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Pooled DNA Resequencing of 68 Myocardial Infarction Candidate Genes in French Canadians

Mélissa Beaudoin, MS*; Ken Sin Lo, BS*; Amidou N'Diaye, PhD; Manuel A. Rivas, BS; Marie-Pierre Dubé, PhD; Nathalie Laplante, PhD; Michael S. Phillips, PhD; John D. Rioux, PhD; Jean-Claude Tardif, MD; Guillaume Lettre, PhD

Background—Familial history is a strong risk factor for coronary artery disease (CAD), especially for early-onset myocardial infarction (MI). Several genes and chromosomal regions have been implicated in the genetic cause of coronary artery disease/MI, mostly through the discovery of familial mutations implicated in hyper-/hypocholesterolemia by linkage studies and single nucleotide polymorphisms by genome-wide association studies. Except for a few examples (eg, PCSK9), the role of low-frequency genetic variation (minor allele frequency [MAF]) ≈0.1%–5% on MI/coronary artery disease predisposition has not been extensively investigated.

Methods and Results—We selected 68 candidate genes and sequenced their exons (394 kb) in 500 early-onset MI cases and 500 matched controls, all of French-Canadian ancestry, using solution-based capture in pools of nonindexed DNA samples. In these regions, we identified 1852 single nucleotide variants (695 novel) and captured 85% of the variants with MAF≥1% found by the 1000 Genomes Project in Europe-ancestry individuals. Using gene-based association testing, we prioritized for follow-up 29 low-frequency variants in 8 genes and attempted to genotype them for replication in 1594 MI cases and 2988 controls from 2 French-Canadian panels. Our pilot association analysis of low-frequency variants in 68 candidate genes did not identify genes with large effect on MI risk in French Canadians.

Conclusions—We have optimized a strategy, applicable to all complex diseases and traits, to discover efficiently and cost-effectively DNA sequence variants in large populations. Resequencing endeavors to find low-frequency variants implicated in common human diseases are likely to require very large sample size. **(*Circ Cardiovasc Genet*. 2012;5:547-554.)**

Key Words: myocardial infarction ■ polymorphism myocardial infarction ■ population ■ single nucleotide ■ polymorphisms ■ coronary artery disease

Coronary artery disease (CAD) and its main clinical manifestation, myocardial infarction (MI), is the leading cause of death and disability worldwide.[1] The main risk factors for MI include old age, male sex, tobacco use, dyslipidemia, obesity, diabetes mellitus, arterial hypertension, and chronic stress.[2] Epidemiological studies in twins and large pedigrees have also established that a positive family history of MI is a strong predictor, indicating that there is an important genetic component to MI pathogenesis.[3,4]

Clinical Perspective on p 554

Recent large meta-analyses of genome-wide association study (GWAS) results have identified over 25 genomic regions that carry common single nucleotide polymorphisms (SNPs) associated with MI risk.[5,6] For many of these MI loci, the gene(s) and causal DNA sequence variant(s) are unknown. Identification of low-frequency and penetrant nonsynonymous variants through exon resequencing of genes within these loci can help address these 2 questions. This approach is supported by recent successes for type 1 diabetes mellitus,[7] fetal hemoglobin,[8] age-related macular degeneration,[9] and Crohn disease.[10] In this study, we sequenced exons from 68 MI candidate genes (394 kb) in 500 early-onset MI cases and 500 matched controls selected from a French–Canadian biobank using pooled sequencing of nonindexed DNA after solution-based target capture. We identified 1852 high-quality single nucleotide variants (SNVs) with low false-positive and negative rates. From the sequence data, we performed gene-based association testing and attempted to replicate the top findings in 2 independent French–Canadian replication panels totaling 1594 MI cases and 2988 controls.

Methods

Participants

Participants in this study were recruited from the Montreal Heart Institute (MHI) Biobank and the Pharmacogenomics of the Toxicity

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From the Montreal Heart Institute, Montreal, Québec, Canada (M.B., K.S.L., A.N.D., M.P.D., N.L., M.S.P., J.D.R., J.C.T., G.L.); Université de Montréal, Montreal, Québec, Canada (M.P.D., M.S.P., J.D.R., J.C.T., G.L.); Nuffield Dept of Clinical Medicine, University of Oxford, Oxford, United Kingdom (M.A.R.); and the Broad Institute of Harvard & MIT, Cambridge, MA (M.A.R.).

*These authors contibuted equally to this article.

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Correspondence to Guillaume Lettre, PhD, or Jean-Claude Tardif, MD, Montreal Heart Institute, 5000 Rue Bélanger, Montréal, Québec, H1T 1C8, Canada. E-mail guillaume.lettre@umontreal.ca or jean-claude.tardif@icm-mhi.org

Table 1. Characteristics of Study Participants Selected From the Montreal Heart Institute (MHI) Biobank and the Pharmacogenomics of the Toxicity of Lipid-Lowering Agents (MHI Statins) Study

	MHI Biobank—Sequencing		MHI Biobank—Replication		MHI Statins Study	
Study	MI cases	Controls	MI cases	Controls	MI cases	Controls
N	500	500	870	1604	724	1384
Mean age, y*	45±7	63±5	58±10	60±13	55±10	58±11
Female sex, %	28	29	17	62	14	45
Hypertension, %†	62	54	73	35	67	42
Diabetes mellitus, %‡	24	17	27	8	22	18
Hypercholesterolemia, %§	92	68	89	36	100	100
Body mass index, kg/m^2	29.3±5.8	28.8±5.2	29.0±5.3	27.8±5.4	28.8±5.0	28.7±5.4

All participants have 4 French–Canadian grandparents. Values with "±" are means and standard deviations.

*Mean age at first myocardial infarction (MI) for cases and at baseline for controls.

†Hypertension is defined as a previous diagnosis of hypertension, on antihypertensive therapy or with systolic blood pressure ≥140 mm Hg or diastolic blood pressure ≥90 mm Hg.

‡Diabetes mellitus is defined as a previous diagnosis of diabetes or treatment with antidiabetic drugs.

§Hypercholesterolemia is defined as a previous diagnosis of hypercholesterolemia or treatment with lipid-lowering drugs.

of Lipid-Lowering Agents Study (thereafter referred to as the MHI Statins Study). All participants had 4 French–Canadian grandparents. Participant characteristics are summarized in Table 1. All cases had documented history of MI. For controls, we excluded patients with MI, percutaneous coronary intervention (PCI), coronary artery bypass graft (CABG) surgery, transient ischemic attack (TIA) or stroke, peripheral vascular disease, congestive heart failure (CHF), and angina. For resequencing, we selected a subgroup totaling 500 early-onset MI cases (<50 years of age for men and <60 years of age for women) because MI events that occur in younger patients are associated with substantially greater heritability[11] and 500 controls matched as best as possible for hypertension, diabetes mellitus and lipid-lowering drugs usage. The controls were selected to be older than the cases (age at baseline between 50 and 70 years of age in men and between 60 and 70 years of age in women). All participants gave written informed consent and the MHI ethics committee approved the project.

DNA Sample Preparation, Gene Selection and Targeted Sequence Enrichment

As part of this targeted DNA resequencing project, we sequenced exons of 68 candidate genes (394 kb) for MI in 500 early-onset MI cases and 500 matched controls. These genes were selected because: (1) there is an OMIM entry (http://www.ncbi.nlm.nih.gov/omim) linking them to MI pathogenesis (often through lipid metabolism), (2) they were identified in previous linkage or candidate gene association studies, or (3) are located near (within recombination hotspots) SNPs associated with MI by GWAS (as of January 2010; online-only Data Supplement Table I).

To minimize costs, we selected an approach using pools of non-indexed (no barcodes) DNA, as previously described.[10] We prepared 20 pools of 50 DNA samples (10 pools of 50 case DNA samples and 10 pools of 50 control DNA samples) at equimolar concentration. Briefly, genomic DNA samples extracted from blood were quantified using picogreen protocols and concentrations were adjusted to 10 ng/μL. Fifty DNA samples were mixed (200 ng of each DNA sample) to achieve a final pooled DNA concentration of 10 ng/μL in 1000 μL; we verified the final concentration of the pools by picogreen.

For target enrichment, we designed a custom-made Agilent SureSelect library for capture in solution (http://www.genomics.agilent.com); see online-only Data Supplement Table II for the coordinates of the targeted exons. DNA pools were sonicated using a Covaris S2 instrument using default settings to obtain 200 base pairs (bp) fragments size and the sheared DNA was quantified on a Bioanalyzer (Agilent). The Illumina Paired-End DNA Sample prep protocol (including end-repaired, A-tailed, and sequencing adapaters ligation) was used for preparing 3.5 μg of the sheared DNA for each pool, following the manufacturer's protocol. Following Agilent's protocol 500 ng of each library was hybridized with our SureSelect library. Captured DNA was eluted in 15 μL of EB buffer and PCR-amplified for 12 cycles.

Next-Generation DNA Resequencing and Data Analysis

We sequenced each library (pool of 50 DNA samples) on 1 lane of an Illumina GAIIx instrument using a 2×76 bp protocol following the manufacturer's recommendations. Analysis of our data is based on a bioinformatic pipeline built around software developed for the 1000 Genomes Project. Briefly, fastq files generated by the sequencers were aligned to the reference human genome (hg18; NCBI Build 36) using BWA.[12] SAMtools[13] was used to convert SAM files to the BAM format, and we used PICARD (http://picard.sourceforge.net) to remove PCR or optical duplicates. We then used the GATK suite[14,15] to recalibrate base quality scores and perform local realignment around indels. We used the Syzygy software with defaults parameters to call variants and estimate allele frequency.[10] Summary statistics relevant to sequence data analysis can be found in online-only Data Supplement Tables III and IV. In this article, we only consider SNVs (we excluded insertions–deletions [indels]) with the highest Syzygy quality score; online-only Data Supplement Table V includes the complete list of the 1852 SNVs identified in this project.

Genotyping for Validation and Replication

We genotyped 45 low-frequency DNA sequence variants (MAF<1%) in the same 1000 DNA samples than those used for sequencing to validate the estimates of allele frequencies from the resequencing results. For independent replication of the MI results, we used a 2-stage design where we attempted to genotype 29 variants in 2474 DNA from the MHI Biobank-replication panel (870 MI cases and 1604 controls; not overlapping with the sequenced DNA samples) and in 2108 DNA from the MHI Statins Study (724 MI cases and 1384 controls; not overlapping with the MHI Biobank samples). For genotyping, we used the Sequenom iPLEX technology. Using the PLINK software,[16] we removed from the analysis individuals with a genotyping success rate <90% and markers with a genotyping success rate <95% or a Hardy–Weinberg $P<0.001$. The genotype concordance rate estimated from DNA triplicates was >99.9%.

Statistical Analysis

Gene-based association statistics, based on allele frequency estimates generated by the Syzygy software, were calculated using the C-alpha statistic as implemented in the Syzygy C-alpha module.[10,17] Many of the existing methods are used to identify gene-based associations between low-frequency variants and phenotypes collapse

low-frequency variants together and test whether there is a burden of these variants in cases versus controls.[18] These tests imply that all genetic variation in a gene act in the same direction on phenotypes. In contrast, the C-alpha statistic considers that there might be risk, protective and neutral low-frequency variants in a given gene that may act together on phenotypes. Instead of focusing on the overall average effect of all low-frequency variants on phenotypes (this is what burden tests do), it considers the distribution (variance) of each low-frequency variant between cases and controls. The C-alpha test quantifies departure from the expected binomial variance across all variants analyzed.[17] For example, a gene has 2 low-frequency variants with nonreference allele counts 0:10 and 10:0 in cases:controls. Whereas burden tests would not detect a signal (count of 10 nonreference alleles in both cases and controls), the C-alpha test would identify a gene-based association signal owing to the presence of strong protective and risk variants. One caveat of the C-alpha statistic is that it cannot adjust for covariates. Our analysis of the genotype data to perform gene-based analysis relied on the sequence kernel association test (SKAT) software, which is a generalized C-alpha test that can take into account covariates.[19] For each analysis with SKAT, we used the default parameters and corrected for covariates that were correlated with MI status: MHI Biobank-sequencing (diabetes mellitus, hypertension, hypercholesterolemia), MHI Biobank-replication (age, sex, diabetes mellitus, hypertension, hypercholesterolemia), and MHI Statins Study (age, sex, diabetes mellitus, hypertension, recruitment site). All *P* values reported in this study are uncorrected for the number of hypotheses tested; the significance threshold is set at $\alpha=7\times10^{-4}$ (Bonferroni correction for 68 genes tested).

Using Syzygy, we estimated that our power to discover singletons with the pool approach in 1000 samples is on average >60% for 80% of all the targeted exonic sequences, although we note pool-to-pool variation (online-only Data Supplement Figure I).[10] We estimated the statistical power of our study design to find gene-based association with MI using the power calculator and reference haplotypes (calibrated based on a coalescent model) provided in the SKAT package for dichotomous traits.[19] Under the following assumptions (gene size: 6 kb, MI prevalence: 2%, proportion of cases: 50%, proportion of causal variants: 10%, MAF cutoff: 5%, proportion of causal variants with effect in the opposite direction: 20%) and averaging across 500 simulations, we calculate that we have 35% power to find a gene with a SKAT $P<0.05$ in the resequencing set (N=1000) and 48% power for the same gene to achieve a SKAT $P<7\times10^{-4}$ (Bonferroni correction for 68 genes tested) in the replication cohorts (N=1594 cases and 2988 controls) (online-only Data Supplement Table VI).

Results

High Sequence Coverage of Targeted Exons

For this project, we targeted 394 kb of exonic sequences from 68 genes selected because they had been linked to MI through linkage, candidate-gene, or GWAS (online-only Data Supplement Tables I and II). For the DNA resequencing phase, we selected 500 early-onset MI cases and 500 matched controls from the MHI Biobank (MHI Biobank-sequencing in Table 1). Our resequencing strategy was based on a protocol recently described to follow-up GWAS results for Crohn disease,[10] with the major modification that we used solution-based capture as opposed to PCR for exon enrichment (Materials and Methods). The major impact of this change was to reduce from weeks to days the time necessary to prepare sequencing libraries, thus reducing costs, without affecting the overall quality of the sequence data (see below). A similar approach was recently described.[20]

Each of the 20 pools of 50 nonindexed DNA samples was sequenced on an Illumina GAIIx lane. After removing sequence duplicates, we generated ≈539 millions paired-end reads, or >76 billions raw bases of sequences. After applying quality-control filters that removed poorly mapped (10%), badly paired (2%), or off-target (60%) reads, we obtained ≈151 millions paired-end reads of high quality. Although the off-target rate is high, this result is not unexpected given the size of the targeted genomic region (394 kb) in comparison with the rest of the human genome (3 gigabases), as previously reported.[21] Nevertheless, because of the throughput of the sequencer, we could achieve our target mean coverage per sample (≥30X, that is 15X per chromosome or 1500X per DNA pool of 50 DNA samples) for all but 6 genes (*APOA1*, *APOE*, *CDKN2BAS*, *CYP20A1*, *SLC5A3*, *TXNDC6*) (Figure 1 and online-only Data Supplement Table III). While inspecting these results, we noticed a difference in mean coverage per sample between cases and controls (54X versus 61X, *t*-test $P=0.01$; Figure 1). For 3 pools of cases, we had to perform 11 cycles of PCR amplification (instead of 8 for the other pools) to have enough DNA materials for exon capture. This resulted in a higher number of read duplicates for these 3 pools of cases (55% versus 42% for the other 17 pools, Wilcoxon's rank sum test $P=0.02$), and therefore overall a lower coverage and reduced discovery power for cases in comparison with controls (online-only Data Supplement Figure I). This systematic difference, which is hard to explain as DNA samples from cases and controls were prepared in the same laboratory using the same protocols, might affect our estimates of allele frequencies in cases and controls from the sequence reads (see below).

Pool Sequencing of Nonindexed DNA Samples is Efficient to Identify Single Nucleotide Variants

We used the Syzygy software to detect high-quality SNVs in the pooled sequence data.[10] To minimize the number of false-positive findings, we focused exclusively on sequence variants with the highest Syzygy score and we excluded all indel calls. In total, Syzygy found 1852 SNVs (including 6 nonsense, 363 missense, and 1 splice site variants), including 695 SNVs not present in dbSNP 135 (38%) (online-only Data Supplement Tables IV and V). As expected, the mean MAF of the novel SNVs identified is significantly less than the mean MAF for the SNVs already present in public databases (0.2% versus 7.9%, *t*-test $P<2.2\times10^{-16}$). The nonsynonymous-to-synonymous and the transition-to-transversion ratios are, respectively, 1.65 (369/223) and 2.43 (1312/540); these numbers are consistent with the analysis of the 1000 Genomes Project (Pilot 3) and the recent Crohn disease exon resequencing experiment (online-only Data Supplement Table IV).[10,22] All these metrics suggest that the list of variants is of high quality.

We were also interested in characterizing our false-negative rate, that is the number of true SNVs missed by our approach. As an imperfect proxy to the overall genetic variation present in the targeted exons of our French–Canadian population, we used the latest variant calls (October 2011) from European populations sequenced by the 1000 Genomes Project.[23] In the European populations, the 1000 Genomes Project identified 1852 SNVs located within the 394 kb of sequence targeted by our exon resequencing experiment, and 977 of those were also present in our dataset (53%). Because rare markers (eg, singletons) are less likely to be observed in other populations (or in other individuals), we also performed the same analysis but limiting our survey to SNVs with a MAF≥1%.

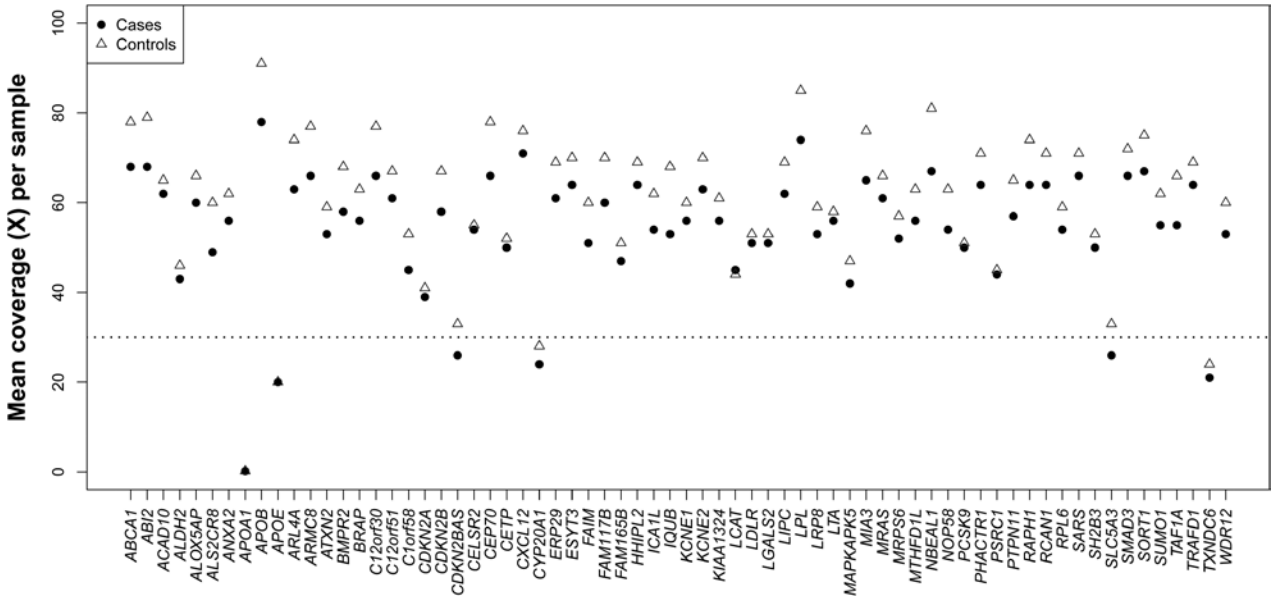

Figure 1. High coverage of targeted exons by pooled sequencing of nonindexed DNA samples. Each pool of 50 DNA samples was sequenced on one Illumina GAIIx lane. We targeted for sequencing exons from 68 genes (394 kb) reported to be implicated in myocardial infarction. Overall, we achieved a mean coverage of 2881X per pool (58X per sample or 29X per chromosome). We did not reach our aimed mean coverage per sample (30X, dashed line) for 6 genes: *APOA1*, *APOE*, *CDKN2BAS*, *CYP20A1*, *SLC5A3*, *TXNDC6*. For *APOA1* and *APOE*, mean coverage in cases and controls are similar and the corresponding symbols overlap.

Across the targeted exons, the 1000 Genomes Project found in the European populations 878 SNVs with a MAF≥1%, and 749 of these variants are in our list of 1852 high-quality SNVs (85%). Therefore, the resequencing strategy using pools of nonindexed DNA combined with solution-based capture is efficient (and cost-effective) to discover SNVs down to a frequency of 1%. For rarer variants, the true–false negative rate of our protocol remains to be determined.

Estimation of Allele Frequencies and Gene-Based Association Testing from Sequence Data

The Syzygy software can accurately estimate allele frequencies from pooled sequence data when using PCR as enrichment method.[10] Because we modified the original protocol by using instead a solution-based strategy to capture exons, we reevaluated Syzygy's performance in estimating allele frequencies. We genotyped 45 randomly selected low-frequency (MAF <1%) SNVs in the same 1000 individuals and observed a strong correlation in the estimates of allele frequencies (r^2=0.90) (Figure 2). However, this correlation is not as strong as previously reported,[10] probably because of 2 main reasons. First, we used the hybridization with RNA baits to capture DNA fragments and this method might be more sensitive than PCR to allele bias. Second, by focusing on low-frequency DNA markers in the validation, even small differences in the number of estimated nonreference alleles will have a strong impact on the correlation; common markers are less sensitive to small differences in allele frequency estimates. For instance, estimating the frequency of a rare variant as a tripleton when the true frequency is a singleton has a more dramatic impact on the correlation of frequency estimates than estimating the frequency of a common marker to 0.5 when its true frequency is 0.51. Because we only validated low-frequency SNVs, our analysis is more sensitive to small allele frequency differences between estimates.

The main aim of our study was to identify new genes involved in MI, or new disease-causing penetrant alleles in known MI genes. For that reason, our variant discovery effort also included a design to perform association testing on sequence data and replication by direct genotyping in large independent cohorts. Because very large GWAS have already tested the role of common genetic variation in CAD and MI,[5,6] we focused our follow-up strategy on markers with a MAF<5%

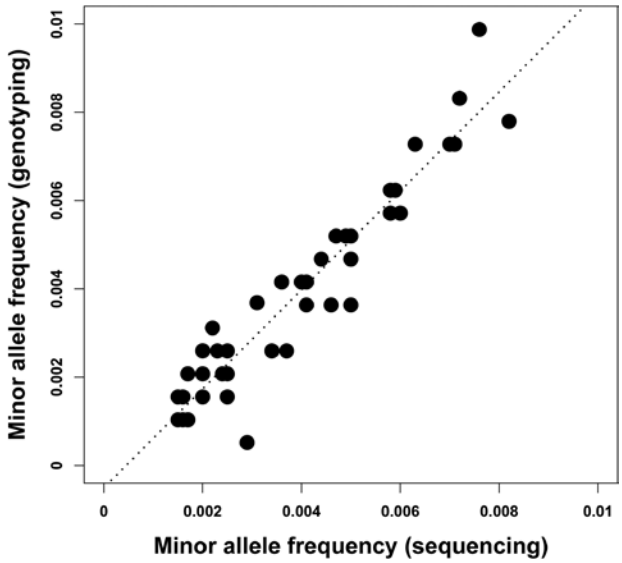

Figure 2. Correlation of allele frequencies estimated from the pooled sequence data or from direct DNA genotyping. For the pooled sequence data, the Syzygy software was used to estimate allele frequencies. We randomly selected 45 low-frequency (minor allele frequency <1%) DNA sequence variants from the resequencing results and genotyped them using the Sequenom platform in the same 1000 individuals used for sequencing. The coefficient of determination is r^2=0.90.

in our combined case–control resequencing panel. Also, to increase the likelihood to find causal MI alleles, we limited a priori our analysis to low-frequency nonsense, splice site and missense variants (Strategy 1) or to low-frequency nonsense, splice site, and missense variants predicted to be damaging (Strategy 2).[24] Our approach was to: (1) perform gene-based association testing with the C-alpha statistic[17] on the sequence data (500 early-onset MI cases and 500 matched controls) and select genes with $P \leq 0.05$, (2) validate the sequence results by genotyping the top genes in the same 1000 DNA samples, and (3) replicate the gene-based association results by genotyping in the DNA of 1594 and 2988 independent MI cases and controls, respectively (Table 1). Under specific assumptions, we estimated the statistical power of our study design: we have ≈48% power to find a gene at $\alpha=7\times10^{-4}$ (Bonferroni correction for 68 genes tested, see online-only Data Supplement Table VI for details).

For each of the 2 strategies described above, we found 4 genes with a C-alpha $P \leq 0.05$ (Strategy 1: *HHIPL2*, *TXNDC6*, *ATXN2*, *ERP29*; Strategy 2: *ICA1L*, *ESYT3*, *ABCA1*, *CXCL12*); the signal in these 8 genes was caused by 29 SNVs (Table 2). Given our results when we considered the correlation of allele frequency estimates for low-frequency variants between sequence and genotype data (Figure 2), we attempted to genotype these 29 SNVs in the same 1000 DNA samples used for resequencing but 5 failed. To facilitate comparison between the sequence- and genotype-based association results, we reran the C-alpha analysis of the sequence data on the 24 SNVs that genotyped

Table 2. Validation of the Sequence-Derived Top Gene-Based Association Results by Direct Genotyping in the Same DNA Samples

				Exon Resequencing (Syzygy/C-alpha)				Genotyping (PLINK/SKAT)		
Gene	rsID	Coordinates (hg19)	Annotation	Freq (cases)	Freq (controls)	*P* Value	*P* Value*	Freq (cases)	Freq (controls)	*P* Value
Strategy 1: All nonsense, missense, and splice site variants with a minor allele frequency <5%.										
HHIPL2	rs144597197	chr1:222696035	Arg695Cys	0.002	0.005	1.9×10^{-4}	—	0.002	0.007	0.067
		chr1:222696080	Arg680Stop	0.001	0.001			0	0.001	
		chr1:222696977	Arg622Gln	0	0.001			0	0.001	
	rs13989312	chr1:222705379	Thr551Met	0.002	0.003			0.002	0.004	
	rs61748612	chr1:222705418	Lys538Thr	0.002	0.012			0.002	0.009	
	rs116359984	chr1:222712108	Leu487Met	0.007	0.004			0.007	0.004	
	rs3811466	chr1:222717132	Val241Met	0.002	0.008			0.002	0.006	
		chr1:222717147	Glu236Lys	0.001	0			0	0	
TXNDC6	rs15184268	chr3:138033228	Asp75His	0.005	0	7.8×10^{-4}	—	0.006	0	0.056
ATXN2	rs14242317	chr12:111902514	Pro1108Ser	0.001	0.003	0.037	0.029	0.001	0.002	0.081
		chr12:111907981	Ala1083Thr	0	0.002			0	0.002	
		chr12:111908041	Pro1063Ser	0.001	0			0.001	0	
	rs14246247	chr12:111923594	Pro954Ser	0.004	0.001			NA	NA	
	rs11785191	chr12:111956226	Asn491Ser	0.004	0			0.003	0	
ERP29	rs14797597	chr12:112460215	Lys182Arg	0.007	0.016	0.034	—	0.009	0.015	0.55
Strategy 2: All nonsense, splice site, and probably and possibly damaging missense variants based on Polyphen-2 predictions. Minor allele frequency <5%.										
ICA1L	rs149686236	chr2:203680632	splice site 5'	0.004	0	0.0072	—	NA	NA	0.36
		chr2:203684596	Arg129His	0.001	0			0.001	0	
ESYT3	rs1541196	chr3:138183187	Gly306Arg	0.007	0.005	2.6×10^{-4}	3.3×10^{-6}	NA	NA	0.0050
	rs6772467	chr3:138186974	Gly416Arg	0.002	0.012			0.002	0.015	
ABCA1		chr9:107558635	Ser1731Cys	0.003	0	2.2×10^{-5}	1.9×10^{-5}	NA	NA	0.043
		chr9:107578504	Glu1220Lys	0.003	0			0.002	0	
		chr9:107578512	Ala1217Gly	0	0.002			0	0.001	
	rs76881554	chr9:107578620	Ser1181Phe	0.001	0.003			0.001	0.002	
		chr9:107583722	Arg965His	0.001	0.001			0.001	0.001	
	rs1388892	chr9:107589238	Lys776Asn	0.022	0.009			0.025	0.009	
	rs9282543	chr9:107599376	Val399Ala	0.006	0.003			NA	NA	
	rs14518323	chr9:107646756	Pro85Leu	0.002	0			0.001	0	
CXCL12		chr10:44873264	Arg119Gln	0	0.001	0.042	—	0	0.001	0.12
		chr10:44873340	Ala94Thr	0	0.003			0	0.002	

Association results for the sequence data was obtained using the C-alpha module implemented in Syzygy. For the genotype data, we use the sequence kernel association test (SKAT) to calculate evidence of gene-based association (with covariate adjustment for diabetes mellitus, hypertension, and hypercholesterolemia status). Because of failure during assay design or genotyping, some markers could not be tested with SKAT (NA, not available). For this reason, we also provide C-alpha results including only markers that were successfully genotyped (found in the *P* value* column). For *ICA1L*, we could not calculate a C-alpha *P* value* because we only successfully genotyped a singleton (chr2:203684596).

Table 3. Gene-Based Replication Results for Variants Selected Using Allele Frequency Estimates From DNA Sequence Data

				MHI Biobank - Replication			MHI Statins Study		
Gene	rsID	Coordinates (hg19)	Annotation	Freq (cases)	Freq (controls)	*P* Value	Freq (cases)	Freq (controls)	*P* Value
Strategy 1: All nonsense, missense, and splice site variants with a minor allele frequency <5%.									
HHIPL2	rs144597197	chr1:222696035	Arg695Cys	0.002	0.001	0.90	0.002	0.005	0.94
		chr1:222696080	Arg680Stop	0	0.001		0	0	
		chr1:222696977	Arg622Gln	0	0		0	0	
	rs13989312	chr1:222705379	Thr551Met	0.002	0.003		0.003	0.004	
	rs61748612	chr1:222705418	Lys538Thr	0.005	0.008		0.010	0.006	
	rs116359984	chr1:222712108	Leu487Met	0.005	0.004		0.003	0.004	
	rs3811466	chr1:222717132	Val241Met	0.001	0.003		0.003	0.003	
		chr1:222717147	Glu236Lys	0	0		0	0	
TXNDC6	rs15184268	chr3:138033228	Asp75His	0.005	0.002	0.63	0.004	0.001	0.25
ATXN2	rs14242317	chr12:111902514	Pro1108Ser	0.002	0.002	1	0.001	0.001	0.57
		chr12:111907981	Ala1083Thr	0.001	0.001		0	0.0004	
		chr12:111908041	Pro1063Ser	0	0		0	0	
	rs14246247	chr12:111923594	Pro954Ser	NA	NA		NA	NA	
	rs11785191	chr12:111956226	Asn491Ser	0.0006	0.0003		0.0007	0.0004	
ERP29	rs14797597	chr12:112460215	Lys182Arg	0.012	0.010	0.86	0.014	0.013	0.74
Strategy 2: All nonsense, splice site, and probably and possibly damaging missense variants based on Polyphen-2 predictions. Minor allele frequency <5%.									
ICA1L	rs149686236	chr2:203680632	splice site 5'	NA	NA	Monomorphic	NA	NA	Monomorphic
		chr2:203684596	Arg129His	0	0		0	0	
ESYT3	rs1541196	chr3:138183187	Gly306Arg	NA	NA	0.50	NA	NA	0.061
	rs6772467	chr3:138186974	Gly416Arg	0.007	0.007		0.003	0.008	
ABCA1		chr9:107558635	Ser1731Cys	NA	NA	0.37	NA	NA	0.43
		chr9:107578504	Glu1220Lys	0	0		0	0	
		chr9:107578512	Ala1217Gly	0	0		0	0.0004	
	rs76881554	chr9:107578620	Ser1181Phe	0.004	0.004		0.003	0.003	
		chr9:107583722	Arg965His	0	0.0003		0	0	
	rs1388892	chr9:107589238	Lys776Asn	0.007	0.012		0.015	0.023	
	rs9282543	chr9:107599376	Val399Ala	NA	NA		NA	NA	
	rs14518323	chr9:107646756	Pro85Leu	0.002	0.001		0.0007	0.001	
CXCL12		chr10:44873264	Arg119Gln	0.0006	0	0.25	0	0.0004	0.89
		chr10:44873340	Ala94Thr	0	0		0.0007	0.0007	

We attempted to genotype 29 single nucleotide variants from eight genes in the DNA of 870 myocardial infarction (MI) cases and 1604 controls from the Montreal Heart Institute (MHI) Biobank—replication and of 724 MI cases and 1384 controls from the MHI Statins Study. We used the sequence kernel association test (SKAT) to perform gene-based association testing between genotypes and MI status while accounting for significant covariates (Materials and Methods). NA indicates not available; these markers could not be genotyped because of assay failure or poor genotyping.

successfully (see *P* value* in Table 2). We used SKAT on genotypes at the 24 SNVs to validate association between MI and these 8 genes; SKAT is a generalized C-alpha test that offers the advantage to control for covariates.[19] Not unexpectedly, 6 of the 8 genes did not have nominally significant SKAT *P* values ($P \leq 0.05$) in the validation experiment on genotyped markers, mostly due to small differences in allele frequency estimates and covariate adjustment (Table 2). Even for the 2 nominally significant genes (*ESYT3*, *ABCA1*), the SKAT *P* values were higher than those calculated with the C-alpha statistic on the sequence data, probably because the C-alpha test cannot accommodate covariates and does require permutations to derive accurate *P* values in the presence of few low-frequency variants, and permutations are not possible with pooled sequence data.[17]

Replicating Gene-Based Association Results in Independent Cohorts

To replicate our findings, we selected an additional 870 MI cases and 1604 controls from the MHI Biobank, and obtained DNA samples from 724 MI cases and 1384 controls from the MHI Statins Study (Table 1). As for the validation, 24 of the 29 prioritized SNVs genotyped well in the replication samples. We tested association at the gene level between these markers and MI status using SKAT while accounting for significant covariates (Materials and Methods). For the 6 genes that did not reach nominal significance in the validation experiment (*HHIPL2*, *TXNDC6*, *ATXN2*, *ERP29*, *ICA1L*, *CXCL12*), results were consistently nonsignificant in the replication panels (Table 3). Similarly, the 2 genes with nominal *P* values ≤0.05 in the validation phase (*ESYT3*, *ABCA1*) did

not replicate in the replication panels (Table 3). However, for *ESYT3* the association signal in the MHI Statins study was almost nominally significant (P=0.061), with the nonreference allele at rs6772467 more frequent in controls than in MI cases, consistent with results observed in the sequencing and validation experiments for this variant (Table 2). Since the gene signal at *ESYT3* is caused by a single probably damaging missense variant (rs6772467, Gly416Arg), we combined evidence of association with MI for this marker across the 3 genotyped panels using the mega-analysis of rare variant (MARV) method.[10] The MARV P value of association between *ESYT3* rs6772467 and MI is P=0.0089, warranting further replication attempts to test this association in additional large cohorts.

Discussion

The focus of this study was to identify new genes and causal DNA sequence variants implicated in the pathogenesis of MI by searching for low-frequency functional genetic variation in the exons of 68 candidate genes. Although linkage studies and targeted resequencing experiments have identified many rare familial mutations associated with MI, and more recently GWAS highlighted many MI-associated common SNPs, few studies have searched specifically the low-frequency allele spectrum (MAF, 0.1%–5%) for MI-associated alleles. One exception is the *PCSK9* gene, which is known to harbor familial, low-frequency and common DNA sequence variants associated with low-density lipoprotein cholesterol (LDL-C) levels and risk of coronary heart disease.[25–29] We resequenced *PCSK9* in our experiment to a mean coverage (per sample) of 50X (Figure 1 and online-only Data Supplement Table III), and identified 5 missense SNVs (online-only Data Supplement Table V). The C-alpha result calculated from the sequence data for these 5 *PCSK9* missense variants was not significant (P=0.74), so markers in *PCSK9* were not genotyped as part of our replication effort. In particular, we identified the *PCSK9* R46L (rs11591147) variant in our sequencing experiment, which has been shown to decrease LDL-C levels and CAD risk in population of European ancestry.[27,30] However, in our samples of 500 early-onset MI cases and 500-matched controls, the allele frequency difference for the leucine 46 allele was not significant (2.0% in cases versus 1.8% in controls, P=0.87).

From the sequence data, we selected for validation and replication SNVs from 8 genes in a total of 2094 MI cases and 3488 controls; all participants had 4 French–Canadian grandparents. Many of the gene-based associations found in the sequence data could not be validated using direct genotype information in the same DNA samples (Table 2). Of the 2 genes with a nominal $P \leq 0.05$ in the validation experiment (*ESYT3*, *ABCA1*), none replicated in the 2 additional French–Canadian case–control panels (Table 3). However, results were modestly encouraging for *ESYT3*-rs6772467, where the P values were P=0.50 in the MHI Biobank-replication panel and P=0.061 in the MHI Statins Study (Table 3). *ESYT3* encodes for the extended synaptotagmin-3 protein, which has no defined biological functions. *ESYT3* was included in our resequencing project because it is located near a SNP in the *MRAS* gene that was found by GWAS to associate with CAD.[31] Interestingly, a recent fine-mapping experiment of the CAD association signal at the 3q22-*MRAS* locus in Han Chinese suggested that SNPs within the *ESYT3* gene are more strongly associated with CAD than the original *MRAS* SNP.[32] This observation, combined with our results, emphasizes the need to attempt to replicate the association between MI and *ESYT3*-rs6772467 in additional large cohorts.

We optimized a protocol, which builds on methods and tools previously described,[10,20] to cost-effectively resequence pools of nonindexed DNA samples following solution-based exon capture. We showed that our method is particularly efficient to discover genetic variation and has a low false-positive rate: of the 69 low-frequency SNVs that we genotyped in the validation set, only one was monomorphic. Despite the success of the discovery phase of our experiment, we met several challenges in using pooled sequencing for association testing: (1) uneven coverage between genes, or between cases and controls, is difficult to account for, (2) genotypes are not available, preventing several downstream analyses (eg, permutations), and (3) difficulty in accurately estimating allele frequencies for low-frequency variants. Other limitations of our study include our difficulty to directly genotype 5 of the variants found by sequencing using the Sequenom platform and the small number of early-onset MI cases in the replication panels (12% versus 100% in the sequencing set). Overall, our pooled, nonindexed DNA resequencing protocol is efficient to discover genetic variants across the allelic spectrum and might be particularly useful to characterize genetic variation at reasonable costs in populations that are not well covered by the HapMap or 1000 Genomes Projects. However, we recommend an initial genotyping-based validation step of interesting variants in the resequenced samples before attempting to find genotype–phenotype associations in replication samples. This step is important to avoid false-positive results due to errors in estimating allele frequencies from sequence data alone.

In conclusion, our targeted exon resequencing experiment in 1000 individuals followed by genotyping in 4582 samples did not identify robust associations with MI. Given our statistical power (Online-only Data Supplement Table VI), our design would have found genes/variants with strong effect sizes on MI, suggesting that such alleles are not present in French Canadians in the exons well covered by DNA resequencing. More generally, our results are consistent with the need for very large sample size to find associations between low-frequency DNA sequence variants and complex human diseases or traits.

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Disclosures

None.

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CLINICAL PERSPECTIVE

Coronary artery disease (CAD) and its main clinical manifestation, myocardial infarction (MI), is the main cause of death and disability in the world. Family history of CAD/MI is a known risk factor, suggesting that this disease has a strong genetic component. Rare familial mutations in genes involved in lipid metabolism and common single nucleotide polymorphisms have been associated with CAD/MI risk, but these genetic variants do not account for all the genetic liability. The role of low-frequency genetic variants, which are not captured by genome-wide association studies (GWAS), in CAD/MI has not been extensively investigated. In our study, we optimized a method to sequence genes in large sample size and applied it to 68 MI candidate genes that were sequenced in 500 early-onset MI cases and 500 matched controls, all of French–Canadian ancestry. The most promising DNA sequence variants were then genotyped in >4500 French Canadians for replication. Our method is efficient and cost-effective to identify low-frequency genetic variants. However, we did not identify new MI-associated variants in these 68 candidate genes in French Canadians. We now have the tools to expand this approach across all the human genes in large populations. Current prevention therapies for CAD/MI consist in controlling lipid levels, heart rate, and blood pressure. The identification of new genes and biological pathways involved in the biology of atherosclerosis using DNA sequencing methods could guide the development of new drugs.

SUPPLEMENTAL MATERIAL

POOLED DNA RE-SEQUENCING OF 68 MYOCARDIAL INFARCTION CANDIDATE GENES IN FRENCH CANADIANS

Mélissa Beaudoin[1,*], MS; Ken Sin Lo[1,*], BS; Amidou N'Diaye[1], PhD; Manuel A. Rivas[3,4], BS; Marie-Pierre Dubé[1,2], PhD; Nathalie Laplante[1], PhD; Michael S. Phillips[1,2], PhD; John D. Rioux[1,2], PhD; Jean-Claude Tardif[1,2,#], MD; Guillaume Lettre[1,2,#], PhD.

[1]Montreal Heart Institute, Montreal, Quebec, Canada.

[2]Université de Montréal, Montreal, Québec, Canada.

[3]Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK.

[4]Broad Institute of Harvard and MIT, Cambridge, Massachussetts, USA.

[*]These authors contributed equally to this work.

[#]Correspondence to:
Guillaume Lettre
Montreal Heart Institute
5000 Rue Bélanger
Montréal, Québec, H1T 1C8, Canada
Phone: 514-376-3330 ext. 2657
Fax: 514-593-2539
Email: guillaume.lettre@umontreal.ca

Jean-Claude Tardif
Montreal Heart Institute
5000 Rue Bélanger
Montréal, Québec, H1T 1C8, Canada
Phone: 514-376-3330 ext. 3612
Fax: 514-593-25009
Email: jean-claude.tardif@icm-mhi.org

Supplementary Table 1. List of the 68 myocardial infarction candidate genes targeted for re-sequencing in this project. OMIM, Online Mendelian Inheritance in Man; GWAS, Genome-wide association study.

Gene	Rationale for inclusion in project
ABCA1	OMIM, Tangier disease
ABI2	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
ACAD10	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
ALDH2	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
ALOX5AP	Linkage study, Helgadottir et al., Nat Genet 36, 233-9 (2004)
ALS2CR8	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
ANXA2	Candidate gene, Poirier et al., J Biol Chem. 284(42):28856-64 (2009)
APOA1	OMIM
APOB	OMIM
APOE	OMIM
ARL4A	GWAS, Samani et al., New England Journal of Medicine 357, 443-453 (2007)
ARMC8	GWAS, Erdmann et al. Nat Genet 41, 280-2 (2009)
ATXN2	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
BMPR2	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
BRAP	Candidate gene, Ozaki et al., Nat Genet 41, 329-33 (2009)
C12orf30	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
C12orf51	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
C1orf58	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
CDKN2A	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
CDKN2B	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
CDKN2BAS	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
CELSR2	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
CEP70	GWAS, Erdmann et al. Nat Genet 41, 280-2 (2009)
CETP	OMIM
CXCL12	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
CYP20A1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
ERP29	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
ESYT3	GWAS, Erdmann et al. Nat Genet 41, 280-2 (2009)
FAIM	GWAS, Erdmann et al. Nat Genet 41, 280-2 (2009)
FAM117B	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
FAM165B	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
HHIPL2	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
ICA1L	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
IQUB	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
KCNE1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
KCNE2	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
KIAA1324	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
LCAT	OMIM
LDLR	OMIM
LGALS2	Candidate gene, Ozaki et al., Nat Genet 41, 329-33 (2009)
LIPC	OMIM

LPL	OMIM
LRP8	OMIM
LTA	Candidate gene, Ozaki et al., Nat Genet 41, 329-33 (2009)
MAPKAPK5	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
MIA3	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
MRAS	GWAS, Erdmann et al. Nat Genet 41, 280-2 (2009)
MRPS6	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
MTHFD1L	GWAS, Samani et al., New England Journal of Medicine 357, 443-453 (2007)
NBEAL1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
NOP58	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
PCSK9	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
PHACTR1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
PSRC1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
PTPN11	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
RAPH1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
RCAN1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
RPL6	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
SARS	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
SH2B3	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
SLC5A3	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
SMAD3	GWAS, Samani et al., New England Journal of Medicine 357, 443-453 (2007)
SORT1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
SUMO1	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
TAF1A	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)
TRAFD1	GWAS, Gudbjartsson et al. Nat Genet 41, 342-7 (2009)
TXNDC6	GWAS, Erdmann et al. Nat Genet 41, 280-2 (2009)
WDR12	GWAS, Kathiresan et al.,Nat Genet 41, 334-41 (2009)

Supplementary Table 2. Gene name, exon numbers and genomic coordinates (hg18, NCBI Build 36) for all regions targeted for DNA re-sequencing in this p

Chromosome	Start (position in bp)	End (position in bp)	Size (bp)	Gene	Feature name
1	53483253	53484633	1380	LRP8	LRP8_exon1
1	53484681	53485161	480	LRP8	LRP8_exon1
1	53485206	53485326	120	LRP8	LRP8_exon1
1	53487620	53487740	120	LRP8	LRP8_exon2
1	53488915	53489155	240	LRP8	LRP8_exon3
1	53493332	53493487	155	LRP8	LRP8_exon4
1	53495491	53495731	240	LRP8	LRP8_exon5
1	53496534	53496774	240	LRP8	LRP8_exon6
1	53498673	53498913	240	LRP8	LRP8_exon7
1	53500276	53500516	240	LRP8	LRP8_exon8
1	53500674	53500853	179	LRP8	LRP8_exon9
1	53502421	53502661	240	LRP8	LRP8_exon10
1	53504699	53504939	240	LRP8	LRP8_exon11
1	53509229	53509635	406	LRP8	LRP8_exon12 LRP8_exon13
1	53513831	53514071	240	LRP8	LRP8_exon14
1	53514904	53515384	480	LRP8	LRP8_exon15
1	53518790	53519030	240	LRP8	LRP8_exon16
1	53527767	53528007	240	LRP8	LRP8_exon17
1	53565101	53565281	180	LRP8	LRP8_exon18
1	53566768	53566948	180		
1	55277298	55278138	840	PCSK9	PCSK9_exon1
1	55278176	55278356	180	PCSK9	PCSK9_exon1
1	55282078	55282318	240	PCSK9	PCSK9_exon2
1	55284724	55284964	240	PCSK9	PCSK9_exon3
1	55290484	55290724	240	PCSK9	PCSK9_exon4
1	55290860	55291100	240	PCSK9	PCSK9_exon5
1	55294231	55294471	240	PCSK9	PCSK9_exon6
1	55295562	55295802	240	PCSK9	PCSK9_exon7
1	55296262	55296502	240	PCSK9	PCSK9_exon8
1	55296713	55296893	180	PCSK9	PCSK9_exon9
1	55297714	55297954	240	PCSK9	PCSK9_exon10
1	55299605	55299845	240	PCSK9	PCSK9_exon11
1	55301602	55302502	900	PCSK9	PCSK9_exon12
1	55302785	55303505	720	PCSK9	PCSK9_exon12
1	109457627	109458527	900	KIAA1324	KIAA1324_exon1
1	109505978	109506218	240	KIAA1324	KIAA1324_exon2
1	109508619	109508859	240	KIAA1324	KIAA1324_exon3
1	109515963	109516203	240	KIAA1324	KIAA1324_exon4
1	109516591	109516752	161	KIAA1324	KIAA1324_exon5

1	109517584	109517757	173	KIAA1324	KIAA1324_exon6
1	109517786	109518026	240	KIAA1324	KIAA1324_exon7
1	109529150	109529315	165	KIAA1324	KIAA1324_exon8
1	109532289	109532529	240	KIAA1324	KIAA1324_exon9
1	109533154	109533394	240	KIAA1324	KIAA1324_exon10
1	109533698	109533863	165	KIAA1324	KIAA1324_exon11
1	109535476	109535649	173	KIAA1324	KIAA1324_exon12
1	109535818	109536058	240	KIAA1324	KIAA1324_exon13
1	109536706	109537066	360	KIAA1324	KIAA1324_exon14
1	109538531	109538771	240	KIAA1324	KIAA1324_exon15
1	109541588	109541828	240	KIAA1324	KIAA1324_exon16
1	109542086	109542255	169	KIAA1324	KIAA1324_exon17
1	109542682	109542853	171	KIAA1324	KIAA1324_exon18
1	109543941	109544412	471	KIAA1324	KIAA1324_exon19 KIAA1324_exon20
1	109544841	109545081	240	KIAA1324	KIAA1324_exon21
1	109547053	109547713	660	KIAA1324	KIAA1324_exon22
1	109548350	109548950	600	KIAA1324	KIAA1324_exon22
1	109549065	109550025	960	KIAA1324	KIAA1324_exon22
1	109550446	109551044	598	KIAA1324	KIAA1324_exon22
1	109551251	109551371	120		
1	109557557	109558277	720	SARS	SARS_exon1
1	109568079	109568234	155	SARS	SARS_exon2
1	109572455	109572616	161	SARS	SARS_exon3
1	109573517	109573757	240	SARS	SARS_exon4
1	109574973	109575213	240	SARS	SARS_exon5
1	109575732	109575972	240	SARS	SARS_exon6
1	109579344	109579584	240	SARS	SARS_exon7
1	109580065	109580305	240	SARS	SARS_exon8
1	109580493	109580733	240	SARS	SARS_exon9
1	109581332	109581572	240	SARS	SARS_exon10
1	109581861	109582821	960	SARS	SARS_exon11
1	109593980	109594220	240	CELSR2	CELSR2_exon1
1	109594300	109597540	3240	CELSR2	CELSR2_exon1
1	109602527	109602827	300	CELSR2	CELSR2_exon2
1	109602862	109603282	420	CELSR2	CELSR2_exon2
1	109605177	109605417	240	CELSR2	CELSR2_exon3
1	109605625	109605803	178	CELSR2	CELSR2_exon4
1	109605913	109606078	165	CELSR2	CELSR2_exon5
1	109606389	109606629	240	CELSR2	CELSR2_exon6
1	109606911	109607151	240	CELSR2	CELSR2_exon7
1	109607228	109607468	240	CELSR2	CELSR2_exon8
1	109607718	109607958	240	CELSR2	CELSR2_exon9

1	109608185	109608545	360	CELSR2	CELSR2_exon10
1	109608565	109608745	180	CELSR2	CELSR2_exon11
1	109608962	109609202	240	CELSR2	CELSR2_exon12
1	109609275	109609515	240	CELSR2	CELSR2_exon13
1	109609850	109610090	240	CELSR2	CELSR2_exon14
1	109610214	109610385	171	CELSR2	CELSR2_exon15
1	109611655	109611822	167	CELSR2	CELSR2_exon16
1	109611979	109612219	240	CELSR2	CELSR2_exon17
1	109612696	109612936	240	CELSR2	CELSR2_exon18
1	109612968	109613208	240	CELSR2	CELSR2_exon19
1	109613224	109613464	240	CELSR2	CELSR2_exon20
1	109613531	109613771	240	CELSR2	CELSR2_exon21
1	109613781	109614021	240	CELSR2	CELSR2_exon22
1	109614057	109614297	240	CELSR2	CELSR2_exon23
1	109614537	109614777	240	CELSR2	CELSR2_exon24
1	109615038	109615215	177	CELSR2	CELSR2_exon25
1	109615320	109615925	605	CELSR2	CELSR2_exon26 CELSR2_exon27 CELSR2_exon28
1	109616365	109616605	240	CELSR2	CELSR2_exon29
1	109616745	109616910	165	CELSR2	CELSR2_exon30
1	109616958	109617078	120	CELSR2	CELSR2_exon31
1	109617275	109617515	240	CELSR2	CELSR2_exon32
1	109617577	109617817	240	CELSR2	CELSR2_exon33
1	109618143	109620423	2280	CELSR2	CELSR2_exon34
1	109623688	109624348	660	PSRC1	PSRC1_exon1
1	109624503	109624670	167	PSRC1	PSRC1_exon2
1	109624918	109625398	480	PSRC1	PSRC1_exon3
1	109625743	109626223	480	PSRC1	PSRC1_exon4
1	109626616	109626765	149	PSRC1	PSRC1_exon5
1	109627166	109627821	655	PSRC1	PSRC1_exon7
1	109653155	109654295	1140	SORT1	SORT1_exon1
1	109654347	109658247	3900	SORT1	SORT1_exon1
1	109658346	109658586	240	SORT1	SORT1_exon2
1	109658782	109658955	173	SORT1	SORT1_exon3
1	109660960	109661135	175	SORT1	SORT1_exon4
1	109661965	109662144	179	SORT1	SORT1_exon5
1	109667050	109667290	240	SORT1	SORT1_exon6
1	109669018	109669258	240	SORT1	SORT1_exon7
1	109671100	109671340	240	SORT1	SORT1_exon8
1	109671608	109671779	171	SORT1	SORT1_exon9
1	109680350	109680523	173	SORT1	SORT1_exon10
1	109684825	109685065	240	SORT1	SORT1_exon11
1	109686110	109686350	240	SORT1	SORT1_exon12

1	109689840	109690080	240	SORT1	SORT1_exon13
1	109691579	109691724	145	SORT1	SORT1_exon14
1	109695031	109695188	157	SORT1	SORT1_exon15
1	109698473	109698713	240	SORT1	SORT1_exon16
1	109699476	109699647	171	SORT1	SORT1_exon17
1	109711510	109711667	157	SORT1	SORT1_exon18
1	109713628	109713778	150	SORT1	SORT1_exon19
1	109741718	109742078	360	SORT1	SORT1_exon20
1	109742106	109742586	480		
1	220762002	220762902	900	HHIPL2	HHIPL2_exon1
1	220763536	220763697	161	HHIPL2	HHIPL2_exon2
1	220766893	220767054	161	HHIPL2	HHIPL2_exon3
1	220771882	220772122	240	HHIPL2	HHIPL2_exon4
1	220778555	220778795	240	HHIPL2	HHIPL2_exon5
1	220779959	220780319	360	HHIPL2	HHIPL2_exon6
1	220781927	220782167	240	HHIPL2	HHIPL2_exon7
1	220783467	220784187	720	HHIPL2	HHIPL2_exon8
1	220787640	220788060	420	HHIPL2	HHIPL2_exon9
1	220788174	220788594	420		
1	220798130	220798490	360	TAF1A	TAF1A_exon1
1	220798505	220798745	240	TAF1A	TAF1A_exon1
1	220801285	220801525	240	TAF1A	TAF1A_exon2
1	220803078	220803318	240	TAF1A	TAF1A_exon3
1	220803979	220804132	153	TAF1A	TAF1A_exon4
1	220809433	220809673	240	TAF1A	TAF1A_exon5
1	220810444	220810684	240	TAF1A	TAF1A_exon6
1	220817388	220817628	240	TAF1A	TAF1A_exon7
1	220819691	220819868	177	TAF1A	TAF1A_exon8
1	220824056	220824296	240	TAF1A	TAF1A_exon9
1	220828348	220828588	240	TAF1A	TAF1A_exon10
1	220829643	220830303	660	TAF1A	TAF1A_exon11
1	220857526	220857826	300		
1	220858053	220858233	180	MIA3	MIA3_exon1
1	220861069	220861309	240	MIA3	MIA3_exon2
1	220864693	220864856	163	MIA3	MIA3_exon3
1	220867506	220870386	2880	MIA3	MIA3_exon4
1	220872089	220872329	240	MIA3	MIA3_exon5
1	220873020	220873260	240	MIA3	MIA3_exon6
1	220885523	220885703	180	MIA3	MIA3_exon7
1	220888738	220888869	131	MIA3	MIA3_exon8
1	220890217	220890382	165	MIA3	MIA3_exon9
1	220890557	220890716	159	MIA3	MIA3_exon10

1	220890724	220890899	175	MIA3	MIA3_exon11
1	220891898	220892054	156	MIA3	MIA3_exon12
1	220892157	220892330	173	MIA3	MIA3_exon13
1	220892913	220893153	240	MIA3	MIA3_exon14
1	220893159	220893335	176	MIA3	MIA3_exon15
1	220894160	220894308	148	MIA3	MIA3_exon16
1	220894315	220894480	165	MIA3	MIA3_exon17
1	220894568	220894808	240	MIA3	MIA3_exon18
1	220898651	220898822	171	MIA3	MIA3_exon19
1	220899371	220899522	151	MIA3	MIA3_exon20
1	220899534	220899808	274	MIA3	MIA3_exon21 MIA3_exon22
1	220899834	220900005	171	MIA3	MIA3_exon23
1	220900089	220900329	240	MIA3	MIA3_exon24
1	220901976	220902131	155	MIA3	MIA3_exon25
1	220902176	220902336	160	MIA3	MIA3_exon26
1	220903917	220904157	240	MIA3	MIA3_exon27
1	220905259	220906699	1440	MIA3	MIA3_exon28
1	220906753	220908493	1740	MIA3	MIA3_exon28
1	220951987	220952947	960	C1orf58	C1orf58_exon1
1	220955616	220955795	179	C1orf58	C1orf58_exon2
1	220958855	220959028	173	C1orf58	C1orf58_exon3
1	220959190	220959359	169	C1orf58	C1orf58_exon4
1	220962346	220962514	168	C1orf58	C1orf58_exon5
1	220964013	220964170	157	C1orf58	C1orf58_exon6
1	220965380	220965553	173	C1orf58	C1orf58_exon7
1	220967094	220967259	165	C1orf58	C1orf58_exon8
1	220968668	220968831	163	C1orf58	C1orf58_exon9
1	220969544	220969705	161	C1orf58	C1orf58_exon10
1	220969946	220970126	180	C1orf58	C1orf58_exon11
1	220971280	220971520	240	C1orf58	C1orf58_exon12
1	220972560	220972980	420	C1orf58	C1orf58_exon13
2	21077648	21079748	2100	APOB	APOB_exon1
2	21080616	21080856	240	APOB	APOB_exon2
2	21080905	21081082	177	APOB	APOB_exon3
2	21081401	21089081	7680	APOB	APOB_exon4
2	21089482	21089962	480	APOB	APOB_exon5
2	21090776	21091016	240	APOB	APOB_exon6
2	21091422	21091662	240	APOB	APOB_exon7
2	21091713	21091953	240	APOB	APOB_exon8
2	21092800	21093040	240	APOB	APOB_exon9
2	21095308	21095548	240	APOB	APOB_exon10
2	21096070	21096310	240	APOB	APOB_exon11

2	21099192	21099432	240	APOB	APOB_exon12
2	21099864	21100104	240	APOB	APOB_exon13
2	21101284	21101524	240	APOB	APOB_exon14
2	21103132	21103372	240	APOB	APOB_exon15
2	21104202	21104442	240	APOB	APOB_exon16
2	21104688	21104928	240	APOB	APOB_exon17
2	21105968	21106208	240	APOB	APOB_exon18
2	21106243	21106422	179	APOB	APOB_exon19
2	21108723	21108963	240	APOB	APOB_exon20
2	21109664	21109904	240	APOB	APOB_exon21
2	21111153	21111316	163	APOB	APOB_exon22
2	21111902	21112142	240	APOB	APOB_exon23
2	21113433	21113673	240	APOB	APOB_exon24
2	21114290	21114530	240	APOB	APOB_exon25
2	21117266	21117506	240	APOB	APOB_exon26
2	21118705	21118883	178	APOB	APOB_exon27
2	21119838	21119977	139	APOB	APOB_exon28
2	21120327	21120987	660	APOB	APOB_exon29
2	202778634	202778754	120		
2	202779068	202780328	1260	SUMO1	SUMO1_exon1
2	202783659	202783815	156	SUMO1	SUMO1_exon2
2	202787283	202787442	159	SUMO1	SUMO1_exon3
2	202792957	202793114	157	SUMO1	SUMO1_exon4
2	202811376	202812096	720	SUMO1	SUMO1_exon5
2	202838575	202838995	420	NOP58	NOP58_exon1
2	202848038	202848197	159	NOP58	NOP58_exon2
2	202850869	202851016	147	NOP58	NOP58_exon3
2	202855258	202855498	240	NOP58	NOP58_exon4
2	202857320	202857500	180	NOP58	NOP58_exon5
2	202860582	202860735	153	NOP58	NOP58_exon6
2	202863237	202863477	240	NOP58	NOP58_exon7
2	202864044	202864284	240	NOP58	NOP58_exon8
2	202865687	202865927	240	NOP58	NOP58_exon9
2	202868602	202868842	240	NOP58	NOP58_exon10
2	202870293	202870533	240	NOP58	NOP58_exon11
2	202870767	202870918	151	NOP58	NOP58_exon12
2	202873147	202873387	240	NOP58	NOP58_exon13
2	202876386	202876866	480	NOP58	NOP58_exon15
2	202876896	202877136	240		
2	202948760	202949060	300		
2	202949245	202949485	240	BMPR2	BMPR2_exon1
2	202949508	202949988	480	BMPR2	BMPR2_exon1

2	202950014	202950554	540	BMPR2	BMPR2_exon1
2	203037741	203037981	240	BMPR2	BMPR2_exon2
2	203040451	203040691	240	BMPR2	BMPR2_exon3
2	203086653	203086828	175	BMPR2	BMPR2_exon4
2	203087817	203087983	166	BMPR2	BMPR2_exon5
2	203091784	203092024	240	BMPR2	BMPR2_exon6
2	203093022	203093199	177	BMPR2	BMPR2_exon7
2	203103721	203103961	240	BMPR2	BMPR2_exon8
2	203105505	203105745	240	BMPR2	BMPR2_exon9
2	203115226	203115466	240	BMPR2	BMPR2_exon10
2	203125649	203125889	240	BMPR2	BMPR2_exon11
2	203128198	203129518	1320	BMPR2	BMPR2_exon12
2	203132652	203135412	2760	BMPR2	BMPR2_exon13
2	203135457	203135577	120	BMPR2	BMPR2_exon13
2	203135616	203135856	240	BMPR2	BMPR2_exon13
2	203136418	203137018	600	BMPR2	BMPR2_exon13
2	203137025	203137745	720	BMPR2	BMPR2_exon13
2	203138308	203140828	2520	BMPR2	BMPR2_exon13
2	203207730	203207970	240		
2	203207974	203208334	360	FAM117B	FAM117B_exon1
2	203208429	203208549	120	FAM117B	FAM117B_exon1
2	203208615	203208795	180	FAM117B	FAM117B_exon1
2	203268803	203269043	240	FAM117B	FAM117B_exon2
2	203297846	203298013	167	FAM117B	FAM117B_exon3
2	203299185	203299362	177	FAM117B	FAM117B_exon4
2	203328456	203328696	240	FAM117B	FAM117B_exon5
2	203330172	203330412	240	FAM117B	FAM117B_exon6
2	203332140	203332380	240	FAM117B	FAM117B_exon7
2	203338360	203339020	660	FAM117B	FAM117B_exon8
2	203339060	203340140	1080	FAM117B	FAM117B_exon8
2	203340417	203341737	1320	FAM117B	FAM117B_exon8
2	203341778	203343278	1500	FAM117B	FAM117B_exon8
2	203346153	203347473	1320	ICA1L	ICA1L_exon1
2	203347863	203348463	600	ICA1L	ICA1L_exon1
2	203348798	203349998	1200	ICA1L	ICA1L_exon1
2	203350342	203350822	480	ICA1L	ICA1L_exon1
2	203351161	203352661	1500	ICA1L	ICA1L_exon1
2	203358847	203359012	165	ICA1L	ICA1L_exon2
2	203361745	203362105	360	ICA1L	ICA1L_exon3
2	203369815	203369972	157	ICA1L	ICA1L_exon4
2	203384663	203384805	142	ICA1L	ICA1L_exon5
2	203387629	203387790	161	ICA1L	ICA1L_exon6

2	203388842	203389011	169	ICA1L	ICA1L_exon7
2	203390327	203390567	240	ICA1L	ICA1L_exon8
2	203392647	203392887	240	ICA1L	ICA1L_exon9
2	203394266	203394506	240	ICA1L	ICA1L_exon10
2	203398472	203398772	300	ICA1L	ICA1L_exon11
2	203401779	203402019	240	ICA1L	ICA1L_exon12
2	203443440	203443680	240	ICA1L	ICA1L_exon14
2	203444118	203444478	360	ICA1L	ICA1L_exon15
2	203444533	203445158	625	ICA1L	ICA1L_exon16
2	203453047	203453227	180		
2	203453545	203453905	360	WDR12	WDR12_exon1
2	203455635	203455792	157	WDR12	WDR12_exon2
2	203456522	203456762	240	WDR12	WDR12_exon3
2	203457131	203457304	173	WDR12	WDR12_exon4
2	203457312	203457552	240	WDR12	WDR12_exon5
2	203465545	203465708	163	WDR12	WDR12_exon6
2	203467499	203467642	143	WDR12	WDR12_exon7
2	203468989	203469229	240	WDR12	WDR12_exon8
2	203470235	203470413	178	WDR12	WDR12_exon9
2	203472464	203472637	173	WDR12	WDR12_exon10
2	203473955	203474122	167	WDR12	WDR12_exon11
2	203480795	203480962	167	WDR12	WDR12_exon12
2	203484342	203484822	480	WDR12	WDR12_exon13
2	203484848	203486108	1260	WDR12	WDR12_exon13 ALS2CR8_exon1 ALS2CR8_exon2
2	203490807	203491047	240	ALS2CR8	ALS2CR8_exon3
2	203514767	203515007	240	ALS2CR8	ALS2CR8_exon5
2	203515700	203515940	240	ALS2CR8	ALS2CR8_exon6
2	203525466	203525706	240	ALS2CR8	ALS2CR8_exon7
2	203526916	203527156	240	ALS2CR8	ALS2CR8_exon8
2	203528601	203528764	163	ALS2CR8	ALS2CR8_exon9
2	203534178	203534418	240	ALS2CR8	ALS2CR8_exon10
2	203539885	203540125	240	ALS2CR8	ALS2CR8_exon11
2	203542837	203543077	240	ALS2CR8	ALS2CR8_exon12
2	203544468	203544708	240	ALS2CR8	ALS2CR8_exon13
2	203547262	203547502	240	ALS2CR8	ALS2CR8_exon14
2	203550191	203550343	152	ALS2CR8	ALS2CR8_exon15
2	203554527	203554707	180	ALS2CR8	ALS2CR8_exon16
2	203554983	203555463	480	ALS2CR8	ALS2CR8_exon17
2	203556415	203556955	540	ALS2CR8	ALS2CR8_exon18
2	203556991	203557591	600	ALS2CR8	ALS2CR8_exon18
2	203557627	203557747	120	ALS2CR8	ALS2CR8_exon18
2	203558136	203558376	240	ALS2CR8	ALS2CR8_exon18

2	203558380	203559820	1440	ALS2CR8	ALS2CR8_exon18
2	203587321	203587983	662	NBEAL1	NBEAL1_exon1
2	203588104	203588464	360		
2	203588767	203589427	660	NBEAL1	NBEAL1_exon2
2	203614694	203614860	166	NBEAL1	NBEAL1_exon3
2	203622741	203622981	240	NBEAL1	NBEAL1_exon4
2	203629354	203629515	161	NBEAL1	NBEAL1_exon5
2	203630236	203630476	240	NBEAL1	NBEAL1_exon6
2	203641320	203641481	161	NBEAL1	NBEAL1_exon7
2	203656159	203656519	360	NBEAL1	NBEAL1_exon9
2	203657396	203657569	173	NBEAL1	NBEAL1_exon10
2	203672556	203672718	162	NBEAL1	NBEAL1_exon11
2	203680351	203680520	169	NBEAL1	NBEAL1_exon12
2	203680565	203681165	600	NBEAL1	NBEAL1_exon13
2	203683063	203683303	240	NBEAL1	NBEAL1_exon14
2	203684915	203685095	180	NBEAL1	NBEAL1_exon15
2	203685953	203686313	360	NBEAL1	NBEAL1_exon16
2	203688913	203689076	163	NBEAL1	NBEAL1_exon17
2	203695183	203695348	165	NBEAL1	NBEAL1_exon18
2	203698283	203698523	240	NBEAL1	NBEAL1_exon19
2	203698873	203699113	240	NBEAL1	NBEAL1_exon20
2	203699483	203699723	240	NBEAL1	NBEAL1_exon21
2	203699756	203699927	171	NBEAL1	NBEAL1_exon22
2	203700706	203700946	240	NBEAL1	NBEAL1_exon23
2	203703244	203703484	240	NBEAL1	NBEAL1_exon24
2	203704899	203705139	240	NBEAL1	NBEAL1_exon25
2	203705986	203706151	165	NBEAL1	NBEAL1_exon26
2	203708631	203709231	600	NBEAL1	NBEAL1_exon27
2	203709533	203709773	240	NBEAL1	NBEAL1_exon28
2	203711085	203711325	240	NBEAL1	NBEAL1_exon29
2	203711531	203711771	240	NBEAL1	NBEAL1_exon30
2	203717539	203717899	360	NBEAL1	NBEAL1_exon31
2	203717992	203718172	180	NBEAL1	NBEAL1_exon32
2	203721916	203722156	240	NBEAL1	NBEAL1_exon33
2	203724374	203724614	240	NBEAL1	NBEAL1_exon34
2	203730609	203730789	180	NBEAL1	NBEAL1_exon35
2	203739070	203739310	240	NBEAL1	NBEAL1_exon36
2	203740140	203740380	240	NBEAL1	NBEAL1_exon37
2	203742679	203742852	173	NBEAL1	NBEAL1_exon38
2	203744858	203745026	168	NBEAL1	NBEAL1_exon39
2	203745638	203745878	240	NBEAL1	NBEAL1_exon40
2	203748064	203748304	240	NBEAL1	NBEAL1_exon41

2	203753294	203753534	240	NBEAL1	NBEAL1_exon42
2	203756213	203756388	175	NBEAL1	NBEAL1_exon43
2	203761467	203761587	120	NBEAL1	NBEAL1_exon44
2	203763223	203763392	169	NBEAL1	NBEAL1_exon45
2	203766730	203766909	179	NBEAL1	NBEAL1_exon46
2	203770231	203770396	165	NBEAL1	NBEAL1_exon47
2	203772272	203772447	175	NBEAL1	NBEAL1_exon48
2	203774476	203774716	240	NBEAL1	NBEAL1_exon49
2	203775617	203775784	167	NBEAL1	NBEAL1_exon50
2	203781572	203781751	179	NBEAL1	NBEAL1_exon51
2	203782088	203782328	240	NBEAL1	NBEAL1_exon52
2	203783879	203784119	240	NBEAL1	NBEAL1_exon53
2	203786432	203786672	240	NBEAL1	NBEAL1_exon54
2	203790178	203791198	1020	NBEAL1	NBEAL1_exon55
2	203791238	203791478	240		
2	203810931	203811051	120		
2	203811616	203812156	540	CYP20A1	CYP20A1_exon1
2	203818765	203818910	145	CYP20A1	CYP20A1_exon2
2	203819685	203819925	240	CYP20A1	CYP20A1_exon3
2	203824885	203825125	240	CYP20A1	CYP20A1_exon4
2	203839444	203839684	240	CYP20A1	CYP20A1_exon5
2	203845596	203845755	159	CYP20A1	CYP20A1_exon6
2	203851508	203851686	178	CYP20A1	CYP20A1_exon7
2	203852979	203853126	147	CYP20A1	CYP20A1_exon8
2	203858519	203858759	240	CYP20A1	CYP20A1_exon9
2	203862699	203862875	176	CYP20A1	CYP20A1_exon10
2	203865184	203865337	153	CYP20A1	CYP20A1_exon11
2	203869403	203869568	165	CYP20A1	CYP20A1_exon12
2	203869689	203870229	540	CYP20A1	CYP20A1_exon13
2	203872055	203872295	240	CYP20A1	CYP20A1_exon13
2	203872423	203872543	120	CYP20A1	CYP20A1_exon13
2	203872856	203873576	720	CYP20A1	CYP20A1_exon13
2	203874528	203874888	360	CYP20A1	CYP20A1_exon13
2	203877482	203877602	120	CYP20A1	CYP20A1_exon13
2	203877918	203878158	240	CYP20A1	CYP20A1_exon13
2	203878504	203878984	480	CYP20A1	CYP20A1_exon13
2	203900695	203901235	540		
2	203901308	203901428	120	ABI2	ABI2_exon1
2	203901477	203901597	120	ABI2	ABI2_exon1
2	203939807	203940047	240	ABI2	ABI2_exon2
2	203953143	203953383	240	ABI2	ABI2_exon3
2	203963977	203964146	169	ABI2	ABI2_exon4

2	203967620	203967860	240	ABI2	ABI2_exon5
2	203968565	203968805	240	ABI2	ABI2_exon6
2	203975502	203975742	240	ABI2	ABI2_exon7
2	203984213	203984376	163	ABI2	ABI2_exon8
2	203989841	203990081	240	ABI2	ABI2_exon9
2	204000093	204002433	2340	ABI2	ABI2_exon10
2	204002735	204004655	1920	ABI2	ABI2_exon10
2	204004681	204005641	960	ABI2	ABI2_exon10
2	204006535	204007015	480	RAPH1	RAPH1_exon1
2	204007032	204008232	1200	RAPH1	RAPH1_exon1
2	204008352	204012192	3840	RAPH1	RAPH1_exon1
2	204012315	204013275	960	RAPH1	RAPH1_exon1
2	204013385	204013985	600	RAPH1	RAPH1_exon1
2	204014059	204014179	120	RAPH1	RAPH1_exon1
2	204014271	204015101	830	RAPH1	RAPH1_exon1 RAPH1_exon2
2	204017786	204018026	240	RAPH1	RAPH1_exon3
2	204020866	204021106	240	RAPH1	RAPH1_exon4
2	204021669	204021838	169	RAPH1	RAPH1_exon5
2	204027364	204027539	175	RAPH1	RAPH1_exon6
2	204028355	204028595	240	RAPH1	RAPH1_exon7
2	204030453	204030606	153	RAPH1	RAPH1_exon8
2	204032814	204033054	240	RAPH1	RAPH1_exon9
2	204034175	204034415	240	RAPH1	RAPH1_exon10
2	204034774	204034933	159	RAPH1	RAPH1_exon11
2	204043164	204043321	157	RAPH1	RAPH1_exon12
2	204050002	204050163	161	RAPH1	RAPH1_exon13
2	204062503	204063103	600	RAPH1	RAPH1_exon14
2	204064147	204064320	173	RAPH1	RAPH1_exon15
2	204068170	204068350	180	RAPH1	RAPH1_exon16
2	204108031	204108211	180	RAPH1	RAPH1_exon17
2	204108569	204108809	240		
3	139388652	139389012	360	ARMC8	ARMC8_exon1
3	139411306	139411465	159	ARMC8	ARMC8_exon3
3	139423414	139423570	156	ARMC8	ARMC8_exon4
3	139424871	139425111	240	ARMC8	ARMC8_exon5
3	139425131	139425300	169	ARMC8	ARMC8_exon6
3	139430411	139430578	167	ARMC8	ARMC8_exon7
3	139436524	139436685	161	ARMC8	ARMC8_exon8
3	139438798	139438956	158	ARMC8	ARMC8_exon9
3	139438975	139439140	165	ARMC8	ARMC8_exon10
3	139440953	139441104	151	ARMC8	ARMC8_exon11
3	139443294	139443534	240	ARMC8	ARMC8_exon12

3	139446558	139448478	1920	ARMC8	ARMC8_exon13
3	139462455	139462815	360		
3	139463087	139464047	960	TXNDC6	TXNDC6_exon1
3	139465230	139465391	161	ARMC8	ARMC8_exon14
3	139465622	139465783	161	ARMC8	ARMC8_exon15
3	139468647	139468810	163	ARMC8	ARMC8_exon16
3	139471533	139471700	167	ARMC8	ARMC8_exon17
3	139474452	139474692	240	ARMC8	ARMC8_exon18
3	139475943	139476111	168	ARMC8	ARMC8_exon19
3	139485925	139486093	168	ARMC8	ARMC8_exon20
3	139490536	139490693	157	ARMC8	ARMC8_exon21
3	139492040	139492207	167	ARMC8	ARMC8_exon22
3	139497371	139498091	720	ARMC8	ARMC8_exon23
3	139498093	139499413	1320	ARMC8	ARMC8_exon23
3	139504986	139505226	240	TXNDC6	TXNDC6_exon2
3	139506361	139506601	240	TXNDC6	TXNDC6_exon3
3	139507497	139507664	167	TXNDC6	TXNDC6_exon4
3	139507889	139508050	161	TXNDC6	TXNDC6_exon5
3	139515821	139515979	158	TXNDC6	TXNDC6_exon6
3	139519636	139519792	156	TXNDC6	TXNDC6_exon7
3	139520974	139521146	172	TXNDC6	TXNDC6_exon8
3	139526358	139526507	149	TXNDC6	TXNDC6_exon9
3	139530782	139530921	139	TXNDC6	TXNDC6_exon11
3	139531305	139531732	427	TXNDC6	TXNDC6_exon12
3	139549485	139549905	420	MRAS	MRAS_exon1
3	139550213	139550333	120	MRAS	MRAS_exon2
3	139574382	139574622	240	MRAS	MRAS_exon3
3	139598811	139599051	240	MRAS	MRAS_exon4
3	139599964	139600134	170	MRAS	MRAS_exon5
3	139602024	139602184	160	MRAS	MRAS_exon6
3	139603662	139604202	540	MRAS	MRAS_exon7
3	139604308	139606108	1800	MRAS	MRAS_exon7
3	139606265	139607225	960	MRAS	MRAS_exon7
3	139607455	139607575	120		
3	139635453	139636113	660	ESYT3	ESYT3_exon1
3	139636161	139636701	540	ESYT3	ESYT3_exon1
3	139653529	139653670	141	ESYT3	ESYT3_exon2
3	139656672	139656912	240	ESYT3	ESYT3_exon3
3	139659057	139659216	159	ESYT3	ESYT3_exon4
3	139660674	139660827	153	ESYT3	ESYT3_exon5
3	139661438	139661603	165	ESYT3	ESYT3_exon6
3	139662095	139662243	148	ESYT3	ESYT3_exon7

3	139663557	139663797	240	ESYT3	ESYT3_exon8
3	139665841	139666081	240	ESYT3	ESYT3_exon9
3	139666830	139666991	161	ESYT3	ESYT3_exon10
3	139669043	139669188	145	ESYT3	ESYT3_exon11
3	139669598	139669763	165	ESYT3	ESYT3_exon12
3	139670141	139670292	151	ESYT3	ESYT3_exon13
3	139670305	139670456	151	ESYT3	ESYT3_exon14
3	139670923	139671078	155	ESYT3	ESYT3_exon15
3	139671552	139671715	163	ESYT3	ESYT3_exon16
3	139672362	139672602	240	ESYT3	ESYT3_exon17
3	139673842	139674442	600	ESYT3	ESYT3_exon18
3	139675031	139675200	169	ESYT3	ESYT3_exon19
3	139675697	139675877	180	ESYT3	ESYT3_exon20
3	139677720	139677893	173	ESYT3	ESYT3_exon21
3	139677926	139678071	145	ESYT3	ESYT3_exon22
3	139678486	139680466	1980	ESYT3	ESYT3_exon23
3	139695331	139696651	1320	CEP70	CEP70_exon1
3	139699521	139699681	160	CEP70	CEP70_exon2
3	139701609	139701786	177	CEP70	CEP70_exon3
3	139701894	139702134	240	CEP70	CEP70_exon4
3	139702219	139702459	240	CEP70	CEP70_exon5
3	139706791	139707031	240	CEP70	CEP70_exon6
3	139709936	139710109	173	CEP70	CEP70_exon7
3	139726979	139727136	157	CEP70	CEP70_exon8
3	139730736	139730856	120	CEP70	CEP70_exon9
3	139730867	139731031	164	CEP70	CEP70_exon10
3	139733998	139734147	149	CEP70	CEP70_exon11
3	139738673	139738913	240	CEP70	CEP70_exon12
3	139771819	139772059	240	CEP70	CEP70_exon13
3	139772506	139772746	240	CEP70	CEP70_exon14
3	139772759	139772924	165	CEP70	CEP70_exon15
3	139774348	139774505	157	CEP70	CEP70_exon16
3	139793350	139793521	171	CEP70	CEP70_exon17
3	139795691	139796346	655	CEP70	CEP70_exon18
3	139809878	139810478	600	FAIM	FAIM_exon1
3	139810565	139810720	155	FAIM	FAIM_exon2
3	139812432	139812612	180	FAIM	FAIM_exon3
3	139821196	139821346	150	FAIM	FAIM_exon4
3	139822884	139823124	240	FAIM	FAIM_exon5
3	139823713	139823953	240	FAIM	FAIM_exon6
3	139830590	139830735	145	FAIM	FAIM_exon7
3	139834451	139835411	960	FAIM	FAIM_exon8

6	12825279	12825999	720	PHACTR1	PHACTR1_exon1
6	12826870	12827110	240	PHACTR1	PHACTR1_exon2
6	12857874	12857994	120	PHACTR1	PHACTR1_exon3
6	13161544	13161784	240	PHACTR1	PHACTR1_exon4
6	13268380	13268541	161	PHACTR1	PHACTR1_exon5
6	13290692	13290932	240	PHACTR1	PHACTR1_exon6
6	13314005	13314365	360	PHACTR1	PHACTR1_exon7
6	13335969	13336269	300	PHACTR1	PHACTR1_exon8
6	13338205	13338445	240	PHACTR1	PHACTR1_exon9
6	13381023	13381171	148	PHACTR1	PHACTR1_exon10
6	13386433	13386584	151	PHACTR1	PHACTR1_exon11
6	13391582	13391822	240	PHACTR1	PHACTR1_exon12
6	13394314	13394473	159	PHACTR1	PHACTR1_exon13
6	13395219	13396059	840	PHACTR1	PHACTR1_exon14
6	31647557	31648196	639	LTA	LTA_exon1-2
6	31648509	31648629	120	LTA	LTA_exon3
6	31648649	31648822	173	LTA	LTA_exon4
6	31649007	31649787	780	LTA	LTA_exon5
6	31649850	31650630	780	LTA	LTA_exon5
6	151228279	151228519	240	MTHFD1L	MTHFD1L_exon1
6	151228571	151228691	120	MTHFD1L	MTHFD1L_exon1
6	151228767	151228887	120	MTHFD1L	MTHFD1L_exon1
6	151238878	151239041	163	MTHFD1L	MTHFD1L_exon2
6	151240414	151240701	287	MTHFD1L	MTHFD1L_exon3 MTHFD1L_exon4
6	151245532	151245772	240	MTHFD1L	MTHFD1L_exon5
6	151248426	151248597	171	MTHFD1L	MTHFD1L_exon6
6	151250621	151250801	180	MTHFD1L	MTHFD1L_exon7
6	151268445	151268621	176	MTHFD1L	MTHFD1L_exon8
6	151281367	151281533	166	MTHFD1L	MTHFD1L_exon9
6	151284997	151285166	169	MTHFD1L	MTHFD1L_exon10
6	151288916	151289156	240	MTHFD1L	MTHFD1L_exon11
6	151299580	151299820	240	MTHFD1L	MTHFD1L_exon12
6	151301478	151301621	143	MTHFD1L	MTHFD1L_exon13
6	151307280	151307454	174	MTHFD1L	MTHFD1L_exon14
6	151308253	151308410	157	MTHFD1L	MTHFD1L_exon15
6	151311824	151311995	171	MTHFD1L	MTHFD1L_exon16
6	151318820	151318940	120	MTHFD1L	MTHFD1L_exon17
6	151323053	151323293	240	MTHFD1L	MTHFD1L_exon18
6	151327753	151327908	155	MTHFD1L	MTHFD1L_exon19
6	151334742	151334918	176	MTHFD1L	MTHFD1L_exon20
6	151372596	151372836	240	MTHFD1L	MTHFD1L_exon21
6	151376557	151376698	141	MTHFD1L	MTHFD1L_exon22

6	151377672	151377843	171	MTHFD1L	MTHFD1L_exon23
6	151378312	151378552	240	MTHFD1L	MTHFD1L_exon24
6	151397287	151397461	174	MTHFD1L	MTHFD1L_exon25
6	151399749	151399989	240	MTHFD1L	MTHFD1L_exon26
6	151455235	151455475	240	MTHFD1L	MTHFD1L_exon27
6	151464304	151465264	960	MTHFD1L	MTHFD1L_exon28
7	12692500	12692980	480		
7	12693043	12693163	120	ARL4A	ARL4A_exon1
7	12693441	12693921	480	ARL4A	ARL4A_exon2
7	12694287	12696387	2100	ARL4A	ARL4A_exon3
7	12696448	12697528	1080	ARL4A	ARL4A_exon3
7	122879272	122880231	959	IQUB	IQUB_exon1
7	122884642	122884882	240	IQUB	IQUB_exon2
7	122888590	122888950	360	IQUB	IQUB_exon3
7	122892090	122892330	240	IQUB	IQUB_exon4
7	122896468	122896648	180	IQUB	IQUB_exon5
7	122907051	122907291	240	IQUB	IQUB_exon6
7	122923970	122924210	240	IQUB	IQUB_exon7
7	122929843	122930083	240	IQUB	IQUB_exon8
7	122930199	122930439	240	IQUB	IQUB_exon9
7	122930451	122930691	240	IQUB	IQUB_exon10
7	122937137	122937377	240	IQUB	IQUB_exon11
7	122939193	122939673	480	IQUB	IQUB_exon12
7	122961730	122961910	180	IQUB	IQUB_exon13
8	19840363	19841323	960	LPL	LPL_exon1
8	19849930	19850170	240	LPL	LPL_exon2
8	19853528	19853768	240	LPL	LPL_exon3
8	19855067	19855243	176	LPL	LPL_exon4
8	19855906	19856146	240	LPL	LPL_exon5
8	19857572	19857932	360	LPL	LPL_exon6
8	19860990	19861230	240	LPL	LPL_exon7
8	19862662	19862902	240	LPL	LPL_exon8
8	19863870	19864043	173	LPL	LPL_exon9
8	19867064	19869584	2520	LPL	LPL_exon10
9	21957197	21957617	420		
9	21957871	21957991	120	CDKN2A	CDKN2A_exon1
9	21958020	21958260	240	CDKN2A	CDKN2A_exon1
9	21960873	21961233	360	CDKN2A	CDKN2A_exon2
9	21964359	21965079	720	CDKN2A	CDKN2A_exon3
9	21984076	21984496	420	CDKN2A	CDKN2A_exon4
9	21984550	21985210	660	CDKN2BAS	CDKN2BAS_exon1
9	21992351	21992891	540		

9	21992946	21993906	960	CDKN2B	CDKN2B_exon1
9	21994154	21995114	960	CDKN2B	CDKN2B_exon1
9	21995153	21996293	1140	CDKN2B	CDKN2B_exon1
9	21998642	21999842	1200	CDKN2B	CDKN2B_exon2
9	22019391	22019631	240	CDKN2BAS	CDKN2BAS_exon2
9	22022620	22022920	300	CDKN2BAS	CDKN2BAS_exon3
9	22036700	22036880	180	CDKN2BAS	CDKN2BAS_exon5
9	22039045	22039285	240	CDKN2BAS	CDKN2BAS_exon6
9	22048337	22048577	240	CDKN2BAS	CDKN2BAS_exon8
9	22051909	22052066	157	CDKN2BAS	CDKN2BAS_exon9
9	22053900	22054057	157	CDKN2BAS	CDKN2BAS_exon10
9	22055623	22055791	168	CDKN2BAS	CDKN2BAS_exon11
9	22087222	22087395	173	CDKN2BAS	CDKN2BAS_exon14
9	22103610	22103850	240	CDKN2BAS	CDKN2BAS_exon16
9	22108583	22108823	240	CDKN2BAS	CDKN2BAS_exon17
9	22110183	22110423	240	CDKN2BAS	CDKN2BAS_exon18
9	22110614	22110734	120	CDKN2BAS	CDKN2BAS_exon19
9	22111081	22111321	240	CDKN2BAS	CDKN2BAS_exon19
9	106582574	106584914	2340	ABCA1	ABCA1_exon1
9	106584952	106586272	1320	ABCA1	ABCA1_exon1
9	106586299	106586599	300	ABCA1	ABCA1_exon1
9	106587438	106587798	360	ABCA1	ABCA1_exon2
9	106588361	106588528	167	ABCA1	ABCA1_exon3
9	106588939	106589111	172	ABCA1	ABCA1_exon4
9	106589968	106590208	240	ABCA1	ABCA1_exon5
9	106590477	106590717	240	ABCA1	ABCA1_exon6
9	106592989	106593162	173	ABCA1	ABCA1_exon7
9	106593992	106594143	151	ABCA1	ABCA1_exon8
9	106594827	106595067	240	ABCA1	ABCA1_exon9
9	106595216	106595456	240	ABCA1	ABCA1_exon10
9	106596429	106596669	240	ABCA1	ABCA1_exon11
9	106598106	106598346	240	ABCA1	ABCA1_exon12
9	106598378	106598556	178	ABCA1	ABCA1_exon13
9	106600490	106600730	240	ABCA1	ABCA1_exon14
9	106601884	106602124	240	ABCA1	ABCA1_exon15
9	106602569	106602726	157	ABCA1	ABCA1_exon16
9	106604121	106604294	173	ABCA1	ABCA1_exon17
9	106605332	106605469	137	ABCA1	ABCA1_exon18
9	106606690	106606857	167	ABCA1	ABCA1_exon19
9	106608316	106608556	240	ABCA1	ABCA1_exon20
9	106611531	106611700	169	ABCA1	ABCA1_exon21
9	106612843	106613083	240	ABCA1	ABCA1_exon22

9	106614629	106614869	240	ABCA1	ABCA1_exon23
9	106616187	106616364	177	ABCA1	ABCA1_exon24
9	106616479	106616624	145	ABCA1	ABCA1_exon25
9	106618225	106618465	240	ABCA1	ABCA1_exon26
9	106619390	106619547	157	ABCA1	ABCA1_exon27
9	106620754	106620994	240	ABCA1	ABCA1_exon28
9	106621635	106621875	240	ABCA1	ABCA1_exon29
9	106621979	106622219	240	ABCA1	ABCA1_exon30
9	106623421	106623661	240	ABCA1	ABCA1_exon31
9	106624562	106624802	240	ABCA1	ABCA1_exon32
9	106626534	106626711	177	ABCA1	ABCA1_exon33
9	106627766	106628006	240	ABCA1	ABCA1_exon34
9	106629039	106629279	240	ABCA1	ABCA1_exon35
9	106631008	106631248	240	ABCA1	ABCA1_exon36
9	106632994	106633234	240	ABCA1	ABCA1_exon37
9	106633705	106633945	240	ABCA1	ABCA1_exon38
9	106634653	106634893	240	ABCA1	ABCA1_exon39
9	106639049	106639228	179	ABCA1	ABCA1_exon40
9	106639478	106639718	240	ABCA1	ABCA1_exon41
9	106642320	106642620	300	ABCA1	ABCA1_exon42
9	106647540	106647707	167	ABCA1	ABCA1_exon43
9	106660591	106660831	240	ABCA1	ABCA1_exon44
9	106663720	106663960	240	ABCA1	ABCA1_exon45
9	106685109	106685288	179	ABCA1	ABCA1_exon46
9	106686478	106686718	240	ABCA1	ABCA1_exon47
9	106691166	106691333	167	ABCA1	ABCA1_exon48
9	106705673	106705913	240	ABCA1	ABCA1_exon49
9	106729985	106730525	540	ABCA1	ABCA1_exon50
9	106730597	106730777	180		
10	44185093	44188813	3720	CXCL12	CXCL12_exon1
10	44191338	44191516	178	CXCL12	CXCL12_exon2
10	44192505	44194185	1680	CXCL12	CXCL12_exon3
10	44196185	44196364	179	CXCL12	CXCL12_exon4
10	44200657	44201077	420		
11	116211157	116212357	1200	APOA1	APOA1_exon1
11	116212884	116213124	240	APOA1	APOA1_exon2
11	116213225	116213376	151	APOA1	APOA1_exon3
11	116213474	116214093	619	APOA1	APOA1_exon4
12	110327593	110328013	420		
12	110328087	110328207	120	SH2B3	SH2B3_exon1
12	110328241	110328361	120	SH2B3	SH2B3_exon1
12	110340435	110340675	240	SH2B3	SH2B3_exon2

12	110340716	110341076	360	SH2B3	SH2B3_exon2
12	110368904	110369075	171	SH2B3	SH2B3_exon3
12	110369090	110369256	166	SH2B3	SH2B3_exon4
12	110369274	110369441	167	SH2B3	SH2B3_exon5
12	110369503	110369743	240	SH2B3	SH2B3_exon6
12	110369807	110370047	240	SH2B3	SH2B3_exon7
12	110370120	110372100	1980	SH2B3	SH2B3_exon8
12	110372446	110374366	1920	SH2B3	SH2B3_exon8
12	110374477	110374597	120	ATXN2	ATXN2_exon1
12	110374652	110375072	420	ATXN2	ATXN2_exon1
12	110375827	110376067	240	ATXN2	ATXN2_exon2
12	110378208	110378448	240	ATXN2	ATXN2_exon3
12	110379352	110379592	240	ATXN2	ATXN2_exon4
12	110386801	110386948	147	ATXN2	ATXN2_exon5
12	110392240	110392480	240	ATXN2	ATXN2_exon6
12	110392716	110392956	240	ATXN2	ATXN2_exon7
12	110407411	110407562	151	ATXN2	ATXN2_exon8
12	110407855	110408095	240	ATXN2	ATXN2_exon9
12	110408902	110409054	152	ATXN2	ATXN2_exon10
12	110410634	110410994	360	ATXN2	ATXN2_exon11
12	110431692	110431847	155	ATXN2	ATXN2_exon12
12	110432043	110432217	174	ATXN2	ATXN2_exon13
12	110432549	110432789	240	ATXN2	ATXN2_exon14
12	110435514	110435754	240	ATXN2	ATXN2_exon15
12	110438324	110438564	240	ATXN2	ATXN2_exon16
12	110440404	110440644	240	ATXN2	ATXN2_exon17
12	110442043	110442283	240	ATXN2	ATXN2_exon18
12	110443030	110443196	166	ATXN2	ATXN2_exon19
12	110447320	110447560	240	ATXN2	ATXN2_exon20
12	110474421	110474661	240	ATXN2	ATXN2_exon21
12	110475049	110475205	156	ATXN2	ATXN2_exon22
12	110476298	110476448	150	ATXN2	ATXN2_exon23
12	110520932	110521112	180	ATXN2	ATXN2_exon25
12	110521378	110521498	120	ATXN2	ATXN2_exon25
12	110521624	110522404	780	ATXN2	ATXN2_exon25
12	110564243	110566760	2517	BRAP	BRAP_exon1
12	110572090	110572262	172	BRAP	BRAP_exon2
12	110577714	110577879	165	BRAP	BRAP_exon3
12	110580889	110581064	175	BRAP	BRAP_exon4
12	110581342	110581582	240	BRAP	BRAP_exon5
12	110582744	110582902	158	BRAP	BRAP_exon6
12	110587779	110588019	240	BRAP	BRAP_exon7

12	110594815	110594992	177	BRAP	BRAP_exon8
12	110601311	110601551	240	BRAP	BRAP_exon9
12	110603802	110604042	240	BRAP	BRAP_exon10
12	110605292	110605532	240	BRAP	BRAP_exon11
12	110607684	110607984	300	BRAP	BRAP_exon12
12	110608029	110608509	480	BRAP	BRAP_exon12 ACAD10_exon1
12	110614862	110615102	240	ACAD10	ACAD10_exon2
12	110624302	110624542	240	ACAD10	ACAD10_exon3
12	110627901	110628141	240	ACAD10	ACAD10_exon4
12	110631671	110631911	240	ACAD10	ACAD10_exon5
12	110634643	110634883	240	ACAD10	ACAD10_exon7
12	110637957	110638197	240	ACAD10	ACAD10_exon8
12	110643813	110643968	155	ACAD10	ACAD10_exon9
12	110650118	110650358	240	ACAD10	ACAD10_exon10
12	110651947	110652187	240	ACAD10	ACAD10_exon11
12	110656061	110656301	240	ACAD10	ACAD10_exon12
12	110658983	110659223	240	ACAD10	ACAD10_exon13
12	110666789	110667269	480	ACAD10	ACAD10_exon14
12	110668280	110668520	240	ACAD10	ACAD10_exon15
12	110669183	110669423	240	ACAD10	ACAD10_exon16
12	110669443	110669608	165	ACAD10	ACAD10_exon17
12	110670462	110670702	240	ACAD10	ACAD10_exon18
12	110671184	110671544	360	ACAD10	ACAD10_exon19
12	110675909	110676149	240	ACAD10	ACAD10_exon20
12	110677813	110677972	159	ACAD10	ACAD10_exon21
12	110678495	110679815	1320	ACAD10	ACAD10_exon22
12	110688667	110689027	360	ALDH2	ALDH2_exon1
12	110689055	110689295	240	ALDH2	ALDH2_exon1
12	110704069	110704242	173	ALDH2	ALDH2_exon2
12	110705294	110705534	240	ALDH2	ALDH2_exon3
12	110707412	110707572	160	ALDH2	ALDH2_exon4
12	110711976	110712152	176	ALDH2	ALDH2_exon5
12	110712564	110712804	240	ALDH2	ALDH2_exon6
12	110713460	110713637	177	ALDH2	ALDH2_exon7
12	110714212	110714383	171	ALDH2	ALDH2_exon8
12	110714756	110714996	240	ALDH2	ALDH2_exon9
12	110720226	110720466	240	ALDH2	ALDH2_exon10
12	110722050	110722290	240	ALDH2	ALDH2_exon11
12	110726013	110726190	177	ALDH2	ALDH2_exon12
12	110731669	110732209	540	ALDH2	ALDH2_exon13
12	110732526	110732706	180		
12	110764152	110764392	240		

12	110764551	110764671	120	MAPKAPK5	MAPKAPK5_exon1
12	110764723	110764963	240	MAPKAPK5	MAPKAPK5_exon1
12	110787394	110787551	157	MAPKAPK5	MAPKAPK5_exon2
12	110788300	110788458	158	MAPKAPK5	MAPKAPK5_exon3
12	110789722	110789891	169	MAPKAPK5	MAPKAPK5_exon4
12	110790905	110791080	175	MAPKAPK5	MAPKAPK5_exon5
12	110792419	110792584	165	MAPKAPK5	MAPKAPK5_exon6
12	110793234	110793402	168	MAPKAPK5	MAPKAPK5_exon7
12	110802592	110802753	161	MAPKAPK5	MAPKAPK5_exon8
12	110805740	110805980	240	MAPKAPK5	MAPKAPK5_exon9
12	110808042	110808282	240	MAPKAPK5	MAPKAPK5_exon10
12	110810619	110810859	240	MAPKAPK5	MAPKAPK5_exon11
12	110811011	110811191	180	MAPKAPK5	MAPKAPK5_exon12
12	110812191	110812364	173	MAPKAPK5	MAPKAPK5_exon13
12	110815149	110815269	120	MAPKAPK5	MAPKAPK5_exon14
12	110815375	110815855	480	MAPKAPK5	MAPKAPK5_exon14
12	110934994	110935834	840	ERP29	ERP29_exon1
12	110941891	110942131	240	ERP29	ERP29_exon2
12	110944281	110945961	1680	ERP29	ERP29_exon3
12	110948412	110949492	1080	C12orf30	C12orf30_exon1
12	110949516	110950356	840	C12orf30	C12orf30_exon1
12	110950423	110950783	360	C12orf30	C12orf30_exon1
12	110950861	110951881	1020	C12orf30	C12orf30_exon1
12	110955372	110955612	240	C12orf30	C12orf30_exon2
12	110961382	110961557	175	C12orf30	C12orf30_exon3
12	110962631	110962800	169	C12orf30	C12orf30_exon4
12	110964181	110964334	153	C12orf30	C12orf30_exon5
12	110965215	110965455	240	C12orf30	C12orf30_exon6
12	110965752	110966112	360	C12orf30	C12orf30_exon7
12	110969793	110970033	240	C12orf30	C12orf30_exon8
12	110970433	110970673	240	C12orf30	C12orf30_exon9
12	110975708	110975878	170	C12orf30	C12orf30_exon10
12	110976544	110976784	240	C12orf30	C12orf30_exon11
12	110982418	110982583	165	C12orf30	C12orf30_exon12
12	110983350	110983590	240	C12orf30	C12orf30_exon13
12	110991033	110991210	177	C12orf30	C12orf30_exon14
12	110994045	110994285	240	C12orf30	C12orf30_exon15
12	110996823	110996988	165	C12orf30	C12orf30_exon16
12	110997831	110998007	176	C12orf30	C12orf30_exon17
12	111000333	111000492	159	C12orf30	C12orf30_exon18
12	111000786	111000960	174	C12orf30	C12orf30_exon19
12	111003204	111003361	157	C12orf30	C12orf30_exon20

12	111009838	111010017	179	C12orf30	C12orf30_exon21
12	111012861	111013101	240	C12orf30	C12orf30_exon22
12	111015198	111015361	163	C12orf30	C12orf30_exon23
12	111030861	111031421	560	C12orf30	C12orf30_exon24
12	111047227	111048187	960	TRAFD1	TRAFD1_exon1
12	111052651	111052800	149	TRAFD1	TRAFD1_exon2
12	111056871	111057111	240	TRAFD1	TRAFD1_exon3
12	111057152	111057299	147	TRAFD1	TRAFD1_exon4
12	111062967	111063447	480	TRAFD1	TRAFD1_exon5
12	111064258	111064498	240	TRAFD1	TRAFD1_exon6
12	111067730	111067889	159	TRAFD1	TRAFD1_exon7
12	111070255	111070495	240	TRAFD1	TRAFD1_exon8
12	111071877	111072117	240	TRAFD1	TRAFD1_exon9
12	111073976	111074336	360	TRAFD1	TRAFD1_exon10
12	111074570	111074727	157	TRAFD1	TRAFD1_exon11
12	111074885	111076325	1440	TRAFD1	TRAFD1_exon12
12	111081944	111082604	660	C12orf51	C12orf51_exon1
12	111082654	111084754	2100	C12orf51	C12orf51_exon1
12	111085219	111085459	240	C12orf51	C12orf51_exon2
12	111085705	111085945	240	C12orf51	C12orf51_exon3
12	111086258	111086498	240	C12orf51	C12orf51_exon4
12	111089493	111089733	240	C12orf51	C12orf51_exon5
12	111089965	111090137	172	C12orf51	C12orf51_exon6
12	111091646	111091886	240	C12orf51	C12orf51_exon7
12	111092488	111092668	180	C12orf51	C12orf51_exon8
12	111093256	111093496	240	C12orf51	C12orf51_exon9
12	111094832	111095072	240	C12orf51	C12orf51_exon10
12	111097863	111098103	240	C12orf51	C12orf51_exon11
12	111098748	111098921	173	C12orf51	C12orf51_exon12
12	111101072	111101312	240	C12orf51	C12orf51_exon13
12	111101351	111101591	240	C12orf51	C12orf51_exon14
12	111105228	111105468	240	C12orf51	C12orf51_exon15
12	111106313	111106493	180	C12orf51	C12orf51_exon16
12	111106550	111107390	840	C12orf51	C12orf51_exon16
12	111107448	111107688	240	C12orf51	C12orf51_exon16
12	111112941	111113181	240	C12orf51	C12orf51_exon17
12	111114728	111114968	240	C12orf51	C12orf51_exon18
12	111115192	111115432	240	C12orf51	C12orf51_exon19
12	111115637	111115877	240	C12orf51	C12orf51_exon20
12	111117041	111117281	240	C12orf51	C12orf51_exon21
12	111122784	111123024	240	C12orf51	C12orf51_exon22
12	111125770	111126010	240	C12orf51	C12orf51_exon23

12	111126620	111126860	240	C12orf51	C12orf51_exon24
12	111130003	111130243	240	C12orf51	C12orf51_exon25
12	111130709	111130829	120	C12orf51	C12orf51_exon26
12	111132199	111132439	240	C12orf51	C12orf51_exon27
12	111134634	111134874	240	C12orf51	C12orf51_exon28
12	111138437	111138597	160	C12orf51	C12orf51_exon29
12	111138913	111139153	240	C12orf51	C12orf51_exon30
12	111139180	111139420	240	C12orf51	C12orf51_exon31
12	111141537	111141709	172	C12orf51	C12orf51_exon32
12	111148797	111148975	178	C12orf51	C12orf51_exon33
12	111150239	111150479	240	C12orf51	C12orf51_exon34
12	111150795	111151035	240	C12orf51	C12orf51_exon35
12	111151855	111152095	240	C12orf51	C12orf51_exon36
12	111152820	111153060	240	C12orf51	C12orf51_exon37
12	111153680	111153920	240	C12orf51	C12orf51_exon38
12	111155150	111155311	161	C12orf51	C12orf51_exon39
12	111157237	111157477	240	C12orf51	C12orf51_exon40
12	111157650	111158010	360	C12orf51	C12orf51_exon41
12	111159087	111159327	240	C12orf51	C12orf51_exon42
12	111161210	111161450	240	C12orf51	C12orf51_exon43
12	111162020	111162260	240	C12orf51	C12orf51_exon44
12	111165502	111165742	240	C12orf51	C12orf51_exon45
12	111165756	111165996	240	C12orf51	C12orf51_exon46
12	111166007	111166247	240	C12orf51	C12orf51_exon47
12	111169054	111169294	240	C12orf51	C12orf51_exon48
12	111169609	111169774	165	C12orf51	C12orf51_exon49
12	111170218	111170391	173	C12orf51	C12orf51_exon50
12	111170482	111170722	240	C12orf51	C12orf51_exon51
12	111172326	111172566	240	C12orf51	C12orf51_exon52
12	111173118	111173358	240	C12orf51	C12orf51_exon53
12	111174557	111174797	240	C12orf51	C12orf51_exon54
12	111176198	111176378	180	C12orf51	C12orf51_exon55
12	111178485	111178725	240	C12orf51	C12orf51_exon56
12	111180646	111180817	171	C12orf51	C12orf51_exon57
12	111181254	111181494	240	C12orf51	C12orf51_exon58
12	111183433	111183673	240	C12orf51	C12orf51_exon59
12	111186214	111186454	240	C12orf51	C12orf51_exon60
12	111187301	111187541	240	C12orf51	C12orf51_exon61
12	111188030	111188203	173	C12orf51	C12orf51_exon62
12	111189055	111189210	155	C12orf51	C12orf51_exon63
12	111191842	111192082	240	C12orf51	C12orf51_exon64
12	111192409	111192649	240	C12orf51	C12orf51_exon65

12	111195791	111196031	240	C12orf51	C12orf51_exon66
12	111201373	111201613	240	C12orf51	C12orf51_exon67
12	111205272	111205512	240	C12orf51	C12orf51_exon68
12	111228236	111228836	600	C12orf51	C12orf51_exon69
12	111326943	111327603	660	RPL6	RPL6_exon1
12	111328011	111328251	240	RPL6	RPL6_exon2
12	111328431	111328576	145	RPL6	RPL6_exon3
12	111328884	111329124	240	RPL6	RPL6_exon4
12	111330390	111330559	169	RPL6	RPL6_exon5
12	111330604	111330844	240	RPL6	RPL6_exon6
12	111331575	111331875	300	RPL6	RPL6_exon7
12	111340833	111341313	480	PTPN11	PTPN11_exon1
12	111368403	111368643	240	PTPN11	PTPN11_exon2
12	111372481	111372721	240	PTPN11	PTPN11_exon3
12	111375357	111375597	240	PTPN11	PTPN11_exon4
12	111376718	111376897	179	PTPN11	PTPN11_exon5
12	111378104	111378281	177	PTPN11	PTPN11_exon6
12	111399796	111399956	160	PTPN11	PTPN11_exon8
12	111400002	111400242	240	PTPN11	PTPN11_exon9
12	111404205	111404445	240	PTPN11	PTPN11_exon10
12	111408618	111408858	240	PTPN11	PTPN11_exon11
12	111410585	111410739	154	PTPN11	PTPN11_exon12
12	111411165	111411405	240	PTPN11	PTPN11_exon13
12	111424297	111424474	177	PTPN11	PTPN11_exon14
12	111426846	111427017	171	PTPN11	PTPN11_exon15
12	111427988	111428288	300	PTPN11	PTPN11_exon16
12	111428387	111428747	360	PTPN11	PTPN11_exon16
12	111429259	111432379	3120	PTPN11	PTPN11_exon16
13	30207329	30207569	240		
13	30207589	30207829	240	ALOX5AP	ALOX5AP_exon1
13	30216160	30216330	170	ALOX5AP	ALOX5AP_exon2
13	30224145	30224300	155	ALOX5AP	ALOX5AP_exon3
13	30228040	30228201	161	ALOX5AP	ALOX5AP_exon4
13	30236074	30236674	600	ALOX5AP	ALOX5AP_exon5
13	30236949	30237069	120		
15	56510928	56511648	720	LIPC	LIPC_exon1
15	56617795	56618035	240	LIPC	LIPC_exon2
15	56621246	56621486	240	LIPC	LIPC_exon3
15	56621993	56622172	179	LIPC	LIPC_exon4
15	56625228	56625468	240	LIPC	LIPC_exon5
15	56627761	56628121	360	LIPC	LIPC_exon6
15	56640382	56640502	120	LIPC	LIPC_exon7

15	56642984	56643224	240	LIPC	LIPC_exon8
15	56648202	56648802	600	LIPC	LIPC_exon9
15	58426092	58426512	420		
15	58426711	58427191	480	ANXA2	ANXA2_exon1
15	58428506	58428746	240	ANXA2	ANXA2_exon2
15	58430637	58430786	149	ANXA2	ANXA2_exon3
15	58431177	58431345	168	ANXA2	ANXA2_exon4
15	58431836	58432003	167	ANXA2	ANXA2_exon5
15	58433598	58433748	150	ANXA2	ANXA2_exon6
15	58435368	58435528	160	ANXA2	ANXA2_exon7
15	58436598	58436763	165	ANXA2	ANXA2_exon8
15	58440399	58440576	177	ANXA2	ANXA2_exon9
15	58443882	58444049	167	ANXA2	ANXA2_exon10
15	58461796	58461966	170	ANXA2	ANXA2_exon11
15	58465472	58465621	149	ANXA2	ANXA2_exon12
15	58469668	58469841	173	ANXA2	ANXA2_exon13
15	58476707	58476868	161	ANXA2	ANXA2_exon14
15	58477329	58477538	209	ANXA2	ANXA2_exon15
15	58477586	58477826	240		
15	58477867	58477987	120		
15	65144737	65144857	120		
15	65145078	65145318	240	SMAD3	SMAD3_exon1
15	65145524	65145764	240	SMAD3	SMAD3_exon1
15	65205061	65205421	360	SMAD3	SMAD3_exon2
15	65217371	65217531	160	SMAD3	SMAD3_exon3
15	65244262	65244502	240	SMAD3	SMAD3_exon4
15	65244589	65244829	240	SMAD3	SMAD3_exon5
15	65245495	65245634	139	SMAD3	SMAD3_exon6
15	65246128	65246285	157	SMAD3	SMAD3_exon7
15	65249897	65250042	145	SMAD3	SMAD3_exon8
15	65260618	65260858	240	SMAD3	SMAD3_exon9
15	65264066	65264306	240	SMAD3	SMAD3_exon10
15	65266708	65266948	240	SMAD3	SMAD3_exon11
15	65269750	65270410	660	SMAD3	SMAD3_exon12
15	65270488	65275108	4620	SMAD3	SMAD3_exon12
16	55553161	55553521	360	CETP	CETP_exon1
16	55554390	55554567	177	CETP	CETP_exon2
16	55560745	55561135	390	CETP	CETP_exon3 CETP_exon4
16	55561287	55561451	164	CETP	CETP_exon5
16	55562402	55562557	155	CETP	CETP_exon6
16	55562687	55562838	151	CETP	CETP_exon7
16	55563366	55563532	166	CETP	CETP_exon8

16	55564712	55564952	240	CETP	CETP_exon9
16	55566465	55566610	145	CETP	CETP_exon10
16	55569465	55569705	240	CETP	CETP_exon11
16	55572526	55572680	154	CETP	CETP_exon12
16	55573007	55573144	137	CETP	CETP_exon13
16	55573534	55573691	157	CETP	CETP_exon14
16	55574699	55574862	163	CETP	CETP_exon15
16	55574943	55575723	780	CETP	CETP_exon16
16	66530919	66531939	1020	LCAT	LCAT_exon1
16	66533758	66533998	240	LCAT	LCAT_exon2
16	66534037	66534205	168	LCAT	LCAT_exon3
16	66534232	66534410	178	LCAT	LCAT_exon4
16	66534417	66534657	240	LCAT	LCAT_exon5
16	66535323	66536043	720	LCAT	LCAT_exon6
19	11060503	11061343	840	LDLR	LDLR_exon1
19	11071839	11072019	180	LDLR	LDLR_exon2
19	11074280	11074520	240	LDLR	LDLR_exon3
19	11076845	11077325	480	LDLR	LDLR_exon4
19	11078181	11078421	240	LDLR	LDLR_exon5
19	11079008	11079248	240	LDLR	LDLR_exon6
19	11082296	11082476	180	LDLR	LDLR_exon7
19	11083131	11083371	240	LDLR	LDLR_exon8
19	11084918	11085158	240	LDLR	LDLR_exon9
19	11085203	11085443	240	LDLR	LDLR_exon10
19	11087738	11087917	179	LDLR	LDLR_exon11
19	11088483	11088723	240	LDLR	LDLR_exon12
19	11091717	11091957	240	LDLR	LDLR_exon13
19	11092001	11092241	240	LDLR	LDLR_exon14
19	11094814	11095054	240	LDLR	LDLR_exon15
19	11099642	11099801	159	LDLR	LDLR_exon16
19	11101146	11101386	240	LDLR	LDLR_exon17
19	11102933	11104073	1140	LDLR	LDLR_exon18
19	11104924	11105164	240	LDLR	LDLR_exon18
19	11105255	11105495	240	LDLR	LDLR_exon18
19	50100555	50100982	427	APOE	APOE_exon1
19	50101654	50101807	153	APOE	APOE_exon2
19	50102832	50103072	240	APOE	APOE_exon3
19	50103583	50104603	1020	APOE	APOE_exon4
21	34367189	34367549	360		
21	34367686	34367926	240	MRPS6	MRPS6_exon1 SLC5A3_exon1
21	34388974	34400674	11700	SLC5A3	SLC5A3_exon2
21	34419459	34419699	240	MRPS6	MRPS6_exon2

21	34436540	34437740	1200	MRPS6	MRPS6_exon3
21	34657922	34658342	420	KCNE2	KCNE2_exon1
21	34664584	34665604	1020	KCNE2	KCNE2_exon2
21	34669097	34669766	669	FAM165B	FAM165B_exon1
21	34673557	34673722	165	FAM165B	FAM165B_exon2
21	34679608	34679848	240	FAM165B	FAM165B_exon3
21	34682754	34682934	180	FAM165B	FAM165B_exon4
21	34683305	34683845	540	FAM165B	FAM165B_exon4
21	34740320	34741940	1620	KCNE1	KCNE1_exon1
21	34742354	34742594	240	KCNE1	KCNE1_exon1
21	34742648	34742768	120	KCNE1	KCNE1_exon1
21	34743242	34743902	660	KCNE1	KCNE1_exon1
21	34749502	34749982	480	KCNE1	KCNE1_exon2
21	34752788	34752963	175	KCNE1	KCNE1_exon3
21	34753654	34753812	158	KCNE1	KCNE1_exon4
21	34805254	34805494	240	KCNE1	KCNE1_exon5
21	34805828	34806008	180		
21	34810148	34812428	2280	RCAN1	RCAN1_exon1
21	34815625	34815865	240	RCAN1	RCAN1_exon2
21	34817670	34817910	240	RCAN1	RCAN1_exon3
21	34820800	34821160	360	RCAN1	RCAN1_exon4
21	34908410	34908650	240	RCAN1	RCAN1_exon5
21	34908892	34909072	180	RCAN1	RCAN1_exon6
21	34909151	34909811	660	RCAN1	RCAN1_exon6
22	36295655	36295835	180		
22	36295895	36296375	480	LGALS2	LGALS2_exon1
22	36296487	36296727	240	LGALS2	LGALS2_exon2
22	36297761	36297922	161	LGALS2	LGALS2_exon3
22	36305821	36306150	329	LGALS2	LGALS2_exon4

Supplementary Table 3. Per gene summary statistics of the sequencing experiment in 500 myocardial MI cases and 500 controls.

Gene name	Size of targeted sequence in bp (# of exons)	Covered sequence at 1X (%)		Mean coverage per DNA sample (X)	
		MI cases	Controls	MI cases	Controls
ABCA1	10411 (50)	100	100	68	78
ABI2	6480 (10)	100	100	68	79
ACAD10	4106 (20)	99.235	99.262	62	65
ALDH2	2400 (13)	93.82	94.025	43	46
ALOX5AP	873 (5)	100	100	60	66
ALS2CR8	5929 (15)	87.452	87.47	49	60
ANXA2	1658 (15)	100	100	56	62
APOA1	897 (4)	10.665	10.53	0.2	0.2
APOB	14121 (29)	99.012	98.92	78	91
APOE	1180 (4)	93.473	92.269	20	20
ARL4A	2956 (3)	100	100	63	74
ARMC8	3832 (22)	96.874	96.823	66	77
ATXN2	4702 (24)	99.062	98.365	53	59
BMPR2	12070 (13)	97.557	97.204	58	68
BRAP	4026 (12)	80.973	80.57	56	63
C12orf30	6102 (24)	100	100	66	77
C12orf51	15336 (69)	100	100	61	67
C1orf58	1681 (13)	98.692	98.643	45	53
CDKN2A	1253 (4)	100	100	39	41
CDKN2B	3984 (2)	100	100	58	67
CDKN2BAS	3832 (14)	69.164	69.561	26	33
CELSR2	10540 (32)	97.482	97.358	54	55
CEP70	2662 (18)	100	100	66	78
CETP	1717 (15)	95.448	95.782	50	52
CXCL12	1201 (4)	97.663	97.845	71	76
CYP20A1	10943 (13)	70.144	71.913	24	28
ERP29	1472 (3)	100	100	61	69
ESYT3	4447 (23)	100	100	64	70
FAIM	1152 (8)	98.554	97.981	51	60
FAM117B	5772 (8)	99.482	99.063	60	70
FAM165B	900 (4)	99.816	99.739	47	51
HHIPL2	2574 (9)	98.616	98.379	64	69
ICA1L	7996 (15)	96.759	96.509	54	62
IQUB	3112 (13)	98.011	98.603	53	68
KCNE1	3321 (5)	99.05	99.457	56	60
KCNE2	803 (2)	99.075	98.83	63	70
KIAA1324	7030 (21)	98.701	98.664	56	61
LCAT	1354 (6)	100	100	45	44
LDLR	5264 (18)	91.887	91.264	51	53
LGALS2	528 (4)	94.315	93.016	51	53
LIPC	1604 (9)	100	100	62	69
LPL	3747 (10)	100	100	74	85
LRP8	4507 (17)	92.207	91.509	53	59
LTA	1459 (4)	99.776	99.731	56	58
MAPKAPK5	2038 (14)	98.093	98.168	42	47
MIA3	8123 (27)	99.328	99.059	65	76
MRAS	4013 (7)	96.035	95.633	61	66
MRPS6	990 (3)	99.885	100	52	57
MTHFD1L	3598 (27)	97.099	97.161	56	63

NBEAL1	9058 (54)	99.578	99.48	67	81
NOP58	1965 (14)	96.137	96.373	54	63
PCSK9	3710 (12)	100	100	50	51
PHACTR1	2150 (14)	100	100	64	71
PSRC1	1744 (6)	89.922	90.719	44	45
PTPN11	6283 (15)	96.96	97.172	57	65
RAPH1	2769 (16)	99.476	99.151	64	74
RCAN1	2406 (6)	100	100	64	71
RPL6	954 (7)	94.636	93.555	54	59
SARS	1938 (11)	100	100	66	71
SH2B3	5405 (8)	98.698	98.151	50	53
SLC5A3	11576 (1)	69.2	69.6	26	33
SMAD3	6235 (12)	98.241	98.717	66	72
SORT1	7018 (20)	99.78	99.082	67	75
SUMO1	1078 (5)	100	99.996	55	62
TAF1A	1879 (11)	96.437	96.134	55	66
TRAFD1	2647 (12)	99.887	99.771	64	69
TXNDC6	2133 (11)	39.785	39.402	21	24
WDR12	2281 (13)	100	100	53	60

Supplementary Table 4. Variant discovery summary.

Category	Statistic
Number of high quality single nucleotide variants identified	1,852
Number of nonsense variants	6
Number of missense variants	363
Number of synonymous variants	223
Number of splice site variants (2 base pairs on either side of exon boundaries)	1
dbSNP 135 (%)	62.5 (1,157/1,852)
Non-synonymous/synonymous ratio	1.65 (369/223)
Transition/Transversion ratio	2.43 (1,312/540)

Supplementary Table 5. List of high quality single nucleotide variants identified by re-sequencing exons from 68 genes in 500 myocardial infarction cases and 500 controls, all of French-Canadian ancestry.

Gene name	Variant ID	Chr	Position (hg18)	Position (hg19)	Ref. allele	Other allele	Other allele frequency (all sequenced)	Other allele frequency (MI cases)	Oher allele frequency (Controls)	Annotation_description	Annotation_details	Variant on Illumina ExomeChip
LRP8	rs61769622	1	53483595	53711007	C	T	0.0582	0.0493	0.067	near_gene_3p_(500_bp)		N
LRP8	rs61769623	1	53483677	53711089	T	C	0.0081	0.0082	0.008	near_gene_3p_(500_bp)		N
LRP8	chr1:53483742	1	53483742	53711154	C	G	0.001	0	0.002	near_gene_3p_(500_bp)		N
LRP8	chr1:53483752	1	53483752	53711164	C	G	0.0005	0	0.001	near_gene_3p_(500_bp)		N
LRP8	rs5177	1	53484323	53711735	G	C	0.3801	0.3805	0.3797	utr_3p		N
LRP8	chr1:53484677	1	53484677	53712089	T	C	0.005	0.0062	0.0038	utr_3p		N
LRP8	chr1:53484959	1	53484959	53712371	C	T	0.0008	0	0.0016	utr_3p		N
LRP8	rs5174	1	53485315	53712727	C	T	0.3694	0.375	0.3638	missense	Arg689Gln (CGA=>CAA) [exon16]	Y
LRP8	rs3737983	1	53489004	53716416	G	A	0.4032	0.4073	0.3991	synonymous	Asp670Asp (GAC=>GAT) [exon15]	Y
LRP8	rs5173	1	53489079	53716491	T	C	0.0005	0	0.001	synonymous	Arg645Arg (AGA=>AGG) [exon15]	N
LRP8	rs2297661	1	53496553	53723965	C	G	0.0032	0.0024	0.004	intron	intron13 bp26	N
LRP8	chr1:53500768	1	53500768	53728180	T	C	0.0037	0.0053	0.002	missense	Asn442Ser (AAC=>AGC) [exon10]	Y
LRP8	rs151161222	1	53502432	53729844	C	T	0.0033	0.0045	0.0021	missense	Arg422Gln (CGA=>CAA) [exon9]	Y
LRP8	chr1:53502590	1	53502590	53730002	A	G	0.0005	0	0.001	synonymous	Ser369Ser (TCT=>TCC) [exon9]	N
LRP8	rs2297660	1	53504903	53732315	G	T	0.369	0.3704	0.3675	synonymous	Gly290Gly (GGC=>GGA) [exon8]	N
LRP8	rs75624781	1	53518908	53746320	C	T	0.0021	0	0.0043	synonymous	Ser145Ser (TCG=>TCA) [exon4]	N
LRP8	rs3820198	1	53565239	53792651	A	C	0.3469	0.3453	0.3485	missense	Asp46Glu (GAT=>GAG) [exon2]	Y
LRP8	chr1:53566833	1	53566833	53794245	C	T	0.0005	0.001	0	near_gene_5p_(2000_bp)		N
LRP8	rs72897412	1	53566846	53794258	A	C	0.0079	0.0051	0.0108	near_gene_5p_(2000_bp)		N
PCSK9	rs72658887	1	55277414	55504826	G	C	0.0014	0.0009	0.002	near_gene_5p_(2000_bp)		N
PCSK9	rs72658888	1	55277812	55505224	G	A	0.0122	0.0127	0.0116	utr_5p		N
PCSK9	rs45448095	1	55278035	55505447	C	T	0.129	0.1179	0.1402	utr_5p		N
PCSK9	rs11591147	1	55278235	55505647	G	T	0.0187	0.0196	0.0178	missense	Arg46Leu (CGT=>CTT) [exon1]	Y
PCSK9	rs28385701	1	55278239	55505651	C	T	0.012	0.0165	0.0074	synonymous	Ser47Ser (TCC=>TCT) [exon1]	N

PCSK9	rs11583680	1	55278256	55505668	C	T	0.1371	0.1313	0.1429	missense	Ala53Val (GCC=>GTC) [exon1]	Y
PCSK9	chr1:55290497	1	55290497	55517909	T	C	0.001	0	0.002	intron	intron3 bp5590	N
PCSK9	rs11800231	1	55290528	55517940	G	A	0.0411	0.0382	0.044	intron	intron3 bp5621	N
PCSK9	rs11800243	1	55290681	55518093	G	A	0.0382	0.0336	0.0429	intron	intron4 bp9	N
PCSK9	rs11800265	1	55290875	55518287	G	A	0.0373	0.0337	0.0409	intron	intron4 bp203	N
PCSK9	rs2483205	1	55290904	55518316	C	T	0.449	0.447	0.451	intron	intron4 bp232	N
PCSK9	rs148195424	1	55290962	55518374	C	T	0.0007	0	0.0014	missense	Arg237Trp (CGG=>TGG) [exon5]	N
PCSK9	rs41297883	1	55290973	55518385	C	T	0.0045	0.0037	0.0053	synonymous	Gly240Gly (GGC=>GGT) [exon5]	N
PCSK9	chr1:55291039	1	55291039	55518451	C	T	0.0007	0	0.0015	synonymous	Ser262Ser (AGC=>AGT) [exon5]	N
PCSK9	rs2495477	1	55291055	55518467	A	G	0.367	0.3726	0.3614	intron	intron5 bp3	N
PCSK9	rs509504	1	55295621	55523033	A	G	0.9892	0.9898	0.9886	synonymous	Gln342Gln (CAA=>CAG) [exon7]	N
PCSK9	rs540796	1	55296785	55524197	A	G	0.8232	0.8175	0.829	synonymous	Val460Val (GTA=>GTG) [exon9]	N
PCSK9	rs562556	1	55296825	55524237	G	A	0.8308	0.8212	0.8404	missense	Val474Ile (GTC=>ATC) [exon9]	Y
PCSK9	chr1:55297782	1	55297782	55525194	C	T	0.0005	0.001	0	synonymous	Asn513Asn (AAC=>AAT) [exon10]	N
PCSK9	rs505151	1	55301775	55529187	G	A	0.944	0.9436	0.9443	missense	Gly670Glu (GGG=>GAG) [exon12]	Y
PCSK9	rs28362287	1	55301920	55529332	C	T	0.0056	0.0039	0.0072	utr_3p		N
PCSK9	chr1:55302016	1	55302016	55529428	C	T	0.0093	0.0101	0.0084	utr_3p		N
PCSK9	rs182138201	1	55302079	55529491	C	T	0.0057	0.005	0.0064	utr_3p		N
PCSK9	chr1:55302156	1	55302156	55529568	C	T	0.0005	0	0.001	utr_3p		N
PCSK9	rs17111555	1	55302190	55529602	C	T	0.0053	0.0036	0.007	utr_3p		N
PCSK9	chr1:55302253	1	55302253	55529665	A	G	0.0032	0.0028	0.0036	utr_3p		N
PCSK9	rs13376071	1	55302259	55529671	C	T	0.005	0.0027	0.0072	utr_3p		N
PCSK9	chr1:55302286	1	55302286	55529698	T	C	0.0005	0	0.001	utr_3p		N
PCSK9	rs662145	1	55302416	55529828	C	T	0.7683	0.7581	0.7784	utr_3p		N
PCSK9	rs17111557	1	55302459	55529871	C	T	0.0046	0.0023	0.0069	utr_3p		N
PCSK9	chr1:55303021	1	55303021	55530433	C	T	0.0007	0.0015	0	utr_3p		N
PCSK9	chr1:55303087	1	55303087	55530499	A	G	0.0005	0.001	0	utr_3p		N
PCSK9	rs560784	1	55303215	55530627	T	G	0.9902	0.9918	0.9886	near_gene_3p_(500_bp)		N
PCSK9	rs9326034	1	55303252	55530664	G	A	0.0056	0.0032	0.008	near_gene_3p_(500_bp)		N
C1orf194	chr1:109457676	1	109457676	109656153	C	A	0.0069	0.009	0.0049	intron	intron1 bp102	N
KIAA1324	rs667524	1	109458469	109656946	T	C	0.011	0.0124	0.0097	synonymous	His47His (CAT=>CAC) [exon1]	N

KIAA1324	rs74920406	1	109506048	109704525	C	T	0.031	0.0302	0.0317	missense	His55Tyr (CAC=>TAC) [exon2]	Y
KIAA1324	rs678238	1	109506141	109704618	A	G	0.9929	0.9929	0.9929	missense	Ile86Val (ATC=>GTC) [exon2]	Y
KIAA1324	rs34364548	1	109516158	109714635	C	T	0.03	0.0252	0.0349	synonymous	Phe205Phe (TTC=>TTT) [exon4]	Y
KIAA1324	rs139330177	1	109529256	109727733	C	T	0.001	0.001	0.001	missense	Thr340Met (ACG=>ATG) [exon8]	Y
KIAA1324	rs139400610	1	109532373	109730850	G	A	0.0015	0.001	0.002	missense	Glu365Lys (GAG=>AAG) [exon9]	N
KIAA1324	rs138845394	1	109533321	109731798	G	A	0.0005	0.001	0	missense	Glu444Lys (GAG=>AAG) [exon10]	N
KIAA1324	chr1:109535845	1	109535845	109734322	G	A	0.0007	0.0014	0	intron	intron12 bp229	N
KIAA1324	chr1:109535854	1	109535854	109734331	G	C	0.0045	0.005	0.004	intron	intron12 bp238	N
KIAA1324	rs41279690	1	109535872	109734349	G	A	0.0048	0.004	0.0057	missense	Gly516Asp (GGT=>GAT) [exon13]	Y
KIAA1324	chr1:109535914	1	109535914	109734391	G	A	0.0005	0	0.001	missense	Gly530Asp (GGT=>GAT) [exon13]	N
KIAA1324	chr1:109536001	1	109536001	109734478	A	G	0.0029	0.0031	0.0027	missense	His559Arg (CAT=>CGT) [exon13]	N
KIAA1324	rs658779	1	109536821	109735298	T	C	0.7124	0.698	0.7268	synonymous	Gly583Gly (GGT=>GGC) [exon14]	N
KIAA1324	rs659543	1	109536939	109735416	A	C	0.7185	0.7056	0.7314	missense	Thr623Pro (ACT=>CCT) [exon14]	Y
KIAA1324	rs659659	1	109537027	109735504	T	C	0.7182	0.7098	0.7266	intron	intron14 bp8	N
KIAA1324	rs2359246	1	109538586	109737063	C	T	0.7243	0.7107	0.738	synonymous	Asn656Asn (AAC=>AAT) [exon15]	N
KIAA1324	rs2359245	1	109538613	109737090	G	A	0.7203	0.7078	0.7327	synonymous	Pro665Pro (CCG=>CCA) [exon15]	N
KIAA1324	rs149034687	1	109538616	109737093	C	G	0.0005	0	0.001	synonymous	Thr666Thr (ACC=>ACG) [exon15]	N
KIAA1324	rs2359244	1	109538655	109737132	T	C	0.7089	0.6961	0.7217	synonymous	Thr679Thr (ACT=>ACC) [exon15]	N
KIAA1324	rs2359243	1	109538695	109737172	C	T	0.7197	0.7063	0.7331	synonymous	Leu693Leu (CTG=>TTG) [exon15]	N
KIAA1324	rs61756684	1	109541651	109740128	C	G	0.0012	0.0024	0	synonymous	Val718Val (GTC=>GTG) [exon16]	N
KIAA1324	chr1:109541696	1	109541696	109740173	T	C	0.0022	0.0022	0.0022	synonymous	Ser733Ser (TCT=>TCC) [exon16]	N
KIAA1324	chr1:109542203	1	109542203	109740680	C	A	0.0005	0.001	0	missense	Asp794Glu (GAC=>GAA) [exon17]	N
KIAA1324	rs41301271	1	109542688	109741165	T	A	0.0157	0.0199	0.0114	intron	intron17 bp468	N
KIAA1324	rs913178	1	109543975	109742452	C	T	0.7547	0.7449	0.7645	intron	intron18 bp1156	N
KIAA1324	rs913179	1	109544008	109742485	G	A	0.7706	0.7628	0.7785	synonymous	Ser837Ser (TCG=>TCA) [exon19]	N
KIAA1324	chr1:109544971	1	109544971	109743448	G	A	0.0005	0	0.001	missense	Glu967Lys (GAG=>AAG) [exon21]	N
KIAA1324	rs1052878	1	109547141	109745618	T	C	0.885	0.8718	0.8982	missense	Leu1009Pro (CTA=>CCA) [exon22]	Y
KIAA1324	chr1:109547214	1	109547214	109745691	C	T	0.0006	0.001	0.0003	utr_3p		N
KIAA1324	chr1:109547322	1	109547322	109745799	C	G	0.0012	0	0.0024	utr_3p		N
KIAA1324	rs587805	1	109548583	109747060	G	A	0.9929	0.9949	0.9909	utr_3p		N
KIAA1324	chr1:109548676	1	109548676	109747153	G	C	0.0005	0	0.001	utr_3p		N

KIAA1324	rs17034539	1	109549158	109747635	C	T	0.1385	0.1348	0.1423	utr_3p		N
KIAA1324	rs17034541	1	109549342	109747819	G	C	0.001	0.002	0	utr_3p		N
KIAA1324	rs3197232	1	109550463	109748940	A	G	0.7358	0.7338	0.7379	utr_3p		N
KIAA1324	rs3197233	1	109550594	109749071	T	C	0.8829	0.8744	0.8914	utr_3p		N
KIAA1324	chr1:109550903	1	109550903	109749380	G	T	0.0098	0.0101	0.0095	utr_3p		N
KIAA1324	rs72701087	1	109551263	109749740	C	T	0.0053	0.004	0.0065	near_gene_3p_(500_bp)		N
SARS	rs71655996	1	109557709	109756186	G	A	0.0189	0.0176	0.0202	near_gene_5p_(2000_bp)		N
SARS	chr1:109557773	1	109557773	109756250	G	A	0.0011	0	0.0023	near_gene_5p_(2000_bp)		N
SARS	chr1:109557960	1	109557960	109756437	T	C	0.0263	0.0268	0.0259	near_gene_5p_(2000_bp)		N
SARS	chr1:109558047	1	109558047	109756524	G	A	0.0054	0.0039	0.0069	utr_5p		N
SARS	rs2182598	1	109568210	109766687	A	T	0.0014	0.0029	0	intron	intron2 bp17	N
SARS	chr1:109572463	1	109572463	109770940	A	T	0.0049	0.0053	0.0045	intron	intron2 bp4270	N
SARS	chr1:109572467	1	109572467	109770944	A	T	0.0022	0.0017	0.0027	intron	intron2 bp4274	N
SARS	rs683182	1	109572586	109771063	T	C	0.8164	0.8239	0.809	intron	intron3 bp9	N
SARS	rs115867281	1	109573748	109772225	C	T	0.0115	0.015	0.008	intron	intron4 bp31	N
SARS	chr1:109574974	1	109574974	109773451	T	A	0.0013	0.0004	0.0021	intron	intron4 bp1257	N
SARS	rs140717526	1	109580596	109779073	G	A	0.0093	0.0089	0.0098	missense	Gly387Glu (GGA=>GAA) [exon9]	Y
SARS	chr1:109581542	1	109581542	109780019	C	T	0.0005	0	0.0011	intron	intron1 bp24	N
SARS	rs11547492	1	109582135	109780612	C	G	0.0207	0.0216	0.0198	utr_5p		N
SARS	chr1:109582147	1	109582147	109780624	C	T	0.0015	0.002	0.001	utr_5p		N
SARS	chr1:109582400	1	109582400	109780877	T	G	0.002	0	0.0039	near_gene_3p_(500_bp)		N
SARS	rs180908904	1	109582480	109780957	C	G	0.0043	0.0027	0.0059	near_gene_3p_(500_bp)		N
SARS	chr1:109582537	1	109582537	109781014	C	G	0.0005	0.001	0	near_gene_3p_(500_bp)		N
SARS	rs191260222	1	109582581	109781058	T	C	0.0041	0.002	0.0062	near_gene_3p_(500_bp)		N
CELSR2	rs62623708	1	109594600	109793077	C	A	0.0044	0	0.0087	missense	Gln126Lys (CAG=>AAG) [exon1]	Y
CELSR2	chr1:109594832	1	109594832	109793309	T	G	0.0005	0.001	0	missense	Leu203Arg (CTG=>CGG) [exon1]	N
CELSR2	chr1:109594851	1	109594851	109793328	C	T	0.0019	0.002	0.0017	synonymous	Asp209Asp (GAC=>GAT) [exon1]	N
CELSR2	rs142745606	1	109595087	109793564	T	C	0.0012	0	0.0024	missense	Val288Ala (GTG=>GCG) [exon1]	Y
CELSR2	rs149311467	1	109595374	109793851	G	T	0.002	0.0021	0.002	missense	Ala384Ser (GCT=>TCT) [exon1]	Y
CELSR2	chr1:109595629	1	109595629	109794106	G	A	0.0005	0	0.001	missense	Glu469Lys (GAG=>AAG) [exon1]	N
CELSR2	rs41279704	1	109595646	109794123	G	C	0.0265	0.0351	0.0179	synonymous	Val474Val (GTG=>GTC) [exon1]	N

CELSR2	rs454107	1	109595775	109794252	T	C	0.9584	0.9648	0.952	synonymous	Ser517Ser (AGT=>AGC) [exon1]	N
CELSR2	rs144228553	1	109595817	109794294	C	T	0.0005	0	0.0011	synonymous	Asp531Asp (GAC=>GAT) [exon1]	N
CELSR2	chr1:109595858	1	109595858	109794335	C	G	0.0005	0	0.001	missense	Ala545Gly (GCT=>GGT) [exon1]	N
CELSR2	rs41279706	1	109596116	109794593	C	T	0.0065	0.0055	0.0075	missense	Thr631Met (ACG=>ATG) [exon1]	Y
CELSR2	chr1:109596167	1	109596167	109794644	C	A	0.0006	0.0012	0	missense	Thr648Asn (ACC=>AAC) [exon1]	N
CELSR2	rs413380	1	109596549	109795026	T	C	0.9579	0.9638	0.952	synonymous	Tyr775Tyr (TAT=>TAC) [exon1]	N
CELSR2	chr1:109596625	1	109596625	109795102	C	T	0.0005	0.001	0	synonymous	Leu801Leu (CTG=>TTG) [exon1]	N
CELSR2	rs437444	1	109597131	109795608	T	C	0.9613	0.9667	0.956	synonymous	Phe969Phe (TTT=>TTC) [exon1]	N
CELSR2	rs115856488	1	109597265	109795742	T	A	0.0036	0.004	0.0033	missense	Leu1014His (CTT=>CAT) [exon1]	N
CELSR2	rs138976507	1	109597416	109795893	T	C	0.0025	0	0.005	synonymous	Phe1064Phe (TTT=>TTC) [exon1]	N
CELSR2	rs684138	1	109602644	109801121	C	T	0.1077	0.1082	0.1072	synonymous	Thr1126Thr (ACC=>ACT) [exon2]	Y
CELSR2	rs75237799	1	109602868	109801345	C	T	0.0175	0.0141	0.0209	missense	Pro1201Leu (CCC=>CTC) [exon2]	Y
CELSR2	rs138543788	1	109603066	109801543	A	G	0.0236	0.0222	0.025	missense	His1267Arg (CAC=>CGC) [exon2]	N
CELSR2	rs115077620	1	109605220	109803697	G	A	0.0025	0	0.0049	missense	Arg1331His (CGT=>CAT) [exon3]	N
CELSR2	chr1:109605336	1	109605336	109803813	C	T	0.0006	0	0.0013	missense	Arg1370Cys (CGC=>TGC) [exon3]	N
CELSR2	chr1:109605789	1	109605789	109804266	C	A	0.0024	0.0019	0.0029	intron	intron4 bp16	N
CELSR2	chr1:109605978	1	109605978	109804455	A	G	0.0005	0.001	0	synonymous	Pro1441Pro (CCA=>CCG) [exon5]	N
CELSR2	rs66795935	1	109606406	109804883	C	G	0.0608	0.0623	0.0592	intron	intron5 bp365	N
CELSR2	rs653635	1	109607836	109806313	T	C	0.0876	0.0933	0.0819	missense	Tyr1639His (TAC=>CAC) [exon9]	Y
CELSR2	rs6698843	1	109608357	109806834	C	T	0.6555	0.6599	0.6511	synonymous	Pro1712Pro (CCC=>CCT) [exon10]	N
CELSR2	rs113593332	1	109608456	109806933	C	T	0.002	0.0021	0.002	synonymous	Gly1745Gly (GGC=>GGT) [exon10]	N
CELSR2	chr1:109608534	1	109608534	109807011	C	A	0.001	0.0017	0.0002	intron	intron10 bp24	N
CELSR2	rs6689614	1	109608622	109807099	G	A	0.5138	0.5143	0.5133	synonymous	Pro1771Pro (CCG=>CCA) [exon11]	N
CELSR2	chr1:109609431	1	109609431	109807908	A	G	0.001	0	0.002	missense	Lys1901Arg (AAG=>AGG) [exon13]	N
CELSR2	rs79762317	1	109609852	109808329	G	A	0.0128	0.0095	0.0161	intron	intron13 bp396	N
CELSR2	rs138787753	1	109609946	109808423	T	G	0.0018	0.001	0.0027	missense	Leu1932Val (TTG=>GTG) [exon14]	Y
CELSR2	rs61761209	1	109611706	109810183	C	T	0.0829	0.0839	0.0819	synonymous	Arg2009Arg (CGC=>CGT) [exon16]	N
CELSR2	chr1:109611787	1	109611787	109810264	C	T	0.0005	0.001	0	synonymous	Phe2036Phe (TTC=>TTT) [exon16]	N
CELSR2	rs2281894	1	109612067	109810544	C	A	0.1361	0.1318	0.1404	synonymous	Arg2060Arg (CGC=>CGA) [exon17]	N
CELSR2	chr1:109612191	1	109612191	109810668	G	A	0.0006	0.0013	0	missense	Val2102Met (GTG=>ATG) [exon17]	N
CELSR2	chr1:109612975	1	109612975	109811452	G	T	0.0017	0.0011	0.0022	intron	intron18 bp66	N

CELSR2	rs148006855	1	109613045	109811522	G	A	0.0026	0.0031	0.002	missense	Asp2175Asn (GAC=>AAC) [exon19]	Y
CELSR2	rs141489111	1	109613615	109812092	G	A	0.0066	0.0071	0.0062	missense	Val2287Ile (GTC=>ATC) [exon21]	Y
CELSR2	chr1:109613707	1	109613707	109812184	C	T	0.0005	0	0.0011	synonymous	Pro2317Pro (CCC=>CCT) [exon21]	N
CELSR2	chr1:109613821	1	109613821	109812298	C	G	0.0005	0	0.001	intron	intron21 bp85	N
CELSR2	rs3895559	1	109614543	109813020	G	A	0.5245	0.5309	0.518	intron	intron23 bp265	N
CELSR2	chr1:109614676	1	109614676	109813153	C	T	0.0009	0.0009	0.001	missense	Arg2472Cys (CGC=>TGC) [exon24]	N
CELSR2	chr1:109615481	1	109615481	109813958	C	G	0.0006	0.0012	0	intron	intron26 bp40	N
CELSR2	chr1:109615504	1	109615504	109813981	G	A	0.0028	0.0022	0.0035	intron	intron26 bp63	N
CELSR2	chr1:109615556	1	109615556	109814033	G	A	0.0015	0.0022	0.0008	missense	Val2568Ile (GTC=>ATC) [exon27]	N
CELSR2	rs4970834	1	109616403	109814880	C	T	0.1596	0.1566	0.1625	intron	intron28 bp536	N
CELSR2	chr1:109616559	1	109616559	109815036	C	T	0.0073	0.0065	0.008	intron	intron29 bp9	N
CELSR2	rs79868705	1	109616597	109815074	G	A	0.0386	0.0336	0.0436	intron	intron29 bp47	N
CELSR2	rs611917	1	109616775	109815252	A	G	0.2578	0.2478	0.2678	intron	intron29 bp225	N
CELSR2	rs6670347	1	109616891	109815368	T	C	0.0353	0.0307	0.04	intron	intron30 bp18	N
CELSR2	rs41279718	1	109616988	109815465	G	A	0.0037	0.0011	0.0062	synonymous	Thr2718Thr (ACG=>ACA) [exon31]	N
CELSR2	rs149569254	1	109617384	109815861	C	T	0.002	0.0013	0.0027	synonymous	Asn2804Asn (AAC=>AAT) [exon32]	N
CELSR2	chr1:109617667	1	109617667	109816144	C	T	0.0012	0.0019	0.0005	missense	Arg2866Trp (CGG=>TGG) [exon33]	N
CELSR2	rs41279720	1	109617712	109816189	C	T	0.027	0.027	0.0271	missense	Arg2881Cys (CGC=>TGC) [exon33]	N
CELSR2	rs74116311	1	109618421	109816898	C	G	0.0029	0	0.0057	utr_3p		N
CELSR2	chr1:109618653	1	109618653	109817130	C	T	0.0018	0.0019	0.0017	utr_3p		N
CELSR2	rs7528419	1	109618715	109817192	A	G	0.1731	0.1606	0.1857	utr_3p		N
CELSR2	rs11102967	1	109618768	109817245	C	T	0.7099	0.7154	0.7045	utr_3p		N
CELSR2	rs41279722	1	109618822	109817299	G	C	0.0068	0.0074	0.0063	utr_3p		N
CELSR2	rs1277917	1	109619002	109817479	G	C	0.1353	0.1317	0.1389	utr_3p		N
CELSR2	rs12740374	1	109619113	109817590	G	T	0.1607	0.1483	0.1731	utr_3p		Y
CELSR2	rs57496540	1	109619156	109817633	A	G	0.0034	0.001	0.0058	utr_3p		N
CELSR2	rs660240	1	109619361	109817838	T	C	0.8027	0.8079	0.7974	utr_3p		N
CELSR2	rs192338753	1	109619388	109817865	G	A	0.002	0.0041	0	utr_3p		N
CELSR2	rs659782	1	109619470	109817947	C	T	0.064	0.0699	0.0581	utr_3p		N
CELSR2	chr1:109619594	1	109619594	109818071	A	G	0.0015	0.002	0.001	utr_3p		N
CELSR2	rs77579579	1	109619651	109818128	C	T	0.0393	0.033	0.0455	utr_3p		N

CELSR2	rs192610782	1	109619762	109818239	A	G	0.001	0.001	0.001	utr_3p		N
CELSR2	rs658437	1	109619786	109818263	G	A	0.9959	0.9959	0.9959	utr_3p		N
CELSR2	rs658435	1	109619793	109818270	C	T	0.1013	0.1081	0.0944	utr_3p		N
CELSR2	rs629301	1	109619829	109818306	G	T	0.8065	0.8186	0.7944	utr_3p		Y
CELSR2	chr1:109619836	1	109619836	109818313	G	A	0.0005	0	0.001	utr_3p		N
CELSR2	chr1:109619978	1	109619978	109818455	C	A	0.0017	0.0014	0.002	near_gene_3p_(500_bp)		N
CELSR2	chr1:109620003	1	109620003	109818480	G	A	0.0005	0	0.001	near_gene_3p_(500_bp)		N
CELSR2	rs646776	1	109620053	109818530	C	T	0.8009	0.8146	0.7873	near_gene_3p_(500_bp)		Y
PSRC1	rs599839	1	109623689	109822166	G	A	0.8082	0.8268	0.7895	near_gene_3p_(500_bp)		Y
PSRC1	chr1:109623911	1	109623911	109822388	T	C	0.0005	0	0.001	utr_3p		N
PSRC1	rs10410	1	109623927	109822404	G	A	0.1064	0.1093	0.1035	utr_3p		N
PSRC1	chr1:109623957	1	109623957	109822434	A	T	0.0006	0.0012	0	utr_3p		N
PSRC1	rs14000	1	109624032	109822509	T	C	0.1056	0.1059	0.1053	utr_3p		N
PSRC1	rs41279724	1	109624159	109822636	G	A	0.0015	0	0.003	utr_3p		N
PSRC1	rs115047241	1	109625032	109823509	C	T	0.0014	0.0018	0.001	missense	Arg265Gln (CGG=>CAG) [exon6]	N
PSRC1	rs76057315	1	109625060	109823537	G	A	0.0095	0.0069	0.012	missense	Pro256Ser (CCT=>TCT) [exon6]	Y
PSRC1	rs35358959	1	109625773	109824250	G	A	0.0485	0.0484	0.0486	synonymous	Asn170Asn (AAC=>AAT) [exon4]	N
PSRC1	chr1:109626078	1	109626078	109824555	G	T	0.0019	0.0025	0.0014	missense	Leu69Ile (CTC=>ATC) [exon4]	N
PSRC1	rs41302083	1	109626203	109824680	C	T	0.0041	0.0051	0.0032	missense	Arg27His (CGT=>CAT) [exon4]	Y
PSRC1	rs12145875	1	109627575	109826052	G	A	0.0038	0.0056	0.0021	near_gene_5p_(2000_bp)		N
PSRC1	rs657420	1	109627659	109826136	C	T	0.5838	0.588	0.5796	near_gene_5p_(2000_bp)		N
PSRC1	chr1:109627788	1	109627788	109826265	T	A	0.0012	0.0013	0.001	near_gene_5p_(2000_bp)		N
	chr1:109653196	1	109653196	109851673	G	A	0.0005	0	0.001	intergenic		N
SORT1	rs72647819	1	109653316	109851793	C	T	0.0141	0.0187	0.0094	near_gene_3p_(500_bp)		N
SORT1	chr1:109654150	1	109654150	109852627	T	A	0.0014	0.0009	0.002	utr_3p		N
SORT1	chr1:109654259	1	109654259	109852736	G	C	0.0005	0	0.001	utr_3p		N
SORT1	rs189679368	1	109654757	109853234	C	G	0.001	0.001	0.001	utr_3p		N
SORT1	chr1:109654918	1	109654918	109853395	C	T	0.0005	0	0.001	utr_3p		N
SORT1	rs1064599	1	109655458	109853935	T	A	0.0095	0.0087	0.0104	utr_3p		N
SORT1	rs72647809	1	109655506	109853983	A	G	0.0015	0.003	0	utr_3p		N
SORT1	chr1:109655617	1	109655617	109854094	G	C	0.0005	0	0.001	utr_3p		N

SORT1	rs66852370	1	109655680	109854157	C	T	0.001	0	0.002	utr_3p		N
SORT1	chr1:109656156	1	109656156	109854633	A	G	0.0005	0	0.001	utr_3p		N
SORT1	rs72647804	1	109656543	109855020	A	G	0.0387	0.0464	0.0309	utr_3p		N
SORT1	rs192172116	1	109656853	109855330	T	C	0.0017	0.001	0.0025	utr_3p		N
SORT1	rs461200	1	109656927	109855404	G	A	0.7292	0.735	0.7235	utr_3p		N
SORT1	chr1:109657126	1	109657126	109855603	A	G	0.0005	0	0.001	utr_3p		N
SORT1	chr1:109657251	1	109657251	109855728	C	T	0.0015	0.0019	0.001	utr_3p		N
SORT1	rs459533	1	109657275	109855752	A	G	0.0062	0.01	0.0025	utr_3p		N
SORT1	chr1:109657438	1	109657438	109855915	A	G	0.0014	0.001	0.0019	utr_3p		N
SORT1	chr1:109657520	1	109657520	109855997	T	C	0.0005	0.001	0	utr_3p		N
SORT1	rs464218	1	109657829	109856306	G	A	0.5892	0.6128	0.5655	utr_3p		N
SORT1	rs150416069	1	109661103	109859580	C	T	0.001	0.001	0.001	synonymous	Arg714Arg (AGG=>AGA) [exon17]	Y
SORT1	chr1:109667164	1	109667164	109865641	C	T	0.0033	0.0025	0.004	missense	Arg646His (CGC=>CAC) [exon15]	N
SORT1	rs67195750	1	109680347	109878824	A	C	0.0016	0.001	0.0021	intron	intron11 bp38	N
SORT1	rs144141753	1	109680416	109878893	T	C	0.001	0.001	0.001	missense	Glu447Gly (GAA=>GGA) [exon11]	Y
SORT1	rs72646568	1	109680426	109878903	C	G	0.0113	0.0104	0.0123	missense	Glu444Gln (GAA=>CAA) [exon11]	Y
SORT1	rs72646566	1	109680528	109879005	T	C	0.0015	0.0031	0	intron	intron10 bp4341	N
SORT1	chr1:109684881	1	109684881	109883358	C	T	0.0005	0.001	0	missense	Val418Met (GTG=>ATG) [exon10]	N
SORT1	rs2228604	1	109686298	109884775	T	G	0.7321	0.7348	0.7295	synonymous	Thr323Thr (ACA=>ACC) [exon9]	N
SORT1	rs141749679	1	109689955	109888432	T	C	0.0031	0.0042	0.002	missense	Lys302Glu (AAA=>GAA) [exon8]	Y
SORT1	rs72646560	1	109698623	109897100	T	C	0.0398	0.0404	0.0393	synonymous	Arg199Arg (AGA=>AGG) [exon5]	N
SORT1	rs11142	1	109698626	109897103	A	G	0.7356	0.7404	0.7308	synonymous	Phe198Phe (TTT=>TTC) [exon5]	N
SORT1	chr1:109698718	1	109698718	109897195	T	G	0.0016	0.0022	0.001	intron	intron4 bp794	N
SORT1	rs61797119	1	109711623	109910100	T	C	0.0097	0.0122	0.0071	missense	Ile124Val (ATT=>GTT) [exon3]	Y
HHIPL2	chr1:220762134	1	220762134	222695511	G	C	0.0021	0.0015	0.0027	near_gene_3p_(500_bp)		N
HHIPL2	rs144597197	1	220762658	222696035	G	A	0.0037	0.002	0.0054	missense	Arg695Cys (CGC=>TGC) [exon9]	Y
HHIPL2	rs146670821	1	220762662	222696039	G	A	0.0011	0.001	0.0012	synonymous	His693His (CAC=>CAT) [exon9]	N
HHIPL2	chr1:220762703	1	220762703	222696080	G	A	0.001	0.0011	0.001	nonsense	Arg680Stop (CGA=>TGA) [exon9]	N
HHIPL2	chr1:220763600	1	220763600	222696977	C	T	0.0005	0	0.001	missense	Arg622Gln (CGG=>CAG) [exon8]	N
HHIPL2	rs1487523	1	220767039	222700416	C	T	0.2639	0.2737	0.2542	intron	intron6 bp4892	N
HHIPL2	rs4846373	1	220771893	222705270	T	C	0.3771	0.3913	0.3629	intron	intron6 bp38	N

HHIPL2	chr1:220771926	1	220771926	222705303	G	T	0.0014	0	0.0028	intron	intron6 bp5	N
HHIPL2	rs139893102	1	220772002	222705379	G	A	0.0026	0.0022	0.0029	missense	Thr551Met (ACG=>ATG) [exon6]	Y
HHIPL2	rs61748612	1	220772041	222705418	T	G	0.0068	0.002	0.0116	missense	Lys538Thr (AAG=>ACG) [exon6]	Y
HHIPL2	rs139585324	1	220772106	222705483	G	A	0.0052	0.0035	0.0069	intron	intron5 bp6507	N
HHIPL2	chr1:220772109	1	220772109	222705486	T	G	0.002	0.002	0.0019	intron	intron5 bp6504	N
HHIPL2	rs116359984	1	220778731	222712108	G	T	0.0055	0.007	0.004	missense	Leu487Met (CTG=>ATG) [exon5]	Y
HHIPL2	rs3748665	1	220780244	222713621	C	T	0.0867	0.0936	0.0797	missense	Arg394Gln (CGG=>CAG) [exon4]	Y
HHIPL2	rs3748666	1	220780254	222713631	G	C	0.2726	0.2869	0.2584	missense	His391Asp (CAT=>GAT) [exon4]	Y
HHIPL2	rs3811466	1	220783755	222717132	C	T	0.005	0.0019	0.008	missense	Val241Met (GTG=>ATG) [exon2]	Y
HHIPL2	chr1:220783770	1	220783770	222717147	C	T	0.0006	0.0012	0	missense	Glu236Lys (GAG=>AAG) [exon2]	N
HHIPL2	rs137934221	1	220787655	222721032	C	A	0.0017	0.0003	0.003	intron	intron1 bp34	N
HHIPL2	rs183510189	1	220787785	222721162	G	A	0.0161	0.0197	0.0124	synonymous	Asp75Asp (GAC=>GAT) [exon1]	N
HHIPL2	rs4846382	1	220787911	222721288	C	T	0.5936	0.5922	0.595	synonymous	Leu33Leu (TTG=>TTA) [exon1]	N
HHIPL2	rs72738203	1	220788210	222721587	C	A	0.0113	0.0102	0.0124	near_gene_5p_(2000_bp)		N
HHIPL2	rs9441911	1	220788296	222721673	T	C	0.819	0.827	0.811	near_gene_5p_(2000_bp)		N
HHIPL2	chr1:220788368	1	220788368	222721745	G	A	0.001	0.002	0	near_gene_5p_(2000_bp)		N
HHIPL2	chr1:220788462	1	220788462	222721839	T	C	0.0005	0	0.001	near_gene_5p_(2000_bp)		N
HHIPL2	rs75926317	1	220788505	222721882	C	G	0.0801	0.0663	0.094	near_gene_5p_(2000_bp)		N
HHIPL2	rs114397514	1	220788562	222721939	T	C	0.0015	0.0017	0.0013	near_gene_5p_(2000_bp)		N
TAF1A	chr1:220798150	1	220798150	222731527	A	G	0.0341	0.0286	0.0396	near_gene_3p_(500_bp)		N
TAF1A	rs67870673	1	220798175	222731552	C	T	0.1043	0.1024	0.1062	near_gene_3p_(500_bp)		N
TAF1A	rs76003336	1	220798650	222732027	T	C	0.0148	0.0155	0.0142	missense	Tyr329Cys (TAC=>TGC) [exon10]	Y
TAF1A	rs143557200	1	220798674	222732051	C	T	0.0109	0.0064	0.0154	missense	Arg321Gln (CGG=>CAG) [exon10]	Y
TAF1A	rs1134898	1	220801426	222734803	G	C	0.4539	0.4543	0.4535	synonymous	Gly267Gly (GGC=>GGG) [exon9]	N
TAF1A	chr1:220801488	1	220801488	222734865	A	G	0.0047	0.0034	0.006	intron	intron8 bp1650	N
TAF1A	rs74148135	1	220803112	222736489	A	G	0.0151	0.0113	0.0189	intron	intron8 bp26	N
TAF1A	rs11485180	1	220803121	222736498	C	T	0.1198	0.1229	0.1167	intron	intron8 bp17	N
TAF1A	chr1:220804093	1	220804093	222737470	G	A	0.0044	0.0035	0.0053	intron	intron6 bp5382	N
TAF1A	rs187439406	1	220804101	222737478	G	A	0.002	0.002	0.002	intron	intron6 bp5374	N
TAF1A	rs17464254	1	220804104	222737481	C	G	0.1074	0.1066	0.1082	intron	intron6 bp5371	N
TAF1A	rs148553032	1	220809636	222743013	A	G	0.0026	0.0042	0.001	intron	intron5 bp864	N

TAF1A	rs141066966	1	220817632	222751009	C	T	0.0113	0.0102	0.0125	intron	intron3 bp2092	N
TAF1A	chr1:220819775	1	220819775	222753152	G	T	0.0005	0	0.001	missense	Phe4Leu (TTC=>TTA) [exon3]	N
TAF1A	rs2270705	1	220828394	222761771	A	G	0.0894	0.1015	0.0773	intron	intron2 bp14	N
TAF1A	rs4846767	1	220829649	222763026	C	T	0.6871	0.6899	0.6842	intron	intron1 bp43	N
TAF1A	chr1:220829731	1	220829731	222763108	T	C	0.0014	0.0028	0	utr_5p		N
TAF1A	rs3008650	1	220829838	222763215	C	G	0.1279	0.1297	0.1262	utr_5p		N
TAF1A	rs3008651	1	220829858	222763235	T	G	0.6869	0.6907	0.683	utr_5p		N
TAF1A	rs3008652	1	220829872	222763249	C	T	0.9949	0.9959	0.9939	utr_5p		N
TAF1A	chr1:220830022	1	220830022	222763399	G	T	0.0005	0.001	0	near_gene_5p_(2000_bp)		N
TAF1A	chr1:220830144	1	220830144	222763521	G	A	0.0013	0.0016	0.0011	near_gene_5p_(2000_bp)		N
TAF1A	rs79187803	1	220830157	222763534	G	C	0.0828	0.0966	0.069	near_gene_5p_(2000_bp)		N
TAF1A	rs2936040	1	220830284	222763661	T	A	0.1355	0.1478	0.1232	near_gene_5p_(2000_bp)		N
MIA3	rs2133186	1	220861078	222794455	T	A	0.0871	0.0912	0.083	intron	intron1 bp2870	N
MIA3	rs3008617	1	220864729	222798106	G	A	0.9964	0.9959	0.9969	intron	intron2 bp3472	N
MIA3	rs17530776	1	220867536	222800913	A	G	0.0773	0.082	0.0726	intron	intron3 bp2717	N
MIA3	rs193055682	1	220867544	222800921	C	T	0.0034	0.0039	0.0029	missense	Thr120Met (ACG=>ATG) [exon4]	Y
MIA3	chr1:220867820	1	220867820	222801197	A	T	0.0015	0.0015	0.0014	missense	His212Leu (CAT=>CTT) [exon4]	N
MIA3	chr1:220867833	1	220867833	222801210	A	C	0.0014	0.0019	0.001	missense	Gln216His (CAA=>CAC) [exon4]	N
MIA3	rs184666801	1	220867858	222801235	G	C	0.005	0.0069	0.0031	missense	Ala225Pro (GCT=>CCT) [exon4]	N
MIA3	rs142088763	1	220868284	222801661	A	T	0.0246	0.0254	0.0238	missense	Thr367Ser (ACT=>TCT) [exon4]	Y
MIA3	rs2936053	1	220868629	222802006	A	G	0.9909	0.9909	0.9909	missense	Lys482Glu (AAG=>GAG) [exon4]	Y
MIA3	rs2936052	1	220868999	222802376	A	G	0.1987	0.1843	0.2131	missense	Lys605Arg (AAA=>AGA) [exon4]	Y
MIA3	rs189013781	1	220869275	222802652	T	C	0.0005	0.001	0	missense	Met697Thr (ATG=>ACG) [exon4]	Y
MIA3	rs3748626	1	220869426	222802803	T	G	0.6714	0.6819	0.6609	synonymous	Pro747Pro (CCT=>CCG) [exon4]	N
MIA3	chr1:220869445	1	220869445	222802822	T	A	0.0009	0.0018	0	missense	Phe754Ile (TTT=>ATT) [exon4]	Y
MIA3	rs3008620	1	220869549	222802926	C	T	0.885	0.8759	0.894	synonymous	Ser788Ser (AGC=>AGT) [exon4]	N
MIA3	rs79054337	1	220869685	222803062	A	G	0.0077	0.0087	0.0068	missense	Ile834Val (ATA=>GTA) [exon4]	Y
MIA3	chr1:220869751	1	220869751	222803128	G	A	0.0021	0.001	0.0032	missense	Asp856Asn (GAC=>AAC) [exon4]	N
MIA3	rs76329326	1	220869822	222803199	C	A	0.001	0.001	0.001	missense	Asp879Glu (GAC=>GAA) [exon4]	Y
MIA3	rs2936051	1	220869827	222803204	A	G	0.19	0.1791	0.2009	missense	Glu881Gly (GAG=>GGG) [exon4]	Y
MIA3	chr1:220869872	1	220869872	222803249	C	T	0.0021	0.0032	0.0009	missense	Ala896Val (GCT=>GTT) [exon4]	Y

MIA3	chr1:220870033	1	220870033	222803410	G	A	0.0005	0.001	0	missense	Ala950Thr (GCC=>ACC) [exon4]	N
MIA3	chr1:220870207	1	220870207	222803584	G	A	0.0015	0.0013	0.0016	missense	Glu1008Lys (GAA=>AAA) [exon4]	N
MIA3	rs3008622	1	220872321	222805698	T	G	0.1875	0.1716	0.2035	intron	intron5 bp30	N
MIA3	rs78391833	1	220872329	222805706	T	G	0.0109	0.0082	0.0136	intron	intron5 bp38	N
MIA3	chr1:220873045	1	220873045	222806422	G	C	0.0011	0.0013	0.001	intron	intron5 bp754	N
MIA3	rs189532371	1	220885699	222819076	A	C	0.0009	0.001	0.0009	intron	intron7 bp49	N
MIA3	chr1:220890292	1	220890292	222823669	A	G	0.0005	0	0.001	missense	Ile1223Val (ATC=>GTC) [exon9]	Y
MIA3	chr1:220890358	1	220890358	222823735	T	C	0.0051	0.0081	0.002	intron	intron9 bp13	N
MIA3	rs67180937	1	220890366	222823743	T	G	0.6831	0.6835	0.6828	intron	intron9 bp21	N
MIA3	chr1:220890375	1	220890375	222823752	T	C	0.0085	0.0083	0.0086	intron	intron9 bp30	N
MIA3	chr1:220891909	1	220891909	222825286	A	G	0.0013	0.0011	0.0015	intron	intron11 bp1041	N
MIA3	rs3002150	1	220892026	222825403	G	A	0.9652	0.9659	0.9644	intron	intron12 bp13	N
MIA3	rs34851033	1	220892038	222825415	G	A	0.0336	0.0329	0.0343	intron	intron12 bp25	N
MIA3	rs2291832	1	220893104	222826481	G	A	0.6966	0.7052	0.6881	intron	intron14 bp9	N
MIA3	chr1:220894654	1	220894654	222828031	A	G	0.0034	0.003	0.0038	synonymous	Ser1501Ser (TCA=>TCG) [exon18]	N
MIA3	chr1:220898762	1	220898762	222832139	G	A	0.0023	0.0014	0.0031	synonymous	Ser1561Ser (TCG=>TCA) [exon19]	N
MIA3	chr1:220899461	1	220899461	222832838	C	T	0.001	0.002	0	missense	Arg1585Trp (CGG=>TGG) [exon20]	N
MIA3	rs189566529	1	220899590	222832967	G	A	0.0022	0.0014	0.003	missense	Ala1592Thr (GCT=>ACT) [exon21]	Y
MIA3	chr1:220899615	1	220899615	222832992	A	C	0.0005	0	0.001	missense	Glu1600Ala (GAA=>GCA) [exon21]	Y
MIA3	chr1:220900091	1	220900091	222833468	T	A	0.002	0.0034	0.0006	intron	intron23 bp120	N
MIA3	rs2291835	1	220900161	222833538	C	G	0.1939	0.1947	0.1932	synonymous	Gly1665Gly (GGC=>GGG) [exon24]	N
MIA3	rs3002153	1	220900224	222833601	T	C	0.9909	0.9918	0.9899	synonymous	Pro1686Pro (CCT=>CCC) [exon24]	N
MIA3	chr1:220900299	1	220900299	222833676	C	G	0.0005	0.001	0	intron	intron24 bp20	N
MIA3	chr1:220902051	1	220902051	222835428	G	A	0.001	0.002	0	missense	Arg1715Gln (CGA=>CAA) [exon25]	N
MIA3	rs189601285	1	220905446	222838823	C	T	0.0024	0.0029	0.002	synonymous	Pro1862Pro (CCC=>CCT) [exon28]	N
MIA3	rs115300624	1	220905838	222839215	C	A	0.0076	0.009	0.0062	utr_3p		N
MIA3	rs74822125	1	220906039	222839416	G	C	0.0005	0	0.001	utr_3p		N
MIA3	chr1:220906219	1	220906219	222839596	G	A	0.001	0.001	0.001	utr_3p		N
MIA3	rs1053316	1	220906461	222839838	A	G	0.8755	0.8692	0.8818	utr_3p		N
MIA3	rs112439912	1	220906508	222839885	T	A	0.0014	0.0019	0.001	utr_3p		N
MIA3	rs192838774	1	220906672	222840049	C	G	0.0593	0.0601	0.0584	utr_3p		N

MIA3	rs75711036	1	220906776	222840153	T	G	0.0709	0.0751	0.0667	utr_3p		N
MIA3	rs188380685	1	220906935	222840312	T	C	0.0036	0.0072	0	utr_3p		N
MIA3	chr1:220907106	1	220907106	222840483	G	A	0.0005	0	0.001	utr_3p		N
MIA3	chr1:220907282	1	220907282	222840659	A	G	0.0027	0.0011	0.0043	utr_3p		N
MIA3	chr1:220907784	1	220907784	222841161	G	T	0.0182	0.0182	0.0182	utr_3p		N
C1orf58	rs3811465	1	220952742	222886119	A	G	0.7987	0.8089	0.7885	utr_5p		N
C1orf58	chr1:220952787	1	220952787	222886164	T	C	0.001	0	0.002	utr_5p		N
C1orf58	rs111319544	1	220952792	222886169	C	A	0.0154	0.01	0.0207	utr_5p		N
C1orf58	rs147480860	1	220971276	222904653	A	G	0.0024	0.001	0.0038	intron	intron11 bp1134	N
C1orf58	rs12043288	1	220972917	222906294	A	G	0.6647	0.6593	0.67	near_gene_3p_(500_bp)		N
	rs10929897	2	14124322	14206871	T	C	0.2214	0.2126	0.2303	intergenic		N
APOB	rs142151703	2	21077928	21224423	G	A	0.0035	0.0021	0.0048	utr_3p		N
APOB	rs72654427	2	21078119	21224614	A	G	0.001	0.002	0	synonymous	Thr4560Thr (ACT=>ACC) [exon29]	N
APOB	chr2:21078303	2	21078303	21224798	A	G	0.0005	0	0.001	missense	Leu4499Pro (CTG=>CCG) [exon29]	N
APOB	rs12713450	2	21078348	21224843	G	A	0.0022	0.0023	0.0021	missense	Thr4484Met (ACG=>ATG) [exon29]	Y
APOB	rs1801695	2	21078358	21224853	C	T	0.0383	0.0394	0.0373	missense	Ala4481Thr (GCC=>ACC) [exon29]	Y
APOB	rs141339310	2	21078779	21225274	A	G	0.0005	0.001	0	synonymous	Tyr4340Tyr (TAT=>TAC) [exon29]	N
APOB	rs1042034	2	21078786	21225281	C	T	0.7845	0.7691	0.7999	missense	Ser4338Asn (AGT=>AAT) [exon29]	Y
APOB	rs72654423	2	21078859	21225354	T	C	0.0117	0.0138	0.0096	missense	Ile4314Val (ATT=>GTT) [exon29]	Y
APOB	rs1801702	2	21078990	21225485	C	G	0.0161	0.0159	0.0163	missense	Arg4270Thr (AGG=>ACG) [exon29]	Y
APOB	rs61743502	2	21079005	21225500	A	G	0.0054	0.0058	0.0049	missense	Val4265Ala (GTA=>GCA) [exon29]	Y
APOB	chr2:21079029	2	21079029	21225524	A	G	0.0005	0	0.001	missense	Leu4257Ser (TTA=>TCA) [exon29]	N
APOB	rs1042031	2	21079258	21225753	C	T	0.1915	0.1836	0.1994	missense	Glu4181Lys (GAA=>AAA) [exon29]	Y
APOB	rs1801703	2	21079417	21225912	C	T	0.0082	0.0143	0.002	missense	Val4128Met (GTG=>ATG) [exon29]	Y
APOB	rs143685680	2	21079451	21225946	A	G	0.0006	0.0012	0	synonymous	Tyr4116Tyr (TAT=>TAC) [exon29]	N
APOB	rs140424976	2	21080708	21227203	C	T	0.0005	0.001	0	missense	Val4009Met (GTG=>ATG) [exon28]	N
APOB	rs12720851	2	21080836	21227331	G	A	0.0026	0.003	0.0021	intron	intron27 bp102	N
APOB	rs1801698	2	21081008	21227503	T	C	0.0037	0.0042	0.0033	missense	Thr3945Ala (ACT=>GCT) [exon27]	Y
APOB	rs61743512	2	21081703	21228198	C	T	0.0005	0.0011	0	missense	Ala3848Thr (GCA=>ACA) [exon26]	N
APOB	rs61744153	2	21081768	21228263	G	A	0.0024	0.0037	0.001	missense	Thr3826Met (ACG=>ATG) [exon26]	Y
APOB	rs12713540	2	21081844	21228339	A	T	0.003	0.003	0.003	missense	Ser3801Thr (TCT=>ACT) [exon26]	Y

APOB	chr2:21081926	2	21081926	21228421	C	T	0.0009	0	0.0018	synonymous	Lys3773Lys (AAG=>AAA) [exon26]	N
APOB	chr2:21081936	2	21081936	21228431	A	C	0.0015	0	0.003	missense	Ile3770Ser (ATC=>AGC) [exon26]	N
APOB	rs1801701	2	21082332	21228827	C	T	0.1024	0.0961	0.1087	missense	Arg3638Gln (CGG=>CAG) [exon26]	Y
APOB	rs12713559	2	21082573	21229068	G	A	0.001	0.002	0	missense	Arg3558Cys (CGC=>TGC) [exon26]	Y
APOB	rs1042023	2	21082951	21229446	G	C	0.0082	0.0075	0.0088	missense	Gln3432Glu (CAA=>GAA) [exon26]	Y
APOB	rs1799812	2	21083114	21229609	C	T	0.0072	0.0124	0.002	synonymous	Leu3377Leu (CTG=>CTA) [exon26]	N
APOB	rs72654403	2	21083390	21229885	G	A	0.0021	0.002	0.0023	synonymous	Ile3285Ile (ATC=>ATT) [exon26]	N
APOB	rs12720854	2	21083410	21229905	T	C	0.002	0.002	0.0021	missense	Ser3279Gly (AGC=>GGC) [exon26]	Y
APOB	rs142422341	2	21083434	21229929	C	T	0.0036	0.0036	0.0035	missense	Gly3271Ser (GGC=>AGC) [exon26]	N
APOB	chr2:21083656	2	21083656	21230151	T	C	0.0016	0.0032	0	missense	Ile3197Val (ATC=>GTC) [exon26]	N
APOB	rs147510760	2	21084140	21230635	A	G	0.0015	0.0021	0.001	synonymous	Asn3035Asn (AAT=>AAC) [exon26]	N
APOB	rs142756262	2	21084363	21230858	T	C	0.0015	0.002	0.001	missense	Asn2961Ser (AAT=>AGT) [exon26]	Y
APOB	chr2:21084390	2	21084390	21230885	C	A	0.0005	0	0.001	missense	Gly2952Val (GGA=>GTA) [exon26]	N
APOB	chr2:21084521	2	21084521	21231016	G	A	0.0005	0	0.001	synonymous	Asn2908Asn (AAC=>AAT) [exon26]	N
APOB	rs148498577	2	21084695	21231190	A	C	0.0016	0	0.0032	missense	Ile2850Met (ATT=>ATG) [exon26]	Y
APOB	rs72653095	2	21084783	21231278	G	A	0.0102	0.0104	0.01	missense	Pro2821Leu (CCG=>CTG) [exon26]	Y
APOB	rs676210	2	21085029	21231524	G	A	0.2061	0.2192	0.1929	missense	Pro2739Leu (CCA=>CTA) [exon26]	Y
APOB	rs6413458	2	21085097	21231592	G	A	0.015	0.016	0.0141	synonymous	Ile2716Ile (ATC=>ATT) [exon26]	N
APOB	chr2:21085153	2	21085153	21231648	C	T	0.0005	0	0.001	missense	Val2698Met (GTG=>ATG) [exon26]	N
APOB	rs1801696	2	21085549	21232044	C	T	0.0005	0.001	0	missense	Glu2566Lys (GAG=>AAG) [exon26]	Y
APOB	rs148170480	2	21085630	21232125	C	T	0.0019	0.0018	0.002	missense	Val2539Ile (GTA=>ATA) [exon26]	Y
APOB	rs72653093	2	21085633	21232128	G	A	0.001	0.002	0	synonymous	Leu2538Leu (CTG=>TTG) [exon26]	N
APOB	rs693	2	21085700	21232195	G	A	0.4952	0.5048	0.4856	synonymous	Thr2515Thr (ACC=>ACT) [exon26]	N
APOB	rs72653092	2	21085960	21232455	A	T	0.0035	0.004	0.003	missense	Ser2429Thr (TCA=>ACA) [exon26]	Y
APOB	rs72653090	2	21086093	21232588	A	G	0.0014	0.0018	0.001	synonymous	Val2384Val (GTT=>GTC) [exon26]	N
APOB	chr2:21087381	2	21087381	21233876	A	G	0.0005	0.001	0	missense	Val1955Ala (GTG=>GCG) [exon26]	N
APOB	rs533617	2	21087477	21233972	T	C	0.0255	0.0269	0.0242	missense	His1923Arg (CAT=>CGT) [exon26]	Y
APOB	rs1801699	2	21087504	21233999	T	C	0.0186	0.0176	0.0197	missense	Asn1914Ser (AAT=>AGT) [exon26]	Y
APOB	chr2:21088207	2	21088207	21234702	C	A	0.0005	0	0.001	missense	Ala1680Ser (GCA=>TCA) [exon26]	N
APOB	rs72653083	2	21088420	21234915	A	G	0.0046	0.0053	0.004	synonymous	Leu1609Leu (TTG=>CTG) [exon26]	N
APOB	chr2:21088719	2	21088719	21235214	G	T	0.0005	0	0.001	missense	Pro1509His (CCT=>CAT) [exon26]	N

APOB	rs568413	2	21088980	21235475	T	C	0.992	0.9922	0.9919	missense	Tyr1422Cys (TAT=>TGT) [exon26]	Y
APOB	chr2:21088988	2	21088988	21235483	T	C	0.0005	0.001	0	synonymous	Thr1419Thr (ACA=>ACG) [exon26]	N
APOB	rs72653082	2	21088994	21235489	C	T	0.0005	0.001	0	synonymous	Thr1417Thr (ACG=>ACA) [exon26]	N
APOB	rs12713771	2	21089070	21235565	C	T	0.0108	0.0123	0.0094	intron	intron25 bp467	N
APOB	rs182531066	2	21089508	21236003	G	A	0.0027	0.0033	0.0021	intron	intron25 bp29	N
APOB	chr2:21089572	2	21089572	21236067	T	C	0.002	0.003	0.0009	missense	Asp1394Gly (GAC=>GGC) [exon25]	N
APOB	chr2:21090943	2	21090943	21237438	A	T	0.0005	0.001	0	missense	Ser1242Thr (TCT=>ACT) [exon24]	Y
APOB	chr2:21091648	2	21091648	21238143	G	A	0.0019	0.0011	0.0028	intron	intron22 bp99	N
APOB	rs72653077	2	21091828	21238323	G	A	0.0031	0.0035	0.0026	missense	Pro1143Ser (CCT=>TCT) [exon22]	Y
APOB	rs12713843	2	21091872	21238367	C	T	0.0056	0.0055	0.0057	missense	Arg1128His (CGT=>CAT) [exon22]	Y
APOB	rs12713844	2	21091918	21238413	C	G	0.0098	0.009	0.0106	missense	Asp1113His (GAC=>CAC) [exon22]	Y
APOB	rs146133928	2	21092948	21239443	G	A	0.001	0.001	0.001	missense	Pro1067Leu (CCG=>CTG) [exon21]	Y
APOB	rs72653071	2	21093032	21239527	C	T	0.0013	0.0025	0	intron	intron20 bp2337	N
APOB	chr2:21095424	2	21095424	21241919	G	T	0.0015	0.002	0.001	synonymous	Leu1022Leu (CTC=>CTA) [exon20]	N
APOB	rs72653070	2	21096258	21242753	G	A	0.0011	0	0.0022	synonymous	Thr947Thr (ACC=>ACT) [exon19]	N
APOB	rs72653069	2	21096301	21242796	A	C	0.001	0	0.002	intron	intron18 bp2907	N
APOB	rs1801700	2	21099318	21245813	G	A	0.0494	0.0511	0.0476	synonymous	Asn902Asn (AAC=>AAT) [exon18]	N
APOB	rs144622446	2	21099413	21245908	C	T	0.0005	0	0.001	missense	Ala871Thr (GCT=>ACT) [exon18]	Y
APOB	rs72653066	2	21099887	21246382	C	G	0.0071	0.0055	0.0086	intron	intron17 bp15	N
APOB	chr2:21103205	2	21103205	21249700	A	T	0.0005	0	0.001	missense	Val735Glu (GTG=>GAG) [exon15]	Y
APOB	rs12691202	2	21103221	21249716	C	T	0.0396	0.0313	0.0479	missense	Val730Ile (GTC=>ATC) [exon15]	N
APOB	chr2:21103252	2	21103252	21249747	C	A	0.0005	0	0.001	missense	Leu719Phe (TTG=>TTT) [exon15]	N
APOB	rs679899	2	21104419	21250914	G	A	0.4462	0.466	0.4263	missense	Ala618Val (GCT=>GTT) [exon14]	Y
APOB	rs12714214	2	21104872	21251367	G	A	0.002	0.002	0.002	missense	Pro554Leu (CCG=>CTG) [exon13]	Y
APOB	chr2:21111214	2	21111214	21257709	T	A	0.0005	0.001	0	missense	Asn295Tyr (AAC=>TAC) [exon8]	N
APOB	rs1800478	2	21113641	21260136	G	A	0.0056	0.0058	0.0053	intron	intron5 bp694	N
APOB	rs1367117	2	21117405	21263900	G	A	0.3386	0.345	0.3322	missense	Thr98Ile (ACC=>ATC) [exon4]	Y
APOB	rs1800480	2	21120437	21266932	G	C	0.005	0.0041	0.006	utr_5p		N
APOB	chr2:21120595	2	21120595	21267090	A	G	0.0085	0.009	0.0081	near_gene_5p_(2000_bp)		N
APOB	rs1800481	2	21120715	21267210	A	G	0.8343	0.8449	0.8236	near_gene_5p_(2000_bp)		N
APOB	rs9282606	2	21120752	21267247	G	T	0.0348	0.0338	0.0359	near_gene_5p_(2000_bp)		N

APOB	rs72653049	2	21120869	21267364	G	A	0.0019	0.003	0.0009	near_gene_5p_(2000_bp)		N
APOB	rs934197	2	21120966	21267461	G	A	0.2898	0.2924	0.2873	near_gene_5p_(2000_bp)		N
	rs17020632	2	81765823	81912312	T	G	0.0023	0.0036	0.001	intergenic		N
SUMO1	rs72923015	2	202779445	203071200	T	A	0.002	0.0023	0.0018	utr_3p		N
SUMO1	chr2:202780172	2	202780172	203071927	T	C	0.001	0.001	0.001	utr_3p		N
SUMO1	chr2:202811608	2	202811608	203103363	A	T	0.0005	0.001	0	near_gene_5p_(2000_bp)		N
SUMO1	rs3754931	2	202811646	203103401	G	A	0.4352	0.4253	0.445	near_gene_5p_(2000_bp)		N
SUMO1	rs183601062	2	202811683	203103438	T	C	0.001	0.001	0.001	near_gene_5p_(2000_bp)		N
NOP58	chr2:202838720	2	202838720	203130475	G	A	0.001	0.001	0.001	near_gene_5p_(2000_bp)		N
NOP58	chr2:202838731	2	202838731	203130486	C	G	0.001	0	0.0021	near_gene_5p_(2000_bp)		N
NOP58	chr2:202838840	2	202838840	203130595	C	G	0.0009	0	0.0018	utr_5p		N
NOP58	chr2:202838865	2	202838865	203130620	C	T	0.0005	0	0.001	utr_5p		N
NOP58	rs148667174	2	202838877	203130632	G	C	0.0408	0.0413	0.0404	utr_5p		N
NOP58	chr2:202848068	2	202848068	203139823	C	A	0.003	0.0033	0.0026	intron	intron1 bp9114	N
NOP58	rs80282360	2	202848089	203139844	T	C	0.1115	0.1194	0.1036	synonymous	Asn18Asn (AAT=>AAC) [exon2]	N
NOP58	chr2:202857348	2	202857348	203149103	T	C	0.0005	0	0.001	synonymous	Val111Val (GTT=>GTC) [exon5]	N
NOP58	chr2:202857472	2	202857472	203149227	G	T	0.0005	0.001	0	intron	intron5 bp23	N
NOP58	rs7572505	2	202860600	203152355	G	A	0.2243	0.2321	0.2165	intron	intron5 bp3151	N
NOP58	rs147158311	2	202864141	203155896	A	C	0.0058	0.0055	0.0061	missense	Glu228Ala (GAA=>GCA) [exon8]	Y
NOP58	rs3731700	2	202864181	203155936	A	C	0.1295	0.1403	0.1186	synonymous	Ser241Ser (TCA=>TCC) [exon8]	N
NOP58	rs16839032	2	202865783	203157538	A	G	0.0176	0.0174	0.0178	synonymous	Glu273Glu (GAA=>GAG) [exon9]	N
NOP58	chr2:202870440	2	202870440	203162195	G	T	0.001	0.001	0.001	missense	Ala389Ser (GCC=>TCC) [exon11]	N
NOP58	rs138554847	2	202873217	203164972	C	T	0.0021	0.0032	0.001	synonymous	Tyr428Tyr (TAC=>TAT) [exon13]	N
NOP58	rs1054446	2	202876418	203168173	C	T	0.1133	0.1088	0.1178	utr_3p		N
NOP58	chr2:202876431	2	202876431	203168186	C	A	0.001	0.0009	0.0011	utr_3p		N
NOP58	rs16841867	2	202876480	203168235	C	G	0.1256	0.1415	0.1098	utr_3p		N
NOP58	rs13029433	2	202876682	203168437	G	A	0.2378	0.2458	0.2298	near_gene_3p_(500_bp)		N
NOP58	chr2:202877038	2	202877038	203168793	T	G	0.0007	0	0.0014	near_gene_3p_(500_bp)		N
BMPR2	chr2:202948829	2	202948829	203240584	G	A	0.0011	0.0013	0.001	near_gene_5p_(2000_bp)		N
BMPR2	rs115604088	2	202949774	203241529	G	A	0.01	0.0076	0.0125	utr_5p		N
BMPR2	rs116154690	2	202950142	203241897	G	A	0.0192	0.0195	0.0189	utr_5p		N

BMPR2	chr2:203087880	2	203087880	203379635	G	A	0.0011	0.001	0.0012	missense	Ser185Asn (AGT=>AAT) [exon5]	N
BMPR2	rs55722784	2	203087926	203379681	A	C	0.0232	0.0203	0.0261	synonymous	Leu200Leu (CTA=>CTC) [exon5]	N
BMPR2	chr2:203091965	2	203091965	203383720	G	C	0.001	0.001	0.001	missense	Arg266Thr (AGA=>ACA) [exon6]	N
BMPR2	rs149225691	2	203103775	203395530	T	C	0.0034	0.003	0.0037	synonymous	Pro327Pro (CCT=>CCC) [exon8]	N
BMPR2	chr2:203128719	2	203128719	203420474	C	T	0.0014	0.0019	0.001	missense	Pro696Ser (CCA=>TCA) [exon12]	N
BMPR2	rs2228545	2	203128957	203420712	G	A	0.0309	0.0265	0.0353	missense	Ser775Asn (AGC=>AAC) [exon12]	Y
BMPR2	chr2:203129267	2	203129267	203421022	C	T	0.001	0	0.002	synonymous	Gly878Gly (GGC=>GGT) [exon12]	N
BMPR2	rs1061157	2	203129444	203421199	G	A	0.1251	0.1381	0.1121	synonymous	Arg937Arg (AGG=>AGA) [exon12]	N
BMPR2	chr2:203132983	2	203132983	203424738	T	A	0.0137	0.014	0.0134	utr_3p		N
BMPR2	rs45502895	2	203133020	203424775	C	T	0.0038	0.0032	0.0045	utr_3p		N
BMPR2	chr2:203133339	2	203133339	203425094	T	C	0.001	0.0021	0	utr_3p		N
BMPR2	chr2:203133402	2	203133402	203425157	C	A	0.002	0.002	0.002	utr_3p		N
BMPR2	chr2:203133502	2	203133502	203425257	C	T	0.0005	0	0.001	utr_3p		N
BMPR2	rs6435156	2	203133720	203425475	C	T	0.243	0.2522	0.2338	utr_3p		N
BMPR2	rs184240459	2	203133729	203425484	C	T	0.002	0.003	0.001	utr_3p		N
BMPR2	rs113305949	2	203134150	203425905	C	A	0.0289	0.0315	0.0263	utr_3p		N
BMPR2	rs17199242	2	203134380	203426135	T	G	0.1236	0.1162	0.131	utr_3p		N
BMPR2	rs115467510	2	203134646	203426401	T	C	0.0165	0.0131	0.0199	utr_3p		N
BMPR2	rs17199249	2	203134913	203426668	T	G	0.1238	0.1166	0.131	utr_3p		N
BMPR2	rs181609907	2	203135087	203426842	A	G	0.001	0.001	0.0009	utr_3p		N
BMPR2	rs149030267	2	203135683	203427438	T	A	0.0032	0.0042	0.0022	utr_3p		N
BMPR2	rs77006932	2	203135747	203427502	G	A	0.0026	0.0043	0.001	utr_3p		N
BMPR2	chr2:203136631	2	203136631	203428386	C	G	0.0005	0.001	0	utr_3p		N
BMPR2	rs6705406	2	203136821	203428576	G	C	0.123	0.1186	0.1274	utr_3p		N
BMPR2	rs191179468	2	203136910	203428665	G	T	0.0005	0.001	0	utr_3p		N
BMPR2	chr2:203137278	2	203137278	203429033	C	T	0.0017	0.0034	0	utr_3p		N
BMPR2	rs1048829	2	203138701	203430456	T	G	0.4807	0.4586	0.5029	utr_3p		N
BMPR2	chr2:203138898	2	203138898	203430653	A	C	0.0005	0.001	0	utr_3p		N
BMPR2	rs7600694	2	203138912	203430667	G	A	0.1278	0.1243	0.1312	utr_3p		N
BMPR2	rs187466173	2	203138915	203430670	T	C	0.0013	0.0016	0.001	utr_3p		N
BMPR2	rs150216929	2	203139545	203431300	C	T	0.0005	0.001	0	utr_3p		N

BMPR2	chr2:203139554	2	203139554	203431309	G	C	0.0005	0	0.001	utr_3p		N
BMPR2	rs138750669	2	203139793	203431548	A	G	0.0031	0.004	0.0022	utr_3p		N
BMPR2	rs3731696	2	203140049	203431804	A	G	0.1193	0.1327	0.1059	utr_3p		N
BMPR2	rs149345058	2	203140302	203432057	C	T	0.0108	0.0108	0.0109	utr_3p		N
BMPR2	chr2:203140737	2	203140737	203432492	T	C	0.0019	0.0029	0.001	near_gene_3p_(500_bp)		N
FAM117B	rs11692610	2	203207757	203499512	T	C	0.2007	0.1983	0.2032	near_gene_5p_(2000_bp)		N
FAM117B	rs933969	2	203207965	203499720	G	A	0.5992	0.5923	0.6062	near_gene_5p_(2000_bp)		N
FAM117B	rs193178985	2	203208194	203499949	G	A	0.0152	0.0144	0.016	synonymous	Pro13Pro (CCG=>CCA) [exon1]	N
FAM117B	chr2:203299191	2	203299191	203590946	G	T	0.0012	0.0024	0	intron	intron3 bp1214	N
FAM117B	rs114146579	2	203338807	203630562	C	T	0.0451	0.0461	0.0441	utr_3p		N
FAM117B	rs138090755	2	203339020	203630775	C	T	0.002	0.0031	0.001	utr_3p		N
FAM117B	rs75456597	2	203339148	203630903	A	T	0.0062	0.0039	0.0084	utr_3p		N
FAM117B	rs11680951	2	203339604	203631359	G	A	0.5817	0.6046	0.5587	utr_3p		N
FAM117B	rs188785525	2	203339639	203631394	G	A	0.0044	0.0041	0.0048	utr_3p		N
FAM117B	rs16839311	2	203339801	203631556	G	A	0.219	0.2205	0.2174	utr_3p		N
FAM117B	chr2:203340041	2	203340041	203631796	G	T	0.0033	0.0044	0.0021	utr_3p		N
FAM117B	chr2:203340606	2	203340606	203632361	C	T	0.0027	0.002	0.0033	utr_3p		N
FAM117B	rs11544338	2	203340755	203632510	T	C	0.5738	0.5913	0.5563	utr_3p		N
FAM117B	rs188944416	2	203341041	203632796	A	T	0.0216	0.0206	0.0225	utr_3p		N
FAM117B	rs182860438	2	203341446	203633201	G	A	0.0146	0.0111	0.018	utr_3p		N
FAM117B	rs17807135	2	203341490	203633245	A	C	0.0973	0.099	0.0956	utr_3p		N
FAM117B	chr2:203341533	2	203341533	203633288	T	C	0.0005	0	0.001	utr_3p		N
FAM117B	chr2:203342102	2	203342102	203633857	A	G	0.0019	0.0019	0.0019	utr_3p		N
FAM117B	rs139674857	2	203342490	203634245	T	C	0.0074	0.0069	0.0079	utr_3p		N
FAM117B	rs150027543	2	203342809	203634564	C	T	0.0092	0.0087	0.0098	near_gene_3p_(500_bp)		N
FAM117B	chr2:203342916	2	203342916	203634671	T	A	0.0009	0.0019	0	near_gene_3p_(500_bp)		N
FAM117B	chr2:203342997	2	203342997	203634752	A	G	0.001	0.0021	0	near_gene_3p_(500_bp)		N
ICA1L	rs7598328	2	203346428	203638183	A	G	0.45	0.4457	0.4543	utr_3p		N
ICA1L	chr2:203346488	2	203346488	203638243	T	C	0.0005	0.001	0	utr_3p		N
ICA1L	chr2:203346555	2	203346555	203638310	G	A	0.0011	0.0022	0	utr_3p		N
ICA1L	chr2:203346760	2	203346760	203638515	A	C	0.0014	0.001	0.0018	utr_3p		N

ICA1L	chr2:203346800	2	203346800	203638555	G	A	0.0005	0	0.001	utr_3p		N
ICA1L	chr2:203346893	2	203346893	203638648	G	A	0.0005	0	0.001	utr_3p		N
ICA1L	chr2:203347016	2	203347016	203638771	T	G	0.0015	0	0.003	utr_3p		N
ICA1L	chr2:203347034	2	203347034	203638789	A	C	0.0014	0.0018	0.001	utr_3p		N
ICA1L	rs4675290	2	203348084	203639839	T	C	0.7429	0.743	0.7427	utr_3p		N
ICA1L	rs72932711	2	203348091	203639846	T	A	0.1447	0.1531	0.1362	utr_3p		N
ICA1L	rs56008729	2	203348128	203639883	C	T	0.0182	0.0131	0.0234	utr_3p		N
ICA1L	chr2:203348384	2	203348384	203640139	T	G	0.0009	0	0.0018	utr_3p		N
ICA1L	rs2036927	2	203348958	203640713	T	C	0.7457	0.746	0.7454	utr_3p		N
ICA1L	rs62194157	2	203349387	203641142	T	C	0.1537	0.1523	0.155	utr_3p		N
ICA1L	rs113452458	2	203349644	203641399	T	C	0.0073	0.0061	0.0086	utr_3p		N
ICA1L	rs62194158	2	203350400	203642155	G	A	0.4599	0.4573	0.4625	utr_3p		N
ICA1L	rs72932716	2	203350489	203642244	T	G	0.1473	0.1556	0.139	utr_3p		N
ICA1L	chr2:203350591	2	203350591	203642346	A	G	0.0072	0.0038	0.0106	utr_3p		N
ICA1L	chr2:203351241	2	203351241	203642996	G	A	0.0019	0.0028	0.001	utr_3p		N
ICA1L	chr2:203351279	2	203351279	203643034	G	C	0.0011	0.0012	0.001	utr_3p		N
ICA1L	rs147850742	2	203351285	203643040	G	A	0.0022	0.0005	0.004	utr_3p		N
ICA1L	rs60785646	2	203351527	203643282	A	T	0.0106	0.0074	0.0137	utr_3p		N
ICA1L	rs72932717	2	203351555	203643310	G	A	0.0183	0.0143	0.0223	utr_3p		N
ICA1L	rs115831835	2	203351584	203643339	T	C	0.0005	0	0.001	utr_3p		N
ICA1L	rs114466346	2	203351685	203643440	T	C	0.0081	0.008	0.0082	utr_3p		N
ICA1L	chr2:203351886	2	203351886	203643641	A	G	0.0017	0.001	0.0025	utr_3p		N
ICA1L	chr2:203352043	2	203352043	203643798	G	A	0.0013	0.0027	0	utr_3p		N
ICA1L	chr2:203352416	2	203352416	203644171	G	A	0.001	0	0.002	utr_3p		N
ICA1L	rs142998309	2	203361832	203653587	A	T	0.0039	0.0048	0.003	missense	Phe403Leu (TTT=>TTA) [exon12]	Y
ICA1L	chr2:203361838	2	203361838	203653593	T	C	0.0006	0	0.0013	synonymous	Gln401Gln (CAA=>CAG) [exon12]	N
ICA1L	rs149686236	2	203388877	203680632	A	G	0.002	0.0041	0	splice_site_5p	exon8	Y
ICA1L	chr2:203390446	2	203390446	203682201	T	C	0.0015	0.001	0.002	synonymous	Lys208Lys (AAA=>AAG) [exon7]	N
ICA1L	rs72932772	2	203390549	203682304	C	G	0.136	0.148	0.124	intron	intron6 bp2120	N
ICA1L	chr2:203392841	2	203392841	203684596	C	T	0.0005	0.0011	0	missense	Arg129His (CGT=>CAT) [exon6]	N
ICA1L	rs114889031	2	203394304	203686059	A	G	0.0132	0.0129	0.0135	intron	intron5 bp22	N

ICA1L	rs144482724	2	203394447	203686202	T	C	0.0054	0.0058	0.0049	missense	Ile80Val (ATA=>GTA) [exon5]	Y
ICA1L	rs1344959	2	203398632	203690387	G	A	0.9513	0.9587	0.9439	utr_3p		N
ICA1L	rs4675296	2	203401804	203693559	C	G	0.9533	0.9637	0.943	intron	intron3 bp12	N
ICA1L	chr2:203401999	2	203401999	203693754	C	T	0.0005	0.001	0	intron	intron2 bp41499	N
ICA1L	chr2:203443545	2	203443545	203735300	T	G	0.0005	0	0.001	utr_5p		N
ICA1L	rs60609531	2	203444341	203736096	G	A	0.0168	0.0161	0.0174	utr_5p		N
ICA1L	rs183813475	2	203444745	203736500	C	T	0.0111	0.0104	0.0118	near_gene_5p_(2000_bp)		N
ICA1L	chr2:203445040	2	203445040	203736795	A	C	0.0063	0.0066	0.0059	near_gene_5p_(2000_bp)		N
WDR12	chr2:203453540	2	203453540	203745295	T	A	0.033	0.0345	0.0314	near_gene_3p_(500_bp)		N
WDR12	rs6722332	2	203453572	203745327	T	C	0.1414	0.1557	0.1271	utr_3p		N
WDR12	rs72934751	2	203455767	203747522	A	G	0.1448	0.1538	0.1358	intron	intron11 bp810	N
WDR12	chr2:203456681	2	203456681	203748436	C	T	0.0026	0.0052	0	synonymous	Thr339Thr (ACG=>ACA) [exon11]	N
WDR12	chr2:203469059	2	203469059	203760814	T	C	0.0005	0	0.001	missense	Ile195Val (ATA=>GTA) [exon6]	N
WDR12	rs35212307	2	203474001	203765756	T	C	0.1435	0.1512	0.1358	missense	Ile75Val (ATC=>GTC) [exon3]	Y
WDR12	rs75565328	2	203474043	203765798	A	G	0.0018	0.0019	0.0017	missense	Phe61Leu (TTT=>CTT) [exon3]	Y
WDR12	chr2:203484375	2	203484375	203776130	A	T	0.001	0	0.0021	intron	intron1 bp29	N
WDR12	chr2:203484404	2	203484404	203776159	T	C	0.0019	0.0018	0.002	missense	Lys14Arg (AAA=>AGA) [exon1]	N
WDR12	chr2:203484545	2	203484545	203776300	T	C	0.0007	0	0.0013	utr_5p		N
WDR12	chr2:203485042	2	203485042	203776797	G	C	0.0087	0.0101	0.0073	utr_5p		N
WDR12	rs192973683	2	203485110	203776865	C	G	0.0188	0.0235	0.014	utr_5p		N
WDR12	rs75366898	2	203485191	203776946	C	T	0.0005	0	0.001	utr_5p		N
WDR12	chr2:203485207	2	203485207	203776962	G	A	0.0015	0.001	0.002	near_gene_5p_(2000_bp)		N
WDR12	rs145281736	2	203485210	203776965	G	C	0.0191	0.0225	0.0157	near_gene_5p_(2000_bp)		N
ALS2CR8	rs149163995	2	203485471	203777226	C	T	0.1256	0.131	0.1202	utr_5p		N
ALS2CR8	rs188957338	2	203486053	203777808	A	C	0.0015	0	0.003	utr_5p		N
ALS2CR8	chr2:203514865	2	203514865	203806620	G	A	0.0005	0	0.001	utr_5p		N
ALS2CR8	rs75869289	2	203514969	203806724	C	T	0.1433	0.1525	0.134	intron	intron4 bp21	N
ALS2CR8	rs115268453	2	203525542	203817297	C	T	0.008	0.0071	0.0089	missense	Pro108Ser (CCA=>TCA) [exon6]	Y
ALS2CR8	rs116945957	2	203527100	203818855	C	T	0.0008	0.0016	0	synonymous	Thr185Thr (ACC=>ACT) [exon7]	N
ALS2CR8	rs72932557	2	203555062	203846817	A	T	0.1426	0.152	0.1332	missense	Tyr571Phe (TAC=>TTC) [exon16]	Y
ALS2CR8	rs75249727	2	203555110	203846865	C	T	0.0005	0	0.001	missense	Pro587Leu (CCG=>CTG) [exon16]	Y

ALS2CR8	chr2:203555177	2	203555177	203846932	G	A	0.0005	0.001	0	synonymous	Leu609Leu (CTG=>CTA) [exon16]	N
ALS2CR8	chr2:203555212	2	203555212	203846967	G	A	0.0005	0.001	0	missense	Cys621Tyr (TGC=>TAC) [exon16]	N
ALS2CR8	chr2:203555253	2	203555253	203847008	C	T	0.001	0.001	0.001	missense	Leu635Phe (CTT=>TTT) [exon16]	Y
ALS2CR8	rs72932561	2	203556647	203848402	G	A	0.1472	0.1541	0.1404	utr_3p		N
ALS2CR8	rs76890136	2	203558256	203850011	C	G	0.1422	0.1511	0.1334	utr_3p		N
ALS2CR8	rs1351825	2	203558712	203850467	G	C	0.951	0.9572	0.9448	utr_3p		N
ALS2CR8	rs1351826	2	203558753	203850508	G	A	0.9524	0.9601	0.9448	utr_3p		N
ALS2CR8	chr2:203558912	2	203558912	203850667	A	G	0.0005	0	0.001	utr_3p		N
ALS2CR8	rs139402208	2	203558981	203850736	A	T	0.0196	0.024	0.0152	utr_3p		N
ALS2CR8	rs13028438	2	203559536	203851291	A	G	0.0264	0.0247	0.0282	near_gene_3p_(500_bp)		N
NBEAL1	rs4675309	2	203587748	203879503	A	G	0.9528	0.9545	0.9511	near_gene_5p_(2000_bp)		N
NBEAL1	rs78115373	2	203588206	203879961	T	G	0.0071	0.0074	0.0067	intron	intron1 bp256	N
NBEAL1	chr2:203588324	2	203588324	203880079	G	A	0.0005	0	0.001	intron	intron1 bp374	N
NBEAL1	chr2:203588442	2	203588442	203880197	C	A	0.0006	0	0.0013	intron	intron1 bp492	N
NBEAL1	chr2:203588934	2	203588934	203880689	A	G	0.001	0	0.002	intron	intron1 bp984	N
NBEAL1	rs4675310	2	203589079	203880834	G	A	0.8481	0.8428	0.8534	intron	intron1 bp1129	N
NBEAL1	rs2351524	2	203589237	203880992	T	C	0.8465	0.8385	0.8545	utr_5p		Y
NBEAL1	chr2:203614836	2	203614836	203906591	C	T	0.0013	0.0015	0.001	intron	intron3 bp12	N
NBEAL1	chr2:203622783	2	203622783	203914538	G	A	0.0005	0	0.001	missense	Val49Ile (GTA=>ATA) [exon4]	N
NBEAL1	chr2:203622808	2	203622808	203914563	C	T	0.0009	0	0.0019	missense	Ser57Phe (TCT=>TTT) [exon4]	N
NBEAL1	chr2:203622876	2	203622876	203914631	G	C	0.0019	0.0008	0.003	missense	Asp80His (GAT=>CAT) [exon4]	N
NBEAL1	rs4673241	2	203629515	203921270	A	G	0.9621	0.9691	0.9551	intron	intron5 bp39	N
NBEAL1	rs146121994	2	203630320	203922075	A	G	0.0027	0.001	0.0045	synonymous	Glu138Glu (GAA=>GAG) [exon6]	N
NBEAL1	chr2:203630336	2	203630336	203922091	T	C	0.0005	0	0.001	missense	Cys144Arg (TGT=>CGT) [exon6]	N
NBEAL1	chr2:203656362	2	203656362	203948117	G	T	0.0005	0.001	0	missense	Arg287Leu (CGT=>CTT) [exon9]	N
NBEAL1	chr2:203681125	2	203681125	203972880	A	G	0.0005	0	0.001	missense	Asn611Asp (AAC=>GAC) [exon13]	N
NBEAL1	chr2:203681165	2	203681165	203972920	A	T	0.0014	0	0.0028	intron	intron13 bp9	N
NBEAL1	rs142193727	2	203684912	203976667	A	G	0.0022	0.0013	0.0031	intron	intron14 bp1662	N
NBEAL1	chr2:203686162	2	203686162	203977917	G	C	0.0009	0	0.0019	missense	Leu765Phe (TTG=>TTC) [exon16]	N
NBEAL1	rs2086833	2	203689013	203980768	A	C	0.0015	0.001	0.0021	missense	Asn827Thr (AAC=>ACC) [exon17]	Y
NBEAL1	rs9941611	2	203698323	203990078	A	G	0.001	0.001	0.001	missense	Ile867Val (ATC=>GTC) [exon19]	Y

NBEAL1	chr2:203698464	2	203698464	203990219	G	A	0.0011	0.0011	0.0011	missense	Val914Ile (GTA=>ATA) [exon19]	N
NBEAL1	rs72934556	2	203699034	203990789	T	G	0.1258	0.1325	0.1192	synonymous	Val957Val (GTT=>GTG) [exon20]	N
NBEAL1	chr2:203699578	2	203699578	203991333	T	G	0.0005	0	0.001	missense	Ile984Met (ATT=>ATG) [exon21]	N
NBEAL1	chr2:203700831	2	203700831	203992586	C	G	0.001	0	0.002	missense	Leu1082Val (CTG=>GTG) [exon23]	N
NBEAL1	chr2:203703280	2	203703280	203995035	T	C	0.0005	0	0.001	intron	intron23 bp2375	N
NBEAL1	rs6748898	2	203705115	203996870	A	G	0.966	0.9679	0.9641	intron	intron25 bp15	N
NBEAL1	rs150176704	2	203708692	204000447	A	G	0.0058	0.0028	0.0087	synonymous	Ser1258Ser (TCA=>TCG) [exon27]	N
NBEAL1	rs182954834	2	203709727	204001482	A	G	0.0005	0	0.001	missense	Asp1488Gly (GAT=>GGT) [exon28]	N
NBEAL1	rs183146311	2	203711223	204002978	G	A	0.0011	0.0011	0.001	synonymous	Leu1524Leu (CTG=>CTA) [exon29]	N
NBEAL1	chr2:203711753	2	203711753	204003508	A	G	0.002	0.001	0.0029	intron	intron30 bp37	N
NBEAL1	rs182529739	2	203717682	204009437	A	G	0.0042	0.0053	0.003	missense	Ile1626Val (ATC=>GTC) [exon31]	Y
NBEAL1	chr2:203742796	2	203742796	204034551	T	C	0.001	0.001	0.001	missense	Phe1998Leu (TTC=>CTC) [exon38]	N
NBEAL1	rs116604257	2	203745687	204037442	G	T	0.0021	0.0033	0.001	intron	intron39 bp696	N
NBEAL1	rs140473940	2	203745778	204037533	A	G	0.0025	0.002	0.003	missense	Ile2065Val (ATT=>GTT) [exon40]	Y
NBEAL1	chr2:203748176	2	203748176	204039931	T	A	0.0007	0.0014	0	missense	Ser2100Thr (TCA=>ACA) [exon41]	N
NBEAL1	rs114408639	2	203766802	204058557	C	G	0.0021	0.001	0.0031	missense	Gln2292Glu (CAG=>GAG) [exon46]	Y
NBEAL1	rs180771101	2	203766870	204058625	T	G	0.002	0.001	0.003	missense	Phe2314Leu (TTT=>TTG) [exon46]	Y
NBEAL1	rs55843049	2	203766900	204058655	A	G	0.0119	0.0092	0.0145	intron	intron46 bp21	N
NBEAL1	rs4675323	2	203770306	204062061	A	G	0.962	0.9644	0.9597	missense	Ile2330Val (ATC=>GTC) [exon47]	Y
NBEAL1	chr2:203770320	2	203770320	204062075	G	T	0.002	0.0011	0.003	missense	Gln2334His (CAG=>CAT) [exon47]	N
NBEAL1	chr2:203772331	2	203772331	204064086	T	C	0.0009	0.0019	0	missense	Ile2356Thr (ATT=>ACT) [exon48]	Y
NBEAL1	rs140112414	2	203781659	204073414	A	G	0.0356	0.0353	0.036	missense	Thr2492Ala (ACC=>GCC) [exon51]	Y
NBEAL1	rs182855092	2	203781680	204073435	G	A	0.0034	0.0047	0.002	missense	Gly2499Ser (GGC=>AGC) [exon51]	Y
NBEAL1	rs7602883	2	203782305	204074060	A	G	0.0068	0.0062	0.0075	intron	intron52 bp15	N
NBEAL1	chr2:203790268	2	203790268	204082023	G	A	0.0008	0.0015	0	synonymous	Arg2677Arg (CGG=>CGA) [exon55]	N
NBEAL1	chr2:203790761	2	203790761	204082516	G	A	0.0005	0.001	0	utr_3p		N
NBEAL1	chr2:203790880	2	203790880	204082635	A	G	0.0005	0.001	0	utr_3p		N
NBEAL1	chr2:203790907	2	203790907	204082662	T	C	0.001	0.001	0.0011	utr_3p		N
CYP20A1	chr2:203811011	2	203811011	204102766	G	A	0.0006	0	0.0013	near_gene_5p_(2000_bp)		N
CYP20A1	chr2:203811711	2	203811711	204103466	G	A	0.0031	0.0052	0.001	utr_5p		N
CYP20A1	chr2:203811750	2	203811750	204103505	G	A	0.0016	0.0022	0.001	utr_5p		N

CYP20A1	chr2:203811975	2	203811975	204103730	G	A	0.0024	0.0015	0.0032	utr_5p		N
CYP20A1	rs116716498	2	203812024	204103779	C	T	0.0017	0.0033	0.0002	utr_5p		N
CYP20A1	rs6435176	2	203819688	204111443	A	G	0.9637	0.9692	0.9582	intron	intron2 bp825	N
CYP20A1	rs3731694	2	203824905	204116660	A	T	0.5302	0.5249	0.5354	intron	intron3 bp5016	N
CYP20A1	rs2043449	2	203824935	204116690	C	T	0.9628	0.9672	0.9583	missense	Ser97Leu (TCG=>TTG) [exon4]	Y
CYP20A1	chr2:203825046	2	203825046	204116801	C	A	0.0011	0.0013	0.0009	missense	Ser134Tyr (TCT=>TAT) [exon4]	N
CYP20A1	chr2:203853007	2	203853007	204144762	A	G	0.0016	0	0.0032	intron	intron7 bp1351	N
CYP20A1	chr2:203858694	2	203858694	204150449	A	G	0.0008	0.001	0.0007	missense	Gln322Arg (CAG=>CGG) [exon9]	N
CYP20A1	rs1048013	2	203862797	204154552	C	T	0.5315	0.5281	0.5349	missense	Leu346Phe (CTT=>TTT) [exon10]	Y
CYP20A1	rs142547646	2	203869467	204161222	G	A	0.003	0.0048	0.0012	missense	Glu392Lys (GAA=>AAA) [exon12]	Y
CYP20A1	chr2:203870141	2	203870141	204161896	A	G	0.001	0.001	0.001	utr_3p		N
CYP20A1	chr2:203872201	2	203872201	204163956	G	T	0.0005	0.0011	0	utr_3p		N
CYP20A1	chr2:203873059	2	203873059	204164814	A	G	0.0005	0.001	0	utr_3p		N
CYP20A1	rs11888559	2	203873416	204165171	T	C	0.9561	0.9576	0.9546	utr_3p		Y
CYP20A1	rs75712716	2	203873509	204165264	A	G	0.0015	0.002	0.001	utr_3p		N
CYP20A1	rs116443099	2	203874527	204166282	C	T	0.0636	0.0667	0.0606	utr_3p		N
CYP20A1	rs6435181	2	203877509	204169264	A	C	0.9638	0.9673	0.9603	utr_3p		N
CYP20A1	rs6435182	2	203877519	204169274	G	A	0.9643	0.9681	0.9606	utr_3p		N
CYP20A1	chr2:203877570	2	203877570	204169325	C	T	0.0005	0.001	0	utr_3p		N
CYP20A1	rs4675331	2	203878075	204169830	T	G	0.9569	0.9594	0.9545	utr_3p		N
CYP20A1	chr2:203878838	2	203878838	204170593	A	G	0.0005	0	0.001	near_gene_3p_(500_bp)		N
CYP20A1	chr2:203878846	2	203878846	204170601	A	G	0.0005	0	0.001	near_gene_3p_(500_bp)		N
ABI2	rs189439296	2	203900893	204192648	C	T	0.004	0.0038	0.0042	near_gene_5p_(2000_bp)		N
ABI2	chr2:203940019	2	203940019	204231774	C	G	0.0005	0	0.001	intron	intron2 bp7	N
ABI2	chr2:203968769	2	203968769	204260524	C	T	0.001	0.001	0.001	intron	intron6 bp21	N
ABI2	rs140793695	2	203975658	204267413	T	A	0.001	0.0011	0.001	missense	Leu316His (CTT=>CAT) [exon7]	Y
ABI2	rs140922536	2	203990003	204281758	T	C	0.003	0.002	0.004	synonymous	Tyr402Tyr (TAT=>TAC) [exon9]	N
ABI2	chr2:203990075	2	203990075	204281830	A	G	0.0008	0	0.0017	intron	intron9 bp26	N
ABI2	chr2:204000356	2	204000356	204292111	T	C	0.0013	0.0017	0.001	utr_3p		N
ABI2	rs141958154	2	204000655	204292410	C	T	0.0042	0.0055	0.003	utr_3p		N
ABI2	rs2469954	2	204000762	204292517	T	C	0.569	0.565	0.5731	utr_3p		N

ABI2	rs187201827	2	204000829	204292584	A	G	0.0019	0.002	0.0018	utr_3p		N
ABI2	rs190838780	2	204000875	204292630	T	A	0.0036	0.0031	0.004	utr_3p		N
ABI2	rs72926403	2	204000998	204292753	G	A	0.0115	0.0081	0.015	utr_3p		N
ABI2	chr2:204001580	2	204001580	204293335	A	G	0.0005	0.001	0	utr_3p		N
ABI2	chr2:204002003	2	204002003	204293758	T	C	0.001	0.002	0	utr_3p		N
ABI2	rs189753033	2	204003112	204294867	G	C	0.0015	0.001	0.0021	utr_3p		N
ABI2	chr2:204003122	2	204003122	204294877	T	C	0.0005	0.001	0	utr_3p		N
ABI2	rs76425803	2	204003429	204295184	G	C	0.0049	0.005	0.0049	utr_3p		N
ABI2	rs141957667	2	204003519	204295274	G	A	0.0005	0	0.001	utr_3p		N
ABI2	chr2:204003606	2	204003606	204295361	C	T	0.0005	0.001	0	utr_3p		N
ABI2	chr2:204004085	2	204004085	204295840	G	T	0.0017	0.0032	0.0001	utr_3p		N
ABI2	chr2:204004601	2	204004601	204296356	C	T	0.0016	0.0033	0	utr_3p		N
ABI2	rs77691082	2	204004656	204296411	A	G	0.0075	0.009	0.006	utr_3p		N
ABI2	rs186073867	2	204004761	204296516	A	G	0.0015	0.0021	0.001	utr_3p		N
ABI2	chr2:204005188	2	204005188	204296943	G	A	0.0005	0	0.001	near_gene_3p_(500_bp)		N
ABI2	rs79799505	2	204005396	204297151	G	A	0.0058	0.0045	0.0072	near_gene_3p_(500_bp)		N
RAPH1	rs77563991	2	204006542	204298297	C	T	0.0082	0.0085	0.0078	near_gene_3p_(500_bp)		N
RAPH1	chr2:204006790	2	204006790	204298545	G	A	0.0015	0.002	0.001	utr_3p		N
RAPH1	chr2:204006809	2	204006809	204298564	T	A	0.0073	0.0083	0.0064	utr_3p		N
RAPH1	chr2:204007001	2	204007001	204298756	C	A	0.0086	0.008	0.0092	utr_3p		N
RAPH1	chr2:204007008	2	204007008	204298763	A	C	0.0592	0.0617	0.0567	utr_3p		N
RAPH1	rs73990636	2	204007012	204298767	C	A	0.015	0.0115	0.0184	utr_3p		N
RAPH1	chr2:204007036	2	204007036	204298791	A	C	0.0146	0.0132	0.0161	utr_3p		N
RAPH1	chr2:204007040	2	204007040	204298795	A	C	0.011	0.0088	0.0133	utr_3p		N
RAPH1	rs145648108	2	204007128	204298883	C	T	0.0033	0.0038	0.0028	utr_3p		N
RAPH1	rs2250800	2	204007501	204299256	C	T	0.0325	0.0285	0.0365	utr_3p		N
RAPH1	rs72926408	2	204007685	204299440	C	T	0.0077	0.0064	0.0089	utr_3p		N
RAPH1	rs77589546	2	204007752	204299507	A	G	0.0275	0.0291	0.0259	utr_3p		N
RAPH1	rs7602076	2	204007785	204299540	A	G	0.008	0.0089	0.007	utr_3p		N
RAPH1	rs148469963	2	204008174	204299929	G	A	0.007	0.0121	0.002	utr_3p		N
RAPH1	chr2:204008236	2	204008236	204299991	T	C	0.0042	0.0065	0.0018	utr_3p		N

RAPH1	rs185693462	2	204008553	204300308	C	T	0.0005	0	0.001	utr_3p		N
RAPH1	chr2:204009361	2	204009361	204301116	G	A	0.0016	0	0.0032	utr_3p		N
RAPH1	chr2:204009420	2	204009420	204301175	C	T	0.0005	0.001	0	utr_3p		N
RAPH1	rs145407977	2	204009441	204301196	A	T	0.0051	0.0041	0.0062	utr_3p		N
RAPH1	rs2250522	2	204009541	204301296	G	A	0.598	0.5979	0.5981	utr_3p		N
RAPH1	rs142410866	2	204009700	204301455	G	A	0.011	0.0105	0.0115	utr_3p		N
RAPH1	chr2:204009719	2	204009719	204301474	A	G	0.0005	0	0.001	utr_3p		N
RAPH1	chr2:204009887	2	204009887	204301642	T	G	0.0005	0	0.001	utr_3p		N
RAPH1	chr2:204010198	2	204010198	204301953	C	T	0.0009	0.0019	0	utr_3p		N
RAPH1	chr2:204010422	2	204010422	204302177	C	G	0.001	0.001	0.001	utr_3p		N
RAPH1	rs192757605	2	204010479	204302234	A	C	0.0022	0.001	0.0034	utr_3p		N
RAPH1	rs140938480	2	204010632	204302387	T	G	0.0149	0.0147	0.015	utr_3p		N
RAPH1	rs2250390	2	204010641	204302396	T	C	0.0298	0.0262	0.0333	utr_3p		N
RAPH1	chr2:204011065	2	204011065	204302820	T	C	0.0009	0.001	0.0009	utr_3p		N
RAPH1	chr2:204011882	2	204011882	204303637	A	G	0.001	0.001	0.001	utr_3p		N
RAPH1	chr2:204012117	2	204012117	204303872	C	T	0.0009	0.0019	0	utr_3p		N
RAPH1	rs2465520	2	204012459	204304214	G	A	0.1097	0.108	0.1114	synonymous	Pro1233Pro (CCC=>CCT) [exon14]	N
RAPH1	chr2:204012476	2	204012476	204304231	T	G	0.0005	0	0.001	missense	Thr1228Pro (ACG=>CCG) [exon14]	N
RAPH1	rs149975027	2	204013518	204305273	A	G	0.0028	0.0001	0.0054	synonymous	Ser880Ser (TCT=>TCC) [exon14]	N
RAPH1	rs114111739	2	204013578	204305333	C	T	0.0021	0.0041	0	synonymous	Ser860Ser (TCG=>TCA) [exon14]	N
RAPH1	rs186567269	2	204013648	204305403	G	A	0.0018	0.0028	0.0008	missense	Pro837Leu (CCG=>CTG) [exon14]	N
RAPH1	chr2:204013665	2	204013665	204305420	A	G	0.0031	0.0021	0.0041	synonymous	Pro831Pro (CCT=>CCC) [exon14]	N
RAPH1	rs140045631	2	204014112	204305867	G	A	0.0016	0.0017	0.0015	synonymous	Ala682Ala (GCC=>GCT) [exon14]	N
RAPH1	rs55881728	2	204014601	204306356	A	G	0.5601	0.5635	0.5568	utr_3p		N
RAPH1	rs2247197	2	204014678	204306433	T	C	0.0249	0.0217	0.0281	utr_3p		Y
RAPH1	rs55915628	2	204014697	204306452	T	C	0.5632	0.5615	0.5649	utr_3p		N
RAPH1	chr2:204014738	2	204014738	204306493	G	A	0.0005	0.001	0	utr_3p		N
RAPH1	chr2:204014802	2	204014802	204306557	T	C	0.0005	0.001	0	utr_3p		N
RAPH1	chr2:204021053	2	204021053	204312808	G	A	0.0005	0	0.001	intron	intron13 bp653	N
RAPH1	chr2:204021725	2	204021725	204313480	T	C	0.0021	0.0032	0.0009	missense	Asn550Ser (AAT=>AGT) [exon13]	Y
RAPH1	rs2469953	2	204030543	204322298	T	C	0.5731	0.5656	0.5807	synonymous	Lys423Lys (AAA=>AAG) [exon10]	N

RAPH1	rs2256340	2	204033018	204324773	G	A	0.0335	0.0285	0.0386	intron	intron8 bp1199	N
RAPH1	rs149371856	2	204062554	204354309	C	T	0.0055	0.0061	0.0049	missense	Glu244Lys (GAG=>AAG) [exon4]	Y
RAPH1	rs2251317	2	204063068	204354823	C	T	0.0304	0.0304	0.0304	intron	intron3 bp1114	N
RAPH1	chr2:204064157	2	204064157	204355912	C	T	0.0014	0.001	0.0018	intron	intron3 bp25	N
	rs16825115	2	229114411	229406167	C	T	0.0018	0.0018	0.0018	intergenic		N
RBMS3	rs1900905	3	29926389	29951385	G	A	0.001	0.0012	0.0009	intron	intron10 bp10139	N
ARMC8	rs141410098	3	139388697	137906007	T	C	0.0198	0.0231	0.0165	near_gene_5p_(2000_bp)		N
ARMC8	chr3:139411451	3	139411451	137928761	A	G	0.0009	0.001	0.0009	intron	intron3 bp26	N
ARMC8	chr3:139424868	3	139424868	137942178	G	A	0.0098	0.0102	0.0094	intron	intron4 bp1339	N
ARMC8	rs112669388	3	139425105	137942415	C	T	0.0005	0.001	0	intron	intron5 bp42	N
ARMC8	rs139183585	3	139446953	137964263	T	G	0.0364	0.0333	0.0395	utr_3p		N
ARMC8	chr3:139447189	3	139447189	137964499	G	A	0.001	0.001	0.001	utr_3p		N
ARMC8	chr3:139447436	3	139447436	137964746	T	C	0.0011	0.0023	0	utr_3p		N
ARMC8	chr3:139447983	3	139447983	137965293	C	T	0.0005	0	0.001	utr_3p		N
TXNDC6	chr3:139463141	3	139463141	137980451	T	C	0.0039	0.0038	0.004	utr_3p		N
TXNDC6	chr3:139463205	3	139463205	137980515	G	A	0.0012	0.0006	0.0019	utr_3p		N
TXNDC6	rs117262498	3	139463429	137980739	A	T	0.0006	0.0012	0	utr_3p		N
TXNDC6	rs139737188	3	139463585	137980895	G	T	0.0053	0.0056	0.005	utr_3p		N
TXNDC6	rs145695620	3	139463894	137981204	G	A	0.0177	0.0164	0.0189	utr_3p		N
ARMC8	chr3:139465234	3	139465234	137982544	A	G	0.0006	0	0.0012	intron	intron13 bp18519	N
ARMC8	rs141072697	3	139468673	137985983	T	C	0.0041	0.0043	0.0039	intron	intron15 bp2929	N
ARMC8	rs183452792	3	139471693	137989003	C	T	0.0026	0.001	0.0043	intron	intron17 bp29	N
ARMC8	chr3:139475953	3	139475953	137993263	T	G	0.0005	0	0.001	intron	intron18 bp1305	N
ARMC8	rs77176250	3	139486081	138003391	C	T	0.0247	0.0282	0.0211	intron	intron20 bp23	N
ARMC8	rs11716014	3	139497639	138014949	G	T	0.008	0.0085	0.0075	utr_3p		N
ARMC8	chr3:139497760	3	139497760	138015070	A	C	0.0005	0.001	0	utr_3p		N
ARMC8	chr3:139497810	3	139497810	138015120	G	A	0.0005	0	0.001	utr_3p		N
ARMC8	chr3:139497823	3	139497823	138015133	G	T	0.0018	0.0026	0.001	utr_3p		N
ARMC8	rs12972	3	139497879	138015189	T	C	0.0873	0.087	0.0877	utr_3p		N
ARMC8	chr3:139498083	3	139498083	138015393	G	A	0.0343	0.0416	0.027	utr_3p		N
ARMC8	rs1054717	3	139498232	138015542	C	T	0.0089	0.0097	0.0082	utr_3p		N

ARMC8	chr3:139498376	3	139498376	138015686	T	C	0.0005	0.001	0	utr_3p		N
TXNDC6	chr3:139499019	3	139499019	138016329	C	T	0.0005	0	0.001	intron	intron11 bp6020	N
TXNDC6	rs80254291	3	139499218	138016528	C	T	0.0007	0.0014	0	intron	intron11 bp5821	N
TXNDC6	chr3:139504999	3	139504999	138022309	C	G	0.0005	0	0.001	intron	intron11 bp40	N
TXNDC6	chr3:139507584	3	139507584	138024894	G	C	0.0005	0	0.001	synonymous	Thr135Thr (ACC=>ACG) [exon9]	N
TXNDC6	chr3:139508043	3	139508043	138025353	G	A	0.0015	0.001	0.002	intron	intron7 bp7821	N
TXNDC6	rs9289556	3	139515871	138033181	C	T	0.7005	0.7009	0.7001	synonymous	Glu90Glu (GAG=>GAA) [exon7]	N
TXNDC6	rs150184268	3	139515918	138033228	C	G	0.0025	0.0051	0	missense	Asp75His (GAT=>CAT) [exon7]	Y
TXNDC6	chr3:139521120	3	139521120	138038430	G	A	0.001	0.001	0.001	intron	intron4 bp5285	N
TXNDC6	rs114184368	3	139531467	138048777	C	T	0.0221	0.0247	0.0196	near_gene_5p_(2000_bp)		N
MRAS	chr3:139549493	3	139549493	138066803	A	G	0.0005	0	0.001	utr_5p		N
MRAS	rs1199333	3	139574391	138091701	G	T	0.8064	0.8063	0.8064	intron	intron1 bp24092	N
MRAS	rs16848033	3	139574592	138091902	A	G	0.0007	0.0015	0	synonymous	Gln59Gln (CAA=>CAG) [exon2]	N
MRAS	chr3:139598815	3	139598815	138116125	G	A	0.0012	0	0.0025	intron	intron2 bp24207	N
MRAS	rs112911445	3	139599054	138116364	C	T	0.0118	0.0087	0.0149	intron	intron3 bp45	N
MRAS	chr3:139602106	3	139602106	138119416	A	G	0.001	0	0.002	missense	Asn163Ser (AAT=>AGT) [exon5]	N
MRAS	rs2279241	3	139603888	138121198	C	T	0.1598	0.1698	0.1498	utr_3p		N
MRAS	rs113798826	3	139603981	138121291	C	T	0.0238	0.0213	0.0263	utr_3p		N
MRAS	chr3:139604072	3	139604072	138121382	G	A	0.0005	0.001	0	utr_3p		N
MRAS	rs9851766	3	139604199	138121509	A	G	0.1485	0.1564	0.1405	utr_3p		N
MRAS	chr3:139604314	3	139604314	138121624	A	C	0.0005	0	0.001	utr_3p		N
MRAS	rs1199332	3	139604382	138121692	C	G	0.001	0.001	0.001	utr_3p		N
MRAS	rs3732837	3	139604610	138121920	A	T	0.1572	0.168	0.1463	utr_3p		N
MRAS	rs9818870	3	139604812	138122122	C	T	0.1648	0.1746	0.1551	utr_3p		Y
MRAS	chr3:139605114	3	139605114	138122424	A	G	0.001	0.001	0.001	utr_3p		N
MRAS	rs2291127	3	139605167	138122477	C	T	0.1691	0.1768	0.1613	utr_3p		N
MRAS	rs40593	3	139605471	138122781	A	G	0.0015	0.001	0.002	utr_3p		N
MRAS	rs147196023	3	139605579	138122889	C	T	0.006	0.0039	0.0081	utr_3p		N
MRAS	chr3:139606043	3	139606043	138123353	G	A	0.0005	0	0.001	utr_3p		N
MRAS	chr3:139606432	3	139606432	138123742	C	T	0.0005	0	0.001	utr_3p		N
MRAS	rs2293252	3	139606544	138123854	C	T	0.6443	0.6326	0.656	utr_3p		N

MRAS	rs2293251	3	139606804	138124114	T	G	0.1519	0.1639	0.1398	utr_3p		N
MRAS	rs10471	3	139606905	138124215	T	A	0.0146	0.015	0.0143	utr_3p		N
MRAS	rs191106596	3	139607064	138124374	C	T	0.0036	0.0042	0.0031	utr_3p		N
ESYT3	chr3:139635478	3	139635478	138152788	C	T	0.0011	0.0022	0	near_gene_5p_(2000_bp)		N
ESYT3	rs34382779	3	139635490	138152800	C	A	0.0422	0.0412	0.0433	near_gene_5p_(2000_bp)		N
ESYT3	chr3:139635518	3	139635518	138152828	C	G	0.0015	0.002	0.001	near_gene_5p_(2000_bp)		N
ESYT3	rs1679181	3	139635630	138152940	A	C	0.0414	0.044	0.0388	near_gene_5p_(2000_bp)		N
ESYT3	chr3:139636002	3	139636002	138153312	T	G	0.0005	0	0.001	near_gene_5p_(2000_bp)		N
ESYT3	rs114100179	3	139636117	138153427	C	G	0.0078	0.0075	0.008	utr_5p		N
ESYT3	chr3:139636349	3	139636349	138153659	T	C	0.0022	0.0025	0.0019	missense	Cys7Arg (TGC=>CGC) [exon1]	N
ESYT3	rs145360949	3	139636576	138153886	C	G	0.0006	0.0001	0.001	synonymous	Arg82Arg (CGC=>CGG) [exon1]	N
ESYT3	rs811794	3	139653651	138170961	C	G	0.0253	0.0242	0.0263	intron	intron2 bp30	N
ESYT3	chr3:139656681	3	139656681	138173991	G	A	0.0013	0.0017	0.001	intron	intron2 bp3060	N
ESYT3	rs114180322	3	139659054	138176364	C	T	0.0238	0.0215	0.0262	intron	intron3 bp2194	N
ESYT3	rs142676392	3	139659104	138176414	C	T	0.0005	0.001	0	missense	Pro170Leu (CCC=>CTC) [exon4]	Y
ESYT3	rs150550932	3	139659109	138176419	G	A	0.0015	0.003	0	missense	Val172Ile (GTC=>ATC) [exon4]	Y
ESYT3	chr3:139659189	3	139659189	138176499	G	A	0.0005	0	0.001	intron	intron4 bp13	N
ESYT3	rs147568505	3	139661489	138178799	C	T	0.0052	0.0068	0.0036	synonymous	Leu221Leu (CTG=>TTG) [exon6]	N
ESYT3	rs144720494	3	139661581	138178891	C	T	0.0051	0.0027	0.0076	intron	intron6 bp15	N
ESYT3	chr3:139663658	3	139663658	138180968	C	T	0.0015	0.002	0.001	missense	His279Tyr (CAC=>TAC) [exon8]	N
ESYT3	rs150411096	3	139665877	138183187	G	C	0.0057	0.0069	0.0045	missense	Gly306Arg (GGG=>CGG) [exon9]	Y
ESYT3	rs143183371	3	139666017	138183327	C	T	0.0026	0.0021	0.003	synonymous	Asn352Asn (AAC=>AAT) [exon9]	N
ESYT3	rs149376068	3	139669165	138186475	C	T	0.0119	0.011	0.0128	intron	intron11 bp24	N
ESYT3	rs6772467	3	139669664	138186974	G	A	0.0072	0.0022	0.0122	missense	Gly416Arg (GGG=>AGG) [exon12]	Y
ESYT3	rs61732466	3	139669706	138187016	G	A	0.034	0.0337	0.0343	missense	Asp430Asn (GAC=>AAC) [exon12]	Y
ESYT3	rs187064724	3	139670167	138187477	G	A	0.0015	0.001	0.002	intron	intron12 bp441	N
ESYT3	rs1679167	3	139670258	138187568	C	T	0.5606	0.5475	0.5736	intron	intron13 bp9	N
ESYT3	chr3:139670931	3	139670931	138188241	A	G	0.0005	0	0.001	intron	intron14 bp518	N
ESYT3	rs112637024	3	139671566	138188876	A	G	0.005	0.0068	0.0032	intron	intron15 bp530	N
ESYT3	chr3:139671678	3	139671678	138188988	G	A	0.0041	0.0005	0.0077	synonymous	Lys530Lys (AAG=>AAA) [exon16]	Y
ESYT3	rs10935282	3	139673922	138191232	G	A	0.4375	0.4226	0.4524	missense	Gly590Arg (GGG=>AGG) [exon18]	Y

ESYT3	rs139504758	3	139674037	138191347	C	T	0.0129	0.0149	0.0109	missense	Pro628Leu (CCA=>CTA) [exon18]	Y
ESYT3	rs35537868	3	139674138	138191448	A	T	0.025	0.0239	0.026	missense	Thr662Ser (ACA=>TCA) [exon18]	Y
ESYT3	chr3:139674203	3	139674203	138191513	G	A	0.0005	0	0.001	synonymous	Lys683Lys (AAG=>AAA) [exon18]	N
ESYT3	chr3:139674388	3	139674388	138191698	T	C	0.0005	0	0.001	missense	Ile745Thr (ATT=>ACT) [exon18]	Y
ESYT3	rs62282906	3	139679000	138196310	A	G	0.0032	0.0032	0.0031	utr_3p		N
ESYT3	rs75399682	3	139679139	138196449	C	T	0.0239	0.0257	0.0221	utr_3p		N
ESYT3	chr3:139679391	3	139679391	138196701	G	A	0.001	0	0.002	utr_3p		N
ESYT3	rs142806572	3	139679451	138196761	G	A	0.006	0.005	0.007	utr_3p		N
ESYT3	rs184436322	3	139679622	138196932	C	A	0.001	0	0.002	utr_3p		N
ESYT3	chr3:139679849	3	139679849	138197159	G	A	0.005	0.0054	0.0046	utr_3p		N
ESYT3	rs189067477	3	139679920	138197230	C	T	0.0005	0	0.001	utr_3p		N
ESYT3	chr3:139680219	3	139680219	138197529	T	G	0.001	0	0.002	near_gene_3p_(500_bp)		N
	chr3:139680448	3	139680448	138197758	G	A	0.001	0	0.002	intergenic		N
CEP70	rs79173240	3	139695466	138212776	G	A	0.0121	0.0096	0.0147	near_gene_3p_(500_bp)		N
CEP70	rs116246525	3	139695815	138213125	A	C	0.0295	0.0368	0.0222	near_gene_3p_(500_bp)		N
CEP70	rs149217389	3	139695839	138213149	T	C	0.0005	0.001	0	near_gene_3p_(500_bp)		N
CEP70	rs2280596	3	139695856	138213166	C	G	0.0227	0.0229	0.0225	near_gene_3p_(500_bp)		N
CEP70	rs9049	3	139695982	138213292	C	T	0.024	0.022	0.026	utr_3p		N
CEP70	rs116839343	3	139696020	138213330	C	T	0.0009	0.001	0.0009	utr_3p		N
CEP70	rs774012	3	139696399	138213709	T	C	0.7275	0.7227	0.7323	utr_3p		N
CEP70	rs112140750	3	139699675	138216985	T	C	0.0126	0.0118	0.0133	intron	intron16 bp1967	N
CEP70	chr3:139701660	3	139701660	138218970	C	G	0.0015	0.003	0	missense	Gly545Ala (GGA=>GCA) [exon16]	N
CEP70	rs35340237	3	139701684	138218994	T	C	0.0243	0.0217	0.0269	missense	Asn537Ser (AAT=>AGT) [exon16]	Y
CEP70	rs114744558	3	139701942	138219252	A	T	0.0038	0.0043	0.0033	missense	Leu509His (CTC=>CAC) [exon15]	Y
CEP70	rs148908930	3	139702043	138219353	C	T	0.0107	0.0105	0.011	synonymous	Lys475Lys (AAG=>AAA) [exon15]	N
CEP70	chr3:139706821	3	139706821	138224131	C	A	0.0011	0.0012	0.001	intron	intron13 bp6	N
CEP70	rs61996332	3	139706964	138224274	G	C	0.0028	0.002	0.0036	missense	Pro362Ala (CCA=>GCA) [exon13]	Y
CEP70	rs9878436	3	139727090	138244400	C	T	0.446	0.4573	0.4347	synonymous	Thr292Thr (ACG=>ACA) [exon11]	N
CEP70	chr3:139738780	3	139738780	138256090	G	A	0.0008	0.0003	0.0012	missense	Arg189Cys (CGC=>TGC) [exon7]	N
CEP70	rs1673608	3	139771853	138289163	T	C	0.5103	0.503	0.5176	synonymous	Leu154Leu (TTA=>TTG) [exon6]	N
CEP70	rs1673607	3	139771911	138289221	C	T	0.5403	0.5325	0.5481	missense	Ser135Asn (AGT=>AAT) [exon6]	Y

CEP70	chr3:139796163	3	139796163	138313473	T	C	0.0047	0.0055	0.004	near_gene_5p_(2000_bp)		N
CEP70	rs13087696	3	139796282	138313592	G	A	0.0393	0.0427	0.0358	near_gene_5p_(2000_bp)		N
FAIM	chr3:139810058	3	139810058	138327368	C	T	0.0061	0.0082	0.004	near_gene_5p_(2000_bp)		N
FAIM	chr3:139810243	3	139810243	138327553	C	A	0.0023	0.0015	0.0031	utr_5p		N
FAIM	rs811322	3	139812552	138329862	G	A	0.5717	0.5587	0.5846	synonymous	Pro21Pro (CCG=>CCA) [exon2]	N
FAIM	chr3:139822972	3	139822972	138340282	C	T	0.0005	0	0.001	synonymous	Leu4Leu (CTC=>CTT) [exon2]	N
FAIM	rs192752865	3	139823716	138341026	G	T	0.0028	0.0017	0.0039	intron	intron2 bp645	N
FAIM	rs641320	3	139830647	138347957	G	A	0.0655	0.0675	0.0636	missense	Ala117Thr (GCT=>ACT) [exon4]	Y
FAIM	rs13043	3	139830678	138347988	T	C	0.0193	0.0136	0.025	missense	Leu127Ser (TTG=>TCG) [exon4]	Y
FAIM	rs116620131	3	139830697	138348007	A	G	0.0047	0.0056	0.0037	intron	intron4 bp9	N
FAIM	chr3:139830719	3	139830719	138348029	C	T	0.0011	0.0002	0.002	intron	intron4 bp31	N
FAIM	rs149453397	3	139834564	138351874	C	T	0.0005	0.001	0	missense	His165Tyr (CAT=>TAT) [exon5]	Y
FAIM	chr3:139834694	3	139834694	138352004	C	T	0.0016	0.001	0.0022	utr_3p		N
FAIM	chr3:139834926	3	139834926	138352236	T	C	0.0015	0.0009	0.002	near_gene_3p_(500_bp)		N
FAIM	chr3:139834941	3	139834941	138352251	G	C	0.0006	0	0.0012	near_gene_3p_(500_bp)		N
FAIM	chr3:139835030	3	139835030	138352340	G	A	0.0005	0.001	0	near_gene_3p_(500_bp)		N
FREM3	rs6840604	4	144812612	144593162	A	G	0.0033	0.001	0.0057	intron	intron2 bp21104	N
PHACTR1	chr6:12825472	6	12825472	12717486	C	A	0.0036	0.0053	0.002	near_gene_5p_(2000_bp)		N
PHACTR1	chr6:12825586	6	12825586	12717600	G	T	0.0125	0.0133	0.0118	near_gene_5p_(2000_bp)		N
PHACTR1	rs141282814	6	13161629	13053643	C	T	0.001	0.001	0.001	synonymous	Val99Val (GTC=>GTT) [exon4]	N
PHACTR1	rs142347332	6	13268543	13160557	T	C	0.0016	0.0012	0.0019	intron	intron5 bp41	N
PHACTR1	rs149759835	6	13268546	13160560	G	A	0.0012	0.0004	0.002	intron	intron5 bp44	N
PHACTR1	rs79308302	6	13290697	13182718	T	G	0.0112	0.0136	0.0088	intron	intron5 bp22195	N
PHACTR1	chr6:13290801	6	13290801	13182822	T	C	0.0007	0.0014	0	missense	Ser190Pro (TCT=>CCT) [exon6]	N
PHACTR1	rs73725623	6	13314261	13206282	C	T	0.0149	0.0162	0.0137	synonymous	Thr300Thr (ACC=>ACT) [exon7]	Y
PHACTR1	rs114091869	6	13314364	13206385	G	A	0.0204	0.0145	0.0264	intron	intron7 bp17	N
PHACTR1	rs7765972	6	13335983	13228004	G	A	0.0563	0.0582	0.0544	intron	intron7 bp21636	N
PHACTR1	rs9395550	6	13335987	13228008	G	C	0.0838	0.0805	0.0871	intron	intron7 bp21640	N
PHACTR1	rs185255302	6	13381067	13273088	G	A	0.0046	0.0034	0.0058	intron	intron9 bp42663	N
PHACTR1	chr6:13386468	6	13386468	13278489	A	T	0.0011	0.0015	0.0006	intron	intron10 bp5342	N
PHACTR1	chr6:13395295	6	13395295	13287316	G	A	0.001	0	0.002	utr_3p		N

PHACTR1	rs186017527	6	13395335	13287356	T	G	0.0059	0.0101	0.0018	utr_3p		N
PHACTR1	rs693758	6	13395379	13287400	G	A	0.0221	0.019	0.0253	utr_3p		N
PHACTR1	chr6:13395927	6	13395927	13287948	C	T	0.0005	0	0.001	near_gene_3p_(500_bp)		N
LTA	chr6:31647586	6	31647586	31539607	C	G	0.001	0.001	0.001	near_gene_5p_(2000_bp)		N
LTA	rs56161754,rs19265943	6	31647714	31539735	C	T	0.001	0.001	0.001	near_gene_5p_(2000_bp)		N
LTA	chr6:31647834	6	31647834	31539855	C	T	0.0009	0	0.0019	near_gene_5p_(2000_bp)		N
LTA	rs145829373	6	31647953	31539974	G	A	0.0022	0.0023	0.002	utr_5p		N
LTA	rs1800683,rs144330064	6	31648050	31540071	G	A	0.3129	0.3049	0.3209	utr_5p		N
LTA	rs2229094,rs142176367	6	31648535	31540556	T	C	0.2622	0.2567	0.2678	missense	Cys13Arg (TGT=>CGT) [exon2]	Y
LTA	rs3093542	6	31648672	31540693	G	C	0.028	0.022	0.0339	intron	intron2 bp75	N
LTA	rs141682185,rs2229092	6	31648736	31540757	A	C	0.0538	0.0591	0.0485	missense	His51Pro (CAC=>CCC) [exon3]	N
LTA	rs1041981,rs142541719	6	31648763	31540784	C	A	0.3259	0.3233	0.3285	missense	Thr60Asn (ACC=>AAC) [exon3]	Y
LTA	rs56285847	6	31648800	31540821	A	G	0.0037	0.0035	0.004	intron	intron3 bp11	N
LTA	rs55749341	6	31649496	31541517	C	G	0.0005	0	0.001	utr_3p		N
LTA	chr6:31649688	6	31649688	31541709	G	A	0.001	0	0.002	utr_3p		N
LTA	rs3093545,rs149469508	6	31649938	31541959	G	C	0.0038	0.001	0.0066	utr_3p		N
TNF	rs4248157	6	31650122	31542143	C	G	0.0014	0.0009	0.0019	near_gene_5p_(2000_bp)		N
TNF	rs1799964	6	31650287	31542308	T	C	0.2203	0.2139	0.2266	near_gene_5p_(2000_bp)		Y
TNF	rs1800630,rs181370386	6	31650455	31542476	C	A	0.1846	0.1954	0.1737	near_gene_5p_(2000_bp)		Y
TNF	rs1799724	6	31650461	31542482	C	T	0.1128	0.1102	0.1153	near_gene_5p_(2000_bp)		N
TNF	rs4248158	6	31650512	31542533	C	T	0.0194	0.0215	0.0172	near_gene_5p_(2000_bp)		N
MTHFD1L	rs77293546	6	151228337	151186644	T	A	0.1131	0.1173	0.1089	near_gene_5p_(2000_bp)		N
MTHFD1L	chr6:151238982	6	151238982	151197289	G	T	0.0006	0.0012	0	missense	Lys97Asn (AAG=>AAT) [exon2]	N
MTHFD1L	rs144673274	6	151239003	151197310	G	A	0.0005	0	0.001	synonymous	Gln104Gln (CAG=>CAA) [exon2]	Y
MTHFD1L	rs2073064	6	151240588	151198895	T	C	0.1328	0.1298	0.1359	intron	intron3 bp75	N
MTHFD1L	rs146351770	6	151240625	151198932	T	C	0.0024	0.001	0.0039	synonymous	Ile129Ile (ATT=>ATC) [exon4]	N
MTHFD1L	rs190251947	6	151281426	151239733	C	T	0.0069	0.0097	0.0042	missense	Pro305Ser (CCA=>TCA) [exon9]	N
MTHFD1L	rs73013121	6	151285141	151243448	G	A	0.0201	0.024	0.0163	intron	intron10 bp10	N
MTHFD1L	rs9478857	6	151285160	151243467	G	A	0.0328	0.0393	0.0264	intron	intron10 bp29	N
MTHFD1L	chr6:151289111	6	151289111	151247418	G	A	0.0005	0.001	0	missense	Val415Ile (GTC=>ATC) [exon11]	N
MTHFD1L	rs803455	6	151289132	151247439	A	G	0.9321	0.9319	0.9324	intron	intron11 bp8	N

MTHFD1L	rs140780101	6	151299678	151257985	C	T	0.0014	0.001	0.0019	synonymous	Ile434Ile (ATC=>ATT) [exon12]	Y
MTHFD1L	rs2073189	6	151299803	151258110	G	T	0.051	0.0533	0.0488	intron	intron12 bp34	N
MTHFD1L	rs742831	6	151299815	151258122	G	A	0.0338	0.0339	0.0337	intron	intron12 bp46	N
MTHFD1L	rs742830	6	151299820	151258127	G	A	0.3107	0.3195	0.3019	intron	intron12 bp51	N
MTHFD1L	rs2073191	6	151308257	151266564	T	C	0.2529	0.2551	0.2506	intron	intron14 bp835	N
MTHFD1L	rs803444	6	151308410	151266717	G	A	0.3065	0.323	0.2899	intron	intron15 bp40	N
MTHFD1L	rs139593487	6	151311840	151270147	T	A	0.0005	0	0.001	intron	intron15 bp3470	N
MTHFD1L	rs61748674	6	151311924	151270231	G	A	0.0137	0.0124	0.0149	missense	Arg563His (CGT=>CAT) [exon16]	Y
MTHFD1L	chr6:151327879	6	151327879	151286186	C	T	0.0021	0.0023	0.002	intron	intron19 bp13	N
MTHFD1L	rs509474	6	151378432	151336739	C	G	0.4425	0.4371	0.4479	synonymous	Ser832Ser (TCC=>TCG) [exon24]	N
MTHFD1L	chr6:151378516	6	151378516	151336823	T	C	0.0009	0	0.0019	synonymous	Asp860Asp (GAT=>GAC) [exon24]	N
MTHFD1L	chr6:151397421	6	151397421	151355728	A	G	0.001	0.002	0	missense	Thr896Ala (ACT=>GCT) [exon25]	N
MTHFD1L	chr6:151399762	6	151399762	151358069	T	A	0.0009	0	0.0018	intron	intron25 bp2333	N
MTHFD1L	rs56120305	6	151399765	151358072	G	A	0.0335	0.0349	0.0321	intron	intron25 bp2336	N
MTHFD1L	chr6:151399825	6	151399825	151358132	A	G	0.0058	0.0053	0.0062	missense	Lys909Arg (AAG=>AGG) [exon26]	N
MTHFD1L	chr6:151399863	6	151399863	151358170	G	A	0.0063	0.006	0.0066	missense	Gly922Ser (GGT=>AGT) [exon26]	N
MTHFD1L	chr6:151399898	6	151399898	151358205	C	T	0.0679	0.069	0.0669	synonymous	Asp933Asp (GAC=>GAT) [exon26]	N
MTHFD1L	chr6:151399906	6	151399906	151358213	C	T	0.1008	0.1022	0.0994	missense	Ala936Val (GCC=>GTC) [exon26]	N
MTHFD1L	rs115732448	6	151399912	151358219	T	C	0.14	0.1436	0.1364	missense	Ile938Thr (ATA=>ACA) [exon26]	N
MTHFD1L	rs114123717	6	151399915	151358222	G	A	0.1496	0.1545	0.1447	missense	Gly939Asp (GGC=>GAC) [exon26]	N
MTHFD1L	rs78374443	6	151399951	151358258	G	A	0.1192	0.1231	0.1153	intron	intron26 bp5	N
MTHFD1L	rs9478918	6	151399992	151358299	T	C	0.848	0.8358	0.8602	intron	intron26 bp46	N
MTHFD1L	rs117969540	6	151455410	151413717	G	T	0.0486	0.0556	0.0415	utr_3p		N
MTHFD1L	rs75272597	6	151455464	151413771	C	T	0.0171	0.0178	0.0164	intron	intron27 bp48	N
MTHFD1L	rs7646	6	151464443	151422750	A	G	0.2489	0.2194	0.2785	utr_3p		N
MTHFD1L	rs1047662	6	151464528	151422835	C	G	0.0789	0.0853	0.0725	utr_3p		N
MTHFD1L	rs7543	6	151464629	151422936	G	A	0.4114	0.4279	0.3949	utr_3p		N
MTHFD1L	rs1047665	6	151464648	151422955	A	G	0.0785	0.0851	0.0718	utr_3p		N
MTHFD1L	rs138693638	6	151464747	151423054	T	C	0.0015	0.001	0.002	near_gene_3p_(500_bp)		N
MTHFD1L	rs41289359	6	151464786	151423093	G	A	0.0308	0.0175	0.0441	near_gene_3p_(500_bp)		N
ARL4A	rs143211563	7	12692540	12726015	T	G	0.002	0.002	0.002	near_gene_5p_(2000_bp)		N

ARL4A	rs13224956	7	12692593	12726068	G	A	0.0641	0.0695	0.0588	near_gene_5p_(2000_bp)		N
ARL4A	rs3757442	7	12692688	12726163	C	T	0.1444	0.1307	0.1582	near_gene_5p_(2000_bp)		N
ARL4A	chr7:12692707	7	12692707	12726182	G	A	0.0042	0.0031	0.0054	near_gene_5p_(2000_bp)		N
ARL4A	rs12699414	7	12692778	12726253	T	C	0.0695	0.0751	0.0639	near_gene_5p_(2000_bp)		N
ARL4A	rs13227823	7	12692975	12726450	A	G	0.0317	0.0312	0.0322	near_gene_5p_(2000_bp)		N
ARL4A	rs117002576	7	12693084	12726559	G	A	0.0459	0.0476	0.0443	utr_5p		N
ARL4A	chr7:12693459	7	12693459	12726934	G	T	0.0011	0.0002	0.0019	intron	intron1 bp266	N
ARL4A	rs138805218	7	12693606	12727081	G	C	0.0081	0.009	0.0073	utr_5p		N
ARL4A	rs2280634	7	12693684	12727159	C	T	0.1397	0.1305	0.1488	utr_5p		N
ARL4A	rs73300788	7	12693715	12727190	C	A	0.0032	0.0019	0.0045	utr_5p		N
ARL4A	rs71536895	7	12693904	12727379	G	A	0.066	0.0725	0.0596	intron	intron1 bp26	N
ARL4A	rs13232089	7	12694306	12727781	C	T	0.0358	0.0431	0.0286	intron	intron1 bp428	N
ARL4A	rs2280633	7	12694351	12727826	G	C	0.6404	0.6095	0.6713	utr_5p		N
ARL4A	rs150387436	7	12694434	12727909	T	C	0.003	0.002	0.0039	synonymous	Ser10Ser (TCT=>TCC) [exon2]	N
ARL4A	rs112853446	7	12695014	12728489	A	G	0.1872	0.1741	0.2003	utr_3p		N
ARL4A	chr7:12695348	7	12695348	12728823	A	G	0.0005	0.001	0	utr_3p		N
ARL4A	rs73300794	7	12695356	12728831	C	T	0.003	0.0021	0.004	utr_3p		N
ARL4A	rs73053484	7	12695387	12728862	C	G	0.0562	0.0537	0.0586	utr_3p		N
ARL4A	rs1058268	7	12695794	12729269	C	G	0.1082	0.1005	0.116	utr_3p		N
ARL4A	rs73053490	7	12696011	12729486	G	C	0.0019	0.0018	0.002	utr_3p		N
ARL4A	rs62449782	7	12696129	12729604	T	G	0.2537	0.2433	0.2642	utr_3p		N
ARL4A	rs73053491	7	12696458	12729933	T	G	0.0326	0.0246	0.0407	utr_3p		N
ARL4A	chr7:12696530	7	12696530	12730005	G	A	0.001	0	0.0019	utr_3p		N
ARL4A	chr7:12696623	7	12696623	12730098	A	G	0.0025	0.003	0.002	utr_3p		N
ARL4A	rs79385141	7	12696806	12730281	G	T	0.179	0.1701	0.1878	utr_3p		N
ARL4A	rs76875269	7	12696842	12730317	A	T	0.187	0.1796	0.1945	utr_3p		N
ARL4A	rs35689560	7	12696887	12730362	A	G	0.4134	0.3995	0.4273	utr_3p		N
ARL4A	rs73678526	7	12697028	12730503	T	G	0.0331	0.0294	0.0369	utr_3p		N
ARL4A	chr7:12697176	7	12697176	12730651	A	G	0.0005	0	0.001	near_gene_3p_(500_bp)		N
IQUB	rs117254414	7	122879356	123092120	G	A	0.0411	0.0356	0.0466	near_gene_3p_(500_bp)		N
IQUB	chr7:122879382	7	122879382	123092146	A	G	0.0005	0	0.001	near_gene_3p_(500_bp)		N

IQUB	chr7:122879392	7	122879392	123092156	T	C	0.0005	0	0.001	near_gene_3p_(500_bp)		N
IQUB	rs7789409	7	122879538	123092302	C	T	0.2907	0.298	0.2835	utr_3p		N
IQUB	chr7:122879919	7	122879919	123092683	C	A	0.0026	0.0034	0.0018	utr_3p		N
IQUB	chr7:122879926	7	122879926	123092690	C	A	0.0017	0.0034	0.0001	utr_3p		N
IQUB	rs189953913	7	122880005	123092769	G	A	0.0011	0.0012	0.001	utr_3p		N
IQUB	rs10234745	7	122884704	123097468	T	C	0.2681	0.2731	0.2631	synonymous	Ala720Ala (GCA=>GCG) [exon12]	N
IQUB	chr7:122884772	7	122884772	123097536	T	C	0.0015	0	0.003	missense	Met698Val (ATG=>GTG) [exon12]	N
IQUB	rs145461420	7	122884819	123097583	G	A	0.0069	0.004	0.0097	missense	Ala682Val (GCG=>GTG) [exon12]	Y
IQUB	chr7:122892188	7	122892188	123104952	C	A	0.0032	0.0028	0.0036	missense	Ala565Ser (GCG=>TCG) [exon10]	N
IQUB	rs10500091	7	122907226	123119990	T	C	0.2833	0.286	0.2805	synonymous	Gln423Gln (CAA=>CAG) [exon8]	N
IQUB	rs143722337	7	122930267	123143031	G	A	0.006	0.0075	0.0044	synonymous	Pro278Pro (CCC=>CCT) [exon5]	N
IQUB	rs146361404	7	122930397	123143161	T	C	0.0042	0.0051	0.0033	missense	Gln235Arg (CAA=>CGA) [exon5]	Y
IQUB	rs140926528	7	122930542	123143306	A	G	0.0005	0	0.001	missense	Ile215Thr (ATA=>ACA) [exon4]	N
IQUB	rs138085330	7	122930600	123143364	C	T	0.0053	0.0065	0.004	missense	Glu196Lys (GAA=>AAA) [exon4]	Y
IQUB	rs10255061	7	122939255	123152019	C	T	0.2723	0.2763	0.2684	missense	Val126Met (GTG=>ATG) [exon2]	Y
IQUB	rs10270705	7	122939271	123152035	T	C	0.3456	0.3471	0.344	synonymous	Glu120Glu (GAA=>GAG) [exon2]	N
IQUB	rs12154584	7	122961769	123174533	T	C	0.342	0.3495	0.3344	intron	intron1 bp13	N
IQUB	chr7:122961868	7	122961868	123174632	T	C	0.0022	0.001	0.0034	utr_5p		N
	rs60350749	8	998927	1011520	C	G	0.0005	0	0.001	intergenic		N
LPL	rs17091742	8	19840410	19796130	C	T	0.021	0.0261	0.016	near_gene_5p_(2000_bp)		N
LPL	chr8:19840432	8	19840432	19796152	G	T	0.0006	0.0012	0	near_gene_5p_(2000_bp)		N
LPL	chr8:19840626	8	19840626	19796346	A	G	0.0015	0.0011	0.0019	near_gene_5p_(2000_bp)		N
LPL	chr8:19841209	8	19841209	19796929	C	T	0.0016	0.0001	0.0031	utr_5p		N
LPL	rs1801177	8	19849988	19805708	G	A	0.0246	0.0281	0.0211	missense	Asp36Asn (GAC=>AAC) [exon2]	Y
LPL	chr8:19850025	8	19850025	19805745	A	T	0.0016	0.0013	0.0019	missense	Asp48Val (GAC=>GTC) [exon2]	N
LPL	rs1121923	8	19853715	19809435	G	A	0.0241	0.0244	0.0238	synonymous	Val135Val (GTG=>GTA) [exon3]	N
LPL	rs343	8	19855067	19810787	C	A	0.0841	0.0721	0.096	intron	intron3 bp1328	N
LPL	rs248	8	19855106	19810826	G	A	0.0677	0.0709	0.0645	synonymous	Glu145Glu (GAG=>GAA) [exon4]	N
LPL	chr8:19855110	8	19855110	19810830	A	C	0.0005	0.001	0	missense	Asn147His (AAC=>CAC) [exon4]	N
LPL	rs118204057	8	19856013	19811733	G	A	0.0025	0.0031	0.002	missense	Gly215Glu (GGG=>GAG) [exon5]	Y
LPL	rs45607438	8	19856056	19811776	T	C	0.0005	0.0011	0	synonymous	His229His (CAT=>CAC) [exon5]	N

LPL	chr8:19857591	8	19857591	19813311	T	C	0.001	0.001	0.001	intron	intron5 bp1447	N
LPL	rs140986245	8	19857642	19813362	G	A	0.0051	0.0051	0.0051	synonymous	Gln262Gln (CAG=>CAA) [exon6]	N
LPL	rs118204068	8	19857685	19813405	G	A	0.0005	0.001	0	missense	Asp277Asn (GAC=>AAC) [exon6]	N
LPL	chr8:19857690	8	19857690	19813410	T	C	0.0006	0.0012	0	synonymous	Ser278Ser (TCT=>TCC) [exon6]	N
LPL	rs268	8	19857809	19813529	A	G	0.0114	0.0095	0.0133	missense	Asn318Ser (AAT=>AGT) [exon6]	Y
LPL	rs190249506	8	19857908	19813628	A	G	0.0026	0.0026	0.0025	intron	intron6 bp34	N
LPL	rs301	8	19861214	19816934	T	C	0.3751	0.372	0.3781	intron	intron7 bp43	Y
LPL	rs316	8	19862716	19818436	C	A	0.1171	0.1206	0.1137	synonymous	Thr388Thr (ACC=>ACA) [exon8]	N
LPL	rs328	8	19864004	19819724	C	G	0.0973	0.0965	0.0982	nonsense	Ser474Stop (TCA=>TGA) [exon9]	Y
LPL	rs11570891	8	19867090	19822810	C	T	0.1067	0.097	0.1164	intron	intron9 bp3080	N
LPL	rs4922115	8	19867110	19822830	G	A	0.1523	0.154	0.1506	utr_3p		N
LPL	rs3289	8	19867472	19823192	T	C	0.0287	0.0257	0.0317	utr_3p		N
LPL	rs11570892	8	19867897	19823617	A	G	0.1481	0.1522	0.144	utr_3p		N
LPL	rs1803924	8	19867954	19823674	C	T	0.1008	0.0932	0.1084	utr_3p		N
LPL	chr8:19868183	8	19868183	19823903	C	G	0.0011	0.0022	0	utr_3p		N
LPL	rs1059507	8	19868243	19823963	C	T	0.1536	0.1561	0.151	utr_3p		N
LPL	rs150252331	8	19868268	19823988	C	A	0.0133	0.0139	0.0126	utr_3p		N
LPL	rs3735964	8	19868325	19824045	C	A	0.1014	0.0947	0.1082	utr_3p		N
LPL	rs3200218	8	19868351	19824071	A	G	0.2534	0.2543	0.2525	utr_3p		N
LPL	rs1803923	8	19868488	19824208	T	C	0.0044	0.002	0.0067	utr_3p		N
LPL	rs58998793	8	19868517	19824237	T	C	0.0005	0.001	0	utr_3p		N
LPL	chr8:19868690	8	19868690	19824410	G	A	0.0006	0.0012	0	utr_3p		N
LPL	rs13702	8	19868772	19824492	T	C	0.2761	0.2749	0.2774	utr_3p		Y
LPL	rs1059611	8	19868843	19824563	T	C	0.0996	0.0928	0.1063	utr_3p		N
LPL	rs3916027	8	19869148	19824868	G	A	0.2577	0.2556	0.2598	near_gene_3p_(500_bp)		N
LPL	rs9644636	8	19869176	19824896	T	G	0.2766	0.2719	0.2813	near_gene_3p_(500_bp)		N
LPL	rs113831503	8	19869335	19825055	C	T	0.0329	0.038	0.0278	near_gene_3p_(500_bp)		N
LPL	rs4921683	8	19869348	19825068	T	A	0.1519	0.159	0.1448	near_gene_3p_(500_bp)		N
LPL	rs76707496	8	19869404	19825124	G	A	0.0005	0.001	0	near_gene_3p_(500_bp)		N
LPL	rs4921684	8	19869408	19825128	C	T	0.1547	0.1576	0.1518	near_gene_3p_(500_bp)		N
	rs80085105	8	19869577	19825297	T	C	0.0084	0.0079	0.0088	intergenic		N

PTPRD	chr9:8669005	9	8669005	8679005	A	C	0.0016	0.0033	0	intron	intron12 bp54775	N
C9orf53	rs112307232	9	21957207	21967207	G	A	0.0081	0.0077	0.0084	utr_5p		N
C9orf53	chr9:21957291	9	21957291	21967291	T	G	0.0064	0.0045	0.0082	utr_5p		N
C9orf53	chr9:21957586	9	21957586	21967586	C	A	0.0005	0.001	0	utr_5p		N
CDKN2A	chr9:21957931	9	21957931	21967931	C	T	0.0005	0.001	0	utr_3p		N
CDKN2A	rs3088440	9	21958159	21968159	G	A	0.0822	0.0764	0.0879	utr_3p		N
CDKN2A	rs11515	9	21958199	21968199	C	G	0.8334	0.8372	0.8295	utr_3p		N
CDKN2A	rs3731249	9	21960916	21970916	C	T	0.0399	0.0384	0.0414	missense	Ala148Thr (GCG=>ACG) [exon2]	Y
CDKN2A	rs45456595	9	21964640	21974640	C	G	0.0021	0.0021	0.0022	missense	Gly63Arg (GGG=>CGG) [exon1]	Y
CDKN2A	rs3814960	9	21965017	21975017	C	T	0.6417	0.6458	0.6377	utr_5p		N
CDKN2BAS	rs55797833	9	21985044	21995044	T	G	0.0209	0.0168	0.025	utr_5p		N
CDKN2BAS	chr9:21992487	9	21992487	22002487	C	A	0.0173	0.0178	0.0169	intron	intron1 bp7327	N
CDKN2BAS	chr9:21992490	9	21992490	22002490	T	C	0.0054	0.0045	0.0063	intron	intron1 bp7330	N
CDKN2BAS	chr9:21992509	9	21992509	22002509	A	G	0.0005	0	0.001	intron	intron1 bp7349	N
CDKN2BAS	rs3217994	9	21992864	22002864	T	C	0.0093	0.0115	0.007	intron	intron1 bp7704	N
CDKN2B	chr9:21992986	9	21992986	22002986	A	G	0.0026	0.0025	0.0028	utr_3p		N
CDKN2B	chr9:21993050	9	21993050	22003050	A	G	0.0008	0	0.0016	utr_3p		N
CDKN2B	rs3217992	9	21993223	22003223	C	T	0.4314	0.4559	0.4069	utr_3p		Y
CDKN2B	rs1063192	9	21993367	22003367	G	A	0.6246	0.6338	0.6154	utr_3p		Y
CDKN2B	chr9:21993417	9	21993417	22003417	A	C	0.0005	0.001	0	utr_3p		N
CDKN2B	rs3217990	9	21993521	22003521	G	T	0.0097	0.012	0.0074	utr_3p		N
CDKN2B	chr9:21993553	9	21993553	22003553	A	G	0.0008	0	0.0017	utr_3p		N
CDKN2B	rs185130567	9	21993591	22003591	T	C	0.0079	0.0067	0.0092	utr_3p		N
CDKN2B	rs41306083	9	21994322	22004322	T	G	0.0036	0.0024	0.0048	utr_3p		N
CDKN2B	chr9:21994542	9	21994542	22004542	C	T	0.0009	0.001	0.0009	utr_3p		N
CDKN2B	chr9:21995293	9	21995293	22005293	T	G	0.001	0.001	0.001	utr_3p		N
CDKN2B	rs3217986	9	21995330	22005330	T	G	0.0674	0.0677	0.0672	utr_3p		N
CDKN2B	rs3217984	9	21995493	22005493	G	C	0.0109	0.0136	0.0082	utr_3p		N
CDKN2B	rs148421170	9	21996147	22006147	C	T	0.0018	0.0024	0.0011	missense	Asp86Asn (GAT=>AAT) [exon2]	N
CDKN2B	rs2069426	9	21996273	22006273	G	T	0.0918	0.0819	0.1018	intron	intron1 bp2524	N
CDKN2B	chr9:21998958	9	21998958	22008958	A	G	0.0007	0.0005	0.001	utr_5p		N

CDKN2B	rs138552700	9	21999040	22009040	C	T	0.0047	0.0012	0.0082	utr_5p		N
CDKN2B	chr9:21999050	9	21999050	22009050	C	G	0.0011	0	0.0022	utr_5p		N
CDKN2BAS	rs2069419	9	21999337	22009337	G	T	0.0015	0.0011	0.002	intron	intron1 bp14177	N
CDKN2BAS	rs116868578	9	21999628	22009628	A	G	0.0045	0.0061	0.003	intron	intron1 bp14468	N
CDKN2BAS	rs2069418	9	21999698	22009698	G	C	0.6043	0.6072	0.6014	intron	intron1 bp14538	N
CDKN2BAS	rs10965215	9	22019445	22029445	G	A	0.526	0.5465	0.5056	utr_5p		N
CDKN2BAS	rs564398	9	22019547	22029547	T	C	0.3392	0.3243	0.3542	utr_5p		Y
CDKN2BAS	rs188942730	9	22022728	22032728	T	C	0.0005	0	0.001	utr_5p		N
CDKN2BAS	rs76521274	9	22022793	22032793	T	C	0.0101	0.0138	0.0065	utr_5p		N
CDKN2BAS	rs10738605	9	22039130	22049130	C	G	0.5195	0.5365	0.5026	utr_5p		N
CDKN2BAS	chr9:22039237	9	22039237	22049237	A	G	0.0009	0.0018	0	intron	intron6 bp10	N
CDKN2BAS	rs78509876	9	22048581	22058581	A	G	0.001	0.001	0.0011	utr_5p		N
CDKN2BAS	rs4977754	9	22052012	22062012	A	C	0.0417	0.0366	0.0468	utr_5p		N
CDKN2BAS	rs77583149	9	22053903	22063903	G	A	0.0072	0.0049	0.0095	intron	intron9 bp1878	N
CDKN2BAS	rs78668487	9	22055620	22065620	A	G	0.0104	0.0069	0.014	intron	intron10 bp1603	N
CDKN2BAS	rs1333039	9	22055657	22065657	G	C	0.6698	0.6723	0.6672	intron	intron10 bp1640	N
CDKN2BAS	chr9:22111149	9	22111149	22121149	A	C	0.001	0	0.0021	near_gene_3p_(500_bp)		N
MAMDC2	chr9:71903354	9	71903354	72713534	T	G	0.0043	0.0026	0.006	intron	intron2 bp53921	N
MAMDC2	rs2997691	9	71903365	72713545	A	C	0.0017	0.0011	0.0023	intron	intron2 bp53932	N
	chr9:106582596	9	106582596	107542775	C	A	0.002	0.002	0.002	intergenic		N
ABCA1	rs188076682	9	106582861	107543040	A	C	0.0033	0.0029	0.0037	near_gene_3p_(500_bp)		N
ABCA1	rs2482432	9	106582993	107543172	T	C	0.4475	0.4607	0.4343	near_gene_3p_(500_bp)		N
ABCA1	rs10991377	9	106583197	107543376	T	C	0.0448	0.0424	0.0473	utr_3p		N
ABCA1	chr9:106583292	9	106583292	107543471	G	T	0.001	0	0.002	utr_3p		N
ABCA1	rs181614282	9	106583388	107543567	T	C	0.0009	0.001	0.0009	utr_3p		N
ABCA1	chr9:106583505	9	106583505	107543684	A	T	0.0011	0.0003	0.002	utr_3p		N
ABCA1	chr9:106583520	9	106583520	107543699	C	T	0.0111	0.0127	0.0094	utr_3p		N
ABCA1	rs75141626	9	106583712	107543891	C	T	0.0011	0.0002	0.0019	utr_3p		N
ABCA1	chr9:106583921	9	106583921	107544100	C	T	0.0005	0	0.001	utr_3p		N
ABCA1	rs4149341	9	106584106	107544285	T	C	0.1809	0.1738	0.1879	utr_3p		N
ABCA1	rs41437944	9	106584494	107544673	T	G	0.0124	0.0123	0.0125	utr_3p		N

ABCA1	rs4149340	9	106584506	107544685	G	A	0.0032	0.0039	0.0024	utr_3p		N
ABCA1	rs363717	9	106584521	107544700	C	T	0.8339	0.8451	0.8228	utr_3p		N
ABCA1	rs4149339	9	106584977	107545156	G	A	0.2803	0.2859	0.2747	utr_3p		N
ABCA1	chr9:106585322	9	106585322	107545501	G	A	0.0059	0.0068	0.005	utr_3p		N
ABCA1	chr9:106585460	9	106585460	107545639	G	A	0.001	0.001	0.001	utr_3p		N
ABCA1	rs4149338	9	106585724	107545903	G	A	0.2817	0.2836	0.2798	utr_3p		N
ABCA1	rs73517870	9	106586022	107546201	A	T	0.0005	0.001	0	utr_3p		N
ABCA1	rs146987516	9	106586075	107546254	C	A	0.0016	0.001	0.0022	utr_3p		N
ABCA1	chr9:106586118	9	106586118	107546297	G	T	0.0015	0.001	0.002	utr_3p		N
ABCA1	chr9:106586211	9	106586211	107546390	A	G	0.0005	0.001	0	utr_3p		N
ABCA1	rs1331924	9	106587443	107547622	C	G	0.1477	0.1605	0.135	intron	intron49 bp55	N
ABCA1	chr9:106587696	9	106587696	107547875	G	A	0.0011	0.0022	0	synonymous	Asn2149Asn (AAC=>AAT) [exon49]	N
ABCA1	rs2066881	9	106588387	107548566	T	C	0.0414	0.0374	0.0453	intron	intron48 bp13	N
ABCA1	rs73517878	9	106589112	107549291	G	A	0.0246	0.0233	0.0259	intron	intron46 bp910	N
ABCA1	rs9282537	9	106590043	107550222	G	A	0.0245	0.0266	0.0224	synonymous	Gly2061Gly (GGC=>GGT) [exon46]	N
ABCA1	rs2020927	9	106593006	107553185	A	G	0.1065	0.0973	0.1158	intron	intron44 bp18	N
ABCA1	rs34078184	9	106594095	107554274	A	G	0.0005	0	0.001	synonymous	Tyr1921Tyr (TAT=>TAC) [exon43]	N
ABCA1	chr9:106596438	9	106596438	107556617	A	G	0.001	0	0.002	intron	intron40 bp51	N
ABCA1	chr9:106598206	9	106598206	107558385	A	G	0.0009	0	0.0018	synonymous	Ile1777Ile (ATT=>ATC) [exon39]	N
ABCA1	chr9:106598456	9	106598456	107558635	G	C	0.0015	0.003	0	missense	Ser1731Cys (TCC=>TGC) [exon38]	N
ABCA1	rs2230808	9	106602625	107562804	T	C	0.7693	0.7815	0.7571	missense	Lys1587Arg (AAA=>AGA) [exon35]	Y
ABCA1	chr9:106602704	9	106602704	107562883	C	G	0.0018	0.0027	0.0009	intron	intron34 bp1452	N
ABCA1	rs2297404	9	106604287	107564466	C	G	0.0641	0.0531	0.0751	intron	intron33 bp1099	N
ABCA1	chr9:106605335	9	106605335	107565514	A	G	0.0005	0.001	0	intron	intron33 bp51	N
ABCA1	chr9:106605444	9	106605444	107565623	C	T	0.001	0.001	0.001	intron	intron32 bp1284	N
ABCA1	rs2777801	9	106606698	107566877	C	A	0.8887	0.8997	0.8778	intron	intron32 bp30	N
ABCA1	rs41277763	9	106606751	107566930	C	A	0.0267	0.0291	0.0242	synonymous	Thr1512Thr (ACG=>ACT) [exon32]	N
ABCA1	rs2066716	9	106608526	107568705	C	T	0.0847	0.0889	0.0805	synonymous	Thr1427Thr (ACG=>ACA) [exon31]	N
ABCA1	chr9:106612885	9	106612885	107573064	G	A	0.0008	0	0.0017	intron	intron29 bp17	N
ABCA1	chr9:106613050	9	106613050	107573229	C	A	0.0046	0.0001	0.009	intron	intron28 bp1626	N
ABCA1	rs115666991	9	106613060	107573239	G	A	0.0025	0.0023	0.0027	intron	intron28 bp1616	N

ABCA1	chr9:106614669	9	106614669	107574848	G	A	0.0005	0	0.001	intron	intron28 bp7	N
ABCA1	rs111337110	9	106616486	107576665	A	G	0.0028	0.0021	0.0035	intron	intron26 bp43	N
ABCA1	rs2234885	9	106618222	107578401	C	T	0.0201	0.0198	0.0204	intron	intron25 bp23	N
ABCA1	rs2230807	9	106618299	107578478	C	T	0.0008	0.0007	0.001	synonymous	Arg1228Arg (CGG=>CGA) [exon25]	N
ABCA1	chr9:106618325	9	106618325	107578504	C	T	0.0013	0.0027	0	missense	Glu1220Lys (GAA=>AAA) [exon25]	N
ABCA1	chr9:106618333	9	106618333	107578512	G	C	0.0009	0	0.0017	missense	Ala1217Gly (GCC=>GGC) [exon25]	N
ABCA1	rs34788556	9	106618350	107578529	T	C	0.004	0.004	0.0041	synonymous	Glu1211Glu (GAA=>GAG) [exon25]	N
ABCA1	rs76881554	9	106618441	107578620	G	A	0.002	0.001	0.003	missense	Ser1181Phe (TCT=>TTT) [exon25]	Y
ABCA1	rs33918808	9	106619453	107579632	C	G	0.0212	0.0206	0.0217	missense	Glu1172Asp (GAG=>GAC) [exon24]	Y
ABCA1	rs55814314	9	106621725	107581904	G	A	0.0009	0	0.0019	synonymous	Arg1068Arg (CGC=>CGT) [exon22]	N
ABCA1	rs35871586	9	106621770	107581949	A	C	0.0132	0.0098	0.0166	synonymous	Val1053Val (GTT=>GTG) [exon22]	N
ABCA1	rs60913410	9	106623459	107583638	C	T	0.0007	0.0003	0.001	intron	intron20 bp18	N
ABCA1	chr9:106623543	9	106623543	107583722	C	T	0.001	0.001	0.001	missense	Arg965His (CGC=>CAC) [exon20]	N
ABCA1	rs2066714	9	106626574	107586753	T	C	0.1351	0.1265	0.1437	missense	Ile883Met (ATA=>ATG) [exon18]	Y
ABCA1	rs2066715	9	106627854	107588033	C	T	0.0605	0.0528	0.0682	missense	Val825Ile (GTC=>ATC) [exon17]	Y
ABCA1	chr9:106627955	9	106627955	107588134	C	G	0.0005	0.001	0	missense	Cys791Ser (TGT=>TCT) [exon17]	N
ABCA1	rs138880920	9	106629059	107589238	C	G	0.0155	0.0224	0.0085	missense	Lys776Asn (AAG=>AAC) [exon16]	Y
ABCA1	rs35819696	9	106629067	107589246	T	G	0.0069	0.0067	0.0071	missense	Thr774Pro (ACA=>CCA) [exon16]	Y
ABCA1	rs2066718	9	106629076	107589255	C	T	0.0326	0.0311	0.0341	missense	Val771Met (GTG=>ATG) [exon16]	N
ABCA1	chr9:106629152	9	106629152	107589331	C	A	0.001	0	0.002	synonymous	Leu745Leu (CTG=>CTT) [exon16]	N
ABCA1	rs2853579	9	106631093	107591272	G	T	0.1335	0.1273	0.1397	synonymous	Ile680Ile (ATC=>ATA) [exon15]	N
ABCA1	rs34083760	9	106631156	107591335	G	A	0.0005	0.001	0	synonymous	Ile659Ile (ATC=>ATT) [exon15]	N
ABCA1	rs4743763	9	106633003	107593182	A	T	0.2454	0.229	0.2617	intron	intron14 bp24	N
ABCA1	rs142342160	9	106634718	107594897	G	A	0.002	0.002	0.002	synonymous	Asn489Asn (AAC=>AAT) [exon12]	N
ABCA1	chr9:106634859	9	106634859	107595038	G	C	0.0005	0	0.001	missense	Ser442Arg (AGC=>AGG) [exon12]	N
ABCA1	rs138487227	9	106639192	107599371	T	G	0.0005	0	0.001	missense	Lys401Gln (AAG=>CAG) [exon11]	N
ABCA1	rs9282543	9	106639197	107599376	A	G	0.004	0.0055	0.0026	missense	Val399Ala (GTG=>GCG) [exon11]	Y
ABCA1	rs2297399	9	106639211	107599390	G	A	0.0668	0.0628	0.0709	intron	intron10 bp319	N
ABCA1	rs2246841	9	106642487	107602666	C	T	0.0966	0.1062	0.0871	synonymous	Gly316Gly (GGG=>GGA) [exon9]	N
ABCA1	rs2274873	9	106642499	107602678	G	A	0.1014	0.0935	0.1093	synonymous	Pro312Pro (CCC=>CCT) [exon9]	N
ABCA1	chr9:106647599	9	106647599	107607778	G	A	0.0006	0.0012	0	missense	Leu265Phe (CTT=>TTT) [exon8]	N

ABCA1	rs2230806	9	106660688	107620867	C	T	0.261	0.2626	0.2595	missense	Arg219Lys (AGG=>AAG) [exon7]	N
ABCA1	chr9:106663827	9	106663827	107624006	T	C	0.0005	0	0.001	missense	Lys166Arg (AAG=>AGG) [exon6]	N
ABCA1	rs2230805	9	106663850	107624029	C	T	0.2431	0.247	0.2392	synonymous	Leu158Leu (CTG=>CTA) [exon6]	N
ABCA1	rs143894099	9	106685116	107645295	G	A	0.0006	0.0012	0	intron	intron5 bp25	N
ABCA1	rs145183203	9	106686577	107646756	G	A	0.0009	0.0018	0	missense	Pro85Leu (CCG=>CTG) [exon4]	Y
ABCA1	rs7341705	9	106691169	107651348	T	C	0.0005	0.001	0	intron	intron3 bp35	N
ABCA1	rs150520154	9	106691178	107651357	C	T	0.0142	0.0158	0.0126	intron	intron3 bp26	N
ABCA1	rs1800978	9	106705799	107665978	C	G	0.0882	0.0713	0.1051	utr_5p		N
ABCA1	rs111292742	9	106730223	107690402	G	C	0.0317	0.0295	0.0339	utr_5p		N
ABCA1	rs1800977	9	106730271	107690450	G	A	0.3785	0.3712	0.3857	near_gene_5p_(2000_bp)		N
ABCA1	rs2740483	9	106730356	107690535	G	C	0.7141	0.7143	0.7139	near_gene_5p_(2000_bp)		N
ABCA1	chr9:106730524	9	106730524	107690703	C	G	0.0006	0	0.0012	near_gene_5p_(2000_bp)		N
ABCA1	rs2246293	9	106730659	107690838	C	G	0.4546	0.4434	0.4659	near_gene_5p_(2000_bp)		N
CXCL12	rs17883339	10	44185157	44865151	G	A	0.089	0.0988	0.0792	near_gene_3p_(500_bp)		N
CXCL12	rs10900030	10	44185273	44865267	G	A	0.0237	0.0268	0.0207	near_gene_3p_(500_bp)		N
CXCL12	rs1804430	10	44185745	44865739	T	C	0.0243	0.0272	0.0215	utr_3p		N
CXCL12	rs10347	10	44185758	44865752	T	C	0.0006	0.001	0.0003	utr_3p		N
CXCL12	rs1804429	10	44185847	44865841	A	C	0.0257	0.028	0.0234	utr_3p		N
CXCL12	chr10:44185961	10	44185961	44865955	G	A	0.0011	0.0013	0.0009	utr_3p		N
CXCL12	rs1065297	10	44185982	44865976	A	G	0.0248	0.0277	0.022	utr_3p		N
CXCL12	rs266093	10	44186214	44866208	C	G	0.6602	0.6588	0.6617	utr_3p		N
CXCL12	rs41459848	10	44186234	44866228	T	A	0.0226	0.0255	0.0196	utr_3p		N
CXCL12	rs17883887	10	44186253	44866247	T	C	0.1872	0.1937	0.1806	utr_3p		N
CXCL12	rs266092	10	44186281	44866275	T	A	0.056	0.0546	0.0574	utr_3p		N
CXCL12	chr10:44186359	10	44186359	44866353	G	A	0.0034	0.0044	0.0024	utr_3p		N
CXCL12	rs186339497	10	44186423	44866417	A	T	0.0025	0.004	0.001	utr_3p		N
CXCL12	rs2839696	10	44186634	44866628	G	A	0.024	0.0276	0.0204	utr_3p		N
CXCL12	rs1029153	10	44187152	44867146	A	G	0.3055	0.3065	0.3045	utr_3p		N
CXCL12	rs2522	10	44187310	44867304	A	G	0.0221	0.0257	0.0184	utr_3p		N
CXCL12	chr10:44187427	10	44187427	44867421	T	C	0.0005	0	0.001	utr_3p		N
CXCL12	rs10900031	10	44187636	44867630	G	A	0.0251	0.0298	0.0204	utr_3p		N

CXCL12	chr10:44187748	10	44187748	44867742	G	A	0.0005	0	0.001	utr_3p		N
CXCL12	rs3740085	10	44187775	44867769	C	G	0.2791	0.2791	0.2791	utr_3p		N
CXCL12	rs17886187	10	44187876	44867870	C	T	0.0033	0.0023	0.0043	utr_3p		N
CXCL12	rs169097	10	44188089	44868083	A	G	0.9887	0.9891	0.9882	utr_3p		N
CXCL12	chr10:44188153	10	44188153	44868147	G	A	0.001	0.001	0.001	utr_3p		N
CXCL12	chr10:44188177	10	44188177	44868171	A	T	0.0005	0	0.001	utr_3p		N
CXCL12	chr10:44188217	10	44188217	44868211	G	T	0.0015	0.002	0.0011	utr_3p		N
CXCL12	rs1801157	10	44188263	44868257	C	T	0.2285	0.2307	0.2263	utr_3p		N
CXCL12	rs12258838	10	44188471	44868465	C	T	0.023	0.025	0.021	utr_3p		N
CXCL12	rs140248633	10	44188550	44868544	T	C	0.0035	0.0051	0.0019	utr_3p		N
CXCL12	chr10:44188600	10	44188600	44868594	A	G	0.0033	0.0027	0.004	utr_3p		N
CXCL12	rs17881575	10	44191352	44871346	G	A	0.0869	0.0955	0.0784	utr_3p		N
CXCL12	rs78342136	10	44191378	44871372	C	T	0.0045	0.0034	0.0056	utr_3p		N
CXCL12	rs147043282	10	44191403	44871397	C	G	0.001	0.001	0.001	missense	Arg117Thr (AGG=>ACG) [exon4]	Y
CXCL12	chr10:44191476	10	44191476	44871470	C	T	0.0052	0.0046	0.0059	missense	Glu93Lys (GAA=>AAA) [exon4]	N
CXCL12	chr10:44192747	10	44192747	44872741	A	G	0.0005	0.001	0	utr_3p		N
CXCL12	chr10:44192805	10	44192805	44872799	C	T	0.0005	0	0.001	utr_3p		N
CXCL12	chr10:44192900	10	44192900	44872894	T	A	0.0011	0	0.0023	utr_3p		N
CXCL12	rs17881297	10	44192931	44872925	G	A	0.0148	0.0117	0.0179	utr_3p		N
CXCL12	chr10:44193043	10	44193043	44873037	C	T	0.0005	0.001	0	utr_3p		N
CXCL12	rs17880170	10	44193206	44873200	C	A	0.0046	0.0062	0.0031	synonymous	Val140Val (GTG=>GTT) [exon4]	N
CXCL12	chr10:44193270	10	44193270	44873264	C	T	0.0005	0	0.001	missense	Arg119Gln (CGG=>CAG) [exon4]	N
CXCL12	chr10:44193346	10	44193346	44873340	C	T	0.0016	0	0.0032	missense	Ala94Thr (GCA=>ACA) [exon4]	N
CXCL12	chr10:44193583	10	44193583	44873577	C	T	0.0016	0.0024	0.0007	utr_3p		N
CXCL12	rs2839695	10	44193855	44873849	A	G	0.1841	0.1874	0.1807	utr_3p		N
CXCL12	chr10:44194002	10	44194002	44873996	C	T	0.0309	0.029	0.0327	utr_3p		N
CXCL12	chr10:44194006	10	44194006	44874000	A	C	0.0132	0.0126	0.0138	utr_3p		N
CXCL12	rs138862128	10	44196265	44876259	A	G	0.0005	0	0.001	missense	Val44Ala (GTC=>GCC) [exon2]	Y
CXCL12	rs2839687	10	44200844	44880838	T	C	0.1752	0.1909	0.1595	near_gene_5p_(2000_bp)		N
CXCL12	rs17880313	10	44200941	44880935	G	A	0.129	0.1288	0.1291	near_gene_5p_(2000_bp)		N
CXCL12	rs17156283	10	44200963	44880957	A	C	0.004	0.0028	0.0053	near_gene_5p_(2000_bp)		N

	rs7122015	11	96455758	96950548	A	G	0.0042	0.0036	0.0048	intergenic		N
	rs550051	11	104224620	104719410	T	G	0.9934	0.9922	0.9945	intergenic		N
	rs142898866	11	104224673	104719463	A	G	0.0065	0.0063	0.0066	intergenic		N
SH2B3	chr12:110327857	12	110327857	111843474	G	C	0.0005	0	0.0011	near_gene_5p_(2000_bp)		N
SH2B3	chr12:110327870	12	110327870	111843487	C	A	0.0007	0.0001	0.0013	near_gene_5p_(2000_bp)		N
SH2B3	rs183913232	12	110340889	111856506	G	T	0.0076	0.0067	0.0086	missense	Ser186Ile (AGC=>ATC) [exon2]	Y
SH2B3	rs3184504	12	110368991	111884608	T	C	0.5081	0.5018	0.5145	missense	Trp262Arg (TGG=>CGG) [exon3]	Y
SH2B3	rs149554298	12	110369001	111884618	G	A	0.0015	0.001	0.002	missense	Arg265Gln (CGG=>CAG) [exon3]	Y
SH2B3	rs148319611	12	110369139	111884756	G	A	0.0005	0	0.001	missense	Arg282Gln (CGG=>CAG) [exon4]	N
SH2B3	chr12:110369297	12	110369297	111884914	C	T	0.001	0	0.002	intron	intron4 bp77	N
SH2B3	rs74163668	12	110369974	111885591	C	T	0.0025	0.002	0.003	synonymous	Val456Val (GTC=>GTT) [exon7]	Y
SH2B3	rs74163669	12	110370187	111885804	C	T	0.0005	0	0.001	missense	Leu476Phe (CTC=>TTC) [exon8]	Y
SH2B3	chr12:110370256	12	110370256	111885873	C	G	0.0015	0.002	0.0009	missense	Pro499Ala (CCC=>GCC) [exon8]	N
SH2B3	chr12:110370464	12	110370464	111886081	T	C	0.0008	0	0.0016	missense	Ile568Thr (ATA=>ACA) [exon8]	Y
SH2B3	rs1107853	12	110370667	111886284	G	A	0.0015	0.0021	0.001	utr_3p		N
SH2B3	chr12:110370746	12	110370746	111886363	G	A	0.0015	0.001	0.002	utr_3p		N
SH2B3	chr12:110371023	12	110371023	111886640	G	A	0.0005	0.001	0	utr_3p		N
SH2B3	rs11065904	12	110371350	111886967	T	A	0.0035	0.0035	0.0036	utr_3p		N
SH2B3	chr12:110371366	12	110371366	111886983	G	A	0.001	0	0.0021	utr_3p		N
SH2B3	chr12:110371440	12	110371440	111887057	A	C	0.0015	0.002	0.001	utr_3p		N
SH2B3	chr12:110371939	12	110371939	111887556	G	A	0.002	0.0031	0.001	utr_3p		N
SH2B3	rs73410519	12	110371955	111887572	G	T	0.0015	0.002	0.001	utr_3p		N
SH2B3	rs739496	12	110372042	111887659	A	G	0.1953	0.1935	0.1971	utr_3p		N
SH2B3	chr12:110372744	12	110372744	111888361	C	T	0.0011	0	0.0023	utr_3p		N
SH2B3	rs11065906	12	110372939	111888556	A	C	0.0015	0.002	0.0009	utr_3p		N
SH2B3	rs144152836	12	110373191	111888808	T	C	0.0198	0.0192	0.0204	utr_3p		N
SH2B3	chr12:110373228	12	110373228	111888845	G	A	0.001	0	0.002	utr_3p		N
SH2B3	rs142759669	12	110373285	111888902	C	A	0.001	0	0.002	utr_3p		N
SH2B3	chr12:110373576	12	110373576	111889193	G	A	0.0005	0	0.001	utr_3p		N
SH2B3	rs14555	12	110373699	111889316	A	T	0.0013	0.0016	0.001	utr_3p		N
SH2B3	chr12:110373718	12	110373718	111889335	T	C	0.0005	0.001	0	utr_3p		N

SH2B3	rs7311116	12	110373924	111889541	C	T	0.0017	0.0025	0.001	near_gene_3p_(500_bp)		N
SH2B3	rs186769121	12	110373992	111889609	T	C	0.0044	0.0047	0.0041	near_gene_3p_(500_bp)		N
ATXN2	chr12:110374602	12	110374602	111890219	C	T	0.0017	0.0013	0.0021	utr_3p		N
ATXN2	chr12:110374773	12	110374773	111890390	C	T	0.0005	0	0.001	utr_3p		N
ATXN2	rs150319790	12	110374817	111890434	C	G	0.0016	0.0033	0	utr_3p		N
ATXN2	rs143166155	12	110378252	111893869	C	T	0.0027	0.0024	0.003	synonymous	Ala1236Ala (GCG=>GCA) [exon23]	N
ATXN2	chr12:110379461	12	110379461	111895078	G	A	0.002	0	0.004	synonymous	Thr1152Thr (ACC=>ACT) [exon22]	N
ATXN2	rs2301622	12	110379586	111895203	C	G	0.2	0.1969	0.2031	intron	intron21 bp7263	N
ATXN2	chr12:110386823	12	110386823	111902440	A	G	0.0027	0.0021	0.0033	intron	intron21 bp26	N
ATXN2	rs140242317	12	110386897	111902514	G	A	0.0017	0.001	0.0025	missense	Pro1108Ser (CCC=>TCC) [exon21]	Y
ATXN2	chr12:110386934	12	110386934	111902551	C	T	0.001	0	0.0021	intron	intron20 bp5361	N
ATXN2	chr12:110392364	12	110392364	111907981	C	T	0.001	0	0.002	missense	Ala1083Thr (GCC=>ACC) [exon20]	N
ATXN2	chr12:110392424	12	110392424	111908041	G	A	0.0005	0.001	0	missense	Pro1063Ser (CCT=>TCT) [exon20]	N
ATXN2	rs142462470	12	110407977	111923594	G	A	0.0023	0.0038	0.0009	missense	Pro954Ser (CCA=>TCA) [exon17]	Y
ATXN2	rs78209549	12	110410638	111926255	T	G	0.0899	0.0926	0.0871	intron	intron15 bp25	N
ATXN2	chr12:110410764	12	110410764	111926381	C	T	0.0005	0	0.001	synonymous	Glu873Glu (GAG=>GAA) [exon15]	N
ATXN2	chr12:110432203	12	110432203	111947820	A	T	0.001	0.001	0.001	intron	intron12 bp369	N
ATXN2	chr12:110435566	12	110435566	111951183	C	T	0.001	0.0021	0	synonymous	Thr672Thr (ACG=>ACA) [exon11]	N
ATXN2	rs16941540	12	110435758	111951375	T	G	0.0011	0.0022	0	intron	intron10 bp2583	N
ATXN2	rs117851901	12	110440609	111956226	T	C	0.002	0.004	0	missense	Asn491Ser (AAT=>AGT) [exon9]	Y
ATXN2	rs192536857	12	110476309	111991926	C	T	0.0042	0.0032	0.0053	intron	intron3 bp36	N
ATXN2	rs117532831	12	110521833	112037450	G	A	0.1264	0.1279	0.1249	utr_5p		N
ATXN2	chr12:110521854	12	110521854	112037471	T	C	0.0027	0.0014	0.004	utr_5p		N
ATXN2	chr12:110521882	12	110521882	112037499	C	T	0.0017	0.0022	0.0013	near_gene_5p_(2000_bp)		N
ATXN2	rs10849962	12	110521909	112037526	A	G	0.7756	0.7771	0.774	near_gene_5p_(2000_bp)		N
ATXN2	rs183901372	12	110522061	112037678	C	G	0.0005	0	0.001	near_gene_5p_(2000_bp)		N
BRAP	rs73203613	12	110565052	112080669	T	C	0.0122	0.0138	0.0106	utr_3p		N
BRAP	chr12:110565341	12	110565341	112080958	A	G	0.0005	0.001	0	utr_3p		N
BRAP	chr12:110565412	12	110565412	112081029	G	T	0.0213	0.0232	0.0193	utr_3p		N
BRAP	rs6416335	12	110565674	112081291	T	C	0.9774	0.978	0.9769	utr_3p		N
BRAP	chr12:110565949	12	110565949	112081566	C	G	0.0021	0.0011	0.0032	utr_3p		N

BRAP	rs151101195	12	110581440	112097057	C	T	0.0035	0.005	0.002	synonymous	Thr355Thr (ACG=>ACA) [exon8]	N
BRAP	chr12:110587839	12	110587839	112103456	A	T	0.0018	0.0015	0.002	missense	Trp295Arg (TGG=>AGG) [exon6]	N
BRAP	rs146356085	12	110601326	112116943	A	G	0.0124	0.0171	0.0076	intron	intron4 bp12	N
BRAP	chr12:110607851	12	110607851	112123468	G	C	0.0006	0	0.0012	intron	intron1 bp47	N
ACAD10	rs141154493	12	110615028	112130645	G	A	0.001	0.001	0.001	synonymous	Ala44Ala (GCG=>GCA) [exon2]	N
ACAD10	rs7132509	12	110615091	112130708	A	G	0.0046	0.0046	0.0047	intron	intron2 bp8	N
ACAD10	chr12:110628102	12	110628102	112143719	C	T	0.0019	0.0028	0.001	missense	Arg172Trp (CGG=>TGG) [exon4]	N
ACAD10	chr12:110634849	12	110634849	112150466	G	A	0.001	0	0.002	intron	intron6 bp5	N
ACAD10	rs143739010	12	110650324	112165941	A	C	0.0019	0.002	0.0019	missense	Lys413Gln (AAG=>CAG) [exon9]	Y
ACAD10	chr12:110652107	12	110652107	112167724	G	A	0.0011	0.0002	0.002	missense	Arg453His (CGT=>CAT) [exon10]	N
ACAD10	rs36046440	12	110652136	112167753	G	A	0.0029	0.0019	0.004	missense	Asp463Asn (GAC=>AAC) [exon10]	N
ACAD10	chr12:110652190	12	110652190	112167807	C	T	0.0005	0	0.001	intron	intron10 bp47	N
ACAD10	chr12:110656123	12	110656123	112171740	G	A	0.0015	0.002	0.001	missense	Val470Met (GTG=>ATG) [exon11]	N
ACAD10	chr12:110666943	12	110666943	112182560	T	G	0.0007	0	0.0015	missense	Phe610Val (TTC=>GTC) [exon13]	N
ACAD10	chr12:110667037	12	110667037	112182654	A	G	0.0005	0.001	0	missense	Glu641Gly (GAA=>GGA) [exon13]	N
ACAD10	rs150349412	12	110668469	112184086	G	A	0.0021	0.0019	0.0022	missense	Glu752Lys (GAG=>AAG) [exon14]	Y
ACAD10	rs186067085	12	110668512	112184129	T	G	0.001	0.002	0	intron	intron14 bp41	N
ACAD10	rs141918583	12	110669549	112185166	A	T	0.0009	0.0019	0	missense	Asn821Ile (AAC=>ATC) [exon16]	Y
ACAD10	rs34245489	12	110670657	112186274	C	T	0.0311	0.0352	0.027	missense	Ala880Val (GCA=>GTA) [exon17]	Y
ACAD10	chr12:110671276	12	110671276	112186893	A	G	0.001	0	0.002	intron	intron17 bp614	N
ACAD10	rs2074055	12	110676024	112191641	G	A	0.005	0.0046	0.0054	synonymous	Ala961Ala (GCG=>GCA) [exon19]	N
ACAD10	rs138539307	12	110678580	112194197	C	T	0.0005	0.0011	0	nonsense	Arg1034Stop (CGA=>TGA) [exon21]	N
ACAD10	rs142030532	12	110678598	112194215	G	A	0.0023	0.0026	0.002	missense	Asp1040Asn (GAC=>AAC) [exon21]	Y
ACAD10	chr12:110678828	12	110678828	112194445	G	A	0.0005	0.001	0	utr_3p		N
ACAD10	chr12:110679068	12	110679068	112194685	C	T	0.0005	0	0.001	utr_3p		N
ACAD10	rs143161383	12	110679264	112194881	A	G	0.0005	0	0.001	utr_3p		N
ACAD10	rs737280	12	110679359	112194976	T	C	0.2297	0.2284	0.2309	near_gene_3p_(500_bp)		N
ACAD10	rs138694729	12	110679606	112195223	A	G	0.0022	0.0011	0.0034	near_gene_3p_(500_bp)		N
ACAD10	chr12:110679712	12	110679712	112195329	C	T	0.0005	0	0.001	near_gene_3p_(500_bp)		N
ACAD10	chr12:110679729	12	110679729	112195346	C	T	0.0009	0	0.0019	near_gene_3p_(500_bp)		N
ALDH2	chr12:110688662	12	110688662	112204279	C	T	0.0005	0	0.001	near_gene_5p_(2000_bp)		N

ALDH2	rs886205	12	110688810	112204427	A	G	0.1622	0.1584	0.166	utr_5p		N
ALDH2	rs149824295	12	110720229	112235846	C	T	0.0024	0.0013	0.0035	intron	intron9 bp5260	N
ALDH2	rs139552439	12	110722070	112237687	C	T	0.0097	0.0089	0.0104	intron	intron10 bp1641	N
ALDH2	rs183108437	12	110722083	112237700	C	T	0.0005	0	0.001	intron	intron10 bp1654	N
ALDH2	chr12:110722098	12	110722098	112237715	C	T	0.0061	0.0064	0.0059	synonymous	Phe418Phe (TTC=>TTT) [exon11]	N
ALDH2	chr12:110731704	12	110731704	112247321	T	C	0.0014	0.0009	0.002	intron	intron12 bp5544	N
ALDH2	chr12:110731708	12	110731708	112247325	G	A	0.0019	0.0018	0.002	intron	intron12 bp5548	N
ALDH2	chr12:110731805	12	110731805	112247422	A	G	0.002	0	0.004	utr_3p		N
ALDH2	chr12:110731843	12	110731843	112247460	C	T	0.0005	0.001	0	utr_3p		N
ALDH2	rs4646780	12	110732575	112248192	C	T	0.0049	0.0039	0.0059	near_gene_3p_(500_bp)		N
ALDH2	rs4646782	12	110732652	112248269	T	G	0.0047	0.0043	0.0051	near_gene_3p_(500_bp)		N
MAPKAPK5	chr12:110792494	12	110792494	112308111	A	C	0.0009	0.0019	0	missense	Ile144Leu (ATT=>CTT) [exon6]	Y
MAPKAPK5	chr12:110792575	12	110792575	112308192	G	A	0.0005	0.001	0	intron	intron6 bp28	N
MAPKAPK5	chr12:110793274	12	110793274	112308891	T	C	0.0016	0.0023	0.0009	synonymous	Asp162Asp (GAT=>GAC) [exon7]	N
MAPKAPK5	chr12:110802625	12	110802625	112318242	T	G	0.0005	0	0.001	intron	intron7 bp9258	N
MAPKAPK5	rs182683312	12	110810833	112326450	C	T	0.001	0.0011	0.0009	intron	intron11 bp28	N
MAPKAPK5	chr12:110811018	12	110811018	112326635	G	A	0.0008	0.0017	0	intron	intron11 bp213	N
MAPKAPK5	chr12:110815651	12	110815651	112331268	A	G	0.0006	0	0.0013	near_gene_3p_(500_bp)		N
MAPKAPK5	chr12:110815679	12	110815679	112331296	A	G	0.0033	0.0041	0.0026	near_gene_3p_(500_bp)		N
MAPKAPK5	rs12580246	12	110815700	112331317	G	A	0.0511	0.0464	0.0558	near_gene_3p_(500_bp)		N
MAPKAPK5	rs111615149	12	110815741	112331358	G	C	0.0471	0.0451	0.0491	near_gene_3p_(500_bp)		N
MAPKAPK5	rs74601291	12	110815858	112331475	G	A	0.0545	0.0561	0.0529	near_gene_3p_(500_bp)		N
TMEM116	chr12:110935077	12	110935077	112450694	C	A	0.0116	0.0114	0.0119	intron	intron1 bp112	N
TMEM116	rs11066128	12	110935137	112450754	T	C	0.0628	0.0549	0.0707	intron	intron1 bp52	N
TMEM116	chr12:110935319	12	110935319	112450936	G	A	0.0005	0.001	0	utr_5p		N
TMEM116	chr12:110935499	12	110935499	112451116	C	G	0.0097	0.0076	0.0118	near_gene_5p_(2000_bp)		N
ERP29	rs10774648	12	110944530	112460147	T	G	0.0046	0.0039	0.0053	synonymous	Pro159Pro (CCT=>CCG) [exon3]	N
ERP29	rs147970597	12	110944598	112460215	A	G	0.0117	0.0074	0.016	missense	Lys182Arg (AAG=>AGG) [exon3]	Y
ERP29	chr12:110945056	12	110945056	112460673	G	A	0.0005	0.0011	0	utr_3p		N
ERP29	chr12:110945083	12	110945083	112460700	T	A	0.0009	0	0.0018	utr_3p		N
ERP29	rs7114	12	110945132	112460749	A	G	0.0702	0.064	0.0764	utr_3p		N

ERP29	chr12:110945145	12	110945145	112460762	T	C	0.0005	0	0.001	utr_3p		N
ERP29	chr12:110945471	12	110945471	112461088	T	G	0.0015	0.002	0.001	near_gene_3p_(500_bp)		N
ERP29	chr12:110945526	12	110945526	112461143	G	A	0.0005	0.001	0	near_gene_3p_(500_bp)		N
ERP29	rs61941310	12	110945574	112461191	A	C	0.0127	0.0154	0.0101	near_gene_3p_(500_bp)		N
ERP29	chr12:110945612	12	110945612	112461229	A	C	0.0006	0.0012	0	near_gene_3p_(500_bp)		N
ERP29	chr12:110945745	12	110945745	112461362	G	A	0.0005	0	0.001	near_gene_3p_(500_bp)		N
ERP29	rs138812716	12	110945775	112461392	A	G	0.0047	0.0052	0.0041	near_gene_3p_(500_bp)		N
ERP29	rs73428236	12	110945788	112461405	A	G	0.0877	0.0894	0.0861	near_gene_3p_(500_bp)		N
NAA25	rs140119108	12	110948673	112464290	C	T	0.0057	0.0043	0.0071	near_gene_3p_(500_bp)		N
NAA25	rs10431388	12	110949014	112464631	C	T	0.0047	0.0043	0.0051	utr_3p		N
NAA25	rs75512100	12	110949167	112464784	T	C	0.0039	0.0021	0.0057	utr_3p		N
NAA25	rs7295294	12	110949276	112464893	C	T	0.0659	0.0578	0.0739	utr_3p		N
NAA25	chr12:110949380	12	110949380	112464997	C	A	0.0098	0.0121	0.0074	utr_3p		N
NAA25	chr12:110949410	12	110949410	112465027	G	A	0.0008	0.0006	0.001	utr_3p		N
NAA25	chr12:110949872	12	110949872	112465489	C	A	0.001	0	0.002	utr_3p		N
NAA25	chr12:110950329	12	110950329	112465946	C	A	0.0005	0.001	0.0001	utr_3p		N
NAA25	chr12:110950743	12	110950743	112466360	A	G	0.0005	0.0011	0	utr_3p		N
NAA25	rs185609164	12	110951586	112467203	C	T	0.0005	0	0.001	utr_3p		N
NAA25	chr12:110951656	12	110951656	112467273	T	C	0.0009	0	0.0019	utr_3p		N
NAA25	rs138476979	12	110951799	112467416	C	T	0.0005	0	0.001	synonymous	Gln946Gln (CAG=>CAA) [exon24]	N
NAA25	rs12298022	12	110955473	112471090	G	T	0.0894	0.093	0.0858	missense	Leu915Ile (CTA=>ATA) [exon23]	Y
NAA25	rs12231744	12	110961438	112477055	T	C	0.0049	0.0046	0.0052	missense	Lys876Arg (AAA=>AGA) [exon22]	Y
NAA25	rs78983078	12	110962699	112478316	G	A	0.0076	0.0043	0.0109	missense	Thr836Ile (ACT=>ATT) [exon21]	Y
NAA25	rs79907395	12	110965894	112481511	C	T	0.0058	0.0087	0.003	missense	Arg723Gln (CGG=>CAG) [exon18]	Y
NAA25	chr12:110965904	12	110965904	112481521	C	T	0.002	0.002	0.002	missense	Val720Ile (GTA=>ATA) [exon18]	N
NAA25	rs149839526	12	110969860	112485477	T	C	0.0015	0.0021	0.001	synonymous	Pro666Pro (CCA=>CCG) [exon17]	N
NAA25	chr12:110969953	12	110969953	112485570	T	C	0.0021	0.002	0.0021	missense	Ile635Met (ATA=>ATG) [exon17]	N
NAA25	rs11066147	12	110994060	112509677	A	C	0.0043	0.0035	0.005	intron	intron10 bp22	N
NAA25	chr12:111000469	12	111000469	112516086	C	A	0.0014	0.0023	0.0005	intron	intron6 bp352	N
NAA25	chr12:111012975	12	111012975	112528592	A	C	0.001	0	0.002	missense	Leu74Arg (CTT=>CGT) [exon3]	N
NAA25	chr12:111015357	12	111015357	112530974	A	G	0.0046	0.005	0.0041	intron	intron1 bp15546	N

NAA25	chr12:111031001	12	111031001	112546618	G	A	0.0029	0.0028	0.003	utr_5p		N
NAA25	rs187284593	12	111031045	112546662	G	T	0.0075	0.0064	0.0086	near_gene_5p_(2000_bp)		N
TRAFD1	chr12:111047634	12	111047634	112563251	G	A	0.0007	0.0015	0	near_gene_5p_(2000_bp)		N
TRAFD1	chr12:111047683	12	111047683	112563300	T	C	0.0005	0	0.001	near_gene_5p_(2000_bp)		N
TRAFD1	chr12:111052649	12	111052649	112568266	T	G	0.0009	0	0.0019	intron	intron1 bp4844	N
TRAFD1	rs114172135	12	111063204	112578821	G	A	0.001	0.002	0	missense	Val146Ile (GTT=>ATT) [exon5]	Y
TRAFD1	rs7970397	12	111064454	112580071	C	T	0.075	0.0662	0.0839	synonymous	Gly274Gly (GGC=>GGT) [exon6]	N
TRAFD1	rs79680080	12	111067830	112583447	A	C	0.0201	0.0188	0.0214	missense	Glu303Ala (GAA=>GCA) [exon7]	Y
TRAFD1	chr12:111070373	12	111070373	112585990	G	C	0.0005	0	0.001	missense	Ser347Thr (AGT=>ACT) [exon8]	N
TRAFD1	chr12:111072039	12	111072039	112587656	G	C	0.001	0.001	0.001	missense	Arg420Ser (AGG=>AGC) [exon9]	N
TRAFD1	rs149284206	12	111075770	112591387	T	C	0.0141	0.0133	0.015	utr_3p		N
TRAFD1	chr12:111075820	12	111075820	112591437	T	C	0.0005	0.001	0	near_gene_3p_(500_bp)		N
TRAFD1	rs17630235	12	111076069	112591686	G	A	0.4378	0.4446	0.4309	near_gene_3p_(500_bp)		N
TRAFD1	rs60549974	12	111076204	112591821	T	C	0.0664	0.0652	0.0675	near_gene_3p_(500_bp)		N
TRAFD1	rs182634285	12	111076237	112591854	T	G	0.004	0	0.008	near_gene_3p_(500_bp)		N
C12orf51	chr12:111082385	12	111082385	112598002	A	G	0.0005	0	0.001	utr_3p		N
C12orf51	chr12:111082407	12	111082407	112598024	G	T	0.0005	0.001	0	utr_3p		N
C12orf51	rs3519	12	111082704	112598321	G	A	0.0522	0.0482	0.0562	utr_3p		N
C12orf51	chr12:111082873	12	111082873	112598490	C	G	0.0005	0.001	0	utr_3p		N
C12orf51	chr12:111082951	12	111082951	112598568	G	C	0.0186	0.0139	0.0233	utr_3p		N
C12orf51	chr12:111082958	12	111082958	112598575	A	G	0.0046	0.0034	0.0057	utr_3p		N
C12orf51	rs28405421	12	111083448	112599065	G	C	0.0541	0.0538	0.0543	utr_3p		N
C12orf51	chr12:111083453	12	111083453	112599070	T	G	0.0104	0.0107	0.0102	utr_3p		N
C12orf51	chr12:111083977	12	111083977	112599594	C	T	0.0064	0.0076	0.0051	utr_3p		N
C12orf51	chr12:111084228	12	111084228	112599845	C	A	0.0005	0.001	0	utr_3p		N
C12orf51	rs183882784	12	111085266	112600883	C	T	0.0036	0.0024	0.0048	synonymous	Pro4189Pro (CCG=>CCA) [exon74]	N
C12orf51	chr12:111085344	12	111085344	112600961	C	A	0.0033	0.0034	0.0032	missense	Lys4163Asn (AAG=>AAT) [exon74]	N
C12orf51	rs189667513	12	111089550	112605167	T	C	0.0041	0.0062	0.002	missense	Gln3991Arg (CAG=>CGG) [exon71]	Y
C12orf51	rs2242496	12	111089994	112605611	T	C	0.0024	0.0015	0.0033	intron	intron70 bp7	N
C12orf51	chr12:111090061	12	111090061	112605678	C	A	0.0011	0.001	0.0012	synonymous	Leu3912Leu (CTG=>CTT) [exon70]	N
C12orf51	rs186884971	12	111092610	112608227	C	T	0.0022	0.0044	0	missense	Val3816Met (GTG=>ATG) [exon68]	Y

C12orf51	chr12:111097904	12	111097904	112613521	C	T	0.0006	0.0013	0	intron	intron65 bp19	N
C12orf51	rs183402588	12	111097998	112613615	A	G	0.0016	0.001	0.0021	missense	Ile3668Thr (ATT=>ACT) [exon65]	Y
C12orf51	rs143848386	12	111098079	112613696	T	C	0.002	0.0017	0.0023	intron	intron64 bp704	N
C12orf51	chr12:111101153	12	111101153	112616770	C	T	0.0029	0.003	0.0029	synonymous	Pro3604Pro (CCG=>CCA) [exon63]	N
C12orf51	chr12:111106427	12	111106427	112622044	G	C	0.0072	0.0056	0.0088	missense	Leu3404Val (CTG=>GTG) [exon60]	Y
C12orf51	chr12:111106926	12	111106926	112622543	G	A	0.0005	0	0.001	synonymous	Asp3237Asp (GAC=>GAT) [exon60]	N
C12orf51	chr12:111107326	12	111107326	112622943	G	A	0.0007	0.0015	0	missense	Thr3104Ile (ACA=>ATA) [exon60]	N
C12orf51	chr12:111107339	12	111107339	112622956	T	C	0.0005	0.001	0	missense	Asn3100Asp (AAC=>GAC) [exon60]	N
C12orf51	rs186329035	12	111117158	112632775	C	T	0.0024	0.0039	0.001	missense	Arg2716His (CGC=>CAC) [exon55]	N
C12orf51	chr12:111117209	12	111117209	112632826	C	T	0.0005	0.0011	0	missense	Arg2699His (CGC=>CAC) [exon55]	N
C12orf51	rs61739678	12	111122869	112638486	G	T	0.0151	0.0158	0.0144	synonymous	Thr2669Thr (ACC=>ACA) [exon54]	N
C12orf51	chr12:111130052	12	111130052	112645669	G	A	0.0034	0.003	0.0038	intron	intron51 bp9	N
C12orf51	chr12:111130176	12	111130176	112645793	G	A	0.002	0.001	0.003	synonymous	Tyr2500Tyr (TAC=>TAT) [exon51]	N
C12orf51	chr12:111141641	12	111141641	112657258	G	A	0.0005	0	0.001	missense	Arg2164Trp (CGG=>TGG) [exon44]	N
C12orf51	rs61748915	12	111141663	112657280	T	C	0.0033	0.0032	0.0034	synonymous	Ala2156Ala (GCA=>GCG) [exon44]	N
C12orf51	rs142382140	12	111148965	112664582	C	T	0.0128	0.0117	0.0139	intron	intron42 bp1311	N
C12orf51	rs1005902	12	111152058	112667675	T	G	0.2332	0.2251	0.2413	synonymous	Arg1944Arg (AGA=>CGA) [exon40]	Y
C12orf51	chr12:111153711	12	111153711	112669328	C	T	0.0018	0.0007	0.003	synonymous	Ser1891Ser (TCG=>TCA) [exon38]	N
C12orf51	rs111790702	12	111157430	112673047	T	A	0.0042	0.001	0.0074	missense	Thr1745Ser (ACC=>TCC) [exon36]	Y
C12orf51	chr12:111157787	12	111157787	112673404	C	G	0.001	0	0.002	missense	Val1705Leu (GTC=>CTC) [exon35]	N
C12orf51	chr12:111158009	12	111158009	112673626	A	G	0.0005	0	0.001	intron	intron34 bp1123	N
C12orf51	rs73207624	12	111159101	112674718	C	T	0.0168	0.0192	0.0145	intron	intron34 bp31	N
C12orf51	chr12:111165563	12	111165563	112681180	C	T	0.0009	0	0.0018	synonymous	Thr1473Thr (ACG=>ACA) [exon31]	N
C12orf51	rs61941332	12	111165634	112681251	C	T	0.002	0.002	0.002	missense	Val1450Met (GTG=>ATG) [exon31]	Y
C12orf51	rs190911302	12	111165760	112681377	C	T	0.0005	0	0.001	intron	intron30 bp47	N
C12orf51	rs147699244	12	111165803	112681420	G	A	0.0039	0.0048	0.003	intron	intron30 bp4	N
C12orf51	rs73423230	12	111166221	112681838	C	T	0.0093	0.0074	0.0113	intron	intron28 bp2867	N
C12orf51	rs7306162	12	111169641	112685258	C	T	0.0041	0.0041	0.0042	intron	intron27 bp8	N
C12orf51	chr12:111170496	12	111170496	112686113	C	T	0.001	0.0021	0	intron	intron25 bp11	N
C12orf51	rs141477684	12	111183501	112699118	C	T	0.0028	0.0035	0.0022	missense	Arg773His (CGT=>CAT) [exon17]	Y
C12orf51	rs9805001	12	111187341	112702958	A	G	0.0087	0.0073	0.0101	intron	intron15 bp21	N

C12orf51	rs2301757	12	111188115	112703732	A	C	0.0046	0.004	0.0053	synonymous	Ala634Ala (GCT=>GCG) [exon14]	N
C12orf51	chr12:111191977	12	111191977	112707594	C	T	0.0005	0	0.001	synonymous	Arg563Arg (CGG=>CGA) [exon12]	N
C12orf51	chr12:111195832	12	111195832	112711449	T	C	0.0005	0.001	0	intron	intron10 bp10	N
C12orf51	rs10492015	12	111201383	112717000	C	T	0.0045	0.0038	0.0052	intron	intron9 bp32	N
C12orf51	chr12:111201488	12	111201488	112717105	A	G	0.0032	0.0034	0.0031	synonymous	Pro394Pro (CCT=>CCC) [exon9]	N
C12orf51	chr12:111201579	12	111201579	112717196	G	A	0.001	0.0021	0	intron	intron8 bp3718	N
C12orf51	chr12:111228791	12	111228791	112744408	T	G	0.0049	0.0042	0.0056	intron	intron6 bp2149	N
RPL6	chr12:111328535	12	111328535	112844152	A	T	0.0012	0.001	0.0014	intron	intron4 bp399	N
RPL6	chr12:111331648	12	111331648	112847265	A	G	0.001	0.002	0	utr_5p		N
RPL6	chr12:111331665	12	111331665	112847282	T	C	0.0013	0.001	0.0016	utr_5p		N
RPL6	chr12:111331767	12	111331767	112847384	T	C	0.0005	0	0.001	utr_5p		N
PTPN11	rs58805176	12	111341026	112856643	G	A	0.0569	0.0533	0.0606	utr_5p		N
PTPN11	rs41304351	12	111375586	112891203	G	C	0.0244	0.0297	0.0191	intron	intron4 bp12	N
PTPN11	rs184804143	12	111376743	112892360	C	A	0.0037	0.0056	0.0018	intron	intron4 bp1169	N
PTPN11	rs79068130	12	111376790	112892407	T	G	0.0296	0.0297	0.0296	missense	Ser189Ala (TCT=>GCT) [exon5]	N
PTPN11	rs76982592	12	111376816	112892433	T	G	0.0356	0.0356	0.0356	nonsense	Tyr197Stop (TAT=>TAG) [exon5]	N
PTPN11	rs78376169	12	111376841	112892458	T	C	0.0214	0.0218	0.0211	synonymous	Leu206Leu (TTG=>CTG) [exon5]	N
PTPN11	rs41279090	12	111399817	112915434	C	T	0.0844	0.0874	0.0815	intron	intron7 bp4590	N
PTPN11	rs12301915	12	111404252	112919869	C	A	0.0097	0.0074	0.012	intron	intron9 bp4050	N
PTPN11	chr12:111404297	12	111404297	112919914	C	T	0.0005	0	0.001	synonymous	Leu377Leu (CTA=>TTA) [exon10]	N
PTPN11	chr12:111404407	12	111404407	112920024	G	A	0.0011	0.0012	0.001	intron	intron10 bp15	N
PTPN11	rs148176616	12	111424389	112940006	C	T	0.0036	0.0041	0.0031	missense	Thr553Met (ACG=>ATG) [exon14]	N
PTPN11	chr12:111424465	12	111424465	112940082	T	G	0.002	0.0023	0.0018	intron	intron14 bp22	N
PTPN11	chr12:111428111	12	111428111	112943728	C	T	0.0005	0	0.001	utr_3p		N
PTPN11	chr12:111428458	12	111428458	112944075	C	T	0.0005	0	0.001	utr_3p		N
PTPN11	rs3240	12	111428478	112944095	G	T	0.0054	0.0062	0.0045	utr_3p		N
PTPN11	chr12:111429392	12	111429392	112945009	A	C	0.0015	0.003	0	utr_3p		N
PTPN11	chr12:111429403	12	111429403	112945020	G	A	0.0005	0	0.001	utr_3p		N
PTPN11	chr12:111430041	12	111430041	112945658	A	T	0.002	0.001	0.003	utr_3p		N
PTPN11	chr12:111430472	12	111430472	112946089	C	T	0.001	0	0.002	utr_3p		N
PTPN11	chr12:111430588	12	111430588	112946205	G	C	0.0005	0	0.001	utr_3p		N

PTPN11	rs141870860	12	111430985	112946602	G	A	0.0133	0.0124	0.0142	utr_3p		N
PTPN11	rs41307084	12	111431022	112946639	C	T	0.0133	0.0128	0.0138	utr_3p		N
PTPN11	chr12:111431299	12	111431299	112946916	A	G	0.0005	0.001	0	utr_3p		N
PTPN11	chr12:111431699	12	111431699	112947316	T	C	0.0012	0.001	0.0014	utr_3p		N
PTPN11	chr12:111431998	12	111431998	112947615	C	T	0.0025	0.002	0.0029	utr_3p		N
ALOX5AP	rs191239739	13	30207336	31309336	C	T	0.0019	0.0026	0.0011	near_gene_5p_(2000_bp)		N
ALOX5AP	rs9550373	13	30207404	31309404	G	A	0.065	0.074	0.056	near_gene_5p_(2000_bp)		N
ALOX5AP	chr13:30207601	13	30207601	31309601	G	A	0.0217	0.0186	0.0247	near_gene_5p_(2000_bp)		N
ALOX5AP	rs4769055	13	30207830	31309830	C	A	0.3153	0.3058	0.3248	intron	intron1 bp18	N
ALOX5AP	rs41351946	13	30216249	31318249	C	T	0.0111	0.0086	0.0136	synonymous	Ser41Ser (AGC=>AGT) [exon2]	N
ALOX5AP	rs143706085	13	30216280	31318280	C	A	0.001	0	0.002	synonymous	Arg52Arg (CGG=>AGG) [exon2]	N
ALOX5AP	rs3803277	13	30216308	31318308	C	A	0.4027	0.4017	0.4036	intron	intron2 bp12	N
ALOX5AP	chr13:30236136	13	30236136	31338136	G	A	0.0005	0	0.001	missense	Val127Ile (GTT=>ATT) [exon5]	N
ALOX5AP	chr13:30236439	13	30236439	31338439	G	A	0.0015	0.001	0.002	utr_3p		N
ALOX5AP	rs1132340	13	30236462	31338462	A	G	0.0459	0.0392	0.0526	utr_3p		N
ALOX5AP	rs41291237	13	30236618	31338618	C	T	0.0035	0.0024	0.0045	near_gene_3p_(500_bp)		N
COL4A1	rs77952604	13	109719846	110921845	A	G	0.0049	0.0058	0.004	intron	intron1 bp37446	N
LIPC	rs1800588	15	56510967	58723675	C	T	0.2177	0.2245	0.211	near_gene_5p_(2000_bp)		Y
LIPC	rs35511894	15	56511001	58723709	C	T	0.0254	0.0255	0.0252	near_gene_5p_(2000_bp)		N
LIPC	rs36021187	15	56511030	58723738	A	G	0.0113	0.0116	0.011	near_gene_5p_(2000_bp)		N
LIPC	rs2070895	15	56511231	58723939	G	A	0.219	0.2238	0.2142	near_gene_5p_(2000_bp)		N
LIPC	chr15:56511292	15	56511292	58724000	T	G	0.0013	0.0017	0.0009	near_gene_5p_(2000_bp)		N
LIPC	chr15:56511367	15	56511367	58724075	G	T	0.0021	0.003	0.0012	near_gene_5p_(2000_bp)		N
LIPC	chr15:56511416	15	56511416	58724124	G	C	0.0005	0	0.001	near_gene_5p_(2000_bp)		N
LIPC	rs6078	15	56621285	58833993	G	A	0.0303	0.0374	0.0232	missense	Val95Met (GTG=>ATG) [exon3]	Y
LIPC	chr15:56621434	15	56621434	58834142	C	T	0.0025	0.0003	0.0046	synonymous	Val144Val (GTC=>GTT) [exon3]	N
LIPC	rs690	15	56622033	58834741	G	T	0.5764	0.5834	0.5693	synonymous	Val155Val (GTG=>GTT) [exon4]	N
LIPC	chr15:56622102	15	56622102	58834810	C	T	0.0005	0	0.001	synonymous	Gly178Gly (GGC=>GGT) [exon4]	N
LIPC	rs6080	15	56625225	58837933	C	A	0.0426	0.0492	0.036	intron	intron4 bp3083	N
LIPC	rs34351746	15	56625246	58837954	G	A	0.0023	0.0012	0.0035	synonymous	Ala196Ala (GCG=>GCA) [exon5]	N
LIPC	rs6082	15	56625249	58837957	A	G	0.0507	0.0505	0.0509	synonymous	Gly197Gly (GGA=>GGG) [exon5]	N

LIPC	rs6083	15	56625302	58838010	A	G	0.3499	0.3553	0.3445	missense	Asn215Ser (AAT=>AGT) [exon5]	Y
LIPC	rs6084	15	56625330	58838038	C	G	0.4971	0.4845	0.5096	synonymous	Thr224Thr (ACC=>ACG) [exon5]	N
LIPC	rs142741286	15	56627993	58840701	C	T	0.0029	0.0036	0.0021	synonymous	His327His (CAC=>CAT) [exon6]	N
LIPC	rs3829461	15	56640401	58853109	A	G	0.9848	0.9822	0.9874	synonymous	Thr366Thr (ACA=>ACG) [exon7]	N
LIPC	rs6074	15	56648255	58860963	C	A	0.1233	0.1124	0.1342	synonymous	Thr479Thr (ACC=>ACA) [exon9]	N
	rs8037661	15	58167085	60379793	T	C	0.0035	0.0051	0.002	intergenic		N
ANXA2	chr15:58426261	15	58426261	60638969	C	T	0.001	0.001	0.001	near_gene_3p_(500_bp)		N
ANXA2	rs79118718	15	58426294	60639002	A	G	0.0165	0.016	0.017	near_gene_3p_(500_bp)		N
ANXA2	rs151000652	15	58426775	60639483	G	A	0.0034	0.0049	0.0019	utr_3p		N
ANXA2	rs11553797	15	58426902	60639610	C	T	0.0204	0.0238	0.0171	utr_3p		N
ANXA2	chr15:58427022	15	58427022	60639730	G	A	0.0005	0	0.0011	utr_3p		N
ANXA2	rs12442554	15	58427166	60639874	G	A	0.0108	0.0109	0.0107	synonymous	Gly325Gly (GGC=>GGT) [exon14]	N
ANXA2	chr15:58428578	15	58428578	60641286	G	A	0.001	0	0.002	synonymous	Tyr316Tyr (TAC=>TAT) [exon13]	N
ANXA2	rs138364945	15	58431956	60644664	G	A	0.0005	0.001	0	synonymous	Asp200Asp (GAC=>GAT) [exon10]	N
ANXA2	rs116367881	15	58431972	60644680	G	A	0.0214	0.0229	0.0199	intron	intron9 bp1673	N
ANXA2	rs12898604	15	58435506	60648214	T	C	0.7959	0.7892	0.8026	intron	intron7 bp1131	N
ANXA2	rs185805389	15	58436742	60649450	G	A	0.001	0.001	0.001	intron	intron6 bp3690	N
ANXA2	chr15:58440427	15	58440427	60653135	T	C	0.0046	0.0046	0.0045	intron	intron6 bp5	N
ANXA2	rs17845226	15	58440497	60653205	C	A	0.1392	0.1337	0.1447	missense	Val98Leu (GTG=>TTG) [exon6]	N
ANXA2	rs3759911	15	58461964	60674672	C	T	0.2656	0.2693	0.2618	intron	intron3 bp3555	N
ANXA2	rs11855679	15	58465590	60678298	T	A	0.8042	0.8006	0.8077	intron	intron2 bp4114	N
ANXA2	chr15:58465609	15	58465609	60678317	G	A	0.0047	0.0059	0.0036	intron	intron2 bp4095	N
ANXA2	rs11858864	15	58465620	60678328	C	T	0.7993	0.794	0.8046	intron	intron2 bp4084	N
ANXA2	rs12904657	15	58477381	60690089	A	G	0.6181	0.6336	0.6027	synonymous	Cys8Cys (TGT=>TGC) [exon1]	N
ANXA2	chr15:58477441	15	58477441	60690149	G	A	0.0094	0.0092	0.0096	utr_5p		N
ANXA2	chr15:58477923	15	58477923	60690631	T	C	0.0007	0	0.0015	near_gene_5p_(2000_bp)		N
ANXA2	chr15:58477937	15	58477937	60690645	A	G	0.0014	0.0007	0.002	near_gene_5p_(2000_bp)		N
SMAD3	rs1061427	15	65145532	67358478	G	A	0.2364	0.2351	0.2377	utr_5p		N
SMAD3	rs145339999	15	65205149	67418095	C	T	0.002	0.002	0.002	utr_5p		N
SMAD3	rs11636161	15	65205158	67418104	G	A	0.301	0.2955	0.3064	utr_5p		N
SMAD3	rs16950635	15	65205259	67418205	G	A	0.0516	0.0538	0.0493	utr_5p		N

SMAD3	rs8028147	15	65205287	67418233	G	A	0.2739	0.2829	0.2649	utr_5p		N
SMAD3	chr15:65205321	15	65205321	67418267	A	T	0.0005	0	0.001	utr_5p		N
SMAD3	rs1065080	15	65244389	67457335	A	G	0.8785	0.872	0.8851	synonymous	Leu103Leu (CTA=>CTG) [exon2]	N
SMAD3	chr15:65244612	15	65244612	67457558	C	G	0.0022	0.0038	0.0006	intron	intron2 bp132	N
SMAD3	rs35874463	15	65244752	67457698	A	G	0.0306	0.0273	0.0338	missense	Ile170Val (ATC=>GTC) [exon3]	N
SMAD3	rs112991343	15	65245582	67458528	G	A	0.002	0.0021	0.002	utr_5p		N
SMAD3	rs117185005	15	65260844	67473790	C	T	0.0294	0.0242	0.0347	synonymous	Ile290Ile (ATC=>ATT) [exon6]	Y
SMAD3	rs150994304	15	65264231	67477177	G	A	0.0026	0.002	0.0031	synonymous	Pro328Pro (CCG=>CCA) [exon7]	N
SMAD3	chr15:65266747	15	65266747	67479693	T	C	0.0006	0.0012	0	intron	intron7 bp2491	N
SMAD3	rs55678244	15	65266924	67479870	A	C	0.0012	0.001	0.0014	intron	intron8 bp23	N
SMAD3	rs72661159	15	65270229	67483175	C	T	0.0015	0.002	0.001	utr_3p		N
SMAD3	rs8025774	15	65270330	67483276	C	T	0.2179	0.214	0.2219	utr_3p		N
SMAD3	rs55970514	15	65270771	67483717	G	A	0.0294	0.0269	0.0318	utr_3p		N
SMAD3	rs8031440	15	65271033	67483979	G	A	0.2269	0.2212	0.2327	utr_3p		N
SMAD3	rs72661160	15	65271109	67484055	C	T	0.0057	0.0063	0.0051	utr_3p		N
SMAD3	rs8031627	15	65271173	67484119	G	A	0.2189	0.2123	0.2255	utr_3p		N
SMAD3	chr15:65271183	15	65271183	67484129	A	G	0.0015	0.002	0.001	utr_3p		N
SMAD3	rs2278670	15	65271351	67484297	C	T	0.2188	0.2121	0.2255	utr_3p		N
SMAD3	chr15:65271511	15	65271511	67484457	T	G	0.0005	0.001	0	utr_3p		N
SMAD3	chr15:65271710	15	65271710	67484656	C	T	0.0005	0.001	0	utr_3p		N
SMAD3	rs12595334	15	65272210	67485156	C	T	0.2216	0.2191	0.2241	utr_3p		N
SMAD3	chr15:65272213	15	65272213	67485159	G	A	0.0005	0.001	0	utr_3p		N
SMAD3	chr15:65272331	15	65272331	67485277	C	T	0.0025	0.003	0.002	utr_3p		N
SMAD3	rs72661161	15	65272475	67485421	C	T	0.0033	0.0039	0.0028	utr_3p		N
SMAD3	chr15:65272505	15	65272505	67485451	C	G	0.0005	0	0.001	utr_3p		N
SMAD3	chr15:65272704	15	65272704	67485650	C	T	0.0006	0.0003	0.001	utr_3p		N
SMAD3	rs3743342	15	65272721	67485667	C	T	0.2202	0.2214	0.219	utr_3p		N
SMAD3	rs145645018	15	65272965	67485911	C	G	0.0049	0.0024	0.0074	utr_3p		N
SMAD3	chr15:65273041	15	65273041	67485987	G	A	0.0005	0.001	0	utr_3p		N
SMAD3	rs62014610	15	65273054	67486000	C	T	0.0049	0.0044	0.0054	utr_3p		N
SMAD3	chr15:65273100	15	65273100	67486046	A	T	0.0387	0.0429	0.0345	utr_3p		N

SMAD3	rs11556089	15	65273132	67486078	G	A	0.0827	0.0856	0.0799	utr_3p		N
SMAD3	chr15:65273179	15	65273179	67486125	T	C	0.0005	0.001	0	utr_3p		N
SMAD3	rs11556090	15	65273437	67486383	A	G	0.5494	0.5508	0.5479	utr_3p		N
SMAD3	rs61740807	15	65273481	67486427	C	G	0.0011	0.001	0.0011	utr_3p		N
SMAD3	rs143991135	15	65273586	67486532	G	A	0.0099	0.01	0.0098	utr_3p		N
SMAD3	rs12900401	15	65273644	67486590	C	T	0.052	0.0519	0.052	utr_3p		N
SMAD3	rs3743343	15	65273829	67486775	T	C	0.226	0.2326	0.2193	utr_3p		N
SMAD3	rs1052488	15	65273901	67486847	T	C	0.2173	0.2228	0.2117	utr_3p		N
SMAD3	chr15:65274174	15	65274174	67487120	G	T	0.0017	0.0024	0.001	utr_3p		N
SMAD3	rs72661162	15	65274329	67487275	T	C	0.0164	0.0174	0.0154	utr_3p		N
SMAD3	rs10438355	15	65274603	67487549	C	G	0.2116	0.2019	0.2212	near_gene_3p_(500_bp)		N
SMAD3	rs189031289	15	65274686	67487632	G	A	0.0015	0.002	0.001	near_gene_3p_(500_bp)		N
CETP	rs34498052	16	55553315	56995814	G	A	0.0013	0	0.0026	near_gene_5p_(2000_bp)		N
CETP	rs1532625	16	55562802	57005301	C	T	0.4348	0.4397	0.4298	intron	intron7 bp8	N
CETP	rs12720872	16	55563383	57005882	C	T	0.0015	0.0011	0.002	intron	intron7 bp589	N
CETP	rs5883	16	55564854	57007353	C	T	0.0533	0.0505	0.0561	synonymous	Phe287Phe (TTC=>TTT) [exon9]	N
CETP	rs11076176	16	55564947	57007446	T	G	0.1564	0.1636	0.1492	intron	intron9 bp24	N
CETP	rs289714	16	55564952	57007451	G	A	0.8293	0.8214	0.8371	intron	intron9 bp29	N
CETP	chr16:55566559	16	55566559	57009058	C	T	0.0011	0.001	0.0012	nonsense	Gln326Stop (CAA=>TAA) [exon10]	N
CETP	chr16:55569469	16	55569469	57011968	C	A	0.0012	0.0021	0.0003	intron	intron10 bp2905	N
CETP	chr16:55569568	16	55569568	57012067	C	A	0.0005	0	0.001	missense	Ser349Tyr (TCC=>TAC) [exon11]	N
CETP	rs34855278	16	55572577	57015076	G	A	0.0015	0	0.003	missense	Val385Met (GTG=>ATG) [exon12]	Y
CETP	rs7192120	16	55572585	57015084	C	G	0.0016	0.0013	0.0019	synonymous	Thr387Thr (ACC=>ACG) [exon12]	N
CETP	rs5880	16	55572592	57015091	G	C	0.0474	0.0449	0.0498	missense	Ala390Pro (GCC=>CCC) [exon12]	Y
CETP	rs5882	16	55573593	57016092	G	A	0.6668	0.6587	0.675	missense	Val422Ile (GTC=>ATC) [exon14]	Y
CETP	rs5886	16	55573628	57016127	G	A	0.0007	0.0004	0.001	synonymous	Val433Val (GTG=>GTA) [exon14]	N
CETP	rs1800777	16	55574820	57017319	G	A	0.035	0.0348	0.0352	missense	Arg468Gln (CGA=>CAA) [exon15]	N
CETP	rs289741	16	55574975	57017474	G	A	0.7079	0.701	0.7148	intron	intron15 bp151	N
CETP	rs1801706	16	55575163	57017662	G	A	0.1941	0.2051	0.1831	utr_3p		N
CETP	rs289742	16	55575263	57017762	C	G	0.8824	0.8816	0.8832	near_gene_3p_(500_bp)		N
CETP	chr16:55575286	16	55575286	57017785	C	G	0.0022	0.0026	0.0018	near_gene_3p_(500_bp)		N

CETP	rs289743	16	55575297	57017796	G	A	0.6433	0.6292	0.6573	near_gene_3p_(500_bp)		N
CETP	rs289744	16	55575603	57018102	G	T	0.6716	0.6546	0.6886	near_gene_3p_(500_bp)		N
CETP	chr16:55575619	16	55575619	57018118	G	T	0.001	0	0.002	near_gene_3p_(500_bp)		N
CETP	chr16:55575670	16	55575670	57018169	G	A	0.0006	0	0.0013	near_gene_3p_(500_bp)		N
LCAT	rs17240406	16	66531008	67973507	A	G	0.0034	0.0032	0.0036	near_gene_3p_(500_bp)		N
LCAT	rs5923	16	66531454	67973953	G	A	0.0551	0.0595	0.0508	synonymous	Leu393Leu (CTG=>TTG) [exon6]	Y
LCAT	rs4986970	16	66533821	67976320	A	T	0.0215	0.0176	0.0253	missense	Ser232Thr (TCT=>ACT) [exon5]	Y
LCAT	chr16:66533897	16	66533897	67976396	G	A	0.0005	0	0.0011	synonymous	Leu206Leu (CTC=>CTT) [exon5]	N
LCAT	chr16:66533903	16	66533903	67976402	G	A	0.0005	0	0.0011	synonymous	His204His (CAC=>CAT) [exon5]	N
LCAT	chr16:66534193	16	66534193	67976692	G	T	0.0052	0.0034	0.007	intron	intron3 bp72	N
LCAT	chr16:66534323	16	66534323	67976822	G	A	0.0005	0.001	0	synonymous	Arg123Arg (CGC=>CGT) [exon3]	N
LCAT	rs35673026	16	66534352	67976851	C	T	0.001	0.0021	0	missense	Val114Met (GTG=>ATG) [exon3]	Y
LCAT	chr16:66534389	16	66534389	67976888	C	G	0.0084	0.0093	0.0075	intron	intron2 bp71	N
SLC12A4	chr16:66535626	16	66535626	67978125	A	G	0.0005	0	0.001	utr_3p		N
SLC12A4	chr16:66535792	16	66535792	67978291	G	T	0.0036	0.0053	0.002	utr_3p		N
SLC12A4	chr16:66535798	16	66535798	67978297	C	T	0.0029	0.0015	0.0044	utr_3p		N
SLC12A4	chr16:66535905	16	66535905	67978404	C	T	0.001	0.002	0	utr_3p		N
	chr16:69909533	16	69909533	71352032	G	A	0.0031	0.0032	0.003	intergenic		N
	rs4477713	16	69909558	71352057	A	T	0.9705	0.9725	0.9686	intergenic		N
LDLR	chr19:11060772	19	11060772	11199772	A	T	0.0005	0.001	0	near_gene_5p_(2000_bp)		N
LDLR	rs147509697	19	11061282	11200282	G	A	0.0011	0.0001	0.0021	missense	Gly20Arg (GGG=>AGG) [exon1]	N
LDLR	chr19:11071864	19	11071864	11210864	G	A	0.0006	0.0012	0	intron	intron1 bp10573	N
LDLR	rs2228671	19	11071912	11210912	C	T	0.1024	0.0952	0.1095	synonymous	Cys27Cys (TGC=>TGT) [exon2]	Y
LDLR	rs137853960	19	11071979	11210979	G	T	0.0024	0.0047	0.0001	missense	Ala50Ser (GCT=>TCT) [exon2]	N
LDLR	rs121908025	19	11074408	11213408	T	G	0.0071	0.0101	0.004	missense	Trp87Gly (TGG=>GGG) [exon3]	N
LDLR	rs10423288	19	11076846	11215846	T	C	0.0131	0.0136	0.0125	intron	intron3 bp2384	N
LDLR	rs13306513	19	11079226	11218226	G	A	0.0408	0.0435	0.0381	intron	intron6 bp36	N
LDLR	rs2738442	19	11082454	11221454	T	C	0.9923	0.9928	0.9919	intron	intron7 bp7	N
LDLR	rs12710260	19	11082457	11221457	G	C	0.4182	0.4211	0.4152	intron	intron7 bp10	N
LDLR	rs72658861	19	11083182	11222182	T	C	0.0074	0.0076	0.0073	intron	intron7 bp735	N
LDLR	rs11669576	19	11083300	11222300	G	A	0.0748	0.061	0.0885	missense	Ala391Thr (GCC=>ACC) [exon8]	Y

LDLR	chr19:11083372	19	11083372	11222372	T	G	0.0017	0.0014	0.002	intron	intron8 bp57	N
LDLR	chr19:11085005	19	11085005	11224005	C	T	0.0005	0	0.001	missense	Thr413Met (ACG=>ATG) [exon9]	N
LDLR	rs6413505	19	11085157	11224157	C	T	0.0077	0.0075	0.0079	intron	intron9 bp32	N
LDLR	rs5930	19	11085265	11224265	A	G	0.599	0.5869	0.6111	synonymous	Arg471Arg (AGA=>AGG) [exon10]	N
LDLR	chr19:11085319	19	11085319	11224319	C	G	0.0011	0.0022	0	nonsense	Tyr489Stop (TAC=>TAG) [exon10]	N
LDLR	rs5929	19	11087800	11226800	C	T	0.0359	0.0338	0.0379	synonymous	Pro539Pro (CCC=>CCT) [exon11]	N
LDLR	rs2738447	19	11088480	11227480	A	C	0.5844	0.5731	0.5958	intron	intron11 bp592	N
LDLR	rs17248882	19	11088525	11227525	G	A	0.0022	0.0024	0.002	intron	intron11 bp637	N
LDLR	rs1799898	19	11088554	11227554	C	T	0.1312	0.1367	0.1257	synonymous	Leu575Leu (CTC=>CTT) [exon12]	N
LDLR	rs688	19	11088602	11227602	C	T	0.4371	0.4367	0.4376	synonymous	Asn591Asn (AAC=>AAT) [exon12]	N
LDLR	chr19:11088613	19	11088613	11227613	G	A	0.0009	0.0018	0	missense	Arg595Gln (CGG=>CAG) [exon12]	N
LDLR	rs5925	19	11091881	11230881	T	C	0.4389	0.4396	0.4381	synonymous	Val653Val (GTT=>GTC) [exon13]	N
LDLR	rs149126953	19	11092113	11231113	G	A	0.0023	0.0036	0.001	synonymous	Pro685Pro (CCG=>CCA) [exon14]	N
LDLR	rs72658867	19	11092203	11231203	G	A	0.0147	0.0166	0.0127	intron	intron14 bp5	N
LDLR	chr19:11094874	19	11094874	11233874	A	G	0.0015	0	0.003	missense	Gln722Arg (CAG=>CGG) [exon15]	N
LDLR	rs45508991	19	11094886	11233886	C	T	0.0074	0.0076	0.0072	missense	Thr726Ile (ACC=>ATC) [exon15]	N
LDLR	rs138477254	19	11094991	11233991	C	T	0.0017	0.0034	0	missense	Thr761Met (ACG=>ATG) [exon15]	N
LDLR	rs41306974	19	11099637	11238637	G	A	0.0244	0.0237	0.0251	intron	intron15 bp4617	N
LDLR	chr19:11099761	19	11099761	11238761	G	A	0.0005	0.0011	0	missense	Val797Met (GTG=>ATG) [exon16]	N
LDLR	rs72658868	19	11099802	11238802	C	A	0.0103	0.0111	0.0095	intron	intron16 bp41	N
LDLR	rs183496025	19	11101173	11240173	G	A	0.0032	0.0045	0.002	intron	intron16 bp1412	N
LDLR	rs56270417	19	11103011	11242011	G	A	0.0015	0.003	0	utr_3p		N
LDLR	rs14158	19	11103044	11242044	G	A	0.2394	0.2407	0.2381	utr_3p		N
LDLR	rs3826810	19	11103133	11242133	G	A	0.0441	0.0467	0.0416	utr_3p		N
LDLR	rs17243011	19	11103215	11242215	G	A	0.0035	0.0003	0.0067	utr_3p		N
LDLR	rs2738464	19	11103307	11242307	G	C	0.8709	0.8906	0.8512	utr_3p		N
LDLR	rs17249029	19	11103330	11242330	G	A	0.002	0.0021	0.0018	utr_3p		N
LDLR	chr19:11103606	19	11103606	11242606	C	T	0.0005	0	0.0011	utr_3p		N
LDLR	rs1433099	19	11103658	11242658	T	C	0.7096	0.7298	0.6895	utr_3p		N
LDLR	rs2738466	19	11103765	11242765	A	G	0.2143	0.2178	0.2109	utr_3p		N
LDLR	rs17242677	19	11103795	11242795	C	T	0.014	0.0128	0.0152	utr_3p		N

LDLR	chr19:11104949	19	11104949	11243949	C	T	0.0009	0	0.0018	utr_3p		N
LDLR	rs72658879	19	11105008	11244008	G	A	0.0252	0.0261	0.0243	utr_3p		N
LDLR	rs184187776	19	11105124	11244124	G	A	0.0029	0.0039	0.002	utr_3p		N
LDLR	rs72658880	19	11105311	11244311	C	G	0.0063	0.0032	0.0094	utr_3p		N
LDLR	chr19:11105338	19	11105338	11244338	C	T	0.0009	0.0019	0	utr_3p		N
LDLR	chr19:11105373	19	11105373	11244373	G	A	0.0005	0.001	0	utr_3p		N
LDLR	chr19:11105401	19	11105401	11244401	T	C	0.0005	0	0.001	utr_3p		N
LDLR	chr19:11105419	19	11105419	11244419	C	T	0.0005	0.001	0	utr_3p		N
APOE	rs405509	19	50100676	45408836	T	G	0.4943	0.503	0.4857	near_gene_5p_(2000_bp)		N
APOE	chr19:50102904	19	50102904	45411064	G	A	0.001	0.0021	0	missense	Glu31Lys (GAG=>AAG) [exon3]	N
APOE	rs429358	19	50103781	45411941	T	C	0.0666	0.0637	0.0696	missense	Cys130Arg (TGC=>CGC) [exon4]	N
APOE	rs7412	19	50103919	45412079	C	T	0.0878	0.0872	0.0885	missense	Arg176Cys (CGC=>TGC) [exon4]	Y
APOE	chr19:50104427	19	50104427	45412587	C	T	0.001	0.001	0.001	utr_3p		N
APOE	chr19:50104577	19	50104577	45412737	C	T	0.0005	0.001	0	near_gene_3p_(500_bp)		N
APOE	rs117656888	19	50104581	45412741	C	G	0.0082	0.0117	0.0048	near_gene_3p_(500_bp)		N
MRPS6	rs11088273	21	34388996	35467126	C	A	0.9944	0.9929	0.9959	intron	intron1 bp21081	N
MRPS6	rs10854370	21	34389018	35467148	C	T	0.9974	0.9979	0.9969	intron	intron1 bp21103	N
SLC5A3	rs8129891	21	34389515	35467645	A	G	0.9929	0.9919	0.9939	missense	Thr50Ala (ACA=>GCA) [exon2]	Y
SLC5A3	chr21:34389937	21	34389937	35468067	G	T	0.0011	0.0002	0.002	synonymous	Leu190Leu (CTG=>CTT) [exon2]	N
SLC5A3	chr21:34390345	21	34390345	35468475	T	C	0.0005	0	0.001	synonymous	Asp326Asp (GAT=>GAC) [exon2]	N
SLC5A3	rs35707420	21	34390475	35468605	G	A	0.0052	0.0045	0.006	missense	Val370Met (GTG=>ATG) [exon2]	Y
SLC5A3	rs4817617	21	34391063	35469193	C	A	0.9929	0.9939	0.9919	missense	Gln566Lys (CAA=>AAA) [exon2]	Y
SLC5A3	rs141933184	21	34391079	35469209	G	A	0.001	0.001	0.001	missense	Ser571Asn (AGC=>AAC) [exon2]	Y
SLC5A3	chr21:34391132	21	34391132	35469262	G	A	0.0015	0.0019	0.0011	missense	Gly589Arg (GGG=>AGG) [exon2]	N
SLC5A3	chr21:34391195	21	34391195	35469325	A	G	0.001	0.0011	0.001	missense	Arg610Gly (AGA=>GGA) [exon2]	N
SLC5A3	rs141909962	21	34391275	35469405	A	G	0.0176	0.0128	0.0225	synonymous	Ala636Ala (GCA=>GCG) [exon2]	N
SLC5A3	rs141529022	21	34391310	35469440	C	T	0.001	0.002	0	missense	Thr648Met (ACG=>ATG) [exon2]	Y
SLC5A3	rs4817618	21	34391722	35469852	C	A	0.9949	0.9959	0.9939	utr_3p		N
SLC5A3	rs190738029	21	34391786	35469916	C	T	0.0036	0.0033	0.004	utr_3p		N
SLC5A3	rs143299811	21	34391878	35470008	T	C	0.0081	0.0101	0.0061	utr_3p		N
SLC5A3	rs4817620	21	34392080	35470210	T	G	0.9914	0.9919	0.9909	utr_3p		N

SLC5A3	rs4817621	21	34392083	35470213	C	A	0.9954	0.9979	0.9929	utr_3p		N
SLC5A3	rs75106434	21	34392263	35470393	T	A	0.0086	0.0079	0.0093	utr_3p		N
SLC5A3	rs78365560	21	34392467	35470597	G	A	0.0068	0.0066	0.0069	utr_3p		N
SLC5A3	chr21:34392543	21	34392543	35470673	T	A	0.001	0	0.0019	utr_3p		N
SLC5A3	chr21:34392971	21	34392971	35471101	G	A	0.001	0.001	0.001	utr_3p		N
SLC5A3	chr21:34393073	21	34393073	35471203	A	T	0.0005	0	0.001	utr_3p		N
SLC5A3	chr21:34393150	21	34393150	35471280	A	G	0.0033	0.0036	0.003	utr_3p		N
SLC5A3	chr21:34393376	21	34393376	35471506	T	A	0.0021	0	0.0042	utr_3p		N
SLC5A3	rs56896967	21	34393586	35471716	T	G	0.0149	0.0156	0.0142	utr_3p		N
SLC5A3	chr21:34393651	21	34393651	35471781	A	G	0.001	0.002	0	utr_3p		N
SLC5A3	chr21:34393707	21	34393707	35471837	T	A	0.0012	0	0.0023	utr_3p		N
SLC5A3	rs118144043	21	34394373	35472503	G	A	0.0084	0.0078	0.0091	utr_3p		N
SLC5A3	chr21:34394387	21	34394387	35472517	C	T	0.0011	0	0.0022	utr_3p		N
SLC5A3	rs116897058	21	34394431	35472561	G	T	0.0068	0.005	0.0086	utr_3p		N
SLC5A3	chr21:34394469	21	34394469	35472599	T	A	0.0028	0.0038	0.0018	utr_3p		N
SLC5A3	chr21:34394656	21	34394656	35472786	C	T	0.0005	0	0.001	utr_3p		N
SLC5A3	rs28570507	21	34394717	35472847	A	G	0.0434	0.0397	0.0471	utr_3p		N
SLC5A3	rs16991200	21	34394725	35472855	T	C	0.0059	0.0059	0.0059	utr_3p		N
SLC5A3	rs62212119	21	34394859	35472989	T	C	0.0622	0.07	0.0544	utr_3p		N
SLC5A3	rs112609870	21	34394887	35473017	C	G	0.0063	0.0051	0.0076	utr_3p		N
SLC5A3	rs16991209	21	34394934	35473064	C	T	0.0062	0.0054	0.0069	utr_3p		N
SLC5A3	rs181051877	21	34394978	35473108	A	G	0.003	0.0011	0.0048	utr_3p		N
SLC5A3	chr21:34395010	21	34395010	35473140	C	T	0.0005	0	0.001	utr_3p		N
SLC5A3	chr21:34395078	21	34395078	35473208	C	A	0.0005	0	0.001	utr_3p		N
SLC5A3	chr21:34395122	21	34395122	35473252	T	C	0.0009	0	0.0019	utr_3p		N
SLC5A3	rs16991212	21	34395388	35473518	T	A	0.0054	0.0043	0.0065	utr_3p		N
SLC5A3	rs187628584	21	34396031	35474161	T	C	0.001	0	0.002	utr_3p		N
SLC5A3	rs2244724	21	34396280	35474410	G	A	0.6763	0.669	0.6836	utr_3p		N
SLC5A3	rs16991220	21	34396322	35474452	T	C	0.0061	0.005	0.0072	utr_3p		N
SLC5A3	rs2032107	21	34396474	35474604	T	C	0.0722	0.0773	0.0672	utr_3p		N
SLC5A3	rs191279650	21	34396477	35474607	A	G	0.0059	0.0068	0.005	utr_3p		N

SLC5A3	rs73899969	21	34396777	35474907	T	C	0.0011	0.001	0.0013	utr_3p		N
SLC5A3	chr21:34397006	21	34397006	35475136	T	G	0.0007	0.0015	0	utr_3p		N
SLC5A3	chr21:34397340	21	34397340	35475470	T	C	0.0005	0.001	0	utr_3p		N
SLC5A3	rs114419906	21	34397693	35475823	G	A	0.0649	0.0696	0.0602	utr_3p		N
SLC5A3	rs184287228	21	34398077	35476207	A	G	0.0005	0	0.001	utr_3p		N
SLC5A3	chr21:34398199	21	34398199	35476329	C	T	0.0005	0	0.001	utr_3p		N
SLC5A3	chr21:34398416	21	34398416	35476546	G	A	0.0008	0	0.0016	utr_3p		N
SLC5A3	chr21:34398870	21	34398870	35477000	T	C	0.001	0.002	0	utr_3p		N
SLC5A3	rs184094254	21	34398970	35477100	C	T	0.0045	0.002	0.0071	utr_3p		N
SLC5A3	chr21:34398985	21	34398985	35477115	T	A	0.0007	0.0014	0	utr_3p		N
SLC5A3	rs140104162	21	34399064	35477194	C	T	0.0039	0.0012	0.0066	utr_3p		N
SLC5A3	rs150052088	21	34399081	35477211	T	G	0.0175	0.0121	0.0229	utr_3p		N
SLC5A3	chr21:34399236	21	34399236	35477366	G	A	0.0005	0.001	0	utr_3p		N
SLC5A3	rs118183140	21	34399356	35477486	C	T	0.0235	0.0138	0.0331	utr_3p		N
SLC5A3	chr21:34399554	21	34399554	35477684	A	G	0.0005	0	0.001	utr_3p		N
SLC5A3	rs9984245	21	34399933	35478063	G	T	0.1848	0.1785	0.1912	utr_3p		N
SLC5A3	rs113414701	21	34399942	35478072	T	G	0.0058	0.0062	0.0054	utr_3p		N
SLC5A3	rs140597425	21	34400003	35478133	G	A	0.0014	0.0018	0.001	utr_3p		N
SLC5A3	chr21:34400064	21	34400064	35478194	A	G	0.0005	0	0.001	utr_3p		N
SLC5A3	chr21:34400143	21	34400143	35478273	A	G	0.0005	0.001	0	utr_3p		N
SLC5A3	chr21:34400245	21	34400245	35478375	G	T	0.001	0.0021	0	utr_3p		N
MRPS6	rs190453891	21	34400665	35478795	T	C	0.002	0.002	0.002	intron	intron1 bp32750	N
MRPS6	chr21:34419633	21	34419633	35497763	G	A	0.0005	0.001	0	synonymous	Gln56Gln (CAG=>CAA) [exon2]	N
MRPS6	chr21:34436604	21	34436604	35514734	C	G	0.0005	0.001	0	missense	Pro71Arg (CCC=>CGC) [exon3]	N
MRPS6	rs61910679	21	34436619	35514749	A	T	0.0165	0.0119	0.0211	missense	Glu76Val (GAA=>GTA) [exon3]	Y
MRPS6	chr21:34436778	21	34436778	35514908	C	T	0.0005	0.001	0	utr_3p		N
MRPS6	chr21:34436804	21	34436804	35514934	T	A	0.0005	0	0.001	utr_3p		N
MRPS6	rs111963757	21	34436864	35514994	A	G	0.0063	0.0061	0.0065	utr_3p		N
MRPS6	rs60826745	21	34436929	35515059	C	T	0.0066	0.006	0.0071	utr_3p		N
MRPS6	chr21:34436979	21	34436979	35515109	A	G	0.0012	0.0025	0	utr_3p		N
MRPS6	rs7115	21	34436987	35515117	G	A	0.6936	0.6952	0.692	utr_3p		N

MRPS6	rs15044	21	34437026	35515156	T	G	0.0065	0.0056	0.0073	utr_3p		N
MRPS6	rs62213666	21	34437092	35515222	G	A	0.0046	0.0042	0.005	utr_3p		N
MRPS6	rs193105407	21	34437145	35515275	G	A	0.0006	0.0012	0	utr_3p		N
MRPS6	rs3746864	21	34437203	35515333	T	C	0.0698	0.0713	0.0683	utr_3p		Y
MRPS6	chr21:34437220	21	34437220	35515350	C	T	0.0005	0	0.001	near_gene_3p_(500_bp)		N
MRPS6	chr21:34437287	21	34437287	35515417	G	T	0.0011	0.001	0.0011	near_gene_3p_(500_bp)		N
MRPS6	chr21:34437429	21	34437429	35515559	G	A	0.0016	0.0023	0.001	near_gene_3p_(500_bp)		N
MRPS6	chr21:34437580	21	34437580	35515710	G	A	0.001	0	0.002	near_gene_3p_(500_bp)		N
KCNE2	rs13048252	21	34658036	35736166	G	A	0.6157	0.6079	0.6235	near_gene_5p_(2000_bp)		N
KCNE2	rs41260744	21	34658254	35736384	G	A	0.0687	0.0634	0.0739	utr_5p		N
KCNE2	rs41314699	21	34658281	35736411	G	A	0.001	0.002	0	utr_5p		N
KCNE2	chr21:34658314	21	34658314	35736444	T	A	0.0009	0	0.0019	utr_5p		N
KCNE2	rs9305548	21	34664592	35742722	C	T	0.1492	0.1509	0.1475	intron	intron1 bp6272	N
KCNE2	rs41314677	21	34664620	35742750	A	G	0.0298	0.0272	0.0325	intron	intron1 bp6300	N
KCNE2	rs2234916	21	34664669	35742799	A	G	0.0069	0.0078	0.006	missense	Thr8Ala (ACA=>GCA) [exon2]	N
KCNE2	chr21:34665065	21	34665065	35743195	G	T	0.0015	0.003	0	utr_3p		N
KCNE2	rs72550218	21	34665081	35743211	G	A	0.001	0.002	0	utr_3p		N
KCNE2	chr21:34665434	21	34665434	35743564	T	C	0.0005	0	0.001	near_gene_3p_(500_bp)		N
FAM165B	rs140767873	21	34669123	35747253	C	G	0.0027	0.0044	0.0009	near_gene_5p_(2000_bp)		N
FAM165B	rs117032621	21	34669305	35747435	C	G	0.0077	0.003	0.0123	near_gene_5p_(2000_bp)		N
FAM165B	rs762159	21	34669659	35747789	C	G	0.9928	0.9908	0.9948	utr_5p		N
FAM165B	rs192071625	21	34669673	35747803	G	A	0.0049	0.007	0.0028	utr_5p		N
FAM165B	chr21:34669680	21	34669680	35747810	C	T	0.0023	0.0018	0.0028	utr_5p		N
FAM165B	rs111297541	21	34679611	35757741	A	T	0.0027	0.0044	0.0009	intron	intron2 bp5926	N
FAM165B	rs61747964	21	34679657	35757787	C	T	0.0298	0.0284	0.0311	synonymous	His8His (CAC=>CAT) [exon3]	N
FAM165B	rs78481066	21	34679732	35757862	T	C	0.0019	0.0029	0.001	synonymous	Tyr33Tyr (TAT=>TAC) [exon3]	N
FAM165B	rs34016792	21	34679785	35757915	A	G	0.0256	0.0249	0.0263	missense	Lys51Arg (AAG=>AGG) [exon3]	Y
FAM165B	rs78181086	21	34683731	35761861	G	A	0.021	0.0223	0.0197	near_gene_3p_(500_bp)		N
FAM165B	chr21:34683744	21	34683744	35761874	G	C	0.0061	0.0064	0.0058	near_gene_3p_(500_bp)		N
FAM165B	rs2012713	21	34683820	35761950	T	G	0.9944	0.9969	0.9919	near_gene_3p_(500_bp)		N
	rs12481822	21	34740317	35818447	T	C	0.4192	0.4162	0.4223	intergenic		N

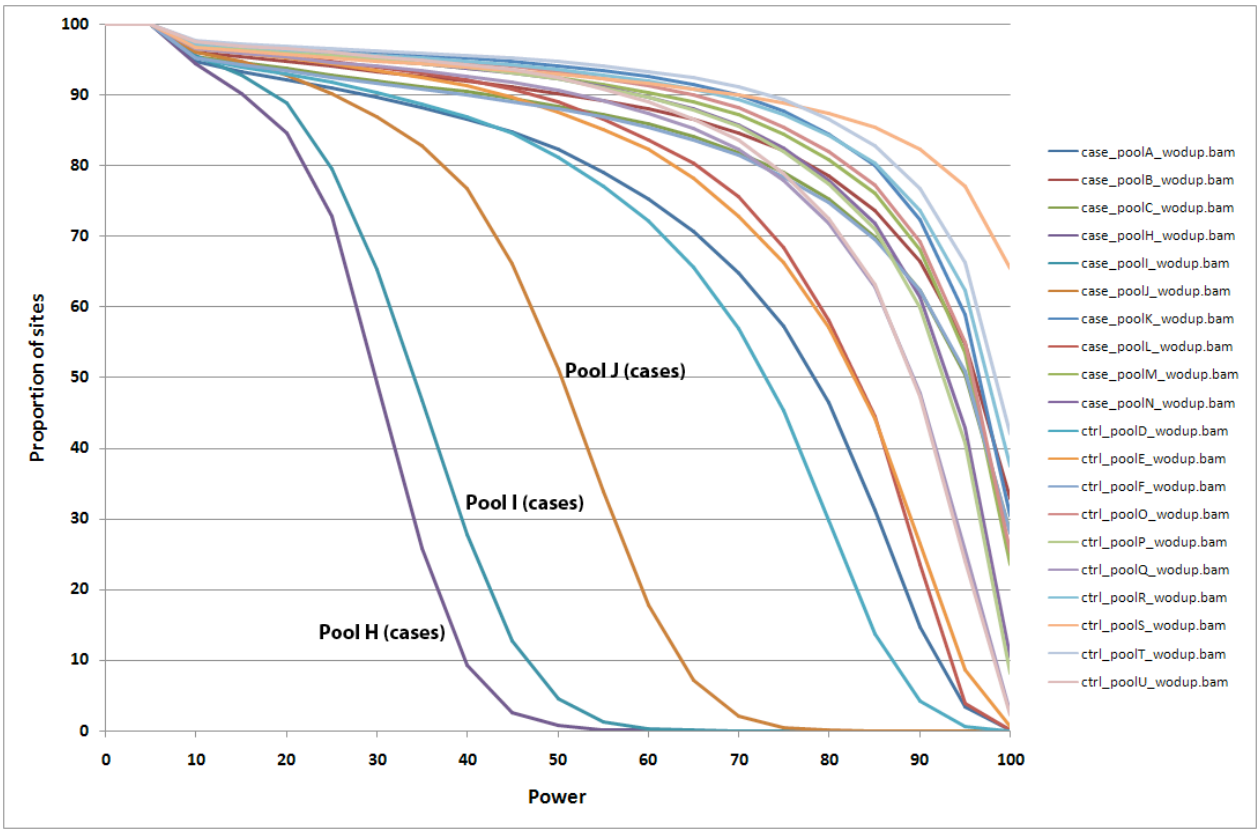
	chr21:34740339	21	34740339	35818469	A	G	0.0193	0.0189	0.0197	intergenic		N
	rs113754577	21	34740342	35818472	T	C	0.0101	0.0093	0.0109	intergenic		N
	rs184706079	21	34740346	35818476	C	T	0.0197	0.0204	0.019	intergenic		N
KCNE1	rs188324232	21	34740401	35818531	G	A	0.0192	0.0173	0.021	near_gene_3p_(500_bp)		N
KCNE1	chr21:34740425	21	34740425	35818555	T	C	0.0134	0.013	0.0138	near_gene_3p_(500_bp)		N
KCNE1	chr21:34740439	21	34740439	35818569	T	C	0.0192	0.0215	0.0168	near_gene_3p_(500_bp)		N
KCNE1	chr21:34740443	21	34740443	35818573	A	G	0.001	0	0.002	near_gene_3p_(500_bp)		N
KCNE1	rs5010906	21	34740460	35818590	G	C	0.3277	0.3399	0.3156	near_gene_3p_(500_bp)		N
KCNE1	chr21:34740710	21	34740710	35818840	C	T	0.001	0.002	0	near_gene_3p_(500_bp)		N
KCNE1	chr21:34740719	21	34740719	35818849	G	T	0.002	0.002	0.002	near_gene_3p_(500_bp)		N
KCNE1	rs73363349	21	34740828	35818958	C	A	0.05	0.052	0.0481	near_gene_3p_(500_bp)		N
KCNE1	rs2834485	21	34740884	35819014	G	A	0.664	0.6692	0.6589	utr_3p		N
KCNE1	rs3453	21	34740933	35819063	T	C	0.5084	0.5098	0.5071	utr_3p		N
KCNE1	rs13050198	21	34740952	35819082	T	C	0.0273	0.0201	0.0345	utr_3p		N
KCNE1	rs41312993	21	34741315	35819445	A	G	0.0227	0.0197	0.0258	utr_3p		N
KCNE1	rs41314799	21	34741412	35819542	C	T	0.0005	0	0.001	utr_3p		N
KCNE1	chr21:34741458	21	34741458	35819588	G	A	0.0005	0	0.0011	utr_3p		N
KCNE1	rs41312369	21	34741575	35819705	A	T	0.001	0.001	0.001	utr_3p		N
KCNE1	chr21:34742402	21	34742402	35820532	C	T	0.0008	0.0005	0.0011	utr_3p		N
KCNE1	rs41314071	21	34743281	35821411	T	C	0.0545	0.0552	0.0539	utr_3p		N
KCNE1	rs2070357	21	34743289	35821419	T	C	0.5142	0.5205	0.508	utr_3p		N
KCNE1	rs1805128	21	34743550	35821680	C	T	0.01	0.0098	0.0102	missense	Asp85Asn (GAT=>AAT) [exon3]	N
KCNE1	chr21:34743664	21	34743664	35821794	C	T	0.0005	0.001	0	missense	Val47Ile (GTC=>ATC) [exon3]	N
KCNE1	rs17846179,rs1805127	21	34743691	35821821	T	C	0.6274	0.6312	0.6235	missense	Ser38Gly (AGT=>GGT) [exon3]	Y
KCNE1	rs17173510	21	34743719	35821849	C	T	0.0085	0.0051	0.0119	synonymous	Ser28Ser (TCG=>TCA) [exon3]	N
KCNE1	rs187686559	21	34743773	35821903	C	T	0.0021	0.001	0.0031	synonymous	Thr10Thr (ACG=>ACA) [exon3]	N
KCNE1	chr21:34749924	21	34749924	35828054	C	A	0.0006	0.0011	0.0001	utr_5p		N
KCNE1	rs8127493	21	34753685	35831815	A	C	0.984	0.9818	0.9862	intron	intron1 bp51584	N
KCNE1	chr21:34805277	21	34805277	35883407	G	A	0.0005	0.001	0	utr_5p		N
KCNE1	rs41315349	21	34805482	35883612	T	C	0.001	0.0011	0.001	utr_5p		N
KCNE1	rs140643652	21	34805965	35884095	G	A	0.0033	0.003	0.0035	near_gene_5p_(2000_bp)		N

RCAN1	rs7276552	21	34810241	35888371	G	A	0.0616	0.0686	0.0546	near_gene_3p_(500_bp)		N
RCAN1	rs62211554	21	34810421	35888551	C	G	0.0344	0.0319	0.0368	near_gene_3p_(500_bp)		N
RCAN1	chr21:34810578	21	34810578	35888708	A	G	0.001	0.001	0.001	near_gene_3p_(500_bp)		N
RCAN1	rs6741	21	34810974	35889104	G	C	0.0529	0.0549	0.051	utr_3p		N
RCAN1	chr21:34811641	21	34811641	35889771	C	T	0.0005	0	0.001	utr_3p		N
RCAN1	rs188641039	21	34811752	35889882	G	A	0.002	0.004	0	utr_3p		N
RCAN1	chr21:34811980	21	34811980	35890110	T	C	0.0005	0.001	0	utr_3p		N
RCAN1	rs62211555	21	34812102	35890232	G	A	0.1375	0.1442	0.1308	utr_3p		N
RCAN1	chr21:34812178	21	34812178	35890308	G	A	0.0005	0.0011	0	utr_3p		N
RCAN1	rs4336020	21	34812243	35890373	C	T	0.0011	0.001	0.0011	utr_3p		N
RCAN1	rs59601528	21	34812279	35890409	C	T	0.0651	0.0635	0.0666	synonymous	Pro244Pro (CCG=>CCA) [exon4]	N
RCAN1	chr21:34815692	21	34815692	35893822	T	C	0.002	0.002	0.002	synonymous	Leu187Leu (TTA=>TTG) [exon3]	N
RCAN1	rs145120179	21	34815795	35893925	G	A	0.0032	0.0035	0.0029	missense	Pro153Leu (CCG=>CTG) [exon3]	Y
RCAN1	rs140946286	21	34815857	35893987	G	C	0.0014	0.0009	0.002	intron	intron2 bp1848	N
RCAN1	rs6517239	21	34817902	35896032	A	G	0.1674	0.1709	0.1639	intron	intron1 bp91027	N
RCAN1	rs147745471	21	34820812	35898942	G	A	0.0019	0.0039	0	intron	intron1 bp88117	N
RCAN1	chr21:34820820	21	34820820	35898950	A	T	0.0022	0.0024	0.0021	intron	intron1 bp88109	N
RCAN1	rs75026481	21	34821118	35899248	C	T	0.0309	0.0349	0.0269	utr_5p		N
RCAN1	rs11909625	21	34908472	35986602	G	A	0.002	0.004	0	utr_5p		N
RCAN1	chr21:34908492	21	34908492	35986622	G	A	0.0005	0.001	0	utr_5p		N
RCAN1	chr21:34908544	21	34908544	35986674	C	T	0.001	0	0.002	utr_5p		N
RCAN1	rs149048873	21	34909315	35987445	G	A	0.1124	0.1196	0.1052	near_gene_5p_(2000_bp)		N
RCAN1	rs765610	21	34909752	35987882	C	T	0.4542	0.4595	0.449	near_gene_5p_(2000_bp)		N
CDC42EP1	rs142982465	22	36295801	37965855	T	C	0.003	0.001	0.005	near_gene_3p_(500_bp)		N
CDC42EP1	rs2235338	22	36295826	37965880	G	A	0.5888	0.5873	0.5904	near_gene_3p_(500_bp)		N
LGALS2	rs2281097	22	36296006	37966060	T	C	0.5514	0.5469	0.5558	near_gene_3p_(500_bp)		N
LGALS2	rs73884089	22	36296077	37966131	G	A	0.0014	0.0029	0	near_gene_3p_(500_bp)		N
LGALS2	chr22:36296585	22	36296585	37966639	A	G	0.001	0.002	0	missense	Trp65Arg (TGG=>CGG) [exon3]	N
LGALS2	rs148503336	22	36296649	37966703	G	T	0.0005	0	0.001	missense	Asn43Lys (AAC=>AAA) [exon3]	Y
LGALS2	chr22:36305880	22	36305880	37975934	C	T	0.0005	0	0.001	utr_5p		N

Supplementary Figure 6. Statistical power to identify gene-associations with myocardial infarction (MI). Power estimates were obtained using references haplotypes calibrated on a coalescence model available in the SKAT package [1]. We used the following assumption: MI prevalence=2%, gene size (average 394kb/68 genes)=6kb, proportion of cases=50%, proportion of causal variants=10%, minor allele frequency cutoff=5%, number of simulation=500, proportion of variants with effect in the opposite direction=20%, effect size is weighted based on allele frequency such that a variant with a frequency of $1x10^{-4}$ has an odds ratio=5. Our experiment-wide statistical threshold to declare significance is $\alpha=7x10^{-4}$ (Bonferroni correction 0.05/68 genes).

		Power (%)		
Study	**Sample size (cases/controls)**	**α=0.05**	**α=0.01**	**α=7x10^{-4}**
MHI Biobank - sequencing	500/500	35	21	11
MHI Biobank - replication	870/1,604	58	44	30
MHI Statins Study	724/1,384	54	39	25
All replication	1,584/2,988	71	60	48

Supplementary Figure 1. Power to detect singletons per sequenced DNA pool. The power to detect singletons is ~50% in cases and ~72% in controls, respectively, at 80% of the targeted sites. We note that three pools of cases (H-I-J) are outliers in this power estimation. These three pools presumable has lower DNA quality because 14 cycle of PCR, instead of 12 for the other pools, were necessary to have enough DNA material for hybridization. As a consequence, the proportion of duplicates is higher in these 3 pools in comparison with the rest of the pools (55% vs. 42%, Wilcoxon's rank sum test P=0.02).



References

1. Wu MC, Lee S, Cai T, Li Y, Boehnke M, Lin X. Rare-variant association testing for sequencing data with the sequence kernel association test. *American journal of human genetics*. 2011;89:82-93