ZDHHHC23			SLAMF1
	ZDHHHC5			SLC12A2
	ZEB1			SLC12A4
	ZFC3H1			SLC12A6
	ZFHX3			SLC12A7
	ZFP36			SLC12A9
	ZFP36L2			SLC15A1
	ZFPL1			SLC16A11
	ZFR			SLC16A3
	ZFYVE21			SLC16A9
	ZFYVE27			SLC18A1
	ZFYVE9			SLC18A2
	ZGPAT			SLC19A1
	ZIC1			SLC1A1
	ZMPSTE24			SLC1A3
	ZMYM2			SLC1A5
	ZMYM3			SLC20A2
	ZMYM4			SLC22A1
	ZMYM5			SLC22A18
	ZMYND12			SLC22A2
	ZMYND19			SLC22A4
	ZMYND8			SLC22A9
	ZNF174			SLC25A1
	ZNF207			SLC25A10

Cohort	Whole	Female	Male	Previous
	ZNF219			SLC25A11
	ZNF223			SLC25A12
	ZNF24			SLC25A13
	ZNF250			SLC25A20
	ZNF263			SLC25A22
	ZNF326			SLC25A24
	ZNF330			SLC25A29
	ZNF335			SLC25A3
	ZNF346			SLC25A30
	ZNF385C			SLC25A4
	ZNF397			SLC25A46
	ZNF414			SLC25A5
	ZNF417			SLC25A51
	ZNF460			SLC25A6
	ZNF467			SLC27A4
	ZNF485			SLC27A6
	ZNF496			SLC29A1
	ZNF512			SLC2A1
	ZNF512B			SLC2A12
	ZNF526			SLC2A2
	ZNF558			SLC2A3
	ZNF572			SLC2A4
	ZNF581			SLC30A1
	ZNF587			SLC30A2
	ZNF593			SLC30A5
	ZNF598			SLC30A6
	ZNF608			SLC30A8
	ZNF655			SLC30A9
	ZNF668			SLC31A1
	ZNF746			SLC31A2
	ZNF764			SLC33A1
	ZNF784			SLC35C1
	ZNF785			SLC35G1
	ZNHIT3			SLC37A3
	ZNRD1ASP			SLC38A1
	ZNRF4			SLC38A7
	ZPR1			SLC39A10
	ZRANB1			SLC39A12
	ZRANB2			SLC39A3
	ZSCAN1			SLC39A4
	ZSCAN23			SLC39A6
	ZSCAN5A			SLC39A7
	ZUP1			SLC39A8
	ZWINT			SLC39A9
	ZYX			SLC3A2
	ZZEF1			SLC43A3
	ZZZ3			SLC4A7
				SLC5A6
				SLC7A1
				SLC7A3
				SLC7A5
				SLC9A1
				SLC9A3R1
				SLC9A6
				SLCO1B1
				SLFN11
				SLIRP
				SLMAP
				SLTM
				SLU7
				SLURP1
				SLX4
				SLX4IP
				SMAD1
				SMAD2
				SMAD3
				SMAD4
				SMAD5
				SMAD7
				SMAD9
				SMAP2
				SMARCA1
				SMARCA2
				SMARCA4
				SMARCA5
				SMARCAD1
				SMARCB1
				SMARCC1
				SMARCC2
				SMARCD1
				SMARCD2
				SMARCD3
				SMARCE1
				SMC1A
				SMC2
				SMC3
				SMC4
				SMCHD1
				SMG7
				SMIM29
				SMN1
				SMNDC1
				SMO
				SMPD1
				SMPD2
				SMPD4

Cohort	Whole	Female	Male	Previous
				SMURF1
				SMURF2
				SMYD3
				SNAI1
				SNAI2
				SNAP23
				SNAP29
				SNAPC4
				SNAPIN
				SNCA
				SND1
				SNHG28
				SNIP1
				SNRNP200
				SNRNP27
				SNRNP70
				SNRPA
				SNRPA1
				SNRPB
				SNRPB2
				SNRPC
				SNRPD1
				SNRPD2
				SNRPD3
				SNRPF
				SNTA1
				SNTB1
				SNTB2
				SNU13
				SNW1
				SNX1
				SNX10
				SNX13
				SNX17
				SNX2
				SNX20
				SNX24
				SNX27
				SNX3
				SNX33
				SNX5
				SNX6
				SNX8
				SNX9
				SOAT1
				SOCs1
				SOCs2
				SOCs3
				SOCs6
				SOCs7
				SOD1
				SOD2
				SOHLH1
				SORBS1
				SORBS3
				SORD
				SORL1
				SORT1
				SOS1
				SOSTDC1
				SOX10
				SOX15
				SOX17
				SOX2
				SOX4
				SOX5
				SOX6
				SOX7
				SOX8
				SOX9
				SP1
				SP100
				SP110
				SP2
				SP3
				SP7
				SPACA1
				SPANXN2
				SPANXN5
				SPART
				SPATA2
				SPATA20
				SPATA5
				SPATA5L1
				SPCS1
				SPDL1
				SPDYE4
				SPECC1L
				SPEN
				SPG21
				SPG7
				SPHK2
				SPINK14
				SPINK2
				SPINT2
				SPNS1

Cohort	Whole	Female	Male	Previous
				SPOP
				SPP1
				SPPL2B
				SPPL3
				SPRED1
				SPRED2
				SPRTN
				SPSB1
				SPSB2
				SPSB4
				SPTA1
				SPTAN1
				SPTB
				SPTBN1
				SPTBN2
				SPTBN5
				SPTLC1
				SPX
				SQSTM1
				SRC
				SRCAP
				SREBF1
				SREBF2
				SRF
				SRGAP2
				SRP14
				SRP68
				SRP72
				SRPK1
				SRPK2
				SRPRB
				SRRM1
				SRRM2
				SRSF1
				SRSF2
				SRSF3
				SRSF4
				SRSF5
				SRSF6
				SRSF7
				SRSF9
				SS18
				SS18L1
				SS18L2
				SSB
				SSBP1
				SSBP2
				SSBP3
				SSC4D
				SSH1
				SSH3
				SSR1
				SSR3
				SSR4
				SSRP1
				SSSCA1
				SSUH2
				SSX2IP
				ST13
				ST14
				ST3GAL2
				ST3GAL4
				ST6GAL1
				ST6GALNAC3
				ST6GALNAC6
				ST7
				ST8SIA4
				STAB1
				STAG2
				STAM
				STAM2
				STAP1
				STARD13
				STARD3
				STAT1
				STAT2
				STAT3
				STAT5A
				STAT5B
				STAT6
				STAU1
				STAU2
				STBD1
				STC2
				STIL
				STIM1
				STIP1
				STK11
				STK16
				STK19
				STK24
				STK25
				STK26
				STK3
				STK36
				STK38

Cohort	Whole	Female	Male	Previous
				STK38L
				STK4
				STK40
				STMN1
				STMN2
				STOML2
				STRAP
				STRBP
				STRIP1
				STRN
				STRN3
				STRN4
				STT3A
				STT3B
				STUB1
				STX10
				STX11
				STX12
				STX1A
				STX2
				STX3
				STX4
				STX6
				STX7
				STX8
				SUB1
				SUDS3
				SUFU
				SUGCT
				SUGP1
				SUGP2
				SUGT1
				SULF1
				SULF2
				SULT1C4
				SUMF1
				SUMO1
				SUMO2
				SUMO3
				SUN1
				SUN2
				SUPT16H
				SUPT5H
				SUPT6H
				SURF6
				SUSD1
				SUV39H1
				SUZ12
				SVIL
				SYCE1
				SYCE3
				SYK
				SYMPK
				SYN1
				SYN2
				SYNCRIP
				SYNE2
				SYNE3
				SYNGR2
				SYNJ2BP
				SYNPO
				SYT1
				SYT4
				SYT6
				SYVN1
				TAB1
				TAB2
				TACO1
				TACR1
				TACSTD2
				TADA2A
				TADA3
				TAF1
				TAF15
				TAF3
				TAF4
				TAF5
				TAF5L
				TAF6
				TAF7
				TAF9
				TAF9B
				TAFA2
				TAFA3
				TAFA4
				TAGLN
				TAGLN2
				TAL1
				TANK
				TAOK2
				TAP1
				TAP2
				TAPBP
				TARBP2
				TARDBP
				TARS2

Cohort	Whole	Female	Male	Previous
				TASOR
				TAX1BP1
				TAZ
				TBC1D1
				TBC1D15
				TBC1D23
				TBC1D4
				TBCA
				TBCCD1
				TBCE
				TBK1
				TBL1X
				TBL1XR1
				TBL2
				TBL3
				TBP
				TBR1
				TBX5
				TBXT
				TCAP
				TCEAL1
				TCEANC
				TCERG1
				TCF12
				TCF15
				TCF20
				TCF25
				TCF3
				TCF4
				TCF7L2
				TCIRG1
				TCL1A
				TCL1B
				TCOF1
				TCP1
				TCTN1
				TCTN2
				TCTN3
				TDGF1
				TDP2
				TDRD3
				TEAD1
				TEAD2
				TEAD3
				TEC
				TECR
				TEK
				TEKT4
				TEKT5
				TELO2
				TENM3
				TENT5A
				TEPSIN
				TERF1
				TERF2
				TERF2IP
				TERT
				TES
				TESK1
				TESPA1
				TET2
				TEX101
				TEX11
				TEX264
				TF
				TFAM
				TFAP2A
				TFAP2D
				TFAP4
				TFB2M
				TFCP2
				TFDP1
				TFDP2
				TFDP3
				TFF1
				TFG
				TFIP11
				TFPT
				TFRC
				TGFB1
				TGFBR1
				TGFBR2
				TGFBR3
				TGM1
				TGM2
				TGM3
				TGM5
				TGOLN2
				THADA
				THAP1
				THAP11
				THBS1
				THBS3
				THOC1
				THOC2
				THOC3

Cohort	Whole	Female	Male	Previous
				THOC6
				THOC7
				THRA
				THRAP3
				THRB
				THRSF
				THSD4
				TIAL1
				TIAM1
				TIFA
				TIFAB
				TIGD5
				TIMD4
				TIMM13
				TIMM29
				TIMM44
				TIMM50
				TIMM8A
				TIMP3
				TINAG
				TINF2
				TJP1
				TK1
				TKT
				TLE1
				TLE3
				TLE4
				TLN1
				TLN2
				TLR2
				TLR3
				TLR9
				TLX1
				TLX2
				TLX3
				TM6SF2
				TM9SF2
				TM9SF3
				TMBIM6
				TMCC2
				TMCO1
				TMED1
				TMED10
				TMED2
				TMED4
				TMED5
				TMED6
				TMED7
				TMED8
				TMED9
				TMEM101
				TMEM106A
				TMEM106B
				TMEM106C
				TMEM120B
				TMEM126B
				TMEM128
				TMEM129
				TMEM130
				TMEM131L
				TMEM14A
				TMEM14B
				TMEM160
				TMEM163
				TMEM17
				TMEM176B
				TMEM179B
				TMEM18
				TMEM184A
				TMEM184B
				TMEM189
				TMEM189-UBI
				TMEM19
				TMEM192
				TMEM203
				TMEM206
				TMEM214
				TMEM216
				TMEM223
				TMEM237
				TMEM246
				TMEM25
				TMEM254
				TMEM259
				TMEM30A
				TMEM30B
				TMEM31
				TMEM33
				TMEM59
				TMEM60
				TMEM63A
				TMEM63B
				TMEM65
				TMEM67
				TMEM72
				TMEM74

Cohort	Whole	Female	Male	Previous
				TMEM87A
				TMEM9
				TMEM94
				TMEM98
				TMLHE
				TMOD1
				TMOD3
				TMPO
				TMPRSS11B
				TMPRSS13
				TMPRSS2
				TMPRSS4
				TMX1
				TNF
				TNFAIP3
				TNFAIP6
				TNFAIP8
				TNFRSF10A
				TNFRSF10B
				TNFRSF13B
				TNFRSF1A
				TNFRSF1B
				TNFRSF8
				TNFSF12
				TNFSF13B
				TNFSF8
				TNFSF9
				TNIK
				TNIP1
				TNIP2
				TNIP3
				TNK2
				TNKS
				TNKS1BP1
				TNKS2
				TNNC2
				TNNI2
				TNPO1
				TNPO2
				TNPO3
				TNRC18
				TNRC6A
				TNRC6B
				TNRC6C
				TNS2
				TNS3
				TNXB
				TOLLIP
				TOM1
				TOM1L2
				TOMM20
				TOMM22
				TOMM34
				TOMM40
				TOMM5
				TOP1
				TOP2A
				TOP2B
				TOP3A
				TOP3B
				TOPBP1
				TOR1A
				TOR1AIP1
				TOR3A
				TOX4
				TP53
				TP53BP1
				TP53BP2
				TP53RK
				TP63
				TP73
				TPCN2
				TPK1
				TPM1
				TPM2
				TPM3
				TPM4
				TPR
				TPRA1
				TPST2
				TPT1
				TPTE
				TPTE2
				TPX2
				TRA
				TRA2B
				TRAF1
				TRAF2
				TRAF3
				TRAF3IP1
				TRAF3IP3
				TRAF4
				TRAF6
				TRAF7
				TRAIP
				TRAK2

Cohort	Whole	Female	Male	Previous
				TRAP1
				TRAV20
				TREM2
				TRIB1
				TRIB2
				TRIB3
				TRIM11
				TRIM13
				TRIM14
				TRIM15
				TRIM2
				TRIM21
				TRIM23
				TRIM24
				TRIM25
				TRIM27
				TRIM28
				TRIM29
				TRIM3
				TRIM32
				TRIM33
				TRIM35
				TRIM37
				TRIM42
				TRIM43
				TRIM5
				TRIM52
				TRIM54
				TRIM55
				TRIM56
				TRIM63
				TRIM66
				TRIM68
				TRIM72
				TRIM74
				TRIOBP
				TRIP10
				TRIP11
				TRIP12
				TRIP13
				TRIP4
				TRIP6
				TRMT1
				TRMT10C
				TRMT112
				TRMT6
				TRMT61A
				TRMU
				TROAP
				TRPC1
				TRPC4
				TRPC4AP
				TRPS1
				TRRAP
				TRUB2
				TSC1
				TSC2
				TSC22D2
				TSC22D3
				TSC22D4
				TSFM
				TSG101
				TSGA10
				TSHR
				TSHZ1
				TSHZ2
				TSN
				TSNAX
				TSPAN15
				TSPAN3
				TSPYL6
				TSR1
				TSSC4
				TSSK6
				TTBK2
				TTC1
				TTC14
				TTC17
				TTC19
				TTC26
				TTC3
				TTC37
				TTC4
				TTF2
				TTI1
				TTI2
				TTK
				TTN
				ITR
				TTYH1
				TUB
				TUBA1A
				TUBA1B
				TUBA1C
				TUBA3D
				TUBA4A

Cohort	Whole	Female	Male	Previous
				TUBAL3
				TUBB
				TUBB2A
				TUBB2B
				TUBB3
				TUBB4A
				TUBB4B
				TUBB6
				TUBB8
				TUBG1
				TUBGCP2
				TUBGCP3
				TUBGCP4
				TUFM
				TUFT1
				TULP3
				TWF1
				TWIST1
				TXK
				TXLNA
				TXN
				TXNDC11
				TXNDC15
				TXNDC16
				TXNDC17
				TXNDC5
				TXNDC9
				TXNIP
				TYK2
				TYRO3
				TYROBP
				TYW1B
				TYW3
				U2AF1
				U2AF2
				U2SURP
				UBA1
				UBA52
				UBA6
				UBALD2
				UBAP2
				UBAP2L
				UBASH3A
				UBASH3B
				UBB
				UBD
				UBE2A
				UBE2D1
				UBE2D2
				UBE2D3
				UBE2D4
				UBE2E1
				UBE2E3
				UBE2G2
				UBE2H
				UBE2I
				UBE2K
				UBE2L3
				UBE2L6
				UBE2M
				UBE2N
				UBE2O
				UBE2S
				UBE2U
				UBE2V2
				UBE2W
				UBE2Z
				UBE3A
				UBE3C
				UBE4A
				UBE4B
				UBIAD1
				UBL4A
				UBN1
				UBN2
				UBOX5
				UBP1
				UBQLN1
				UBQLN2
				UBQLN4
				UBR1
				UBR2
				UBR3
				UBR4
				UBR5
				UBTF
				UBXN6
				UBXN7
				UCHL1
				UCHL3
				UCHL5
				UCKL1
				UCN3
				UFD1
				UFL1
				UFSP2

Cohort	Whole	Female	Male	Previous
				UGGT1
				UGGT2
				UGP2
				UGT1A7
				UGT8
				UHKM1
				UHRF1
				UHRF2
				UIMC1
				ULK1
				ULK2
				UNC119
				UNC5B
				UNC93B1
				UNK
				UNKL
				UPF1
				UPF2
				UPK1A
				UPK2
				UPP1
				UPRT
				UQCC1
				UQCRB
				UQCRC1
				UQCRC2
				UQCRCF1
				URI1
				USF1
				USHBP1
				USO1
				USP1
				USP10
				USP11
				USP13
				USP14
				USP15
				USP2
				USP20
				USP21
				USP25
				USP28
				USP3
				USP30
				USP32
				USP36
				USP38
				USP39
				USP4
				USP44
				USP46
				USP47
				USP5
				USP7
				USP8
				USP9X
				UTP14A
				UTP3
				UTP6
				UTRN
				UXS1
				UXT
				VAC14
				VAMP2
				VAMP3
				VAMP5
				VANGL2
				VAPA
				VAPB
				VARS
				VASN
				VASP
				VAV1
				VAV3
				VBP1
				VCAM1
				VCAN
				VCL
				VCP
				VCPIP1
				VDAC1
				VDAC2
				VDAC3
				VDR
				VEGFA
				VEGFB
				VHL
				VIM
				VIPR1
				VIPR2
				VIRMA
				VKORC1
				VLDLR
				VMA21
				VMAC
				VMP1

Cohort	Whole	Female	Male	Previous
				VPS11
				VPS13A
				VPS28
				VPS29
				VPS33A
				VPS33B
				VPS35
				VPS36
				VPS37C
				VPS50
				VPS51
				VPS52
				VPS53
				VPS54
				VPS72
				VRK1
				VRK2
				VRK3
				VSIG1
				VSIG4
				VSX1
				VTa1
				VTI1B
				VTN
				VWA2
				VWA8
				WVC2
				WWCE
				WWDE
				WAPL
				WARS
				WASF1
				WASF3
				WASHC1
				WASHC3
				WASL
				WBP11
				WDFY3
				WDHD1
				WDR1
				WDR3
				WDR44
				WDR48
				WDR5
				WDR59
				WDR6
				WDR61
				WDR73
				WDR74
				WDR76
				WDR77
				WDR82
				WDR83
				WDYHV1
				WFDC2
				WFS1
				WHAMMP3
				WIF1
				WIZ
				WLS
				WNK1
				WNK4
				WNT3A
				WNT4
				WNT5A
				WNT9A
				WRN
				WT1
				WTAP
				WWOX
				WWP1
				WWP2
				XAB2
				XAGE1B
				XPB1
				XIAP
				XPC
				XPNPEP3
				XPO1
				XPO4
				XPO6
				XPOT
				XRCC1
				XRCC3
				XRCC5
				XRCC6
				XRN1
				XRN2
				YAF2
				YAP1
				YARS
				YBX1
				YBX3
				YEATS2
				YEATS4
				YES1

Cohort	Whole	Female	Male	Previous
				YIF1A
				YIPF3
				YJU2
				YLP1
				YPEL3
				YTHDC2
				YTHDF1
				YTHDF2
				YTHDF3
				YWHAB
				YWHAE
				YWHAG
				YWHAH
				YWHAQ
				YWHAZ
				YY1
				ZAP70
				ZAR1L
				ZBBX
				ZBTB1
				ZBTB10
				ZBTB14
				ZBTB16
				ZBTB2
				ZBTB21
				ZBTB24
				ZBTB3
				ZBTB32
				ZBTB33
				ZBTB34
				ZBTB42
				ZBTB46
				ZBTB5
				ZBTB6
				ZBTB7A
				ZBTB8A
				ZBTB9
				ZC2HC1C
				ZC3H10
				ZC3H11A
				ZC3H12C
				ZC3H13
				ZC3H14
				ZC3H15
				ZC3H18
				ZC3H3
				ZC3H4
				ZC3H7A
				ZC3H8
				ZC3HAV1
				ZC4H2
				ZCCHC10
				ZCCHC12
				ZCCHC14
				ZCCHC8
				ZCRB1
				ZDHHC11
				ZDHHC12
				ZDHHC17
				ZDHHC18
				ZDHHC23
				ZDHHC5
				ZEB1
				ZEB2
				ZFC3H1
				ZFHX3
				ZFHX4
				ZFP36
				ZFP36L2
				ZFPL1
				ZFPM2
				ZFR
				ZFYVE27
				ZFYVE9
				ZHX1
				ZHX1-C8orf76
				ZHX2
				ZKSCAN8
				ZMIZ2
				ZMPSTE24
				ZMYM1
				ZMYM2
				ZMYM3
				ZMYM4
				ZMYM5
				ZMYM6
				ZMYND12
				ZMYND19
				ZMYND8
				ZNF131
				ZNF143
				ZNF148
				ZNF207
				ZNF219
				ZNF232
				ZNF24

Cohort	Whole	Female	Male	Previous
				ZNF263
				ZNF296
				ZNF318
				ZNF326
				ZNF330
				ZNF331
				ZNF346
				ZNF384
				ZNF398
				ZNF414
				ZNF417
				ZNF44
				ZNF444
				ZNF445
				ZNF451
				ZNF462
				ZNF471
				ZNF496
				ZNF512
				ZNF512B
				ZNF521
				ZNF526
				ZNF550
				ZNF581
				ZNF592
				ZNF598
				ZNF608
				ZNF609
				ZNF622
				ZNF629
				ZNF638
				ZNF644
				ZNF646
				ZNF652
				ZNF664
				ZNF668
				ZNF687
				ZNF746
				ZNF747
				ZNF76
				ZNF764
				ZNF774
				ZNF777
				ZNF784
				ZNF785
				ZNF787
				ZNF827
				ZNF830
				ZNHIT1
				ZNHIT3
				ZNRF4
				ZRANB1
				ZRANB2
				ZSCAN1
				ZSCAN26
				ZSCAN5A
				ZUP1
				ZW10
				ZWINT
				ZYX
				ZZEF1
				ZZZ3

Supplementary Table 33. Summary of top variants in the *GCKR*, *MLXIPL*, *APOA5*, and *APOC1* gene clusters exhibiting genome-wide significance for blood glucose, HDL-C, and TG, identified in the GWAS by Sinnott-Armstrong N et al.

PUBMEDID	FIRST AUTHOR	JOURNAL	DISEASE/TRAIT	CHR_ID	CHR_POS	REPORTED GENE(S)	MAPPED_GENE	STRONGEST SNP-RISK ALLELE	SNPS	SNP_ID_CURRENT	CONTEXT	P-VALUE	OR or BETA	95% CI (TEXT)
33462484	Sinnott-Armstrong N	Nat Genet	Blood glucose levels	2	26,930,006	NR	DPYSL5	rs1371614-T	rs1371614	1371614	intron_variant	2.00E-15	0.023	[0.017-0.029] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Blood glucose levels	2	27,368,937	NR	EIF2B4	rs80051818-C	rs8005181	80051818	non_coding_transcript_exon_variant	2.00E-16	0.022	[0.017-0.027] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Blood glucose levels	2	27,518,370	NR	GCKR	rs780094-C	rs780094	780094	intron_variant	4.00E-53	0.0394	[0.034-0.044] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	7	73,440,219	NR	FZD9 - BAZ1B	rs71556711-T	rs7155671	71556711	intergenic_variant	2.00E-16	0.0361	[0.027-0.045] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	7	73,605,971	NR	MLXIPL	rs799157-C	rs799157	799157	synonymous_variant	7.00E-12	0.0421	[0.03-0.054] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	7	73,645,676	NR	MLXIPL - VPS37D	rs799160-T	rs799160	799160	intergenic_variant	3.00E-12	0.0174	[0.013-0.022] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,746,524	NR	LINC02702 - BUD13	rs11216126-C	rs1121612	11216126	intergenic_variant	5.00E-27	0.0395	[0.032-0.047] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,789,970	NR	APOA5	rs2266788-A	rs2266788	2266788	3_prime_UTR_variant	3.00E-138	0.123	[0.11-0.13] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,790,940	NR	APOA5	rs201079485-A	rs2010794	201079485	stop_gained	5.00E-14	0.5502	[0.41-0.69] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,791,691	NR	APOA5	rs3135506-C	rs3135506	3135506	missense_variant	9.00E-98	0.1076	[0.098-0.118] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,794,837	NR	APOA5 - LNC-RHL1	rs17520254-G	rs1752025	17520254	intergenic_variant	7.00E-46	0.0759	[0.066-0.086] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,821,577	NR	APOA4	rs12721043-A	rs1272104	12721043	missense_variant	9.00E-81	0.2281	[0.2-0.25] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,822,638	NR	APOA4	rs5093	rs5093	5093	intron_variant	3.00E-16	0.0738	[0.056-0.091] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,823,155	NR	APOA4	rs12721041-T	rs1272104	12721041	missense_variant	4.00E-20	0.0915	[0.072-0.111] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,830,844	NR	APOC3	rs147210663-A	rs1472106	147210663	missense_variant	7.00E-12	0.4213	[0.3-0.54] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,837,023	NR	APOA1, APOA1-AS	rs1997591	rs1997591	199759119	missense_variant	5.00E-32	0.4724	[0.39-0.55] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	116,878,138	NR	SIK3	rs73023045-G	rs7302304	73023045	intron_variant	2.00E-13	0.0292	[0.021-0.037] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,171,692	NR	PAFAH1B2	rs186808413-T	rs1868084	186808413	missense_variant	5.00E-81	0.2302	[0.21-0.25] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,191,654	NR	SIDT2	rs1242229-C	rs1242229	1242229	non_coding_transcript_exon_variant	4.00E-14	0.031	[0.023-0.039] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,223,001	NR	PCSK7	rs73008592-C	rs7300859	73008592	non_coding_transcript_exon_variant	2.00E-11	0.0266	[0.019-0.034] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,230,595	NR	PCSK7	rs74988348-T	rs7498834	74988348	intron_variant	2.00E-25	0.0726	[0.059-0.086] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,304,942	NR	BACE1	rs116987336-A	rs1169873	116987336	intron_variant	5.00E-23	0.0788	[0.063-0.094] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,390,772	NR	CEP164	rs897837-G	rs897837	897837	splice_region_variant	1.00E-10	0.0215	[0.015-0.028] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	High density lipoprotein cholesterol levels	11	117,395,596	NR	CEP164	rs2305830-G	rs2305830	2305830	missense_variant	3.00E-11	0.0179	[0.013-0.023] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	26,902,327	NR	DPYSL5	rs62128447-G	rs6212844	62128447	intron_variant	8.00E-13	0.0422	[0.031-0.054] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	26,930,006	NR	DPYSL5	rs1371614-T	rs1371614	1371614	intron_variant	2.00E-16	0.0227	[0.017-0.028] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	26,953,226	NR	DPYSL5 - MAPRE3	rs115268969-T	rs1152689	115268969	intron_variant	4.00E-09	0.0499	[0.033-0.067] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	26,969,239	NR	DPYSL5 - MAPRE3	rs76471230-C	rs7647123	76471230	intron_variant	3.00E-14	0.0427	[0.032-0.054] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,051,205	NR	AGBL5	rs72808941-A	rs7280894	72808941	intron_variant	1.00E-21	0.0565	[0.045-0.068] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,101,095	NR	CGREF1	rs76649658-G	rs7664965	76649658	3_prime_UTR_variant	7.00E-14	0.0421	[0.031-0.053] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,103,199	NR	CGREF1	rs116170113-A	rs1161701	116170113	intron_variant	5.00E-22	0.0943	[0.075-0.114] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,142,724	NR	PRR30 - TCF23	rs35803469-T	rs3580346	35803469	intergenic_variant	1.00E-10	0.0496	[0.035-0.065] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,145,720	NR	PRR30 - TCF23	rs28489942-C	rs2848994	28489942	intergenic_variant	8.00E-23	0.0246	[0.02-0.029] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,185,172	NR	TCF23 - SLC5A6	rs77585907-T	rs7758590	77585907	regulatory_region_variant	8.00E-11	0.0738	[0.052-0.096] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,247,663	NR	CAD - SLC30A3	rs75252677-A	rs7525267	75252677	intergenic_variant	1.00E-15	0.063	[0.048-0.078] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,268,243	NR	SLC30A3	rs11682713-C	rs1168271	11682713	intron_variant	7.00E-31	0.0452	[0.038-0.053] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,293,422	NR	TRIM54	rs74564095-T	rs7456409	74564095	intron_variant	9.00E-25	0.085	[0.069-0.101] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,303,595	NR	TRIM54	rs116708757-C	rs1167087	116708757	intron_variant	4.00E-09	0.0439	[0.029-0.059] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,316,334	NR	MPV17	rs76898938-A	rs7689893	76898938	intron_variant	4.00E-18	0.0657	[0.051-0.081] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,324,380	NR	MPV17	rs76164683-C	rs7616468	76164683	intron_variant	1.00E-12	0.0633	[0.046-0.081] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,356,305	NR	GTF3C2, GTF3C2-AS2	rs73921514-C	rs7392151	73921514	5_prime_UTR_variant	2.00E-26	0.0645	[0.053-0.076] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,367,799	NR	EIF2B4	rs41288829-T	rs4128882	41288829	missense_variant	6.00E-24	0.0757	[0.061-0.09] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,368,937	NR	EIF2B4	rs80051818-C	rs8005181	80051818	non_coding_transcript_exon_variant	3.00E-103	0.0552	[0.05-0.06] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,371,530	NR	SNX17	rs76476582-T	rs7647658	76476582	non_coding_transcript_exon_variant	7.00E-18	0.0455	[0.035-0.056] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,388,587	NR	PPM1G	rs114439706-T	rs1144397	114439706	intron_variant	4.00E-22	0.0761	[0.061-0.092] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,389,973	NR	PPM1G	rs1647280-G	rs1647280	1647280	intron_variant	9.00E-16	0.0566	[0.043-0.07] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,434,814	NR	NRBP1	rs77005271-T	rs7700527	77005271	non_coding_transcript_exon_variant	5.00E-14	0.0306	[0.023-0.039] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,489,962	NR	IFT172 - FNDC4	rs149117895-A	rs1491178	149117895	TF_binding_site_variant	7.00E-13	0.0918	[0.067-0.117] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,518,370	NR	GCKR	rs780094-C	rs780094	780094	intron_variant	8E-404	0.1053	[0.1-0.111] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,525,082	NR	GCKR - C2orf16	rs71441083-A	rs7144108	71441083	intergenic_variant	2.00E-26	0.0707	[0.058-0.084] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,556,452	NR	C2orf16	rs115960647-T	rs1159606	115960647	intron_variant	1.00E-12	0.07	[0.051-0.089] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,684,577	NR	SLC4A1AP	rs77532628-C	rs7753262	77532628	intron_variant	7.00E-29	0.0604	[0.05-0.071] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,706,156	NR	LINC01460	rs35315097-C	rs3531509	35315097	non_coding_transcript_exon_variant	9.00E-39	0.0697	[0.059-0.08] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,710,734	NR	LINC01460	rs76870318-A	rs7687031	76870318	intron_variant	7.00E-17	0.0711	[0.054-0.088] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,796,957	NR	MRPL33, RBKS	rs114308869-A	rs1143088	114308869	intron_variant	7.00E-20	0.0778	[0.061-0.094] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,820,524	NR	RBKS, MRPL33	rs74994332-C	rs7499433	74994332	intron_variant	2.00E-10	0.042	[0.029-0.055] unit decrease

PUBMEDID	FIRST AUTHOR	JOURNAL	DISEASE/TRAIT	CHR_ID	CHR_POS	REPORTED GENE(S)	MAPPED_GENE	STRONGEST SNP-RISK ALLELE	SNPS	SNP_ID_CURRENT	CONTEXT	P-VALUE	OR or BETA	95% CI (TEXT)
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	27,900,023	NR	MRPL33, BABAM2	rs76260822-T	rs7626082	76260822	intron_variant	4.00E-12	0.0651	[0.047-0.084] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	28,032,027	NR	BABAM2	rs79468673-G	rs7946867	79468673	intron_variant	8.00E-29	0.0732	[0.06-0.086] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	28,092,903	NR	BABAM2	rs13016086-C	rs1301608	13016086	intron_variant	2.00E-26	0.04	[0.033-0.047] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	28,136,149	NR	BABAM2	rs72814468-C	rs7281446	72814468	intron_variant	3.00E-34	0.0443	[0.037-0.051] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	28,150,711	NR	BABAM2	rs79635514-G	rs7963551	79635514	intron_variant	8.00E-14	0.0549	[0.041-0.069] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	28,241,331	NR	BABAM2	rs28997579-T	rs2899757	28997579	synonymous_variant	5.00E-10	0.0525	[0.036-0.069] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	2	28,241,423	NR	BABAM2	rs114295720-T	rs1142957	114295720	intron_variant	3.00E-11	0.0608	[0.043-0.079] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	72,891,942	NR	POM121	rs62463394-G	rs6246339	62463394	intron_variant	2.00E-20	0.0333	[0.026-0.04] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,343,059	NR	FKBP6	rs111423741-A	rs1114237	111423741	intron_variant	3.00E-11	0.0656	[0.046-0.085] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,440,219	NR	FZD9 - BAZ1B	rs71556711-T	rs7155671	71556711	intergenic_variant	1.00E-213	0.1306	[0.12-0.14] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,482,906	NR	BAZ1B	rs117528284-A	rs1175282	117528284	intron_variant	5.00E-09	0.0373	[0.025-0.05] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,509,734	NR	BAZ1B	rs113296769-G	rs1132967	113296769	intron_variant	5.00E-36	0.1085	[0.091-0.126] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,605,971	NR	MLXIPL	rs799157-C	rs799157	799157	synonymous_variant	3.00E-57	0.0935	[0.082-0.105] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,645,676	NR	MLXIPL - VPS37D	rs799160-T	rs799160	799160	intergenic_variant	2.00E-70	0.0424	[0.038-0.047] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,652,697	NR	MLXIPL - VPS37D	rs6956862-G	rs6956862	6956862	intergenic_variant	5.00E-30	0.0286	[0.024-0.033] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,672,124	NR	VPS37D - DNAJC30	rs13242693-T	rs1324269	13242693	intergenic_variant	9.00E-56	0.1032	[0.09-0.116] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	7	73,672,394	NR	VPS37D - DNAJC30	rs11133121-G	rs1113312	111331221	intergenic_variant	7.00E-12	0.0414	[0.03-0.053] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,750,907	NR	BUD13	rs74496689-A	rs7449668	74496689	intron_variant	5.00E-21	0.0853	[0.067-0.103] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,765,235	NR	BUD13	rs79610135-C	rs7961013	79610135	intron_variant	1.00E-10	0.0414	[0.029-0.054] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,789,970	NR	APOA5	rs2266788-A	rs2266788	3_prime_UTR_variant	6E-790	0.2817	[0.27-0.29] unit decrease	
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,790,406	NR	APOA5	rs149808404-A	rs1498084	149808404	stop_gained	4.00E-13	0.8253	[0.6-1.05] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,790,940	NR	APOA5	rs201079485-A	rs2010794	201079485	stop_gained	8.00E-39	0.9193	[0.78-1.06] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,791,691	NR	APOA5	rs3135506-C	rs3135506	3135506	missense_variant	4E-537	0.2429	[0.23-0.25] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,794,837	NR	APOA5 - LNC-RHL1	rs17520254-G	rs1752025	17520254	intergenic_variant	2.00E-62	0.085	[0.075-0.095] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,798,712	NR	APOA5 - LNC-RHL1	rs35412484-C	rs3541248	35412484	intergenic_variant	3.00E-47	0.0456	[0.039-0.052] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,803,787	NR	APOA5 - LNC-RHL1	rs625524-A	rs625524	625524	intergenic_variant	2.00E-09	0.0446	[0.03-0.059] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,821,577	NR	APOA4	rs12721043-A	rs1272104	12721043	missense_variant	8.00E-83	0.2209	[0.2-0.24] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,823,155	NR	APOA4	rs12721041-T	rs1272104	12721041	missense_variant	2.00E-91	0.193	[0.17-0.21] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,826,365	NR	APOA4 - APOC3	rs150555490-T	rs1505554	150555490	intergenic_variant	1.00E-19	0.0467	[0.037-0.057] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,830,844	NR	APOC3	rs14721063-A	rs1472106	147210663	missense_variant	3.00E-22	0.5668	[0.45-0.68] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,835,003	NR	APOC3 - APOA1	rs12718462-C	rs1271846	12718462	regulatory_region_variant	2.00E-24	0.049	[0.04-0.058] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,892,113	NR	SIK3	rs75158858-A	rs7515885	75158858	intron_variant	8.00E-60	0.0629	[0.055-0.071] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	116,982,584	NR	SIK3	rs12804297-A	rs1280429	12804297	intron_variant	3.00E-10	0.0282	[0.019-0.037] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,002,160	NR	SIK3	rs77585745-C	rs7758574	77585745	intron_variant	5.00E-11	0.059	[0.041-0.077] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,045,364	NR	SIK3	rs56121615-A	rs5612161	56121615	intron_variant	5.00E-19	0.0477	[0.037-0.058] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,171,692	NR	PAFAH1B2	rs18680843-T	rs1868084	18680843	missense_variant	1.00E-80	0.2196	[0.2-0.24] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,190,751	NR	SIDT2	rs17120419-T	rs1712041	17120419	non_coding_transcript_exon_variant	9.00E-12	0.0406	[0.029-0.052] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,191,654	NR	SIDT2	rs1242229-C	rs1242229	1242229	non_coding_transcript_exon_variant	7.00E-204	0.1192	[0.11-0.13] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,206,256	NR	PCSK7, TAGLN	rs45574931-A	rs4557493	45574931	missense_variant	2.00E-20	0.0464	[0.037-0.056] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,229,313	NR	PCSK7	rs4938362-A	rs4938362	4938362	intron_variant	3.00E-31	0.0382	[0.032-0.045] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,230,404	NR	PCSK7	rs36066272-C	rs3606627	36066272	5_prime_UTR_variant	5.00E-12	0.0558	[0.04-0.072] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,255,777	NR	RNF214	rs112357006-A	rs1123570	112357006	intron_variant	1.00E-12	0.0425	[0.031-0.054] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,304,942	NR	BACE1	rs116987336-A	rs1169873	116987336	intron_variant	1.00E-140	0.1921	[0.18-0.21] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,375,850	NR	CEP164	rs112933729-A	rs1129337	112933729	intron_variant	7.00E-10	0.0381	[0.026-0.05] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,377,567	NR	CEP164	rs117619191-C	rs1176191	117619191	intron_variant	2.00E-24	0.0855	[0.069-0.102] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,390,772	NR	CEP164	rs897837-G	rs897837	897837	splice_region_variant	2.00E-10	0.0203	[0.014-0.027] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	11	117,431,102	NR	DSCAML1	rs4356265-T	rs4356265	4356265	intron_variant	1.00E-11	0.0245	[0.017-0.032] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,860,563	NR	NECTIN2	rs138607350-G	rs1386073	138607350	intron_variant	1.00E-11	0.0889	[0.063-0.115] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,867,581	NR	NECTIN2	rs12610605-A	rs1261060	12610605	intron_variant	5.00E-13	0.0236	[0.017-0.03] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,867,684	NR	NECTIN2	rs41290100-T	rs4129010	41290100	intron_variant	4.00E-10	0.0466	[0.032-0.061] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,869,072	NR	NECTIN2	rs17561351-G	rs1756135	17561351	intron_variant	4.00E-15	0.0402	[0.03-0.05] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,878,035	NR	NECTIN2	rs150639620-T	rs1506396	150639620	intron_variant	3.00E-25	0.0589	[0.048-0.07] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,883,211	NR	NECTIN2	rs142042446-GTAA	rs1420424	142042446	intron_variant	2.00E-37	0.0454	[0.038-0.052] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,885,967	NR	NECTIN2	rs283814-G	rs283814	283814	synonymous_variant	1.00E-40	0.0597	[0.051-0.069] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,886,339	NR	NECTIN2	rs7254892-A	rs7254892	7254892	intron_variant	7.00E-66	0.1136	[0.1-0.13] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,892,587	NR	TOMM40	rs34095326-A	rs3409532	34095326	intron_variant	8.00E-15	0.0311	[0.023-0.039] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,896,639	NR	TOMM40	rs76366838-A	rs7636683	76366838	intron_variant	2.00E-28	0.0859	[0.071-0.101] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,900,667	NR	TOMM40	rs1160984-T	rs1160984	1160984	intron_variant	5.00E-14	0.0404	[0.03-0.051] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,901,175	NR	TOMM40	rs117264457-A	rs1172644	117264457	intron_variant	5.00E-11	0.051	[0.036-0.066] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,901,434	NR	TOMM40	rs405697-G	rs405697	405697	3_prime_UTR_variant	4.00E-70	0.0497	[0.044-0.055] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,906,745	NR	APOE	rs769449-A	rs769449	769449	non_coding_transcript_exon_variant	1.00E-60	0.0596	[0.053-0.067] unit increase

PUBMEDID	FIRST AUTHOR	JOURNAL	DISEASE/TRAIT	CHR_ID	CHR_POS	REPORTED GENE(S)	MAPPED_GENE	STRONGEST SNP-RISK ALLELE	SNPS	SNP_ID_CURRENT	CONTEXT	P-VALUE	OR or BETA	95% CI (TEXT)
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,908,822	NR	APOE	rs7412-T	rs7412	7412	missense_variant	7.00E-136	0.1152	[0.11-0.12] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,911,135	NR	APOE - APOC1	rs72654472-T	rs7265447	72654472	non_coding_transcript_exon_variant	4.00E-17	0.063	[0.048-0.078] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,912,921	NR	APOE - APOC1	rs483082-T	rs483082	483082	non_coding_transcript_exon_variant	2.00E-219	0.0934	[0.088-0.099] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,913,221	NR	APOE - APOC1	rs584007-G	rs584007	584007	non_coding_transcript_exon_variant	7.00E-193	0.0777	[0.073-0.083] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,919,304	NR	APOC1	rs1064725-G	rs1064725	1064725	3_prime_UTR_variant	3.00E-22	0.0605	[0.048-0.073] unit decrease
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,919,689	NR	APOC1 - APOC1P1	rs4420638-G	rs4420638	4420638	regulatory_region_variant	3.00E-69	0.0534	[0.048-0.059] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,923,535	NR	APOC1 - APOC1P1	rs141622900-A	rs1416229	141622900	intergenic_variant	3.00E-124	0.1325	[0.12-0.14] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,926,451	NR	APOC1 - APOC1P1	rs60049679-C	rs6004967	60049679	intergenic_variant	3.00E-39	0.0604	[0.051-0.069] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,929,300	NR	APOC1P1, APOC1P1	rs7259004-C	rs7259004	7259004	intron_variant	2.00E-117	0.0885	[0.081-0.096] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,942,260	NR	APOC4-APOC2, APOC4	rs79429216-A	rs7942921	79429216	5_prime_UTR_variant	1.00E-13	0.0782	[0.058-0.099] unit increase
33462484	Sinnott-Armstrong N	Nat Genet	Triglyceride levels	19	44,943,964	NR	APOC4, APOC4-APOC2	rs12721109-A	rs1272110	12721109	intron_variant	1.00E-09	0.0462	[0.031-0.061] unit increase

Supplementary Table 34. Top 20 SNPs after clumping for TyG with DM samples and TyG without DM samples.

TyG with DM			
CHR	SNP	Pos	P
11	rs7350481	116715567	< E-300
11	chr11:116741689_AACACACACACACAC_A	116741689	< E-300
11	rs61905084	116739578	1.10E-261
11	rs7927820	116811440	1.70E-248
11	rs603446	116783719	9.00E-225
2	rs1260326	27508073	4.30E-204
8	rs75278536	19963914	2.00E-153
19	rs483082	44912921	1.30E-123
11	rs1784128	116667972	1.20E-112
11	chr11:117120044_G_GAAAC	117120044	1.80E-109
7	rs3812316	73606007	8.50E-105
11	rs75955612	116759802	7.10E-82
8	rs1534650	20020643	2.00E-72
11	rs182500870	116755846	7.90E-71
11	rs499563	116652244	1.90E-68
11	rs11216100	116701814	3.30E-67
19	rs157580	44892009	2.20E-64
11	rs12276805	117008043	8.40E-61
11	rs141882698	116730622	2.90E-60
19	rs7259004	44929300	2.00E-59

TyG without DM			
CHR	SNP	Pos	P
11	rs7350481	116715567	< E-300
11	chr11:116741689_AACACACACACACAC_A	116741689	< E-300
11	rs61905084	116739578	2.70E-257
11	rs7927820	116811440	1.20E-245
11	rs603446	116783719	7.60E-222
2	rs1260326	27508073	1.50E-209
8	rs12679834	19962922	5.50E-151
19	rs483082	44912921	6.10E-120
11	rs1784128	116667972	1.10E-111
11	chr11:117120044_G_GAAAC	117120044	1.30E-106
7	rs3812316	73606007	4.10E-98
11	rs75955612	116759802	5.80E-83
11	rs182500870	116755846	1.70E-72
8	rs285	19957678	3.10E-70
11	rs499563	116652244	2.10E-65
11	rs11216100	116701814	3.50E-63
19	rs157580	44892009	1.20E-62
11	rs12276805	117008043	1.10E-61
11	rs200405951	116780493	1.30E-59
8	rs2954021	125469835	1.50E-59

DM = diabetes mellitus.

CHR = chromosome, P = p-value, Pos = position

This GWAS analysis utilized BOLT-LMM's mixed linear models with a two-sided chi-square test.

The conventional genome-wide significance threshold of $P < 5 \times 10^{-8}$ was applied.