Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

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1. Abbreviations

AGES	Aging Gene-Environment Study
ARFGAP2	ADP-ribosylation factor GTPase activating protein 2
API5	Apoptosis Inhibitor 5
ARIC	Atherosclerosis Risk in Communities
AVEN	apoptosis caspase activation inhibitor
BBS10	Bardet-Biedl syndrome 10
C1QTNF7	C1q and tumor necrosis factor related protein 7
C5orf23	chromosome 5 open reading frame 23
C8orf79	chromosome 8 open reading frame 79
C10orf88	chromosome 10 open reading frame 88
C11orf 49	chromosome 11 open reading frame 49
CD36	CD36 molecule (thrombospondin receptor)
CHARGE	Cohorts for Heart and Aging Research in Genomic Epidemiology
CHS	Cardiovascular Health Study
CI	Confidence Interval
CKAP5	cytoskeleton associated protein 5
CPEB2	cytoplasmic polyadenylation element binding protein 2
DDB2	Damage-specific DNA binding protein 2
DLC1	deleted in liver cancer 1
EFCAB4B	EF-hand calcium binding domain 4B
F2	coagulation factor II (thrombin)
FAM24A	family with sequence similarity 24, member A
FHS	Framingham Heart Study
FIP1L1	FIP1 like 1 (S. cerevisiae)
FUT8	fucosyltransferase 8
GWAS	Genome Wide Association Study
GPHN	gephyrin
HNT	neurotrimin
HR	Hazard Ratio
LD	Linkage Disequilibrium
LNX1	ligand of numb-protein X 1
LRP4	Low density lipoprotein receptor-related protein
LRRC4C	leucine rich repeat containing 4C
MA	Minor Allele
MAF	Minor Allele Frequency
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
MPDZ	multiple PDZ domain protein
NFIB	nuclear factor I/B
NINJ2	ninjurin 2
NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic

	peptide receptor C)
OPCML	opioid binding protein/cell adhesion molecule-like
OSBPL8	oxysterol binding protein-like 8
P2RY5	purinergic receptor P2Y, G-protein coupled, 5
PACSIN3	Protein kinase C and casein kinase substrate in neurons 3
PAR	Population Attributable Risk
PARP11	poly (ADP-ribose) polymerase family, member 11
QC	Quality Control
RB1	retinoblastoma 1
RYR3	ryanodine receptor 3
SD	Standard Deviation
SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
SNP	Single Nucleotide Polymorphism
TP63	tumor protein p63
TPRG1	tumor protein p63 regulated 1
WNK1	WNK lysine deficient protein kinase 1

2. Consortium organization and Sample selection

We combined data from white participants in four large, prospective population-based cohort studies: the Atherosclerosis Risk in Communities (ARIC) Study,[1] the Cardiovascular Health Study (CHS),[2] the Framingham Heart Study (FHS),[3, 4] and the Rotterdam Study[5] to study the genetics of stroke. Together with the Aging Gene-Environment Susceptibility- Reykjavik Study (AGES-RS)[6] these studies form the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium.[7] However, the AGES-RS does not have data on incident stroke and hence did not contribute to this meta-analysis.

All participating studies approved guidelines for collaboration, and a neurology working-group arrived at a consensus on phenotype harmonization, covariate selection and analytic plans for within-study analyses and meta-analysis of results. Each study has an Institutional Review Board that approved the consent procedures, examination and surveillance components, data security processes, genotyping protocols and current study design.

ARIC:

The ARIC study is a prospective population-based study of atherosclerosis and clinical atherosclerotic diseases in 15,792 men and women, including 11,478 non-Hispanic white participants, drawn from 4 U.S. communities (Suburban Minneapolis, Minnesota; Washington County, Maryland; Forsyth County, North Carolina, and Jackson, Mississippi). In the first three communities, the sample reflects the demographic composition of the community. In Jackson, only black residents were enrolled. Ancestry

was self-reported during an interview. Participants were handed a card and asked to tell the interviewer which best described his or her race. Choices offered were: white, black, american indian/ alaskan native, asian/pacific islander, other: specify. Over 99% identified as either white or black. Only self-identified whites were included in the discovery cohort. Participants were between age 45 and 64 years at their baseline examination in 1987-1989 when blood was drawn for DNA extraction and participants consented to genetic testing.[1] Genotyping was performed at the Broad Institute using the Affymetrix® Genome-Wide Human SNP Array 6.0. As of June 2008, genotyping had been completed on 8,861 white participants. Individuals with and without genotype data did not significantly differ with regards to baseline CVD risk factors (not shown). Only individuals free of stroke or TIA at baseline were included (n=8,377). We excluded individuals with a sex mismatch (n=40), those who were discordant for more than 5% of genotypes among 47 previously genotyped overlapping SNPs (n=157), persons who were 1st degree relatives (n=314), those who were outliers based on average identity by state (n=131) or based on Eigenstrat clustering (n=250), or persons who had an incident SAH (n=18); some individuals met more than one exclusion criterion. In total, 7,686 individuals were included in the present analyses.

CHS

The CHS is a population-based cohort study of risk factors for coronary heart disease (CHD) and stroke in adults ≥65 years conducted across four field centers in the United States.[2] The original predominantly white cohort of 5,201 persons (4,964 whites) was recruited in 1989-1990 from a random sample of people on Medicare eligibility lists and

an additional 687 blacks were enrolled subsequently (1992-93) for a total sample of 5,888. As in the ARIC cohort, race was determined by self-identification at interview. In addition to the 5 categories used in the ARIC study, participants were also asked a second question as to whether they considered themselves to be of Hispanic origin. Only self-identified blacks were excluded from the discovery cohort. DNA was extracted from blood samples drawn on all participants who consented to genetic testing at their baseline examination. In 2007-2008, genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai using the Illumina 370CNV Duo® BeadChip system on the first 2,427 of 3,980 CHS participants who were free of CVD at baseline. The 1,908 persons excluded for prevalent CVD had prevalent coronary heart disease (n=1195), congestive heart failure (n=86), peripheral vascular disease (n=93), valvular heart disease (n=20), stroke (n=166) or transient ischemic attack (n=56). Some persons had more than one reason to be excluded and for these individuals only the initial exclusionary event is listed. The 2,427 participants who had been genotyped by July 2008(time of the meta-analysis) were a stratified probability sample that included all cases of myocardial infarction (MI), stroke, atrial fibrillation, dementia, and heart failure, and a selection of controls sampled based on the age-, and sex-distribution of MI cases. Sampling weights were used in the analysis to account for the study design and to weight back to the underlying cohort selected for genotyping (N=3,980). Because the other cohorts were predominantly white, the African American participants were excluded from the initial meta-analysis to limit the potential for false positive associations due to population stratification. At the time of the meta-analysis, genotyping had been attempted in 2,101 white participants, and was successful in 2,022

persons; the latter constitute the CHS sample for this study. QC criteria used to define successful genotyping are listed in Section 3, 35 persons were excluded for a subject-specific call rate ≤95%.

FHS

The FHS is a three-generation, single-site, community-based, ongoing cohort study that was initiated in 1948 to investigate prospectively the risk factors for CVD including stroke. It now comprises 3 generations of participants (N=10,333): the Original cohort followed since 1948;[3] their Offspring and spouses of the Offspring, followed since 1971;[4] and children from the largest Offspring families enrolled in 2000 (Gen 3).[8] Gen 3 participants were not included in this analysis since they are young (mean age 40±9 years) and few have suffered strokes. The Original cohort enrolled 5209 men and women who comprised two-thirds of the adult population then residing in Framingham, MA. Survivors continue to receive biennial examinations. The Offspring cohort comprises 5124 persons (including 3514 biological offspring) who have been examined approximately once every 4 years. The population of Framingham was virtually entirely white (Europeans of English, Scots, Irish and Italian descent) in 1948 when the Original cohort was recruited. At the initial examination participants were asked for country of birth and whether or not they had any Italian ancestry. At a later examination (the 8th) the Offspring cohort participants were asked to identify their race from the following choices: Caucasian or white, African-American or black, Asian, Native Hawaiian or other Pacific Islander, American Indian or Alaska native or 'prefer not to answer'. They were also asked to identify their ethnicity as either 'Hispanic or Latino' or neither. Almost all

the FHS Original and Offspring participants are white/Caucasian and none were excluded from the discovery cohort. FHS participants had DNA extracted and provided consent for genotyping in the 1990s. All available eligible participants were genotyped at Affymetrix (Santa Clara, CA) through an NHLBI funded SNP-Health Association Resource (SHARe) project using the Affymetrix GeneChip® Human Mapping 500K Array Set and 50K Human Gene Focused Panel.® In 272 persons (31 with stroke), small amounts of DNA were extracted from stored whole blood and required whole genome amplification prior to genotyping. Cell lines were available for most of the remaining participants. Genotyping was attempted in 5293 participants, and 4,519 persons met QC criteria. Failures (call rate <97%, extreme heterozygosity or high Mendelian error rate) were largely restricted to persons with whole-genome amplified DNA and DNA extracted from stored serum samples. We also excluded 156 participants who were less than 45 years old at the time of the DNA draw, 135 persons with prevalent stroke and 97 persons who did not have stroke surveillance on follow-up after genotyping; the remaining 4,131 subjects constitute the FHS sample for this study.

Rotterdam Study

The Rotterdam Study is a population-based cohort study among inhabitants of a district of Rotterdam (Ommoord), The Netherlands, and aims to examine the determinants of disease and health in the elderly with a focus on neurogeriatric, cardiovascular, bone, and eye disease.[5] All inhabitants aged ≥55 years (n = 10,275) were invited and the participation rate was 78%, yielding a total of 7983 subjects. All participants gave written informed consent to retrieve information from treating physicians. Baseline

measurements were obtained from 1990 to 1993 and consisted of an interview at home and two visits to the research center for physical examination. At this baseline examination ancestry was determined by self-report. Participants were asked to identify with one of the following categories that best described their ancestry: Dutch, Caucasian, Asian, Indian, Indonesian, Mediterranean, Negroid. Less than 1% of participants chose an ancestry other than Dutch or Caucasian. All Rotterdam study participants were included in the discovery cohort. Survivors have been re-examined three times: in 1993-1995, 1997-1999, and 2002-2004. All persons attending the baseline examination in 1990-93 consented to genotyping and had DNA extracted. This DNA was genotyped using the Illumina Infinium II HumanHap550chip v3.0® array in 2007-2008 according to the manufacturer's protocols. Genotyping was attempted in persons with high-quality extracted DNA (n=6449). From these 6449, samples with low call rate (<97.5%, n=209), with excess autosomal heterozygosity (> 0.336, n=21), with sex-mismatch (n=36), or if there were outliers identified by the IBS clustering analysis (>3 standard deviations from population mean, n=102 or IBS probabilities > 97%, n=129) were excluded from the study population with some persons meeting more than one exclusion criterion; in total, 5974 samples were available with good quality genotyping data. Of these, 170 persons were excluded for prevalent stroke and 41 persons for lack of adequate follow-up after genotyping. The remaining 5763 persons constitute the Rotterdam Study sample for the present analyses.

3**. Stroke surveillance and classification**

Stroke Surveillance

ARIC:

Persons were screened for possible stroke events through annual phone interviews, follow-up examinations, community hospital surveillance, and death certificates. Any reported hospitalization led to screening and, if suitable, to medical record abstraction. Potential stroke events were selected for abstraction of records if the discharge diagnosis included a cerebrovascular disease code (International Classification of Diseases, 9th Revision, codes 430 to 438), if a cerebrovascular procedure was mentioned in the discharge summary, or if the CT or MRI report showed evidence of acute cerebrovascular disease.[9] All suspected events were classified by computer algorithm and also by an expert physician reviewer, blinded to the automated results. A second physician reviewer adjudicated disagreements between the computer and the initial reviewer.

CHS

Participants were examined annually from enrollment to 1999, and since then continue to be under surveillance for stroke.[10, 11] Since baseline, participants have also been contacted twice a year to identify potential cardiovascular events, including stroke. In addition, all hospitalizations were screened for potential stroke events. For suspected events, information was collected from the participant or next of kin, from medical records, and, if needed, from the participant's physician. When available, CT and/or MRI scans or reports were reviewed centrally. Final adjudication of the occurrence of stroke, stroke

types, and subtypes was undertaken by vascular neurologists at a consensus conference using all available information.

FHS

At each clinic exam, participants receive questionnaires, physical examinations and laboratory testing; between examinations they remain under surveillance (regardless of whether or not they live in the vicinity) via physician referrals, record linkage and annual telephone health history updates. Incident strokes have been identified since 1948 through this ongoing system of FHS clinic and local hospital surveillance and methods used have been detailed previously;[12-14] they include review of medical records and collaboration with local general practitioners, emergency rooms and imaging facilities. If a participant saw a physician or was admitted to the hospital, visited an emergency room or obtained any brain imaging between biennial examinations for symptoms suggestive of TIA or stroke, a stroke neurologist from the Heart Study attempted to visit the person within 48 hours and recorded a complete history and neurological examination; this was repeated at 1, 3 and 6 months. All medical records from practitioners, hospitals, imaging centers, rehabilitation centers and nursing homes were procured for review. A panel of 3 investigators (at least 2 neurologists) adjudicated the diagnosis of stroke and determined stroke subtype in each case based on the Framingham evaluations and external records. The recruitment of Original and Offspring cohort participants at FHS had occurred long before the DNA collection with the result that a large number of stroke events in the FHS (although ascertained prospectively) were prevalent at the time of DNA collection and

were excluded from these analyses. While this reduced the sample size from FHS, the meta-analyses presented here focused on incident events.

Rotterdam

All participants have been continuously monitored for major events (including stroke) through automated linkage of the study database with files from general practitioners and the municipality. In addition physician files from nursing homes and general practitioner records of participants who moved out of the Ommoord district were reviewed twice a year. For suspected stroke and TIA events, additional information (including neuroimaging) was obtained from hospital records and research physicians discussed available information with an experienced stroke neurologist to verify all diagnoses.[15, 16]

Stroke Classification

Strokes were classified as ischemic if there was imaging (CT or MRI within 4 weeks), surgical or autopsy evidence excluding a hemorrhage, or in the absence of such direct evidence (in <10% of cases in FHS and Rotterdam, none in CHS) if the preponderance of indirect evidence (e.g. deficit limited to one limb or completely resolved within 72 hours, atrial fibrillation in persons not on anticoagulants) suggested the event was an ischemic rather than a hemorrhagic stroke. A stroke was classified as hemorrhagic if there was imaging, surgical, lumbar puncture or autopsy evidence of hemorrhage, and in the absence of direct evidence to the contrary, when the participant

lost consciousness permanently or died within hours after onset of focal signs. The stroke type was defined as unknown if there was insufficient information available to categorize the event as ischemic or hemorrhagic. All ischemic and hemorrhagic strokes and strokes of unknown type were included in the analyses of total stroke with one exception: subarachnoid hemorrhages (n=28 across all studies) were excluded from these analyses since the heritability, risk factors and pathophysiologic mechanisms underlying subarachnoid hemorrhages are distinctly different from other stroke subtypes. Persons with a subarachnoid hemorrhage were censored at the time of the event.

Only known ischemic strokes were included in the analysis of ischemic stroke. In secondary analyses we related those SNPs which reached genome-wide significance in our initial GWAS to the specific ischemic stroke subtype of atherothrombotic stroke, also called atherothrombotic brain infarction (ABI). We used the best available definitions of definite and possible ABI in each cohort; both large artery atherosclerotic strokes and small-vessel or lacunar strokes were included in this phenotype, events known to be cardioembolic were excluded. In the Rotterdam study which did not subtype ischemic strokes as ABI or cardiomebolic, we excluded those ischemic strokes that occurred in the presence of concomitant atrial fibrillation. For the analysis of ABI, participants were censored in the ARIC, CHS and FHS when they developed an alternative type of stroke and in the Rotterdam study if they developed atrial fibrillation.

Neuroimaging was available for 98% of all events in ARIC, 87% of all events in CHS, 90% of all events in FHS and 65% of all events in the Rotterdam study. In the current analyses we included events through December 31st 2004 for ARIC and the Rotterdam Study, and through December 31st 2005 for the CHS and FHS studies.

4. Genotyping quality control filters and imputation:

Subject specific quality control filters included filters for call rate, heterozygosity, and number of Mendelian errors per individual. SNP specific quality control filters included filters for call rate, minor allele frequency, Hardy-Weinberg equilibrium, and differential missingness by outcome or genotype (mishap test in PLINK); http://pngu.mgh.harvard.edu/purcell/plink/).

Imputation

The set of genotyped input SNPs used for imputation in each study was selected based on their highest quality GWA data. We used a callrate >95% in CHS and ARIC; >97% in FHS and >98% in Rotterdam; a minor allele frequency >0.01 in each study; a Hardy-Weinberg p>1x10-5 in CHS and $p>1x10^{-6}$ in ARIC, FHS, and Rotterdam; and a test of differential missingness by the "mishap" test in PLINK $p>1x10^{-9}$ in each study. We used either the Markov Chain Haplotyping (MaCH) package (http://www.sph.umich.edu/csg/abecasis/MACH) version 1.0.15 software (ARIC, FHS and Rotterdam; imputed to plus strand of NCBI build 36, HapMap release #22) or BIM-BAM[17] (CHS, imputed to plus strand of NCBI build 35) programs. For each imputed SNP a reliability of imputation was estimated (as the ratio of the empirically observed dosage variance to the expected binomial dosage variance: O/E ratio). For the primary meta-analysis using inverse-variance weighting less weight is given to imputed SNPs with low observed dosage variance (resulting in higher variance of the estimate). For the secondary meta- analysis using the inverse square root (N) weighting the ratio was used to compute an effective sample size.

Direct Genotyping

We used the Taqman system to directly genotype SNPs that reached genome-wide significance in the initial GWAS. Rs 11833579 had been imputed in all 4 cohorts and although the estimated reliability of the imputation had been high in three of the four cohorts (O/E ratio: 0.94 to 0.97) we directly genotyped this SNP in all 4 discovery cohorts and in the ARIC African-American replication sample. Rs1245791 had been genotyped by the platforms used in the ARIC, FHS and Rotterdam studies and imputed in the CHS alone (O/E ratio of 0.47), hence it was directly genotyped in CHS. Both SNPs were also genotyped in a small sample of 574 CHS African-Americans and in the white clinical case-control series. Primers and probe sequences may be obtained from the authors on request.

5. Screening for latent population substructure

All four discovery cohorts were screened for latent population substructure (including cryptic relatedness) using suitable programs (i.e, EIGENSTRAT in ARIC and FHS,[18, 19] an IBD matrix in Rotterdam,[20] and using principal components analysis in CHS) and either found no evidence of occult population admixture, or found that the principal components identified were not related to the stroke phenotype.

We studied quantile-quantile (Q-Q) plots to ensure that the p-value distributions in each of the four cohorts conformed to a null distribution at all but the extreme tail. We also calculated the genomic inflation factor (λ), which measures over-dispersion of test-statistics from association tests indicating population stratification and can be used to apply genomic control.[21] The λ for total stroke was 1.010 for ARIC, 1.053 for CHS, 1.029 for FHS, and 0.999 for the Rotterdam Study. For ischemic stroke it was 1.009 for ARIC, 1.064 for CHS, 1.037 for FHS, and 1.003 for the Rotterdam Study.

6. Meta-analysis techniques

After quality control and filtering within each study, the ARIC had either genotyped or imputed data for 2,448,797 SNPS, CHS for 2,531,169 SNPs, the FHS for 2,540,223 SNPs, and the Rotterdam study for 2,543,887 SNPs. SNPs with a minor allele frequency ≤0.005 were excluded. We restricted the present meta-analysis to the 2,194,468 autosomal SNPs common to all 4 studies. Our primary meta-analysis technique was inverse-variance weighting (also known as fixed-effects meta-analysis) after applying genomic control within each individual study. Beta estimates were weighted by their inverse variance and a combined estimate was obtained by summing the weighted betas and dividing by the summed weights. Hence results for SNPs imputed with low certainty were down-weighted because the low reliability-of-imputation (see Section 4) ensures a large variance. In contrast, studies with large sample sizes and with directly genotyped or well-imputed SNPs had a greater effect on the meta-analysis p-value because of small variances. For verification purposes we also undertook meta-analyses using inverse square root (N) weighting without genomic control and these results are included in the Supplementary tables 1 and 2. We undertook the meta-analyses at the Rotterdam study using the R-library, MetABEL (http://mga.bionet.nsc.ru/~yurii/ABEL/).[22]

We estimated the genomic inflation factor (λ) after meta-analysis. The estimate of λ was 1.012 for total stroke and 1.006 for ischemic stroke indicating no significant inflation of p-values. The quantile-quantile (Q-Q) plot of our inverse variance meta-analysis results for total stroke (Figure 1A) and ischemic stroke (Figure 1B) show the distribution of the observed test statistic (negative log of p-values, on the *y*-axis) plotted

against the distribution of test statistic expected under the null-hypothesis (on the *x*-axis).The observed p-values conform to the null distribution across the entire range until $p<1.0x10^{-5}$; we expect that true positive associations reside beyond this region and that population substructure is negligible.

7. Replication Samples:

Our original African-American replication sample consisted of a subset of the cohort of 4,266 African-American participants from the ARIC study. The overall design of the ARIC study is described in Section 2, and the methods used for stroke surveillance and classification are described in Section 3 of the Supplementary Appendix.[1,7] As of June 2008, genotyping had been completed on a sample of 2,572 African-American participants drawn randomly from the total ARIC African-American cohort. Only individuals free of stroke or TIA at baseline were included in the analyses (n=2,483). An additional 8 individuals were excluded for incident SAH Finally, 45 individuals were excluded for failure to meet QC criteria; these individuals had a sex mismatch or were discordant for more than 5% of 47 previously genotyped SNPs. The remaining 2,430 individuals were used in the replication analyses.

Our second replication sample comprised 652 persons with prevalent stroke (313 women, mean age 76.5 ± 7.1, 501 of these persons had an ischemic type of stroke and of these 400 had an atherothrombotic stroke) and age-matched controls. The stroke cases included persons with prevalent stroke in the Rotterdam Study at baseline, and a clinical series of ischemic strokes obtained from three hospitals. The first was the Erasmus MC University Medical Center, Rotterdam (n=271, 246 atherothrombotic), the second was the St Elisabeth Hospital, Tilburg (n=99, of which 76 were atherothrombotic), and the third was the TweeSteden Hospital, Tilburg (n=131, of which 31 were atherothrombotic). These clinical databases aim to collect clinical information, blood samples and DNA in all ischemic stroke patients evaluated at these hospitals. Controls were drawn from the group of Rotterdam Study participants who were stroke-free at baseline and were within

the same age range as the cases. These persons contributed one set of person-years to the prevalent analysis and a second, non-overlapping set of person-years to the incident analyses. Therefore the two analyses are independent of each other, this was confirmed with simulation experiments. A third, small and underpowered sample that was genotyped consisted of 574 African-Americans in the CHS who were free of prevalent cardiovascular disease at baseline and had been followed prospectively for incident stroke. Over a 10 year follow-up period a total of 85 incident strokes (68 ischemic, 57 atherothrombotic) were observed. Baseline characteristics of the replication cohorts are shown in Supplementary Table 4.

8. Candidate genes: selection and results

SNP selection

We searched Pubmed for original articles published before July 1st 2008, which reported statistically significant associations between specific genotypes and stroke. Since over 200 putative candidate genes for stroke have been described in the literature, we focused on genes identified as potential candidates for total stroke and ischemic stroke in whites by meta-analyses of the published literature. We used the search terms *meta-analysis*, *stroke* and *gene* and identified a total of 41 publications; we retrieved and reviewed all of them. We identified 12 meta-analyses,[23-34] each of which studied white participants, and reported a significant association of at least one SNP within a gene with the risk of either total stroke or ischemic stroke in the pooled analyses. A total of 9 candidate genes were identified by this process. We selected SNPs that had been specifically examined in these meta-analyses, ignoring data based on linkage studies. Based on these criteria we studied selected SNPs in the following genes: 5,10-methylene tetrahydrofolate reductase (*MTHFR*),[24] Factor 5 Leiden (*F5*),[24] phosphodiesterase D *(PDE4D*)[31, 33, 34], plasminogen activator inhibitor type 1 or serpin peptidase inhibitor (*SERPINE1*),[23, 29] prothrombin (*F2*),[24] glycoprotein 1b alpha (*GP1BA*),[27]arachidonate 5-lipooxygenase-activating protein (*ALOX5AP*), apolipoprotein E (*APOE*).[28, 32, 34] We also selected a proxy SNP for the ACE insertion/deletion that has been associated with the risk of ischemic stroke.[35] Finally, we selected two intergenic SNPs at chromosome 4q25 and 9p21 that have been related previously to atrial fibrillation and coronary artery disease, respectively, and more recently to cardioembolic (rs2200733)[36] and thrombotic (rs1537378) strokes.

Results are presented in Supplementary Table 6 below. Rs16954257 in the *GPIBA* gene, a proxy SNP for rs2243093 previously associated with stroke, [27] was significantly associated with total stroke (p=0.02) and ischemic stroke (p=0.02) in our meta-analysis. For the prothrombin (*F2)* gene neither the reported SNP nor a proxy SNP with LD>0.8 was genotyped or imputed in our dataset. [24] However, six other SNPs within that gene (rs3136447, rs2070852, rs5896, rs3136457, rs3136480 and rs2282687) reached $p<10^{-4}$ for total stroke (see Supplementary Table 1 rows 206 to 211).

9. Population attributable risk

Population attributable risk is an index incorporating both frequency of a risk factor and the risk ratio of outcome with and without the risk factor. It represents the proportion of a specific disease in the population attributable to this risk factor. Estimation of PAR is usually more accurate in cohort studies than in case/control studies where the odds-ratio may overestimate risk. The PAR for individual SNPs such as rs11833579 and rs12425791 was calculated as follows:

$$PAR = 1 - \frac{1}{q^2 + 2pq(HR) + p^2(HR^2)}$$

where q = major allele frequency; p = minor allele frequency and HR =the hazard ratio from the meta-analysis based on an additive model for increasing dose of the risk allele.[37]

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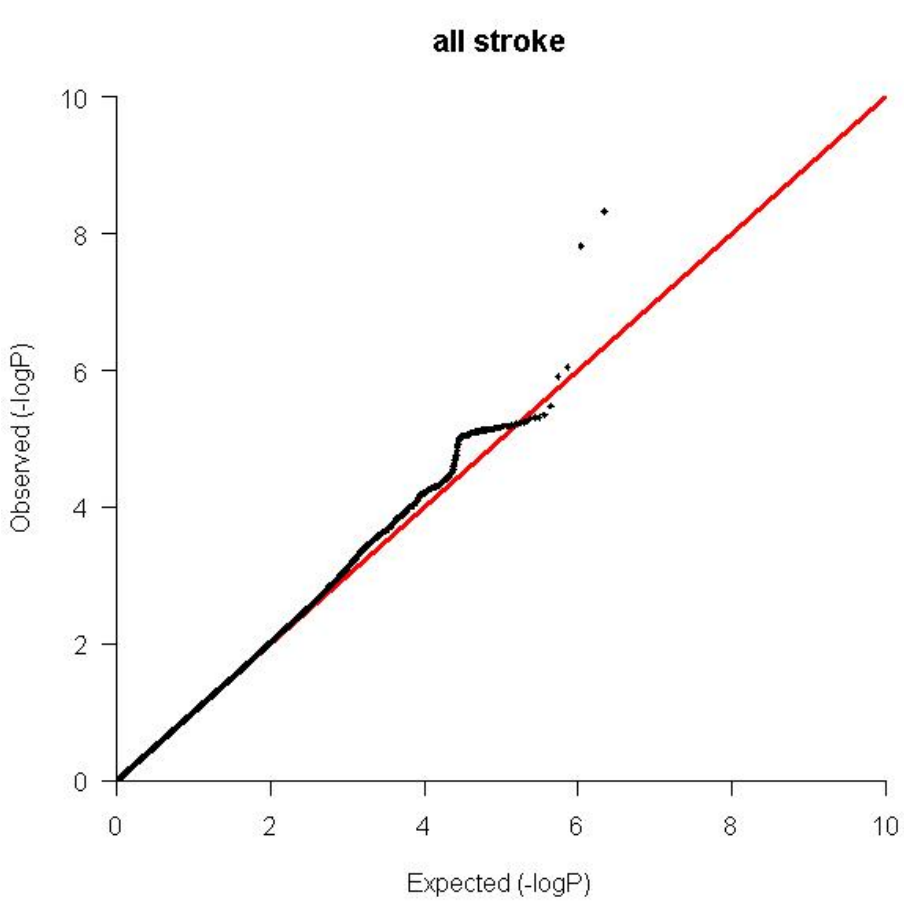
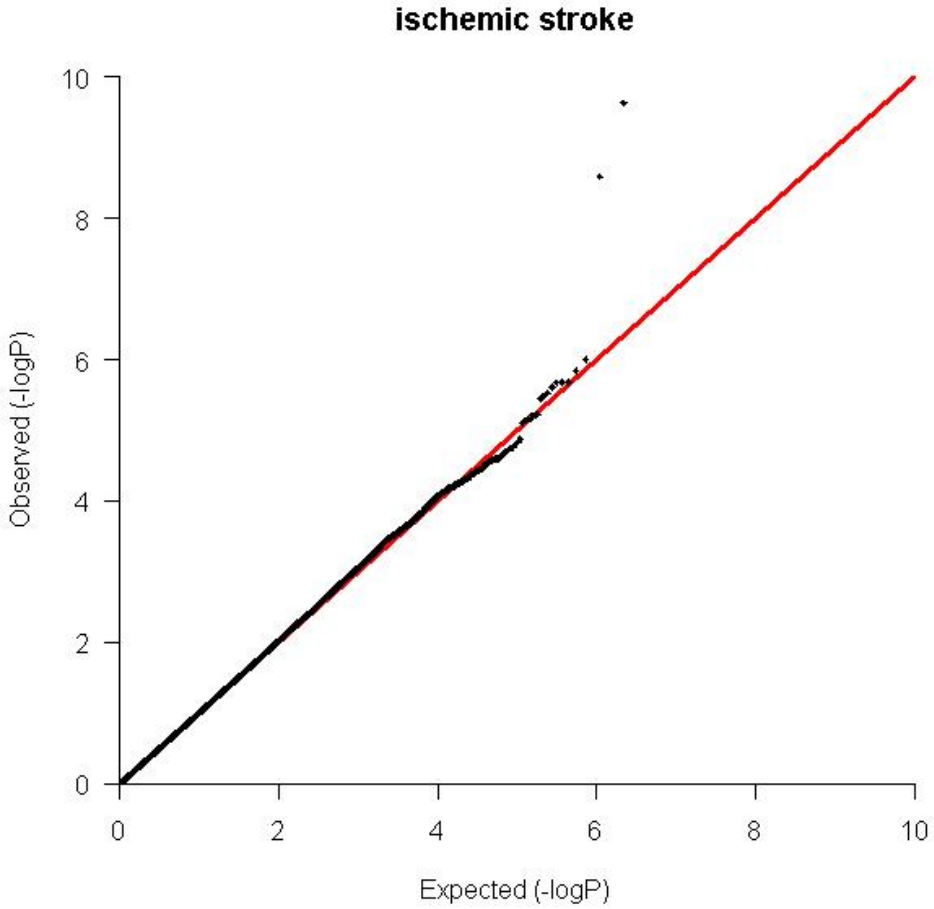
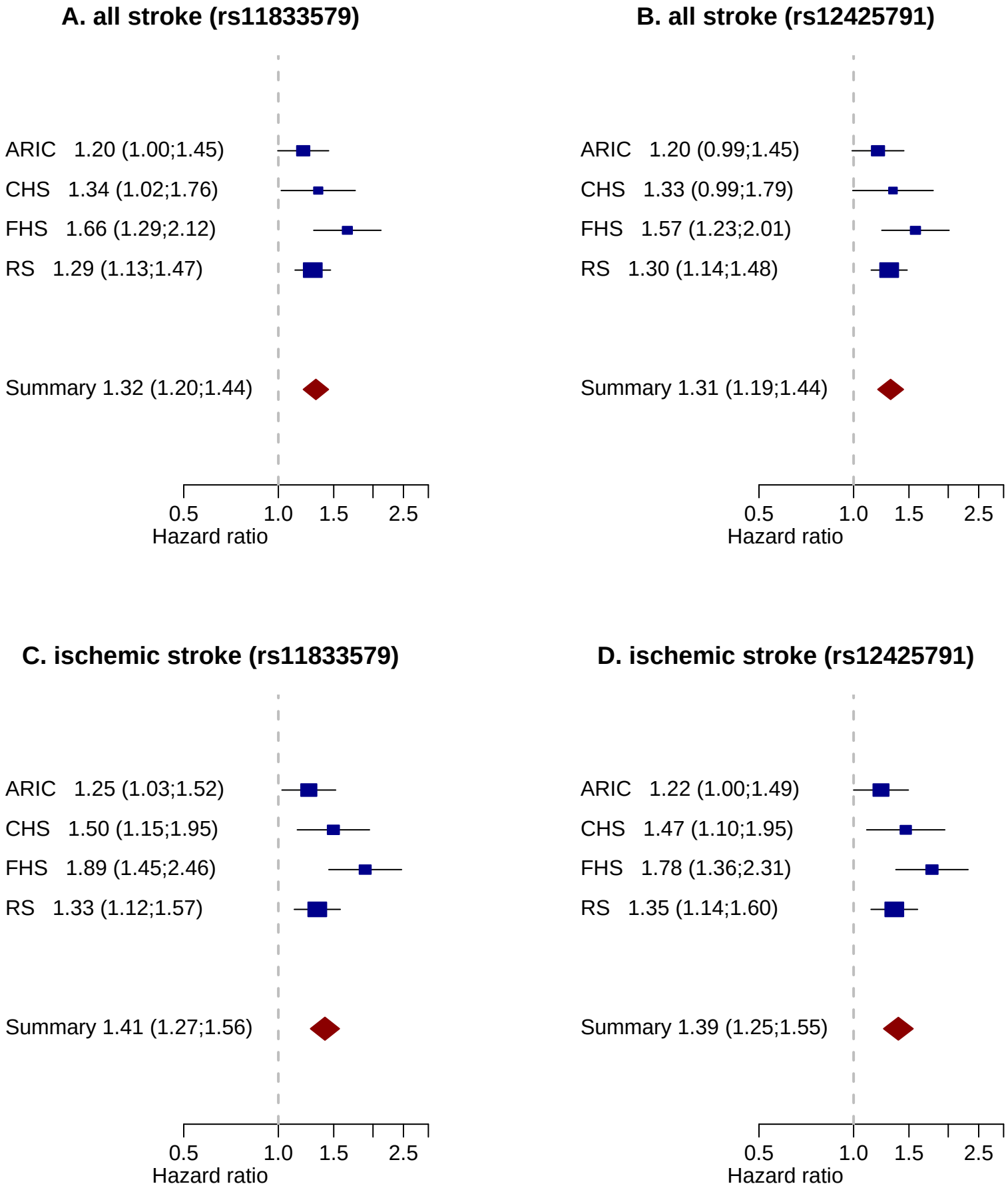
Figures 1A and 1B. Quantile-quantile (QQ)-plot showing the observed versus the expected p-values after meta-analysis for total stroke and ischemic stroke respectively. The red line shows the distribution under the null-hypothesis (also uploaded as separate figures).

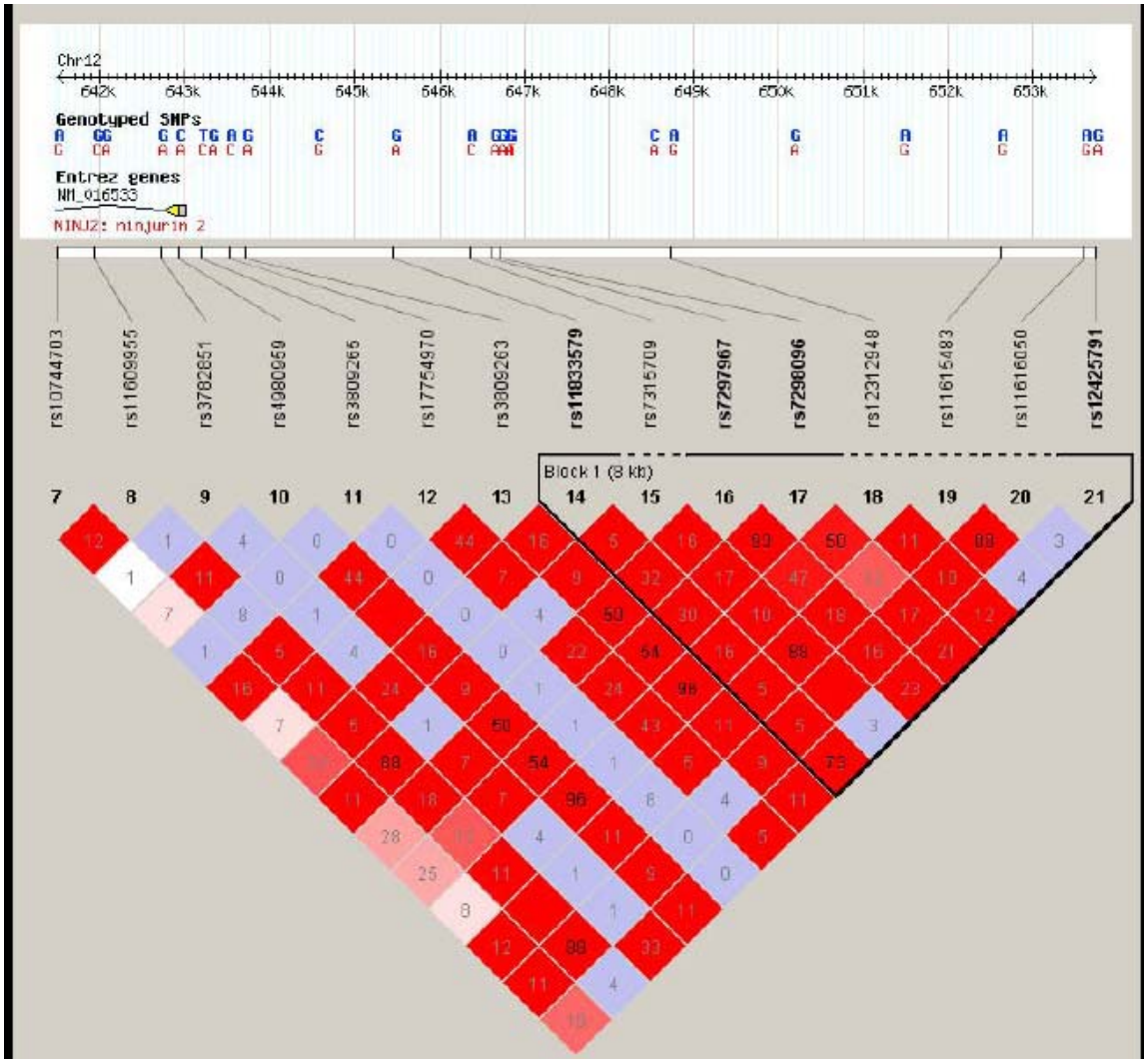






Supplementary Appendix: Figure 2: Forest plots based on initial GWAS for total stroke: rs11833579 (A) and rs12425791 (B) and for ischemic stroke: rs11833579 (C) and rs12425791 (D).

Figure 3: Linkage-disequilibrium plot of SNPs adjacent to the *NINJ2* gene that were significantly associated with total stroke and ischemic stroke and SNPs at the 5′ end of the *NINJ2* gene (also uploaded as separate figure). SNPs in bold are those that were significantly associated with total stroke and ischemic stroke



Tables 1 (total stroke) and 2 (ischemic stroke): results for all associations with a meta-analysis p-value lower than 10^{-4}

Results are ordered by chromosomal number and position. The table provides details specific to the individual participating cohorts including whether SNP was genotyped with sufficient reliability to be used in imputation [1] or was imputed [0], and the hazard ratios (with 95% confidence intervals) and p-values within each participating cohort. It also provides hazard ratios (95% confidence intervals) and p-values based on fixed–effects (inverse variance-weighted) meta-analysis and Z-test statistics and p-values based on inverse square root (N) weighting meta-analysis. The Human Gene Organization (HUGO) Gene Nomenclature System symbols for the two genes located closest to each SNP and the distance of the associated SNP from the 5′ end (start) of the gene are also shown. Standardized gene annotations for all SNP results were derived programatically from the UCSC Genome Browser RefSeq gene track (hg18). Distances to genes are given in kilo-base (kb) pairs, based on NCBI build #36.

Supplementary Appendix: Table 1: Single nucleotide polymorphism (SNP)-phenotype associations at meta-analysis for total stroke; all associations with p-value lower than 10^{-4}

name	chromosome	position	strand	allele1	allele2	minor allele (coded allele)	minor allele frequency	meta-beta inverse variance	meta-se inverse variance	hazard ratio inverse variance	lower bound	upper bound	chi2 statistic inverse variance	p-value inverse variance
rs11247752	1	28298588	+	T	G	G	0.32	0.19	0.048	1.2	1.1	1.3	16.02	6.3x10^{-5}
rs3762318	1	67369707	+	A	G	G	0.16	-0.23	0.055	0.79	0.71	0.88	17.90	2.3x10^{-5}
rs165005	1	91297228	+	A	G	G	0.18	-0.25	0.063	0.78	0.69	0.88	15.42	8.6x10^{-5}
rs12127189	1	117044963	+	T	C	T	0.20	-0.24	0.061	0.79	0.70	0.89	15.50	8.3x10^{-5}
rs12077203	1	163383874	+	T	C	T	0.10	0.27	0.067	1.3	1.2	1.5	16.54	4.8x10^{-5}
rs181131	2	8194011	+	A	C	A	0.39	-0.16	0.041	0.85	0.78	0.92	16.37	5.2x10^{-5}
rs181132	2	8200640	+	A	T	T	0.42	-0.18	0.042	0.84	0.77	0.91	18.46	1.7x10^{-5}
rs181134	2	8202599	+	T	C	C	0.38	-0.17	0.041	0.84	0.78	0.91	17.23	3.3x10^{-5}
rs6735812	2	46434578	+	G	C	C	0.50	-0.15	0.038	0.86	0.80	0.93	15.53	8.1x10^{-5}
rs4953358	2	46434957	+	G	C	C	0.50	-0.15	0.038	0.86	0.80	0.93	15.53	8.1x10^{-5}
rs4953359	2	46435147	+	T	C	C	0.50	-0.15	0.038	0.86	0.80	0.93	15.51	8.2x10^{-5}
rs6743991	2	46436739	+	A	C	C	0.50	-0.15	0.039	0.86	0.80	0.93	15.55	8.0x10^{-5}
rs6707241	2	46438356	+	T	C	C	0.50	-0.15	0.038	0.86	0.80	0.93	15.24	9.5x10^{-5}
rs6740096	2	46439392	+	A	T	A	0.50	-0.15	0.038	0.86	0.80	0.93	15.23	9.5x10^{-5}
rs17819022	2	46704075	+	A	G	A	0.31	0.16	0.041	1.2	1.1	1.3	15.50	8.2x10^{-5}
rs12105006	2	46716090	+	T	C	C	0.32	0.16	0.041	1.2	1.1	1.3	15.42	8.6x10^{-5}
rs350796	2	52765746	+	T	C	T	0.12	0.24	0.058	1.3	1.1	1.4	16.99	3.8x10^{-5}
rs17017029	2	79470375	+	A	G	G	0.09	-0.41	0.099	0.67	0.55	0.81	16.81	4.1x10^{-5}
rs13389286	2	144081346	+	T	C	T	0.36	0.17	0.043	1.2	1.1	1.3	15.31	9.1x10^{-5}
rs1440063	2	223560597	+	A	G	G	0.43	-0.16	0.040	0.85	0.78	0.92	17.27	3.3x10^{-5}
rs17693703	3	35309402	+	T	G	T	0.16	0.21	0.053	1.2	1.1	1.4	16.22	5.6x10^{-5}
rs12492172	3	35320076	+	T	C	T	0.16	0.21	0.052	1.2	1.1	1.4	16.54	4.8x10^{-5}
rs7615446	3	35330281	+	G	C	C	0.16	0.21	0.052	1.2	1.1	1.4	16.46	5.0x10^{-5}
rs697331	3	38321783	+	T	C	T	0.06	0.29	0.075	1.3	1.2	1.6	15.36	8.9x10^{-5}
rs7648153	3	120057225	+	T	C	C	0.38	0.16	0.041	1.2	1.1	1.3	15.23	9.5x10^{-5}
rs1589440	3	120068428	+	G	C	G	0.37	0.16	0.040	1.2	1.1	1.3	15.84	6.9x10^{-5}
rs1402578	3	120076823	+	A	G	G	0.37	0.16	0.040	1.2	1.1	1.3	16.64	4.5x10^{-5}
rs10511381	3	120077681	+	T	C	T	0.37	0.16	0.040	1.2	1.1	1.3	16.61	4.6x10^{-5}
rs6449093	4	14571594	+	A	G	G	0.09	0.28	0.063	1.3	1.2	1.5	19.55	9.8x10^{-6}
rs2259467	4	36342124	+	A	G	G	0.30	0.17	0.042	1.2	1.1	1.3	16.39	5.2x10^{-5}
rs2376008	4	36346259	+	A	C	A	0.30	0.17	0.042	1.2	1.1	1.3	16.36	5.2x10^{-5}
rs9654211	4	134242407	+	A	G	A	0.44	-0.16	0.040	0.85	0.79	0.92	16.20	5.7x10^{-5}
rs2901012	4	134244291	+	T	C	C	0.47	-0.17	0.040	0.85	0.78	0.91	17.50	2.9x10^{-5}
rs6854421	4	134245759	+	A	G	A	0.45	-0.16	0.040	0.85	0.79	0.92	16.17	5.8x10^{-5}
rs962104	4	134248128	+	A	G	A	0.45	-0.16	0.040	0.85	0.79	0.92	16.12	5.9x10^{-5}
rs13136511	4	134251362	+	T	C	C	0.48	-0.17	0.040	0.84	0.78	0.91	17.86	2.4x10^{-5}
rs951744	4	134252369	+	T	G	G	0.45	-0.16	0.040	0.85	0.79	0.92	16.21	5.7x10^{-5}
rs951743	4	134252488	+	A	T	A	0.45	-0.16	0.040	0.85	0.79	0.92	16.27	5.5x10^{-5}
rs7673582	4	134254664	+	G	C	G	0.45	-0.16	0.040	0.85	0.78	0.92	16.41	5.1x10^{-5}
rs1396014	4	134256267	+	A	T	A	0.45	-0.16	0.040	0.85	0.78	0.92	16.31	5.4x10^{-5}
rs17586065	4	134259146	+	A	G	A	0.45	-0.16	0.040	0.85	0.78	0.92	16.26	5.5x10^{-5}
rs7660183	4	134259868	+	A	C	A	0.48	-0.17	0.040	0.85	0.78	0.91	17.70	2.6x10^{-5}
rs17526785	4	134260101	+	A	G	G	0.45	-0.16	0.040	0.85	0.79	0.92	16.15	5.9x10^{-5}
rs7664058	4	134265424	+	T	C	T	0.48	-0.17	0.040	0.85	0.78	0.92	17.38	3.1x10^{-5}
rs13134791	4	134265703	+	T	C	T	0.47	-0.17	0.040	0.85	0.78	0.92	17.39	3.0x10^{-5}
rs4404561	4	134266380	+	A	C	A	0.44	-0.16	0.040	0.85	0.79	0.92	15.87	6.8x10^{-5}
rs906471	4	134269858	+	A	G	G	0.48	-0.17	0.040	0.85	0.78	0.92	17.32	3.2x10^{-5}
rs17586357	4	134278376	+	A	G	G	0.45	-0.16	0.040	0.85	0.79	0.92	15.92	6.6x10^{-5}
rs10010228	4	134279734	+	T	C	T	0.48	-0.17	0.040	0.85	0.78	0.92	17.23	3.3x10^{-5}
rs1396013	4	134281275	+	T	C	C	0.45	-0.16	0.040	0.85	0.79	0.92	15.90	6.7x10^{-5}
rs1507839	4	134282468	+	T	G	T	0.48	-0.16	0.041	0.85	0.78	0.92	15.95	6.5x10^{-5}
rs7720944	5	25554215	+	T	C	C	0.07	0.29	0.073	1.3	1.2	1.5	15.75	7.2x10^{-5}
rs7712047	5	25570111	+	T	C	C	0.07	0.31	0.075	1.4	1.2	1.6	17.16	3.4x10^{-5}
rs7714983	5	25605083	+	G	C	G	0.07	0.31	0.076	1.4	1.2	1.6	16.15	5.9x10^{-5}
rs7701270	5	25605373	+	T	G	G	0.07	0.31	0.076	1.4	1.2	1.6	16.16	5.8x10^{-5}
rs10051348	5	25608147	+	T	C	T	0.07	0.31	0.076	1.4	1.2	1.6	16.26	5.5x10^{-5}
rs10942129	5	25653431	+	A	T	A	0.07	0.33	0.075	1.4	1.2	1.6	19.36	1.1x10^{-5}
rs10462272	5	25672155	+	T	G	T	0.30	-0.17	0.044	0.84	0.77	0.92	15.41	8.7x10^{-5}
rs10061512	5	25678572	+	G	C	C	0.28	-0.19	0.045	0.83	0.76	0.91	17.15	3.5x10^{-5}
rs7733598	5	25679112	+	T	C	C	0.28	-0.19	0.045	0.83	0.76	0.91	17.11	3.5x10^{-5}
rs7734006	5	25679977	+	T	C	T	0.30	-0.18	0.043	0.84	0.77	0.91	16.95	3.8x10^{-5}
rs7729848	5	25679999	+	A	T	A	0.30	-0.18	0.043	0.84	0.77	0.91	16.93	3.9x10^{-5}
rs12188325	5	25692113	+	A	C	C	0.30	-0.18	0.044	0.83	0.77	0.91	17.05	3.6x10^{-5}
rs4867131	5	33047743	+	A	C	A	0.11	0.34	0.071	1.4	1.2	1.6	23.54	1.2x10^{-6}
rs2656989	5	82226475	+	T	C	T	0.16	0.20	0.052	1.2	1.1	1.4	15.28	9.3x10^{-5}
rs2060210	5	151069895	+	A	T	T	0.43	-0.16	0.041	0.85	0.78	0.92	16.21	5.7x10^{-5}
rs10062868	5	151074333	+	A	T	T	0.42	-0.16	0.041	0.85	0.79	0.92	15.71	7.4x10^{-5}
rs13175452	5	164367746	+	T	C	C	0.47	0.17	0.042	1.2	1.1	1.3	16.36	5.3x10^{-5}
rs851880	6	67120634	+	A	G	G	0.12	0.22	0.055	1.2	1.1	1.4	15.64	7.7x10^{-5}
rs1634186	6	67126785	+	A	G	A	0.12	0.23	0.057	1.3	1.1	1.4	16.57	4.7x10^{-5}
rs1708563	6	67127808	+	A	G	A	0.12	0.23	0.057	1.3	1.1	1.4	16.60	4.6x10^{-5}
rs6956537	7	64051842	+	A	G	A	0.09	-0.31	0.077	0.73	0.63	0.85	16.52	4.8x10^{-5}
rs3211928	7	80135656	+	G	C	G	0.45	-0.19	0.041	0.83	0.77	0.90	20.37	6.4x10^{-6}
rs3211931	7	80136109	+	T	C	T	0.44	-0.19	0.041	0.83	0.77	0.90	20.14	7.2x10^{-6}
rs3211932	7	80136823	+	T	C	C	0.44	-0.19	0.041	0.83	0.77	0.90	20.12	7.3x10^{-6}
rs3173804	7	80137786	+	A	T	A	0.45	-0.18	0.041	0.83	0.77	0.90	19.82	8.5x10^{-6}
rs3173805	7	80138940	+	T	C	C	0.45	-0.18	0.041	0.83	0.77	0.90	19.81	8.6x10^{-6}
rs3211958	7	80142008	+	A	G	G	0.45	-0.18	0.041	0.83	0.77	0.90	19.62	9.4x10^{-6}
rs3211960	7	80142548	+	A	G	G	0.45	-0.18	0.041	0.83	0.77	0.90	19.72	9.0x10^{-6}
rs7755	7	80144207	+	A	G	A	0.45	-0.18	0.041	0.83	0.77	0.90	19.70	9.1x10^{-6}
rs13246513	7	80144687	+	T	C	T	0.44	-0.19	0.041	0.83	0.77	0.90	19.94	8.0x10^{-6}
rs12706949	7	80145160	+	T	G	T	0.45	-0.18	0.041	0.83	0.77	0.90	19.95	7.9x10^{-6}
rs13223096	7	80145560	+	T	C	T	0.44	-0.19	0.042	0.83	0.77	0.90	20.12	7.3x10^{-6}
rs13230419	7	80147221	+	T	C	T	0.44	-0.18	0.042	0.83	0.77	0.90	19.70	9.1x10^{-6}
rs17266080	7	80148267	+	A	G	A	0.44	-0.18	0.041	0.83	0.77	0.90	19.82	8.5x10^{-6}
rs10954289	7	80164219	+	A	G	G	0.44	-0.18	0.041	0.83	0.77	0.90	19.83	8.5x10^{-6}
rs12534038	7	80167036	+	G	C	G	0.44	-0.18	0.041	0.83	0.77	0.90	19.91	8.1x10^{-6}
rs713536	8	12943177	+	T	C	T	0.47	0.21	0.042	1.2	1.1	1.3	24.12	9.1x10^{-7}
rs7012771	8	29487626	+	T	G	T	0.40	-0.17	0.041	0.84	0.78	0.92	16.84	4.1x10^{-5}
rs12546690	8	29503055	+	A	T	T	0.41	-0.16	0.040	0.85	0.78	0.92	16.54	4.8x10^{-5}
rs12546462	8	29507407	+	A	C	C	0.42	-0.16	0.040	0.85	0.79	0.92	16.11	6.0x10^{-5}
rs4131179	8	29508328	+	A	G	G	0.42	-0.16	0.040	0.85	0.79	0.92	16.41	5.1x10^{-5}
rs1527939	8	117391083	+	A	G	G	0.13	0.22	0.054	1.2	1.1	1.4	16.46	5.0x10^{-5}
rs2225173	9	13425926	+	G	C	C	0.38	-0.18	0.047	0.83	0.76	0.91	15.30	9.2x10^{-5}
rs10961053	9	13434573	+	G	C	G	0.36	0.17	0.042	1.2	1.1	1.3	16.84	4.1x10^{-5}
rs10491751	9	13434932	+	A	G	A	0.35	0.17	0.042	1.2	1.1	1.3	16.16	5.8x10^{-5}
rs973321	9	13437632	+	A	T	A	0.37	0.17	0.041	1.2	1.1	1.3	17.24	3.3x10^{-5}
rs1556577	9	13443984	+	T	G	G	0.39	0.18	0.040	1.2	1.1	1.3	19.70	9.1x10^{-6}
rs1333992	9	13444817	+	A	C	C	0.33	0.17	0.041	1.2	1.1	1.3	16.75	4.3x10^{-5}
rs7853368	9	13447920	+	G	C	G	0.39	0.18	0.040	1.2	1.1	1.3	19.98	7.8x10^{-6}
rs11788445	9	100305153	+	A	T	T	0.12	0.24	0.061	1.3	1.1	1.4	15.53	8.1x10^{-5}
rs10082493	10	58519754	+	A	T	A	0.23	0.18	0.045	1.2	1.1	1.3	16.07	6.1x10^{-5}
rs11005634	10	58525034	+	T	C	T	0.23	0.18	0.044	1.2	1.1	1.3	16.38	5.2x10^{-5}
rs11005635	10	58525230	+	A	G	A	0.23	0.18	0.044	1.2	1.1	1.3	16.38	5.2x10^{-5}
rs11005636	10	58525500	+	T	C	T	0.23	0.18	0.044	1.2	1.1	1.3	16.38	5.2x10^{-5}
rs12258368	10	58537901	+	T	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.39	5.2x10^{-5}
rs12256850	10	58537981	+	A	T	T	0.23	0.18	0.044	1.2	1.1	1.3	16.41	5.1x10^{-5}
rs4130804	10	58538106	+	T	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.41	5.1x10^{-5}
rs7900082	10	58540334	+	A	T	A	0.25	0.18	0.044	1.2	1.1	1.3	16.20	5.7x10^{-5}
rs12256059	10	58542546	+	T	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.78	4.2x10^{-5}
rs11005649	10	58546057	+	T	C	T	0.23	0.18	0.044	1.2	1.1	1.3	16.85	4.1x10^{-5}
rs3105310	10	58546660	+	A	G	A	0.30	0.16	0.040	1.2	1.1	1.3	16.09	6.0x10^{-5}
rs12767717	10	58547094	+	T	C	T	0.22	0.19	0.046	1.2	1.1	1.3	16.66	4.5x10^{-5}
rs3104627	10	58551576	+	A	G	G	0.30	0.16	0.041	1.2	1.1	1.3	15.69	7.5x10^{-5}
rs11005650	10	58551611	+	T	C	T	0.23	0.18	0.044	1.2	1.1	1.3	17.35	3.1x10^{-5}
rs17608226	10	58552764	+	T	C	C	0.23	0.18	0.043	1.2	1.1	1.3	17.02	3.7x10^{-5}
rs7079891	10	58558159	+	G	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.98	3.8x10^{-5}
rs7092768	10	58558872	+	G	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.99	3.8x10^{-5}
rs11005656	10	58563099	+	T	C	T	0.23	0.18	0.044	1.2	1.1	1.3	16.90	3.9x10^{-5}
rs7080809	10	58572176	+	A	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.49	4.9x10^{-5}
rs12269040	10	58575853	+	T	G	T	0.23	0.18	0.044	1.2	1.1	1.3	16.47	5x10^{-5}
rs7906620	10	58576055	+	T	C	T	0.23	0.18	0.044	1.2	1.1	1.3	16.43	5.0x10^{-5}
rs7086024	10	58577000	+	A	G	A	0.23	0.18	0.044	1.2	1.1	1.3	16.48	4.9x10^{-5}
rs11005665	10	58583657	+	A	G	G	0.23	0.18	0.044	1.2	1.1	1.3	16.51	4.9x10^{-5}
rs12783597	10	58588647	+	G	C	G	0.23	0.18	0.044	1.2	1.1	1.3	16.42	5.1x10^{-5}
rs11005673	10	58591018	+	A	T	T	0.23	0.18	0.044	1.2	1.1	1.3	16.47	4.9x10^{-5}
rs1394112	10	58592427	+	T	C	T	0.24	0.17	0.043	1.2	1.1	1.3	15.20	9.7x10^{-5}
rs1394111	10	58592645	+	A	T	A	0.24	0.17	0.044	1.2	1.1	1.3	15.17	9.8x10^{-5}
rs12247842	10	58592863	+	T	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.17	9.8x10^{-5}
rs12253024	10	58592900	+	G	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.18	9.8x10^{-5}
rs7100491	10	58593290	+	A	T	A	0.24	0.17	0.044	1.2	1.1	1.3	15.19	9.7x10^{-5}
rs7078639	10	58593429	+	A	G	A	0.24	0.17	0.044	1.2	1.1	1.3	15.14	10.x10^{-5}
rs12248271	10	58593596	+	T	C	C	0.23	0.18	0.044	1.2	1.1	1.3	16.41	5.1x10^{-5}
rs1915694	10	58594479	+	A	G	A	0.24	0.17	0.044	1.2	1.1	1.3	15.20	9.7x10^{-5}
rs1915693	10	58594589	+	A	C	A	0.24	0.17	0.044	1.2	1.1	1.3	15.22	9.6x10^{-5}
rs1847409	10	58595019	+	A	T	A	0.23	0.18	0.044	1.2	1.1	1.3	16.40	5.1x10^{-5}
rs7077008	10	58595853	+	T	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.19	9.7x10^{-5}
rs11005676	10	58596784	+	T	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.17	9.8x10^{-5}
rs12261393	10	58597134	+	G	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.18	9.8x10^{-5}
rs12256612	10	58600062	+	A	G	A	0.24	0.17	0.044	1.2	1.1	1.3	15.22	9.6x10^{-5}
rs7080282	10	58601726	+	T	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.19	9.7x10^{-5}
rs11005681	10	58602218	+	T	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.17	9.8x10^{-5}
rs11005682	10	58602460	+	T	C	T	0.24	0.17	0.044	1.2	1.1	1.3	15.18	9.8x10^{-5}
rs11005683	10	58602596	+	A	G	A	0.24	0.17	0.044	1.2	1.1	1.3	15.19	9.7x10^{-5}
rs11005684	10	58602621	+	G	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.21	9.6x10^{-5}
rs7093642	10	58603997	+	T	G	G	0.24	0.17	0.044	1.2	1.1	1.3	15.15	9.9x10^{-5}
rs7072641	10	58604102	+	G	C	G	0.24	0.17	0.044	1.2	1.1	1.3	15.18	9.8x10^{-5}
rs7093904	10	58604159	+	T	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.19	9.7x10^{-5}
rs7072950	10	58604303	+	T	C	T	0.24	0.17	0.044	1.2	1.1	1.3	15.18	9.8x10^{-5}
rs7072214	10	58604500	+	A	G	A	0.24	0.17	0.044	1.2	1.1	1.3	15.18	9.8x10^{-5}
rs7073369	10	58604574	+	A	C	A	0.24	0.17	0.044	1.2	1.1	1.3	15.21	9.6x10^{-5}
rs7921321	10	58604882	+	A	T	A	0.24	0.17	0.044	1.2	1.1	1.3	15.22	9.6x10^{-5}
rs7918221	10	58604990	+	A	C	C	0.24	0.17	0.044	1.2	1.1	1.3	15.21	9.6x10^{-5}
rs7901155	10	58605048	+	A	G	A	0.24	0.17	0.044	1.2	1.1	1.3	15.20	9.7x10^{-5}
rs12262199	10	58605607	+	T	G	G	0.24	0.17	0.044	1.2	1.1	1.3	15.19	9.7x10^{-5}
rs12263813	10	58605867	+	T	C	C	0.23	0.18	0.045	1.2	1.1	1.3	16.37	5.2x10^{-5}
rs11818432	10	58609677	+	T	G	T	0.23	0.18	0.045	1.2	1.1	1.3	15.57	7.9x10^{-5}
rs7076261	10	58610276	+	T	C	T	0.30	0.16	0.041	1.2	1.1	1.3	15.81	7.0x10^{-5}

name	genotyped ARIC	hazard ratio ARIC	lower bound ARIC	upper bound ARIC	p-value ARIC	genotyped CHS	hazard ratio CHS	lower bound CHS	upper bound CHS	p-value CHS	genotypedFHS	hazard ratio FHS	lower bound FHS	upper bound FHS	p-value FHS
rs11247752	1	1.4	1.1	1.6	9.6x10^{-4}	0	0.93	0.65	1.4	7.2x10^{-1}	0	1.1	0.82	1.5	4.9x10^{-1}
rs3762318	1	1.00	0.80	1.2	9.7x10^{-1}	1	0.73	0.58	0.92	7.1x10^{-3}	1	0.62	0.44	0.87	5.4x10^{-3}
rs165005	0	0.86	0.68	1.1	2.2x10^{-1}	0	0.81	0.64	1.0	9.5x10^{-2}	0	0.81	0.57	1.1	2.3x10^{-1}
rs12127189	0	0.74	0.59	0.93	8.8x10^{-3}	0	0.99	0.71	1.4	9.4x10^{-1}	0	0.81	0.57	1.1	2.4x10^{-1}
rs12077203	0	1.5	1.1	1.9	2.6x10^{-3}	0	1.5	0.99	2.3	5.7x10^{-2}	0	1.1	0.70	1.6	8.0x10^{-1}
rs181131	1	0.93	0.79	1.1	3.8x10^{-1}	0	0.85	0.71	1.0	8.2x10^{-2}	1	0.85	0.67	1.1	2.0x10^{-1}
rs181132	1	0.90	0.77	1.1	2.1x10^{-1}	0	0.84	0.69	1.0	5.9x10^{-2}	0	0.83	0.64	1.1	1.7x10^{-1}
rs181134	0	0.92	0.77	1.1	3.3x10^{-1}	1	0.85	0.72	1.0	6.9x10^{-2}	0	0.85	0.66	1.1	2.1x10^{-1}
rs6735812	0	0.94	0.81	1.1	4.5x10^{-1}	0	0.80	0.68	0.95	9.8x10^{-3}	0	0.74	0.59	0.92	6.1x10^{-3}
rs4953358	0	0.94	0.81	1.1	4.5x10^{-1}	0	0.80	0.68	0.95	9.7x10^{-3}	0	0.74	0.59	0.92	6.1x10^{-3}
rs4953359	0	0.94	0.81	1.1	4.5x10^{-1}	0	0.80	0.68	0.95	9.6x10^{-3}	0	0.74	0.59	0.92	6.1x10^{-3}
rs6743991	0	0.94	0.81	1.1	4.5x10^{-1}	0	0.80	0.67	0.95	9.1x10^{-3}	0	0.74	0.60	0.93	7.9x10^{-3}
rs6707241	1	0.95	0.81	1.1	4.8x10^{-1}	0	0.80	0.68	0.95	9.3x10^{-3}	1	0.74	0.60	0.92	6.3x10^{-3}
rs6740096	0	0.95	0.81	1.1	4.8x10^{-1}	0	0.80	0.68	0.95	9.3x10^{-3}	0	0.74	0.60	0.92	6.3x10^{-3}
rs17819022	0	1.2	1.0	1.4	2.6x10^{-2}	0	1.1	0.93	1.3	2.6x10^{-1}	0	1.3	1.0	1.6	3.1x10^{-2}
rs12105006	1	1.2	1.0	1.4	1.4x10^{-2}	0	1.1	0.93	1.3	2.3x10^{-1}	1	1.2	0.96	1.6	1.0x10^{-1}
rs350796	1	1.3	1.0	1.6	3.3x10^{-2}	0	1.6	1.1	2.3	7.1x10^{-3}	1	1.3	0.95	1.8	9.8x10^{-2}
rs17017029	0	0.66	0.46	0.94	2.3x10^{-2}	0	0.80	0.46	1.4	4.4x10^{-1}	0	0.66	0.38	1.2	1.4x10^{-1}
rs13389286	0	1.2	0.99	1.4	7.4x10^{-2}	0	1.2	0.95	1.5	1.2x10^{-1}	0	1.3	1.0	1.7	3.0x10^{-2}
rs1440063	1	0.75	0.64	0.88	5.8x10^{-4}	1	0.79	0.67	0.93	5.3x10^{-3}	0	1.00	0.77	1.3	9.9x10^{-1}
rs17693703	0	1.3	1.1	1.6	3.4x10^{-3}	0	1.1	0.79	1.5	5.5x10^{-1}	0	1.4	1.1	1.8	8.3x10^{-3}
rs12492172	0	1.3	1.1	1.6	3.2x10^{-3}	0	1.1	0.83	1.5	4.5x10^{-1}	0	1.4	1.1	1.8	8.3x10^{-3}
rs7615446	0	1.3	1.1	1.6	3.3x10^{-3}	0	1.1	0.83	1.5	4.5x10^{-1}	0	1.4	1.1	1.8	8.2x10^{-3}
rs697331	1	1.5	1.1	2.0	4.2x10^{-3}	1	1.2	0.86	1.7	2.9x10^{-1}	0	1.3	0.82	2.1	2.6x10^{-1}
rs7648153	1	1.1	0.91	1.3	3.9x10^{-1}	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.3	0.98	1.7	6.8x10^{-2}
rs1589440	0	1.1	0.91	1.3	3.8x10^{-1}	0	1.2	0.98	1.4	9.3x10^{-2}	0	1.3	0.98	1.7	6.8x10^{-2}
rs1402578	0	1.1	0.92	1.3	3.4x10^{-1}	1	1.2	0.99	1.4	5.7x10^{-2}	0	1.3	0.98	1.7	7.0x10^{-2}
rs10511381	0	1.1	0.92	1.3	3.3x10^{-1}	0	1.2	0.99	1.4	6.1x10^{-2}	0	1.3	0.98	1.7	7.0x10^{-2}
rs6449093	0	1.3	0.97	1.7	7.6x10^{-2}	1	1.5	1.1	1.9	5.6x10^{-3}	0	1.1	0.71	1.8	6.3x10^{-1}
rs2259467	0	1.1	0.97	1.3	1.2x10^{-1}	0	1.3	1.1	1.6	6.6x10^{-3}	0	1.3	1.0	1.7	3.9x10^{-2}
rs2376008	0	1.1	0.96	1.3	1.2x10^{-1}	1	1.3	1.1	1.6	6.0x10^{-3}	0	1.3	1.0	1.7	3.9x10^{-2}
rs9654211	0	0.89	0.76	1.1	1.8x10^{-1}	0	0.79	0.66	0.96	1.8x10^{-2}	0	1.00	0.78	1.3	9.8x10^{-1}
rs2901012	0	0.87	0.74	1.0	8.3x10^{-2}	0	0.80	0.66	0.97	2.1x10^{-2}	0	0.97	0.76	1.2	8.1x10^{-1}
rs6854421	1	0.89	0.76	1.0	1.6x10^{-1}	0	0.80	0.66	0.97	2.0x10^{-2}	1	1.00	0.78	1.3	9.8x10^{-1}
rs962104	0	0.89	0.76	1.0	1.6x10^{-1}	0	0.79	0.65	0.96	2.0x10^{-2}	0	1.00	0.78	1.3	9.8x10^{-1}
rs13136511	1	0.86	0.74	1.0	7.3x10^{-2}	0	0.80	0.66	0.97	2.3x10^{-2}	1	0.96	0.76	1.2	7.7x10^{-1}
rs951744	0	0.89	0.76	1.0	1.6x10^{-1}	0	0.79	0.65	0.97	2.1x10^{-2}	0	1.00	0.78	1.3	9.7x10^{-1}
rs951743	0	0.89	0.76	1.0	1.6x10^{-1}	0	0.79	0.65	0.97	2.1x10^{-2}	0	1.00	0.78	1.3	9.7x10^{-1}
rs7673582	1	0.89	0.76	1.0	1.6x10^{-1}	0	0.79	0.65	0.97	2.1x10^{-2}	0	0.99	0.78	1.3	9.7x10^{-1}
rs1396014	0	0.89	0.76	1.0	1.7x10^{-1}	0	0.79	0.65	0.97	2.1x10^{-2}	0	0.99	0.78	1.3	9.6x10^{-1}
rs17586065	1	0.89	0.76	1.1	1.7x10^{-1}	0	0.79	0.65	0.97	2.1x10^{-2}	1	0.99	0.78	1.3	9.6x10^{-1}
rs7660183	0	0.87	0.74	1.0	9.1x10^{-2}	0	0.80	0.66	0.97	2.5x10^{-2}	0	0.96	0.76	1.2	7.7x10^{-1}
rs17526785	0	0.90	0.77	1.1	2.0x10^{-1}	0	0.80	0.66	0.97	2.2x10^{-2}	0	0.99	0.78	1.3	9.6x10^{-1}
rs7664058	1	0.88	0.75	1.0	1.1x10^{-1}	0	0.81	0.67	0.97	2.6x10^{-2}	1	0.96	0.76	1.2	7.6x10^{-1}
rs13134791	1	0.88	0.75	1.0	1.1x10^{-1}	0	0.81	0.67	0.97	2.6x10^{-2}	1	0.96	0.76	1.2	7.6x10^{-1}
rs4404561	0	0.90	0.77	1.1	2.3x10^{-1}	0	0.79	0.65	0.97	2.3x10^{-2}	0	0.99	0.78	1.3	9.3x10^{-1}
rs906471	0	0.88	0.75	1.0	1.1x10^{-1}	0	0.81	0.67	0.98	2.8x10^{-2}	0	0.96	0.76	1.2	7.6x10^{-1}
rs17586357	0	0.90	0.77	1.1	2.2x10^{-1}	0	0.79	0.65	0.97	2.2x10^{-2}	0	0.99	0.78	1.3	9.5x10^{-1}
rs10010228	0	0.88	0.75	1.0	1.1x10^{-1}	0	0.81	0.66	0.98	2.9x10^{-2}	0	0.96	0.76	1.2	7.6x10^{-1}
rs1396013	0	0.90	0.77	1.1	2.2x10^{-1}	0	0.79	0.65	0.97	2.3x10^{-2}	0	0.99	0.78	1.3	9.5x10^{-1}
rs1507839	0	0.88	0.75	1.0	1.4x10^{-1}	0	0.81	0.65	1.00	5.0x10^{-2}	0	0.97	0.76	1.2	7.8x10^{-1}
rs7720944	0	1.1	0.84	1.6	4.1x10^{-1}	1	1.1	0.81	1.6	4.5x10^{-1}	0	1.7	1.1	2.8	1.7x10^{-2}
rs7712047	1	1.1	0.84	1.6	3.9x10^{-1}	0	1.2	0.82	1.9	3.2x10^{-1}	0	1.7	1.1	2.7	1.7x10^{-2}
rs7714983	0	1.1	0.83	1.6	3.9x10^{-1}	0	1.2	0.77	1.8	4.4x10^{-1}	0	1.8	1.1	2.8	1.1x10^{-2}
rs7701270	0	1.1	0.83	1.6	3.9x10^{-1}	0	1.2	0.77	1.8	4.5x10^{-1}	0	1.8	1.1	2.8	1.1x10^{-2}
rs10051348	0	1.2	0.84	1.6	3.6x10^{-1}	0	1.2	0.78	1.7	4.7x10^{-1}	0	1.8	1.1	2.8	1.0x10^{-2}
rs10942129	0	1.3	0.97	1.7	7.6x10^{-2}	0	1.3	0.62	2.8	4.7x10^{-1}	0	1.7	1.1	2.5	1.4x10^{-2}
rs10462272	0	0.93	0.78	1.1	4.2x10^{-1}	0	0.72	0.59	0.88	1.1x10^{-3}	0	0.83	0.63	1.1	1.6x10^{-1}
rs10061512	0	0.87	0.72	1.0	1.3x10^{-1}	0	0.71	0.58	0.86	5.9x10^{-4}	0	0.82	0.64	1.1	1.4x10^{-1}
rs7733598	1	0.87	0.72	1.0	1.3x10^{-1}	0	0.71	0.58	0.86	6.1x10^{-4}	1	0.82	0.64	1.1	1.4x10^{-1}
rs7734006	0	0.93	0.78	1.1	3.9x10^{-1}	1	0.73	0.61	0.88	8.6x10^{-4}	0	0.81	0.63	1.1	1.1x10^{-1}
rs7729848	0	0.93	0.78	1.1	3.9x10^{-1}	0	0.73	0.60	0.88	8.4x10^{-4}	0	0.81	0.63	1.1	1.1x10^{-1}
rs12188325	1	0.91	0.76	1.1	2.9x10^{-1}	0	0.73	0.60	0.88	1.3x10^{-3}	0	0.82	0.63	1.1	1.2x10^{-1}
rs4867131	0	1.3	1.0	1.7	4.0x10^{-2}	0	2.8	1.6	4.8	2.2x10^{-4}	0	1.6	1.1	2.4	1.4x10^{-2}
rs2656989	0	1.4	1.2	1.7	5.1x10^{-4}	0	1.2	0.91	1.5	2.1x10^{-1}	0	1.2	0.86	1.5	3.3x10^{-1}
rs2060210	1	0.87	0.74	1.0	8.8x10^{-2}	0	0.86	0.72	1.0	1.0x10^{-1}	1	0.78	0.62	1.00	4.6x10^{-2}
rs10062868	0	0.88	0.74	1.0	1.3x10^{-1}	0	0.86	0.72	1.0	9.8x10^{-2}	0	0.80	0.63	1.0	8.4x10^{-2}
rs13175452	1	1.2	1.0	1.4	1.7x10^{-2}	0	1.1	0.89	1.4	3.5x10^{-1}	1	1.1	0.90	1.4	2.9x10^{-1}
rs851880	0	1.2	0.93	1.5	1.9x10^{-1}	1	1.2	0.98	1.6	6.8x10^{-2}	0	1.4	1.0	1.9	2.3x10^{-2}
rs1634186	1	1.2	0.94	1.5	1.7x10^{-1}	0	1.3	0.99	1.7	5.6x10^{-2}	1	1.4	1.1	1.9	1.8x10^{-2}
rs1708563	0	1.2	0.94	1.5	1.6x10^{-1}	0	1.3	0.99	1.7	5.5x10^{-2}	0	1.4	1.1	1.9	1.8x10^{-2}
rs6956537	0	0.91	0.67	1.2	5.6x10^{-1}	1	0.65	0.48	0.89	7.2x10^{-3}	0	0.79	0.51	1.2	3.1x10^{-1}
rs3211928	1	0.82	0.69	0.96	1.5x10^{-2}	0	0.92	0.75	1.1	4.0x10^{-1}	1	0.79	0.61	1.0	6.2x10^{-2}
rs3211931	1	0.82	0.70	0.96	1.6x10^{-2}	0	0.91	0.74	1.1	3.9x10^{-1}	1	0.79	0.62	1.0	7.1x10^{-2}
rs3211932	1	0.82	0.70	0.96	1.6x10^{-2}	0	0.91	0.74	1.1	3.9x10^{-1}	1	0.79	0.62	1.0	7.1x10^{-2}
rs3173804	0	0.82	0.70	0.97	1.8x10^{-2}	0	0.92	0.75	1.1	4.0x10^{-1}	0	0.79	0.62	1.0	7.0x10^{-2}
rs3173805	0	0.82	0.70	0.97	1.8x10^{-2}	0	0.92	0.75	1.1	4.0x10^{-1}	0	0.79	0.62	1.0	7.0x10^{-2}
rs3211958	0	0.82	0.70	0.97	2.1x10^{-2}	0	0.92	0.75	1.1	4.0x10^{-1}	0	0.79	0.61	1.0	6.8x10^{-2}
rs3211960	0	0.82	0.70	0.97	2.1x10^{-2}	0	0.91	0.75	1.1	3.9x10^{-1}	0	0.79	0.61	1.0	6.7x10^{-2}
rs7755	1	0.83	0.70	0.97	2.1x10^{-2}	0	0.92	0.75	1.1	3.9x10^{-1}	0	0.79	0.61	1.0	6.7x10^{-2}
rs13246513	0	0.83	0.70	0.97	2.2x10^{-2}	0	0.91	0.74	1.1	3.6x10^{-1}	0	0.78	0.60	1.0	6.6x10^{-2}
rs12706949	0	0.82	0.70	0.97	2.1x10^{-2}	0	0.92	0.75	1.1	3.9x10^{-1}	0	0.78	0.60	1.0	6.5x10^{-2}
rs13223096	0	0.83	0.70	0.97	2.2x10^{-2}	0	0.91	0.74	1.1	3.6x10^{-1}	0	0.78	0.60	1.0	6.6x10^{-2}
rs13230419	0	0.83	0.70	0.98	2.7x10^{-2}	0	0.91	0.75	1.1	3.7x10^{-1}	0	0.79	0.60	1.0	8.7x10^{-2}
rs17266080	0	0.83	0.70	0.98	2.4x10^{-2}	0	0.91	0.75	1.1	3.6x10^{-1}	0	0.79	0.60	1.1	1.1x10^{-1}
rs10954289	0	0.83	0.70	0.97	2.3x10^{-2}	1	0.92	0.76	1.1	3.8x10^{-1}	0	0.79	0.60	1.1	1.1x10^{-1}
rs12534038	1	0.83	0.70	0.98	2.4x10^{-2}	0	0.91	0.75	1.1	3.6x10^{-1}	0	0.79	0.60	1.1	1.1x10^{-1}
rs713536	0	1.1	0.93	1.4	2.3x10^{-1}	1	1.4	1.2	1.7	1.0x10^{-4}	0	1.2	0.89	1.7	2.2x10^{-1}
rs7012771	0	0.86	0.73	1.0	8.3x10^{-2}	0	0.83	0.69	1.0	6.0x10^{-2}	0	0.96	0.76	1.2	7.5x10^{-1}
rs12546690	1	0.85	0.72	1.0	5.2x10^{-2}	0	0.86	0.71	1.0	9.6x10^{-2}	0	0.97	0.77	1.2	7.7x10^{-1}
rs12546462	0	0.85	0.72	1.00	4.4x10^{-2}	0	0.88	0.74	1.0	1.5x10^{-1}	1	1.00	0.79	1.3	9.9x10^{-1}
rs4131179	0	0.84	0.71	0.99	3.7x10^{-2}	0	0.88	0.74	1.0	1.5x10^{-1}	0	0.99	0.79	1.3	9.6x10^{-1}
rs1527939	0	1.3	1.0	1.6	4.6x10^{-2}	0	1.0	0.78	1.3	9.1x10^{-1}	0	1.1	0.78	1.6	5.9x10^{-1}
rs2225173	1	0.83	0.70	0.98	2.5x10^{-2}	0	0.72	0.52	1.0	5.9x10^{-2}	1	0.90	0.69	1.2	4.2x10^{-1}
rs10961053	0	1.2	0.98	1.4	8.9x10^{-2}	0	1.2	0.96	1.4	1.2x10^{-1}	0	1.2	0.88	1.6	2.6x10^{-1}
rs10491751	1	1.1	0.97	1.4	1.1x10^{-1}	0	1.2	0.95	1.4	1.4x10^{-1}	0	1.1	0.84	1.5	4.4x10^{-1}
rs973321	0	1.2	1.0	1.4	1.3x10^{-2}	0	1.1	0.95	1.3	1.8x10^{-1}	0	1.1	0.83	1.5	4.8x10^{-1}
rs1556577	0	1.3	1.1	1.5	5.1x10^{-3}	1	1.1	0.96	1.4	1.3x10^{-1}	0	1.2	0.90	1.6	2.1x10^{-1}
rs1333992	1	1.3	1.1	1.5	2.2x10^{-3}	0	1.1	0.92	1.3	2.8x10^{-1}	1	1.2	0.91	1.6	1.9x10^{-1}
rs7853368	0	1.3	1.1	1.5	4.8x10^{-3}	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	0.90	1.6	2.1x10^{-1}
rs11788445	1	1.3	1.1	1.7	1.1x10^{-2}	0	1.1	0.78	1.7	5.1x10^{-1}	1	1.1	0.82	1.6	4.2x10^{-1}
rs10082493	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.3	1.0	1.6	2.1x10^{-2}	0	1.00	0.73	1.4	10.x10^{-1}
rs11005634	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.5	2.4x10^{-2}	0	1.0	0.73	1.4	9.9x10^{-1}
rs11005635	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.5	2.4x10^{-2}	0	1.0	0.73	1.4	9.9x10^{-1}
rs11005636	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.5	2.4x10^{-2}	0	1.0	0.73	1.4	9.9x10^{-1}
rs12258368	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.5	2.5x10^{-2}	0	1.0	0.73	1.4	9.8x10^{-1}
rs12256850	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.5	2.5x10^{-2}	0	1.0	0.73	1.4	9.7x10^{-1}
rs4130804	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.5	2.5x10^{-2}	0	1.0	0.73	1.4	9.7x10^{-1}
rs7900082	0	1.1	0.92	1.3	2.7x10^{-1}	0	1.2	1.0	1.5	2.5x10^{-2}	0	1.0	0.77	1.4	7.7x10^{-1}
rs12256059	0	1.2	0.96	1.4	1.3x10^{-1}	0	1.2	1.0	1.5	2.1x10^{-2}	0	1.0	0.73	1.4	9.7x10^{-1}
rs11005649	0	1.2	0.96	1.4	1.2x10^{-1}	0	1.2	1.0	1.5	2.2x10^{-2}	0	1.0	0.73	1.4	9.7x10^{-1}
rs3105310	0	1.2	1.0	1.4	1.9x10^{-2}	1	1.1	0.97	1.4	1.0x10^{-1}	0	1.1	0.78	1.4	7.4x10^{-1}
rs12767717	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.3	1.0	1.5	2.2x10^{-2}	0	1.0	0.73	1.4	9.4x10^{-1}
rs3104627	0	1.2	1.0	1.4	4.4x10^{-2}	0	1.1	0.96	1.4	1.3x10^{-1}	0	1.1	0.79	1.4	6.9x10^{-1}
rs11005650	0	1.2	0.96	1.4	1.2x10^{-1}	1	1.2	1.0	1.5	1.6x10^{-2}	0	1.0	0.73	1.4	9.7x10^{-1}
rs17608226	1	1.2	0.96	1.4	1.2x10^{-1}	0	1.2	1.0	1.5	2.0x10^{-2}	1	1.0	0.73	1.4	9.7x10^{-1}
rs7079891	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.5	2.1x10^{-2}	0	1.0	0.74	1.4	9.4x10^{-1}
rs7092768	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.5	2.1x10^{-2}	0	1.0	0.74	1.4	9.4x10^{-1}
rs11005656	1	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.5	2.3x10^{-2}	1	1.0	0.74	1.4	9.4x10^{-1}
rs7080809	1	1.1	0.94	1.4	1.8x10^{-1}	0	1.2	1.0	1.5	2.3x10^{-2}	1	1.0	0.74	1.4	9.5x10^{-1}
rs12269040	0	1.1	0.94	1.4	1.8x10^{-1}	0	1.2	1.0	1.5	2.3x10^{-2}	0	1.0	0.74	1.4	9.5x10^{-1}
rs7906620	1	1.1	0.94	1.4	1.9x10^{-1}	0	1.2	1.0	1.5	2.3x10^{-2}	1	1.0	0.74	1.4	9.5x10^{-1}
rs7086024	0	1.1	0.94	1.4	1.9x10^{-1}	0	1.2	1.0	1.5	2.3x10^{-2}	0	1.0	0.74	1.4	9.5x10^{-1}
rs11005665	1	1.1	0.94	1.4	1.9x10^{-1}	0	1.2	1.0	1.5	2.4x10^{-2}	0	1.0	0.74	1.4	9.5x10^{-1}
rs12783597	0	1.1	0.94	1.4	2.0x10^{-1}	0	1.2	1.0	1.5	2.4x10^{-2}	0	1.0	0.74	1.4	9.1x10^{-1}
rs11005673	0	1.1	0.94	1.4	2.0x10^{-1}	0	1.2	1.0	1.5	2.3x10^{-2}	0	1.0	0.74	1.4	9.1x10^{-1}
rs1394112	1	1.1	0.95	1.4	1.6x10^{-1}	1	1.2	1.0	1.4	4.3x10^{-2}	1	1.00	0.72	1.4	9.9x10^{-1}
rs1394111	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.4x10^{-2}	0	1.00	0.72	1.4	9.9x10^{-1}
rs12247842	1	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.4x10^{-2}	0	1.00	0.72	1.4	9.9x10^{-1}
rs12253024	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.3x10^{-2}	0	1.00	0.72	1.4	9.9x10^{-1}
rs7100491	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.3x10^{-2}	0	1.00	0.72	1.4	9.9x10^{-1}
rs7078639	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.5x10^{-2}	0	1.00	0.71	1.4	9.9x10^{-1}
rs12248271	0	1.1	0.94	1.4	1.9x10^{-1}	0	1.2	1.0	1.5	2.4x10^{-2}	0	1.0	0.74	1.4	9.2x10^{-1}
rs1915694	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.4x10^{-2}	0	1.00	0.72	1.4	9.9x10^{-1}
rs1915693	0	1.1	0.95	1.4	1.6x10^{-1}	0	1.2	1.0	1.4	4.4x10^{-2}	0	1.00	0.72	1.4	9.9x10^{-1}
rs1847409	0	1.1	0.94	1.4	1.9x10^{-1}	0	1.2	1.0	1.5	2.5x10^{-2}	0	1.0	0.74	1.4	9.2x10^{-1}
rs7077008	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.5x10^{-2}	0	1.00	0.71	1.4	9.8x10^{-1}
rs11005676	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.5x10^{-2}	0	1.00	0.71	1.4	9.8x10^{-1}
rs12261393	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.5x10^{-2}	0	1.00	0.71	1.4	9.8x10^{-1}
rs12256612	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.5x10^{-2}	0	1.00	0.71	1.4	9.8x10^{-1}
rs7080282	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.7x10^{-2}	0	0.99	0.71	1.4	9.8x10^{-1}
rs11005681	0	1.1	0.95	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.8x10^{-2}	0	0.99	0.71	1.4	9.8x10^{-1}
rs11005682	0	1.1	0.96	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.8x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs11005683	0	1.1	0.96	1.4	1.5x10^{-1}	0	1.2	1.0	1.4	4.7x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs11005684	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	4.7x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs7093642	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	5.0x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs7072641	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	4.9x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs7093904	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	4.9x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs7072950	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	4.9x10^{-2}	0	0.99	0.71	1.4	9.7x10^{-1}
rs7072214	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	5.0x10^{-2}	0	0.99	0.71	1.4	9.6x10^{-1}
rs7073369	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	5.0x10^{-2}	0	0.99	0.71	1.4	9.6x10^{-1}
rs7921321	1	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	4.9x10^{-2}	1	0.99	0.71	1.4	9.6x10^{-1}
rs7918221	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.0	1.4	5.0x10^{-2}	0	0.99	0.71	1.4	9.6x10^{-1}
rs7901155	0	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.00	1.4	5.0x10^{-2}	0	0.99	0.71	1.4	9.6x10^{-1}
rs12262199	1	1.1	0.96	1.4	1.4x10^{-1}	0	1.2	1.00	1.4	5.0x10^{-2}	0	0.99	0.71	1.4	9.6x10^{-1}
rs12263813	0	1.1	0.95	1.4	1.7x10^{-1}	0	1.2	1.0	1.5	2.9x10^{-2}	0	1.0	0.74	1.4	9.4x10^{-1}
rs11818432	0	1.1	0.95	1.4	1.7x10^{-1}	0	1.2	1.0	1.5	4.9x10^{-2}	0	1.0	0.74	1.4	9.5x10^{-1}
rs7076261	0	1.2	1.0	1.4	2.7x10^{-2}	0	1.1	0.94	1.3	2.0x10^{-1}	0	1.1	0.79	1.5	6.6x10^{-1}

name	genotyped RS	hazard ratio RS	lower bound RS	upper bound RS	p-value RS	z-score N-weighting meta-analysis	p-value N-weighting meta-analysis	closest gene	distance from closest gene (kb)	second closest gene	distance from second closest gene (kb)
rs11247752	1	1.2	1.1	1.4	4.0x10^{-3}	3.81	1.4x10^{-4}	EYA3	10.9	PTAFR	49.9
rs3762318	1	0.77	0.65	0.91	1.8x10^{-3}	-3.90	9.6x10^{-5}	C1orf141	2.9	IL23R	35.0
rs165005	0	0.70	0.57	0.86	6.5x10^{-4}	-3.74	1.8x10^{-4}	ZNF644	37.0	HFM1	201.7
rs12127189	0	0.76	0.64	0.90	2.0x10^{-3}	-3.95	7.7x10^{-5}	IGSF3	33.1	CD2	53.6
rs12077203	0	1.3	1.1	1.5	1.2x10^{-2}	3.92	8.9x10^{-5}	LMX1A	53.9	RXRG	253.1
rs181131	0	0.81	0.72	0.91	3.7x10^{-4}	-3.65	2.6x10^{-4}	ID2	545.6	KIDINS220	592.5
rs181132	0	0.80	0.71	0.91	3.7x10^{-4}	-3.98	6.8x10^{-5}	ID2	538.9	KIDINS220	585.9
rs181134	1	0.81	0.72	0.91	3.5x10^{-4}	-3.74	1.9x10^{-4}	ID2	537.0	KIDINS220	583.9
rs6735812	0	0.88	0.79	0.99	2.7x10^{-2}	3.79	1.5x10^{-4}	EPAS1	within gene	ATP6V1E2	157.9
rs4953358	0	0.88	0.79	0.99	2.8x10^{-2}	3.79	1.5x10^{-4}	EPAS1	within gene	ATP6V1E2	157.5
rs4953359	0	0.88	0.79	0.99	2.8x10^{-2}	-3.79	1.5x10^{-4}	EPAS1	within gene	ATP6V1E2	157.3
rs6743991	0	0.88	0.78	0.98	2.5x10^{-2}	-3.78	1.5x10^{-4}	EPAS1	within gene	ATP6V1E2	155.8
rs6707241	0	0.88	0.79	0.99	3.0x10^{-2}	-3.75	1.8x10^{-4}	EPAS1	within gene	ATP6V1E2	154.1
rs6740096	0	0.88	0.79	0.99	3.0x10^{-2}	-3.75	1.8x10^{-4}	EPAS1	within gene	ATP6V1E2	153.1
rs17819022	0	1.2	1.0	1.3	1.5x10^{-2}	4.08	4.6x10^{-5}	CRIPT	within gene	PIGF	6.3
rs12105006	1	1.2	1.0	1.3	1.4x10^{-2}	4.02	5.8x10^{-5}	CRIPT	10.4	PIGF	18.3
rs350796	0	1.2	1.0	1.4	2.6x10^{-2}	4.17	3.1x10^{-5}	ASB3	984.9	CHAC2	1082.7
rs17017029	0	0.64	0.48	0.85	2.2x10^{-3}	-4.10	4.1x10^{-5}	CTNNA2	123.3	REG3A	230.0
rs13389286	1	1.2	1.0	1.3	1.5x10^{-2}	3.95	7.7x10^{-5}	ARHGAP15	within gene	GTDC1	338.7
rs1440063	1	0.90	0.80	1.0	7.3x10^{-2}	-4.08	4.5x10^{-5}	ACSL3	44.2	KCNE4	64.5
rs17693703	0	1.2	0.99	1.3	6.5x10^{-2}	4.21	2.5x10^{-5}	ARPP-21	349.5	STAC	1087.7
rs12492172	0	1.2	0.99	1.3	6.6x10^{-2}	4.27	1.9x10^{-5}	ARPP-21	338.8	STAC	1077.0
rs7615446	0	1.1	0.99	1.3	6.6x10^{-2}	-4.27	2.0x10^{-5}	ARPP-21	328.6	STAC	1066.8
rs697331	1	1.3	1.1	1.7	1.6x10^{-2}	3.88	1.0x10^{-4}	SLC22A14	0.7	SLC22A13	27.0
rs7648153	0	1.2	1.1	1.4	8.8x10^{-4}	3.68	2.4x10^{-4}	IGSF11	44.9	C3orf30	290.5
rs1589440	0	1.2	1.1	1.4	9.7x10^{-4}	-3.73	1.9x10^{-4}	IGSF11	33.7	C3orf30	279.3
rs1402578	1	1.2	1.1	1.4	1.2x10^{-3}	3.82	1.3x10^{-4}	IGSF11	25.3	C3orf30	270.9
rs10511381	0	1.2	1.1	1.4	1.2x10^{-3}	3.83	1.3x10^{-4}	IGSF11	24.5	C3orf30	270.0
rs6449093	1	1.3	1.1	1.6	1.9x10^{-3}	3.90	9.5x10^{-5}	CPEB2	43.0	C1QTNF7	379.1
rs2259467	0	1.1	1.0	1.3	3.6x10^{-2}	3.96	7.4x10^{-5}	CENTD1	419.8	C4orf19	789.8
rs2376008	1	1.1	1.0	1.3	3.7x10^{-2}	3.95	7.7x10^{-5}	CENTD1	423.9	C4orf19	785.7
rs9654211	0	0.82	0.73	0.92	6.5x10^{-4}	-3.49	4.8x10^{-4}	PCDH10	47.5	C4orf33	3989.1
rs2901012	0	0.83	0.74	0.93	9.6x10^{-4}	-3.76	1.7x10^{-4}	PCDH10	45.6	C4orf33	3991.0
rs6854421	0	0.82	0.73	0.92	6.7x10^{-4}	-3.51	4.6x10^{-4}	PCDH10	44.2	C4orf33	3992.5
rs962104	0	0.82	0.73	0.92	6.6x10^{-4}	-3.51	4.5x10^{-4}	PCDH10	41.8	C4orf33	3994.8
rs13136511	0	0.83	0.74	0.93	8.9x10^{-4}	-3.82	1.3x10^{-4}	PCDH10	38.6	C4orf33	3998.1
rs951744	0	0.82	0.73	0.92	6.2x10^{-4}	-3.52	4.3x10^{-4}	PCDH10	37.6	C4orf33	3999.1
rs951743	0	0.82	0.73	0.92	6.0x10^{-4}	-3.52	4.3x10^{-4}	PCDH10	37.4	C4orf33	3999.2
rs7673582	0	0.82	0.73	0.92	5.5x10^{-4}	3.54	4.0x10^{-4}	PCDH10	35.3	C4orf33	4001.4
rs1396014	0	0.82	0.73	0.92	5.4x10^{-4}	-3.53	4.2x10^{-4}	PCDH10	33.7	C4orf33	4003.0
rs17586065	0	0.82	0.73	0.92	5.2x10^{-4}	-3.52	4.3x10^{-4}	PCDH10	30.8	C4orf33	4005.9
rs7660183	0	0.83	0.74	0.92	7.2x10^{-4}	-3.78	1.6x10^{-4}	PCDH10	30.1	C4orf33	4006.6
rs17526785	0	0.82	0.73	0.92	4.9x10^{-4}	-3.49	4.9x10^{-4}	PCDH10	29.8	C4orf33	4006.8
rs7664058	0	0.82	0.74	0.92	6.7x10^{-4}	-3.72	2.0x10^{-4}	PCDH10	24.5	C4orf33	4012.1
rs13134791	1	0.82	0.74	0.92	6.6x10^{-4}	-3.72	2.0x10^{-4}	PCDH10	24.2	C4orf33	4012.4
rs4404561	1	0.82	0.73	0.92	4.9x10^{-4}	-3.44	5.8x10^{-4}	PCDH10	23.5	C4orf33	4013.1
rs906471	0	0.82	0.74	0.92	6.5x10^{-4}	-3.72	2.0x10^{-4}	PCDH10	20.1	C4orf33	4016.6
rs17586357	0	0.82	0.73	0.91	4.5x10^{-4}	-3.45	5.6x10^{-4}	PCDH10	11.5	C4orf33	4025.1
rs10010228	0	0.82	0.74	0.92	6.5x10^{-4}	-3.71	2.1x10^{-4}	PCDH10	10.2	C4orf33	4026.4
rs1396013	0	0.82	0.73	0.91	4.5x10^{-4}	-3.45	5.6x10^{-4}	PCDH10	8.6	C4orf33	4028.0
rs1507839	0	0.82	0.73	0.92	6.3x10^{-4}	-3.57	3.6x10^{-4}	PCDH10	7.5	C4orf33	4029.2
rs7720944	1	1.4	1.2	1.7	4.4x10^{-4}	3.77	1.6x10^{-4}	CDH10	873.5	CDH9	1362.3
rs7712047	0	1.4	1.2	1.8	3.9x10^{-4}	3.89	1.0x10^{-4}	CDH10	889.4	CDH9	1346.4
rs7714983	0	1.4	1.2	1.7	7.1x10^{-4}	-3.80	1.5x10^{-4}	CDH10	924.4	CDH9	1311.4
rs7701270	0	1.4	1.2	1.7	7.1x10^{-4}	3.80	1.5x10^{-4}	CDH10	924.7	CDH9	1311.1
rs10051348	0	1.4	1.2	1.7	7.5x10^{-4}	3.83	1.3x10^{-4}	CDH10	927.5	CDH9	1308.3
rs10942129	0	1.4	1.1	1.7	1.1x10^{-3}	4.23	2.4x10^{-5}	CDH10	972.8	CDH9	1263.0
rs10462272	0	0.86	0.75	0.97	1.7x10^{-2}	-3.54	4.0x10^{-4}	CDH10	991.5	CDH9	1244.3
rs10061512	0	0.87	0.77	0.99	4.1x10^{-2}	3.89	9.9x10^{-5}	CDH10	997.9	CDH9	1237.9
rs7733598	0	0.87	0.77	0.99	4.1x10^{-2}	-3.88	1.0x10^{-4}	CDH10	998.4	CDH9	1237.4
rs7734006	1	0.85	0.75	0.97	1.4x10^{-2}	-3.71	2.1x10^{-4}	CDH10	999.3	CDH9	1236.5
rs7729848	0	0.85	0.75	0.97	1.4x10^{-2}	-3.72	2.0x10^{-4}	CDH10	999.3	CDH9	1236.5
rs12188325	0	0.85	0.75	0.97	1.4x10^{-2}	-3.80	1.4x10^{-4}	CDH10	1011.4	CDH9	1224.4
rs4867131	0	1.3	1.1	1.6	7.7x10^{-3}	5.06	4.2x10^{-7}	C5orf23	220.2	NPR3	224.7
rs2656989	0	1.2	1.00	1.3	5.7x10^{-2}	4.01	6.2x10^{-5}	TMEM167	161.3	XRCC4	182.6
rs2060210	0	0.85	0.76	0.96	7.3x10^{-3}	-4.00	6.5x10^{-5}	SPARC	23.2	ATOX1	32.7
rs10062868	0	0.84	0.75	0.95	4.7x10^{-3}	-3.85	1.2x10^{-4}	SPARC	27.6	ATOX1	28.2
rs13175452	0	1.2	1.1	1.4	2.4x10^{-3}	3.96	7.6x10^{-5}	MAT2B	1488.8	HMMR	1516.2
rs851880	1	1.2	1.0	1.5	1.2x10^{-2}	3.83	1.3x10^{-4}	EGFL11	774.2	BAI3	2281.7
rs1634186	0	1.2	1.1	1.5	1.1x10^{-2}	3.96	7.5x10^{-5}	EGFL11	780.4	BAI3	2275.6
rs1708563	0	1.2	1.1	1.5	1.1x10^{-2}	3.96	7.4x10^{-5}	EGFL11	781.4	BAI3	2274.5
rs6956537	1	0.67	0.53	0.85	8.9x10^{-4}	-3.54	4.1x10^{-4}	ZNF117	20.4	ZNF273	22.5
rs3211928	0	0.82	0.73	0.92	7.4x10^{-4}	4.52	6.2x10^{-6}	CD36	within gene	SEMA3C	74.1
rs3211931	0	0.82	0.73	0.92	7.6x10^{-4}	-4.47	7.7x10^{-6}	CD36	within gene	SEMA3C	73.7
rs3211932	0	0.82	0.73	0.92	7.6x10^{-4}	-4.47	7.8x10^{-6}	CD36	within gene	SEMA3C	73.0
rs3173804	0	0.82	0.73	0.92	7.4x10^{-4}	-4.44	9.0x10^{-6}	CD36	within gene	SEMA3C	72.0
rs3173805	0	0.82	0.73	0.92	7.4x10^{-4}	-4.44	9.0x10^{-6}	CD36	within gene	SEMA3C	70.9
rs3211958	0	0.82	0.73	0.92	7.5x10^{-4}	-4.42	1.0x10^{-5}	CD36	within gene	SEMA3C	67.8
rs3211960	0	0.82	0.73	0.92	7.5x10^{-4}	-4.43	9.6x10^{-6}	CD36	within gene	SEMA3C	67.2
rs7755	1	0.82	0.73	0.92	7.5x10^{-4}	-4.42	9.7x10^{-6}	CD36	within gene	SEMA3C	65.6
rs13246513	0	0.82	0.73	0.92	7.1x10^{-4}	-4.44	9.1x10^{-6}	CD36	0.4	SEMA3C	65.1
rs12706949	0	0.82	0.73	0.92	6.6x10^{-4}	-4.45	8.5x10^{-6}	CD36	0.9	SEMA3C	64.6
rs13223096	0	0.82	0.73	0.92	6.5x10^{-4}	-4.46	8.3x10^{-6}	CD36	1.3	SEMA3C	64.2
rs13230419	0	0.82	0.73	0.91	4.9x10^{-4}	-4.38	1.2x10^{-5}	CD36	3.0	SEMA3C	62.6
rs17266080	0	0.81	0.73	0.91	4.2x10^{-4}	-4.39	1.1x10^{-5}	CD36	4.0	SEMA3C	61.5
rs10954289	1	0.81	0.73	0.91	3.8x10^{-4}	-4.41	1.1x10^{-5}	CD36	20.0	SEMA3C	45.6
rs12534038	0	0.81	0.73	0.91	4.0x10^{-4}	4.40	1.1x10^{-5}	CD36	22.8	SEMA3C	42.8
rs713536	1	1.2	1.1	1.3	2.3x10^{-3}	4.26	2.1x10^{-5}	C8orf79	11.5	DLC1	42.1
rs7012771	0	0.81	0.72	0.92	6.0x10^{-4}	-3.73	1.9x10^{-4}	DUSP4	223.5	KIF13B	311.1
rs12546690	0	0.82	0.73	0.92	6.8x10^{-4}	-3.76	1.7x10^{-4}	DUSP4	239.0	KIF13B	326.5
rs12546462	1	0.81	0.72	0.91	4.0x10^{-4}	-3.68	2.4x10^{-4}	DUSP4	243.3	KIF13B	330.9
rs4131179	1	0.81	0.72	0.91	4.3x10^{-4}	-3.73	1.9x10^{-4}	DUSP4	244.2	KIF13B	331.8
rs1527939	1	1.4	1.2	1.6	5.3x10^{-5}	3.70	2.2x10^{-4}	EIF3H	335.2	C8orf53	456.8
rs2225173	0	0.84	0.74	0.95	7.8x10^{-3}	3.87	1.1x10^{-4}	MPDZ	185.6	C9orf150	612.9
rs10961053	0	1.2	1.1	1.4	1.1x10^{-3}	-3.86	1.2x10^{-4}	MPDZ	194.2	C9orf150	621.5
rs10491751	0	1.2	1.1	1.4	7.2x10^{-4}	3.68	2.3x10^{-4}	MPDZ	194.6	C9orf150	621.9
rs973321	0	1.2	1.1	1.3	2.1x10^{-3}	3.99	6.6x10^{-5}	MPDZ	197.3	C9orf150	624.6
rs1556577	1	1.2	1.1	1.3	3.3x10^{-3}	4.43	9.6x10^{-6}	MPDZ	203.6	NFIB	627.9
rs1333992	0	1.2	1.0	1.3	1.2x10^{-2}	4.22	2.4x10^{-5}	MPDZ	204.5	NFIB	627.0
rs7853368	0	1.2	1.1	1.3	2.8x10^{-3}	-4.46	8.4x10^{-6}	MPDZ	207.6	NFIB	623.9
rs11788445	0	1.3	1.1	1.5	2.9x10^{-3}	3.75	1.7x10^{-4}	GABBR2	within gene	ANKS6	229.0
rs10082493	0	1.2	1.1	1.4	1.0x10^{-3}	3.43	6.0x10^{-4}	ZWINT	728.7	IPMK	1105.9
rs11005634	0	1.2	1.1	1.4	9.4x10^{-4}	3.46	5.5x10^{-4}	ZWINT	734.0	IPMK	1100.6
rs11005635	0	1.2	1.1	1.4	9.4x10^{-4}	3.46	5.5x10^{-4}	ZWINT	734.2	IPMK	1100.4
rs11005636	0	1.2	1.1	1.4	9.4x10^{-4}	3.46	5.5x10^{-4}	ZWINT	734.5	IPMK	1100.1
rs12258368	0	1.2	1.1	1.4	9.5x10^{-4}	3.47	5.3x10^{-4}	ZWINT	746.9	IPMK	1087.7
rs12256850	0	1.2	1.1	1.4	9.5x10^{-4}	3.47	5.3x10^{-4}	ZWINT	746.9	IPMK	1087.6
rs4130804	0	1.2	1.1	1.4	9.6x10^{-4}	3.47	5.2x10^{-4}	ZWINT	747.1	IPMK	1087.5
rs7900082	0	1.2	1.1	1.4	5.6x10^{-4}	3.43	6.1x10^{-4}	ZWINT	749.3	IPMK	1085.3
rs12256059	0	1.2	1.1	1.4	9.8x10^{-4}	3.51	4.5x10^{-4}	ZWINT	751.5	IPMK	1083.1
rs11005649	0	1.2	1.1	1.4	10.x10^{-4}	3.52	4.3x10^{-4}	ZWINT	755.0	IPMK	1079.6
rs3105310	1	1.2	1.1	1.3	3.3x10^{-3}	3.75	1.8x10^{-4}	ZWINT	755.6	IPMK	1079.0
rs12767717	0	1.2	1.1	1.4	8.1x10^{-4}	3.49	4.9x10^{-4}	ZWINT	756.1	IPMK	1078.5
rs3104627	0	1.2	1.1	1.4	1.6x10^{-3}	3.64	2.7x10^{-4}	ZWINT	760.5	IPMK	1074.0
rs11005650	0	1.2	1.1	1.4	9.9x10^{-4}	3.56	3.7x10^{-4}	ZWINT	760.6	IPMK	1074.0
rs17608226	0	1.2	1.1	1.4	9.9x10^{-4}	3.53	4.1x10^{-4}	ZWINT	761.7	IPMK	1072.9
rs7079891	0	1.2	1.1	1.4	7.3x10^{-4}	-3.52	4.4x10^{-4}	ZWINT	767.1	IPMK	1067.5
rs7092768	0	1.2	1.1	1.4	7.3x10^{-4}	-3.52	4.3x10^{-4}	ZWINT	767.8	IPMK	1066.7
rs11005656	0	1.2	1.1	1.4	7.2x10^{-4}	3.51	4.5x10^{-4}	ZWINT	772.1	IPMK	1062.5
rs7080809	0	1.2	1.1	1.4	7.2x10^{-4}	3.45	5.7x10^{-4}	ZWINT	781.1	IPMK	1053.4
rs12269040	1	1.2	1.1	1.4	7.2x10^{-4}	3.44	5.8x10^{-4}	ZWINT	784.8	IPMK	1049.8
rs7906620	0	1.2	1.1	1.4	7.0x10^{-4}	3.44	5.9x10^{-4}	ZWINT	785.0	IPMK	1049.6
rs7086024	0	1.2	1.1	1.4	6.9x10^{-4}	3.44	5.8x10^{-4}	ZWINT	786.0	IPMK	1048.6
rs11005665	1	1.2	1.1	1.4	6.6x10^{-4}	3.45	5.7x10^{-4}	ZWINT	792.6	IPMK	1042.0
rs12783597	0	1.2	1.1	1.4	6.8x10^{-4}	-3.44	5.8x10^{-4}	ZWINT	797.6	IPMK	1037.0
rs11005673	0	1.2	1.1	1.4	6.8x10^{-4}	3.45	5.6x10^{-4}	ZWINT	800.0	IPMK	1034.6
rs1394112	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.1x10^{-4}	ZWINT	801.4	IPMK	1033.2
rs1394111	0	1.2	1.1	1.4	1.0x10^{-3}	3.31	9.2x10^{-4}	ZWINT	801.6	IPMK	1033.0
rs12247842	0	1.2	1.1	1.4	1.0x10^{-3}	3.31	9.2x10^{-4}	ZWINT	801.8	IPMK	1032.8
rs12253024	0	1.2	1.1	1.4	1.0x10^{-3}	-3.31	9.2x10^{-4}	ZWINT	801.9	IPMK	1032.7
rs7100491	0	1.2	1.1	1.4	1.0x10^{-3}	3.31	9.2x10^{-4}	ZWINT	802.3	IPMK	1032.3
rs7078639	0	1.2	1.1	1.4	9.7x10^{-4}	3.31	9.5x10^{-4}	ZWINT	802.4	IPMK	1032.2
rs12248271	0	1.2	1.1	1.4	6.7x10^{-4}	3.44	5.7x10^{-4}	ZWINT	802.6	IPMK	1032.0
rs1915694	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.1x10^{-4}	ZWINT	803.4	IPMK	1031.1
rs1915693	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.1x10^{-4}	ZWINT	803.5	IPMK	1031.0
rs1847409	0	1.2	1.1	1.4	6.7x10^{-4}	3.45	5.7x10^{-4}	ZWINT	804.0	IPMK	1030.6
rs7077008	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.1x10^{-4}	ZWINT	804.8	IPMK	1029.8
rs11005676	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.2x10^{-4}	ZWINT	805.7	IPMK	1028.8
rs12261393	0	1.2	1.1	1.4	1.0x10^{-3}	-3.32	9.1x10^{-4}	ZWINT	806.1	IPMK	1028.5
rs12256612	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.0x10^{-4}	ZWINT	809.0	IPMK	1025.6
rs7080282	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.0x10^{-4}	ZWINT	810.7	IPMK	1023.9
rs11005681	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.0x10^{-4}	ZWINT	811.2	IPMK	1023.4
rs11005682	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.0x10^{-4}	ZWINT	811.4	IPMK	1023.2
rs11005683	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	8.9x10^{-4}	ZWINT	811.6	IPMK	1023.0
rs11005684	0	1.2	1.1	1.4	1.0x10^{-3}	-3.33	8.9x10^{-4}	ZWINT	811.6	IPMK	1023.0
rs7093642	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	9.0x10^{-4}	ZWINT	813.0	IPMK	1021.6
rs7072641	0	1.2	1.1	1.4	1.0x10^{-3}	-3.32	8.9x10^{-4}	ZWINT	813.1	IPMK	1021.5
rs7093904	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	8.9x10^{-4}	ZWINT	813.1	IPMK	1021.5
rs7072950	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	8.9x10^{-4}	ZWINT	813.3	IPMK	1021.3
rs7072214	0	1.2	1.1	1.4	1.0x10^{-3}	3.32	8.9x10^{-4}	ZWINT	813.5	IPMK	1021.1
rs7073369	0	1.2	1.1	1.4	1.0x10^{-3}	3.33	8.8x10^{-4}	ZWINT	813.5	IPMK	1021.0
rs7921321	0	1.2	1.1	1.4	1.0x10^{-3}	3.33	8.7x10^{-4}	ZWINT	813.8	IPMK	1020.7
rs7918221	0	1.2	1.1	1.4	1.0x10^{-3}	3.33	8.7x10^{-4}	ZWINT	814.0	IPMK	1020.6
rs7901155	0	1.2	1.1	1.4	1.0x10^{-3}	3.33	8.8x10^{-4}	ZWINT	814.0	IPMK	1020.6
rs12262199	0	1.2	1.1	1.4	1.0x10^{-3}	3.33	8.8x10^{-4}	ZWINT	814.6	IPMK	1020.0
rs12263813	0	1.2	1.1	1.4	6.6x10^{-4}	3.46	5.4x10^{-4}	ZWINT	814.8	IPMK	1019.8
rs11818432	0	1.2	1.1	1.4	6.6x10^{-4}	3.38	7.2x10^{-4}	ZWINT	818.6	IPMK	1015.9
rs7076261	0	1.2	1.1	1.4	1.6x10^{-3}	3.71	2.1x10^{-4}	ZWINT	819.2	IPMK	1015.3

name	chromosome	position	strand	allele1	allele2	minor allele (coded allele)	minor allele frequency	meta-beta inverse variance	meta-se inverse variance	hazard ratio inverse variance	lower bound	uoper bound	ch2 statistic inverse variance	p-value inverse variance	genotyped ARIC	hazard ratio ARIC	lower bound ARIC	upper bound ARIC	p-value ARIC	genotyped CHS	hazard ratio CHS	lower bound CHS	upper bound CHS	p-value CHS	genotyped FHS	hazard ratio FHS	lower bound FHS	upper bound FHS	p-value FHS	genotyped RS	hazard ratio RS	lower bound RS	upper bound RS	p-value RS	z-score N-weighting meta-analysis	p-value N-weighting meta-analysis	closest gene	distance from closest gene (kb)	second closest gene	distance from second closest gene (kb)
rs4578668	16	63193838	+	T	C	C	0.43	-0.16	0.040	0.85	0.79	0.92	16.28	5.5x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	1	0.84	0.70	0.99	4.3x10^{-2}	0	0.89	0.71	1.1	3.8x10^{-1}	1	0.82	0.73	0.92	7.4x10^{-4}	-3.63	2.9x10^{-4}	CDH11	344.5	LOC283867	682.3
rs857368	16	63193222	+	T	C	C	0.43	-0.16	0.040	0.85	0.79	0.92	16.33	5.3x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	0	0.84	0.70	0.99	4.2x10^{-2}	0	0.90	0.71	1.1	3.6x10^{-1}	0	0.82	0.73	0.92	7.3x10^{-4}	-3.63	2.8x10^{-4}	CDH11	339.0	LOC283867	676.7
rs8053218	16	63214709	+	A	G	G	0.43	-0.16	0.040	0.85	0.79	0.92	16.37	5.2x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.7x10^{-1}	0	0.82	0.73	0.92	7.2x10^{-4}	-3.64	2.8x10^{-4}	CDH11	323.5	LOC283867	661.2
rs8050250	16	63219190	+	A	G	A	0.43	-0.16	0.040	0.85	0.79	0.92	16.37	5.2x10^{-5}	0	0.91	0.78	1.1	2.5x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.7x10^{-1}	0	0.82	0.73	0.92	7.2x10^{-4}	-3.64	2.8x10^{-4}	CDH11	319.0	LOC283867	656.7
rs6469853	16	63220023	+	G	C	G	0.43	-0.16	0.040	0.85	0.79	0.92	15.99	6.4x10^{-5}	1	0.92	0.78	1.1	2.9x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.8x10^{-1}	0	0.82	0.73	0.92	7.5x10^{-4}	3.58	3.4x10^{-4}	CDH11	318.2	LOC283867	655.9
rs9931297	16	63222408	+	A	C	A	0.43	-0.16	0.040	0.85	0.79	0.92	16.37	5.2x10^{-5}	0	0.91	0.77	1.1	2.5x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.8x10^{-1}	0	0.82	0.73	0.92	7.2x10^{-4}	-3.64	2.8x10^{-4}	CDH11	315.8	LOC283867	653.5
rs9931299	16	63222422	+	A	C	A	0.43	-0.16	0.040	0.85	0.79	0.92	16.36	5.2x10^{-5}	0	0.91	0.77	1.1	2.5x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.8x10^{-1}	0	0.82	0.73	0.92	7.2x10^{-4}	-3.64	2.8x10^{-4}	CDH11	315.8	LOC283867	653.5
rs6469954	16	63225065	+	A	G	A	0.43	-0.16	0.040	0.85	0.79	0.92	16.33	5.3x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.8x10^{-1}	0	0.82	0.73	0.92	7.3x10^{-4}	-3.63	2.9x10^{-4}	CDH11	313.1	LOC283867	650.8
rs4371172	16	63228618	+	T	C	T	0.43	-0.16	0.040	0.85	0.79	0.92	16.37	5.2x10^{-5}	1	0.91	0.78	1.1	2.6x10^{-1}	1	0.83	0.70	0.99	3.7x10^{-2}	1	0.90	0.71	1.1	3.9x10^{-1}	1	0.82	0.73	0.92	7.3x10^{-4}	-3.63	2.9x10^{-4}	CDH11	309.3	LOC283867	647.0
rs7184090	16	63230221	+	T	C	T	0.43	-0.16	0.040	0.85	0.79	0.92	16.25	5.8x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	0	0.83	0.70	0.99	4.1x10^{-2}	0	0.90	0.71	1.1	3.9x10^{-1}	0	0.82	0.73	0.92	7.3x10^{-4}	-3.62	3.0x10^{-4}	CDH11	308.0	LOC283867	645.7
rs4447450	16	63233858	+	G	C	G	0.43	-0.16	0.040	0.85	0.79	0.92	16.40	5.1x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	0	0.83	0.70	0.99	4.2x10^{-2}	0	0.90	0.70	1.1	3.7x10^{-1}	0	0.82	0.73	0.92	6.9x10^{-4}	3.64	2.7x10^{-4}	CDH11	304.2	LOC283867	641.9
rs4389164	16	63234858	+	G	C	C	0.43	-0.16	0.040	0.85	0.79	0.92	16.42	5.1x10^{-5}	0	0.91	0.78	1.1	2.6x10^{-1}	0	0.83	0.70	0.99	4.2x10^{-2}	0	0.90	0.70	1.1	3.6x10^{-1}	0	0.82	0.73	0.92	6.8x10^{-4}	3.64	2.7x10^{-4}	CDH11	303.3	LOC283867	641.0
rs16960253	16	81931015	+	A	T	T	0.20	0.20	0.050	1.2	1.1	1.3	15.55	8.0x10^{-5}	1	1.2	1.0	1.4	4.9x10^{-2}	0	1.1	0.78	1.6	5.6x10^{-1}	1	1.0	0.76	1.3	9.9x10^{-1}	0	1.3	1.1	1.5	1.5x10^{-4}	3.47	5.3x10^{-4}	CDH13	within gene	HSBP1	468.1
rs918766	16	81932846	+	T	C	T	0.20	0.21	0.049	1.2	1.1	1.4	18.71	1.5x10^{-5}	1	1.3	1.0	1.5	1.4x10^{-2}	0	1.1	0.81	1.6	4.6x10^{-1}	0	0.97	0.74	1.3	8.5x10^{-1}	1	1.3	1.1	1.5	6.3x10^{-4}	3.84	1.3x10^{-4}	CDH13	within gene	HSBP1	468.2
rs7209766	17	761070	+	T	C	C	0.49	0.18	0.044	1.2	1.1	1.3	16.15	5.9x10^{-5}	0	1.5	0.93	2.4	9.4x10^{-2}	1	1.3	1.1	1.6	8.8x10^{-4}	0	1.4	1.1	1.7	7.2x10^{-4}	1	1.1	0.97	1.2	1.7x10^{-1}	4.15	3.4x10^{-5}	NXN	within gene	TIMM22	86.0
rs9903227	17	761168	+	T	C	T	0.49	0.18	0.044	1.2	1.1	1.3	16.09	6.1x10^{-5}	0	1.5	0.93	2.4	9.4x10^{-2}	0	1.4	1.1	1.6	8.5x10^{-4}	0	1.4	1.1	1.7	7.1x10^{-4}	1	1.1	0.97	1.2	1.7x10^{-1}	4.15	3.3x10^{-5}	NXN	within gene	TIMM22	85.9
rs4968129	17	762373	+	T	C	T	0.39	-0.19	0.048	0.82	0.75	0.90	16.42	5.1x10^{-5}	0	0.91	0.85	1.3	5.9x10^{-1}	0	0.71	0.57	0.87	1.3x10^{-3}	0	0.69	0.51	0.94	1.7x10^{-2}	0	0.88	0.78	0.99	2.9x10^{-2}	-3.69	2.2x10^{-4}	NXN	within gene	TIMM22	84.7
rs12037685	17	2755942	+	T	C	C	0.45	0.18	0.044	1.2	1.1	1.3	16.92	3.9x10^{-5}	0	1.1	0.89	1.4	3.0x10^{-1}	1	1.3	1.1	1.6	2.4x10^{-3}	0	1.4	0.82	2.4	2.1x10^{-1}	1	1.2	1.0	1.3	9.0x10^{-3}	3.64	2.7x10^{-4}	GARNL4	within gene	OR1D5	156.8
rs4795707	17	27925363	+	A	G	A	0.04	0.41	0.10	1.5	1.2	1.8	15.88	6.8x10^{-5}	1	1.4	0.95	2.0	9.2x10^{-2}	0	1.2	0.57	2.6	6.0x10^{-1}	1	2.0	1.2	3.3	1.2x10^{-2}	0	1.5	1.1	2.0	4.8x10^{-3}	3.88	1.0x10^{-4}	MYO1D	within gene	CDK5R1	83.0
rs7224636	17	60693981	+	T	C	T	0.10	-0.27	0.070	0.76	0.67	0.87	15.20	9.7x10^{-5}	0	0.81	0.61	1.1	1.6x10^{-1}	0	0.72	0.55	0.96	2.3x10^{-2}	0	0.70	0.45	1.1	1.1x10^{-1}	0	0.77	0.63	0.95	1.5x10^{-2}	-3.74	1.9x10^{-4}	RGS9	39.7	GNA13	210.8
rs17690085	17	60697876	+	A	G	A	0.10	-0.27	0.070	0.76	0.66	0.87	15.35	9x10^{-5}	1	0.81	0.61	1.1	1.6x10^{-1}	0	0.72	0.55	0.96	2.3x10^{-2}	1	0.68	0.44	1.1	9.7x10^{-2}	0	0.77	0.63	0.95	1.4x10^{-2}	-3.77	1.7x10^{-4}	RGS9	43.8	GNA13	214.7
rs10420013	19	36618843	+	A	G	A	0.40	-0.17	0.044	0.84	0.77	0.92	15.52	8.2x10^{-5}	0	0.79	0.67	0.93	6.5x10^{-3}	0	0.79	0.57	1.1	1.8x10^{-1}	0	0.93	0.74	1.2	5.7x10^{-1}	1	0.85	0.76	0.96	7.6x10^{-3}	-3.93	8.7x10^{-5}	TSHZ3	84.8	ZNF536	876.0
rs3786949	19	44518319	+	A	G	A	0.07	0.29	0.069	1.3	1.2	1.5	17.58	2.8x10^{-5}	0	1.5	1.2	2.0	2.1x10^{-3}	1	0.90	0.65	1.2	5.2x10^{-1}	0	1.1	0.70	1.7	7.4x10^{-1}	1	1.5	1.2	1.8	4.4x10^{-5}	3.99	6.7x10^{-5}	GMFG	0.3	SAMD4B	6.6
rs2179450	20	1073924	+	T	C	T	0.23	-0.20	0.047	0.82	0.75	0.90	16.93	3.9x10^{-5}	1	0.92	0.76	1.1	3.6x10^{-1}	0	0.70	0.57	0.85	4.4x10^{-4}	0	0.91	0.67	1.2	5.3x10^{-1}	0	0.82	0.72	0.95	5.9x10^{-3}	-3.52	4.3x10^{-4}	PSMF1	within gene	C20orf46	35.3
rs1983522	20	1074724	+	A	G	G	0.23	-0.19	0.047	0.82	0.75	0.90	16.91	3.9x10^{-5}	0	0.92	0.76	1.1	3.6x10^{-1}	1	0.70	0.57	0.86	5.0x10^{-4}	0	0.91	0.67	1.2	5.2x10^{-1}	1	0.82	0.72	0.94	5.8x10^{-3}	-3.52	4.3x10^{-4}	PSMF1	within gene	C20orf46	34.5
rs2251251	20	8894471	+	T	C	T	0.25	0.18	0.044	1.2	1.1	1.3	16.15	5.9x10^{-5}	1	1.2	1.0	1.5	1.5x10^{-2}	0	1.5	1.2	1.8	8.5x10^{-4}	0	1.4	1.1	1.8	8.5x10^{-4}	0	1.0	0.89	1.2	8.5x10^{-1}	4.12	3.8x10^{-5}	PLCB1	80.9	PLCB4	130.5
rs1534941	20	8897872	+	T	G	T	0.24	0.19	0.045	1.2	1.1	1.3	16.80	4.2x10^{-5}	1	1.2	1.0	1.5	1.6x10^{-2}	0	1.5	1.2	1.8	8.4x10^{-4}	0	1.4	1.0	1.8	2.7x10^{-2}	0	1.0	0.91	1.2	5.7x10^{-1}	4.12	3.7x10^{-5}	PLCB1	84.3	PLCB4	127.1
rs13047582	21	19634014	+	A	G	A	0.09	0.26	0.065	1.3	1.1	1.5	15.44	8.5x10^{-5}	1	1.2	0.92	1.6	1.8x10^{-1}	0	1.2	0.89	1.6	2.4x10^{-1}	0	1.1	0.55	2.2	8.0x10^{-1}	0	1.4	1.2	1.7	2.1x10^{-4}	3.34	8.5x10^{-4}	PRSS7	937.1	CHODL	1073.4
rs13040780	21	19638152	+	A	G	G	0.09	0.26	0.065	1.3	1.1	1.5	16.44	5.0x10^{-5}	0	1.2	0.92	1.6	1.9x10^{-1}	1	1.2	0.93	1.6	1.6x10^{-1}	0	1.1	0.55	2.2	8.0x10^{-1}	1	1.4	1.2	1.6	2.1x10^{-4}	3.44	5.9x10^{-4}	PRSS7	940.3	CHODL	1076.6
rs13052992	21	19638238	+	A	T	A	0.06	0.33	0.082	1.4	1.2	1.6	16.43	5.1x10^{-5}	1	1.4	1.0	1.8	4.9x10^{-2}	0	1.2	0.87	1.8	2.3x10^{-1}	0	1.2	0.59	2.6	5.9x10^{-1}	0	1.5	1.2	1.9	6.1x10^{-4}	3.89	2.3x10^{-4}	PRSS7	940.4	CHODL	1076.7
rs9807721	22	39192086	+	A	G	G	0.16	0.20	0.050	1.2	1.1	1.3	16.55	4.7x10^{-5}	0	1.3	1.0	1.5	2.9x10^{-2}	1	1.2	0.96	1.5	1.2x10^{-1}	0	1.5	1.1	1.9	1.3x10^{-2}	1	1.2	1.0	1.4	2.6x10^{-2}	4.20	2.6x10^{-5}	SGSM3	within gene	MKL1	55.8

Supplementary Appendix: Table 2: Single nucleotide polymorphism (SNP)-phenotype associations at meta-analysis for ischemic stroke; all associations with p-value lower than 10^{-4}

name	chromosome	position	strand	allele1	allele2	minor allele (coded allele)	minor allele frequency	meta-beta inverse variance	meta-se inverse variance	hazard ratio inverse variance	lower bound	upper bound	chi2 statistic inverse variance	p-value inverse variance	genotyped ARIC	hazard ratio ARIC	lower bound ARIC	upper bound ARIC	p-value ARIC
rs760601	1	25973531	+	G	C	G	0.37	0.19	0.046	1.2	1.1	1.3	16.38	$5.2x10^{-5}$	0	1.4	1.1	1.6	$5.4x10^{-4}$
rs760600	1	25973750	+	G	C	C	0.36	0.19	0.046	1.2	1.1	1.3	16.42	$5.1x10^{-5}$	1	1.4	1.1	1.6	$5.4x10^{-4}$
rs760599	1	25978819	+	A	G	G	0.37	0.19	0.046	1.2	1.1	1.3	17.36	$3.1x10^{-5}$	1	1.4	1.2	1.6	$2.0x10^{-4}$
rs11247752	1	28298588	+	T	G	G	0.32	0.22	0.056	1.2	1.1	1.4	15.50	$8.3x10^{-5}$	1	1.5	1.2	1.8	$7.9x10^{-5}$
rs12743340	1	41228619	+	A	G	G	0.11	0.29	0.071	1.3	1.2	1.5	17.01	$3.7x10^{-5}$	0	1.6	1.3	2.0	$9.2x10^{-5}$
rs12047657	1	41234100	+	G	C	C	0.11	0.30	0.072	1.3	1.2	1.6	17.39	$3.0x10^{-5}$	0	1.6	1.3	2.0	$9.1x10^{-5}$
rs12023079	1	41242698	+	A	G	A	0.11	0.30	0.070	1.3	1.2	1.5	17.77	$2.5x10^{-5}$	0	1.6	1.3	2.0	$6.8x10^{-5}$
rs11209363	1	41257664	+	T	C	C	0.11	0.29	0.069	1.3	1.2	1.5	16.96	$3.8x10^{-5}$	0	1.6	1.2	2.0	$1.1x10^{-4}$
rs3738369	1	41258995	+	A	G	A	0.11	0.30	0.070	1.3	1.2	1.5	17.74	$2.5x10^{-5}$	0	1.6	1.3	2.0	$7.2x10^{-5}$
rs12031277	1	41264388	+	A	G	G	0.11	0.28	0.067	1.3	1.2	1.5	16.85	$4.0x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs16911	1	41270608	+	T	C	T	0.11	0.27	0.066	1.3	1.1	1.5	16.34	$5.3x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs2300658	1	41277609	+	A	G	A	0.11	0.26	0.064	1.3	1.1	1.5	15.72	$7.4x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs10489521	1	41281077	+	T	C	T	0.10	0.29	0.071	1.3	1.2	1.5	16.88	$4.0x10^{-5}$	0	1.6	1.3	2.1	$8.6x10^{-5}$
rs12729448	1	41282421	+	A	G	A	0.11	0.26	0.065	1.3	1.1	1.5	15.68	$7.5x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs2268678	1	41283640	+	A	G	A	0.11	0.26	0.065	1.3	1.1	1.5	15.66	$7.6x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs10489520	1	41284342	+	A	C	A	0.11	0.26	0.065	1.3	1.1	1.5	15.65	$7.6x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs12406620	1	41285251	+	A	T	T	0.11	0.26	0.065	1.3	1.1	1.5	15.65	$7.6x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs12729586	1	41294964	+	A	C	A	0.11	0.28	0.068	1.3	1.2	1.5	16.94	$3.9x10^{-5}$	0	1.6	1.3	2.0	$9.3x10^{-5}$
rs12742379	1	41298968	+	A	G	G	0.11	0.28	0.068	1.3	1.2	1.5	16.99	$3.8x10^{-5}$	0	1.6	1.3	2.0	$9.3x10^{-5}$
rs12045171	1	41301392	+	A	G	A	0.11	0.26	0.065	1.3	1.1	1.5	15.69	$7.5x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs16827876	1	41312123	+	T	G	G	0.11	0.26	0.065	1.3	1.1	1.5	15.69	$7.5x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs12022978	1	41326675	+	A	G	G	0.11	0.26	0.065	1.3	1.1	1.5	15.92	$6.6x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs2300649	1	41341790	+	T	C	C	0.11	0.26	0.066	1.3	1.1	1.5	16.01	$6.3x10^{-5}$	0	1.6	1.2	1.9	$1.2x10^{-4}$
rs11209531	1	41343608	+	T	C	T	0.11	0.26	0.066	1.3	1.1	1.5	15.99	$6.4x10^{-5}$	1	1.6	1.2	1.9	$1.1x10^{-4}$
rs11209576	1	41358616	+	T	C	C	0.11	0.26	0.066	1.3	1.1	1.5	15.99	$6.4x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs12759023	1	41376565	+	T	C	C	0.12	0.26	0.066	1.3	1.1	1.5	15.79	$7.1x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs12744845	1	41415287	+	G	C	G	0.11	0.26	0.065	1.3	1.1	1.5	15.84	$6.9x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs12408956	1	41424539	+	A	G	A	0.11	0.26	0.064	1.3	1.1	1.5	15.78	$7.1x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs12044539	1	41434319	+	A	C	C	0.11	0.26	0.065	1.3	1.1	1.5	15.96	$6.5x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs11209734	1	41470661	+	T	C	T	0.12	0.27	0.066	1.3	1.1	1.5	16.52	$4.8x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs12037037	1	41470843	+	T	C	T	0.12	0.27	0.066	1.3	1.2	1.5	16.54	$4.8x10^{-5}$	0	1.6	1.2	1.9	$1.1x10^{-4}$
rs8179465	1	41474334	+	A	G	A	0.12	0.27	0.066	1.3	1.2	1.5	16.58	$4.7x10^{-5}$	1	1.6	1.2	1.9	$1.1x10^{-4}$
rs4131949	1	41511224	+	T	C	T	0.11	0.28	0.069	1.3	1.2	1.5	16.67	$4.5x10^{-5}$	0	1.6	1.2	1.9	$1.4x10^{-4}$
rs16828019	1	41517622	+	T	C	T	0.11	0.28	0.069	1.3	1.2	1.5	16.65	$4.5x10^{-5}$	0	1.6	1.2	2.0	$1.4x10^{-4}$
rs595662	1	70383935	+	A	G	A	0.08	0.33	0.082	1.4	1.2	1.6	16.10	$6.0x10^{-5}$	0	1.1	0.82	1.6	$4.2x10^{-1}$
rs2182325	1	71144008	+	A	G	A	0.32	0.24	0.061	1.3	1.1	1.4	15.14	$10.x10^{-5}$	0	1.2	0.92	1.4	$2.2x10^{-1}$
rs2275254	1	111663497	+	T	C	T	0.41	0.18	0.043	1.2	1.1	1.3	16.37	$5.2x10^{-5}$	0	1.0	0.85	1.2	$9.0x10^{-1}$
rs342105	2	20518263	+	T	C	C	0.39	-0.20	0.051	0.82	0.74	0.91	15.14	$10.x10^{-5}$	1	0.79	0.66	0.95	$1.1x10^{-2}$
rs342109	2	20523343	+	T	G	G	0.39	-0.20	0.051	0.82	0.74	0.91	15.15	$9.9x10^{-5}$	0	0.79	0.66	0.95	$1.1x10^{-2}$
rs342125	2	20534771	+	T	C	T	0.39	-0.20	0.050	0.82	0.74	0.91	15.54	$8.1x10^{-5}$	1	0.79	0.66	0.94	$9.3x10^{-3}$
rs10191091	2	46426714	+	T	C	T	0.47	0.18	0.046	1.2	1.1	1.3	15.49	$8.3x10^{-5}$	1	1.0	0.88	1.2	$6.7x10^{-1}$
rs4953356	2	46432428	+	T	G	T	0.50	0.18	0.045	1.2	1.1	1.3	16.41	$5.1x10^{-5}$	0	1.1	0.90	1.3	$4.8x10^{-1}$
rs6756667	2	46432913	+	A	G	A	0.50	-0.18	0.045	0.83	0.76	0.91	16.24	$5.6x10^{-5}$	1	0.95	0.80	1.1	$5.1x10^{-1}$
rs1562452	2	46433948	+	A	G	A	0.48	0.18	0.045	1.2	1.1	1.3	15.35	$8.9x10^{-5}$	0	1.0	0.88	1.2	$6.8x10^{-1}$
rs1562453	2	46433978	+	T	C	T	0.49	-0.18	0.045	0.84	0.77	0.91	15.99	$6.4x10^{-5}$	0	0.95	0.80	1.1	$5.2x10^{-1}$
rs6735812	2	46434578	+	G	C	C	0.50	-0.18	0.045	0.83	0.76	0.91	16.48	$4.9x10^{-5}$	0	0.95	0.80	1.1	$5.1x10^{-1}$
rs4953358	2	46434957	+	G	C	C	0.50	-0.18	0.045	0.83	0.76	0.91	16.48	$4.9x10^{-5}$	0	0.95	0.80	1.1	$5.1x10^{-1}$
rs4953359	2	46435147	+	T	C	C	0.50	-0.18	0.045	0.83	0.76	0.91	16.49	$4.9x10^{-5}$	0	0.95	0.80	1.1	$5.1x10^{-1}$
rs6743991	2	46436739	+	A	C	C	0.50	-0.18	0.045	0.83	0.76	0.91	16.33	$5.3x10^{-5}$	0	0.95	0.80	1.1	$5.3x10^{-1}$
rs6707241	2	46438356	+	T	C	C	0.50	-0.18	0.045	0.84	0.77	0.91	15.95	$6.5x10^{-5}$	1	0.95	0.81	1.1	$5.8x10^{-1}$
rs6740096	2	46439392	+	A	T	A	0.50	-0.18	0.045	0.84	0.77	0.91	15.94	$6.5x10^{-5}$	0	0.95	0.81	1.1	$5.8x10^{-1}$
rs350795	2	52765124	+	T	C	C	0.14	0.25	0.064	1.3	1.1	1.5	15.47	$8.4x10^{-5}$	1	1.2	0.94	1.5	$1.7x10^{-1}$
rs350796	2	52765746	+	T	C	T	0.12	0.27	0.067	1.3	1.1	1.5	16.33	$5.3x10^{-5}$	1	1.3	1.0	1.6	$2.6x10^{-2}$
rs12467772	2	53166535	+	A	G	A	0.18	0.25	0.064	1.3	1.1	1.5	15.22	$9.6x10^{-5}$	0	1.0	0.80	1.4	$7.7x10^{-1}$
rs4664033	2	161610770	+	G	C	C	0.21	-0.25	0.064	0.78	0.68	0.88	15.89	$6.7x10^{-5}$	0	0.69	0.55	0.88	$2.9x10^{-3}$
rs4347769	2	237158333	+	A	G	G	0.05	0.40	0.095	1.5	1.2	1.8	17.34	$3.1x10^{-5}$	0	1.7	1.2	2.3	$6.8x10^{-4}$
rs13002508	2	237162595	+	T	C	T	0.06	0.38	0.094	1.5	1.2	1.8	15.84	$6.9x10^{-5}$	0	1.7	1.2	2.3	$7.5x10^{-4}$
rs17693202	3	35261617	+	T	C	C	0.19	0.22	0.057	1.3	1.1	1.4	15.30	$9.2x10^{-5}$	1	1.3	1.1	1.6	$3.4x10^{-3}$
rs17744129	3	35261638	+	A	C	A	0.19	0.22	0.057	1.3	1.1	1.4	15.33	$9.0x10^{-5}$	0	1.3	1.1	1.6	$3.3x10^{-3}$
rs17693703	3	35309402	+	T	G	T	0.16	0.24	0.060	1.3	1.1	1.4	15.91	$6.6x10^{-5}$	0	1.3	1.1	1.7	$5.7x10^{-3}$
rs12492172	3	35320076	+	T	C	T	0.16	0.24	0.059	1.3	1.1	1.4	15.85	$6.9x10^{-5}$	0	1.3	1.1	1.7	$5.6x10^{-3}$
rs7615446	3	35330281	+	G	C	C	0.16	0.23	0.059	1.3	1.1	1.4	15.59	$7.9x10^{-5}$	0	1.3	1.1	1.7	$5.7x10^{-3}$
rs697331	3	38321783	+	T	C	T	0.06	0.32	0.083	1.4	1.2	1.6	15.16	$9.9x10^{-5}$	1	1.4	1.1	1.9	$2.0x10^{-2}$
rs11712040	3	40602103	+	T	C	C	0.35	-0.19	0.048	0.83	0.75	0.91	15.45	$8.5x10^{-5}$	1	0.80	0.67	0.96	$1.8x10^{-2}$
rs11708971	3	40602833	+	T	C	T	0.35	-0.19	0.048	0.83	0.75	0.91	15.60	$7.8x10^{-5}$	0	0.80	0.67	0.96	$1.7x10^{-2}$
rs9844961	3	40603026	+	T	C	C	0.39	-0.18	0.046	0.83	0.76	0.91	15.37	$8.8x10^{-5}$	0	0.78	0.65	0.93	$5.3x10^{-3}$
rs11709108	3	40603213	+	G	C	G	0.35	-0.19	0.048	0.83	0.75	0.91	15.81	$7.0x10^{-5}$	0	0.80	0.66	0.96	$1.5x10^{-2}$
rs12496162	3	40604695	+	A	G	G	0.35	-0.19	0.048	0.83	0.75	0.91	15.87	$6.8x10^{-5}$	1	0.80	0.66	0.96	$1.4x10^{-2}$
rs7612798	3	40605696	+	A	G	G	0.35	-0.19	0.048	0.83	0.75	0.91	15.76	$7.2x10^{-5}$	0	0.80	0.66	0.96	$1.6x10^{-2}$
rs6599111	3	40606352	+	A	G	G	0.35	-0.19	0.048	0.83	0.75	0.91	15.70	$7.4x10^{-5}$	0	0.80	0.66	0.96	$1.6x10^{-2}$
rs7645790	3	40606562	+	T	G	G	0.35	-0.19	0.048	0.83	0.75	0.91	15.73	$7.3x10^{-5}$	0	0.80	0.66	0.96	$1.6x10^{-2}$
rs4256101	3	40608924	+	T	G	T	0.35	-0.19	0.048	0.83	0.75	0.91	15.60	$7.8x10^{-5}$	1	0.80	0.67	0.96	$1.8x10^{-2}$
rs11717510	3	40616009	+	G	C	G	0.37	-0.20	0.048	0.82	0.75	0.90	16.77	$4.2x10^{-5}$	0	0.76	0.64	0.92	$4.1x10^{-3}$
rs6599113	3	40624764	+	G	C	G	0.39	-0.20	0.048	0.82	0.75	0.90	16.52	$4.8x10^{-5}$	0	0.77	0.64	0.92	$3.6x10^{-3}$
rs4626072	3	40636641	+	T	G	T	0.38	-0.20	0.050	0.81	0.74	0.90	16.63	$4.5x10^{-5}$	1	0.78	0.65	0.93	$6.0x10^{-3}$
rs6790549	3	59915184	+	A	G	A	0.05	0.38	0.092	1.5	1.2	1.8	17.13	$3.5x10^{-5}$	0	1.4	1.0	1.9	$4.7x10^{-2}$
rs13088412	3	152203265	+	A	G	G	0.45	0.18	0.045	1.2	1.1	1.3	16.21	$5.7x10^{-5}$	1	1.3	1.1	1.5	$8.9x10^{-3}$
rs9840169	3	152204090	+	T	C	T	0.45	0.18	0.045	1.2	1.1	1.3	16.12	$5.9x10^{-5}$	0	1.3	1.1	1.5	$8.9x10^{-3}$
rs2121720	3	162062558	+	T	C	T	0.28	0.23	0.053	1.3	1.1	1.4	18.95	$1.3x10^{-5}$	0	1.3	1.1	1.6	$1.5x10^{-2}$
rs1965186	3	162062797	+	A	G	A	0.26	0.20	0.050	1.2	1.1	1.3	16.60	$4.6x10^{-5}$	0	1.2	1.0	1.5	$3.5x10^{-2}$
rs1001190	3	184693666	+	T	C	C	0.26	-0.21	0.054	0.81	0.73	0.90	15.28	$9.3x10^{-5}$	1	0.86	0.71	1.1	$1.5x10^{-1}$
rs1979983	3	184693685	+	T	G	T	0.26	-0.21	0.054	0.81	0.73	0.90	15.28	$9.3x10^{-5}$	1	0.86	0.71	1.1	$1.5x10^{-1}$
rs13097268	3	184694221	+	A	G	A	0.26	-0.21	0.054	0.81	0.73	0.90	15.29	$9.2x10^{-5}$	1	0.86	0.71	1.1	$1.5x10^{-1}$
rs3821514	3	184694381	+	G	C	C	0.26	-0.21	0.054	0.81	0.73	0.90	15.36	$8.9x10^{-5}$	1	0.86	0.71	1.1	$1.5x10^{-1}$
rs7626216	3	184710314	+	A	G	A	0.21	-0.26	0.059	0.77	0.69	0.87	18.72	$1.5x10^{-5}$	0	0.79	0.63	0.99	$4.2x10^{-2}$
rs10513838	3	190715335	+	A	G	G	0.06	0.37	0.083	1.4	1.2	1.7	19.94	$8.0x10^{-6}$	1	1.4	0.99	1.9	$5.5x10^{-2}$
rs1364595	3	190715520	+	G	C	C	0.04	0.37	0.094	1.4	1.2	1.7	15.29	$9.2x10^{-5}$	0	1.4	0.97	2.0	$7.1x10^{-2}$
rs1813739	3	190722401	+	A	T	A	0.04	0.39	0.097	1.5	1.2	1.8	16.24	$5.6x10^{-5}$	0	1.4	0.98	2.0	$6.7x10^{-2}$
rs17429019	3	190727839	+	A	G	G	0.06	0.40	0.086	1.5	1.3	1.8	21.44	$3.6x10^{-6}$	0	1.4	0.99	1.9	$5.9x10^{-2}$
rs16864503	3	190728050	+	T	C	C	0.04	0.42	0.10	1.5	1.2	1.8	17.06	$3.6x10^{-5}$	0	1.3	0.91	1.9	$1.5x10^{-1}$
rs9814173	3	194242151	+	A	G	A	0.24	0.22	0.053	1.2	1.1	1.4	17.57	$2.8x10^{-5}$	1	1.3	1.1	1.6	$1.1x10^{-2}$
rs11934728	4	17756249	+	T	C	C	0.07	0.34	0.087	1.4	1.2	1.7	15.82	$7.0x10^{-5}$	1	1.4	1.0	1.8	$4.0x10^{-2}$
rs7681205	4	17757562	+	A	G	G	0.07	0.34	0.086	1.4	1.2	1.7	15.80	$7.0x10^{-5}$	1	1.4	1.0	1.8	$4.5x10^{-2}$
rs10939767	4	17760447	+	G	C	C	0.07	0.35	0.086	1.4	1.2	1.7	16.08	$6.1x10^{-5}$	0	1.4	1.0	1.8	$4.5x10^{-2}$
rs7698465	4	17765350	+	A	G	G	0.07	0.35	0.086	1.4	1.2	1.7	16.15	$5.9x10^{-5}$	0	1.4	1.0	1.8	$4.5x10^{-2}$
rs17660253	4	54109122	+	T	G	T	0.28	0.21	0.048	1.2	1.1	1.4	20.19	$7.0x10^{-6}$	0	1.3	1.1	1.6	$3.0x10^{-3}$
rs6820391	4	54109453	+	A	C	A	0.28	0.22	0.048	1.2	1.1	1.4	20.21	$7x10^{-6}$	1	1.3	1.1	1.6	$2.9x10^{-3}$
rs2280119	4	54110195	+	T	C	T	0.28	0.21	0.048	1.2	1.1	1.4	20.12	$7.3x10^{-6}$	0	1.3	1.1	1.6	$3.2x10^{-3}$
rs4864801	4	54136939	+	T	C	T	0.24	0.20	0.050	1.2	1.1	1.3	15.95	$6.5x10^{-5}$	0	1.3	1.0	1.5	$1.7x10^{-2}$
rs10016971	4	54139549	+	G	C	C	0.24	0.20	0.050	1.2	1.1	1.3	15.69	$7.5x10^{-5}$	0	1.2	1.0	1.5	$2.0x10^{-2}$
rs6826933	4	54140472	+	T	C	T	0.24	0.20	0.049	1.2	1.1	1.3	15.69	$7.5x10^{-5}$	1	1.2	1.0	1.5	$2.1x10^{-2}$
rs1002824	4	54140737	+	A	C	A	0.24	0.20	0.050	1.2	1.1	1.3	15.68	$7.5x10^{-5}$	1	1.2	1.0	1.5	$2.1x10^{-2}$
rs4418038	4	54141059	+	A	G	G	0.24	0.20	0.050	1.2	1.1	1.3	16.00	$6.3x10^{-5}$	0	1.2	1.0	1.5	$2.1x10^{-2}$
rs1369355	4	54141617	+	A	G	A	0.24	0.20	0.050	1.2	1.1	1.3	16.14	$5.9x10^{-5}$	0	1.2	1.0	1.5	$2.1x10^{-2}$
rs1369354	4	54142731	+	T	G	T	0.24	0.20	0.050	1.2	1.1	1.3	16.17	$5.8x10^{-5}$	0	1.2	1.0	1.5	$2.1x10^{-2}$
rs1567654	4	54142934	+	T	C	T	0.24	0.20	0.050	1.2	1.1	1.3	16.04	$6.2x10^{-5}$	0	1.2	1.0	1.5	$2.1x10^{-2}$
rs4867131	5	33047743	+	A	C	A	0.11	0.40	0.082	1.5	1.3	1.8	23.95	$9.9x10^{-7}$	0	1.4	1.0	1.8	$2.6x10^{-2}$
rs11743048	5	62574013	+	A	G	G	0.11	0.29	0.071	1.3	1.2	1.5	17.11	$3.5x10^{-5}$	0	1.4	0.94	2.0	$1.1x10^{-1}$
rs7714581	5	62655546	+	G	C	G	0.18	0.21	0.055	1.2	1.1	1.4	15.15	$10x10^{-5}$	0	1.3	1.0	1.5	$2.9x10^{-2}$
rs4958347	5	152938349	+	A	G	A	0.12	0.29	0.070	1.3	1.2	1.5	17.06	$3.6x10^{-5}$	0	1.1	0.82	1.4	$6.6x10^{-1}$
rs778816	5	152948351	+	T	C	T	0.12	0.29	0.069	1.3	1.2	1.5	17.85	$2.4x10^{-5}$	1	1.1	0.86	1.4	$4.4x10^{-1}$
rs17624906	6	53973495	+	A	T	A	0.26	0.20	0.050	1.2	1.1	1.3	15.64	$7.7x10^{-5}$	0	1.1	0.95	1.4	$1.6x10^{-1}$
rs4540322	7	37792486	+	A	G	A	0.03	0.45	0.11	1.6	1.3	2.0	16.55	$4.7x10^{-5}$	0	1.9	1.3	2.7	$1.0x10^{-3}$
rs9639775	7	37795475	+	A	C	C	0.03	0.50	0.13	1.7	1.3	2.1	15.41	$8.6x10^{-5}$	0	1.9	1.3	2.7	$1.0x10^{-3}$
rs6467098	7	126213849	+	A	T	T	0.07	0.35	0.085	1.4	1.2	1.7	16.66	$4.5x10^{-5}$	0	1.3	0.99	1.8	$5.6x10^{-2}$
rs10503266	8	4475454	+	T	C	C	0.08	0.32	0.079	1.4	1.2	1.6	16.30	$5.4x10^{-5}$	1	1.2	0.93	1.6	$1.6x10^{-1}$
rs713536	8	12943177	+	T	C	T	0.47	0.23	0.049	1.3	1.1	1.4	21.65	$3.3x10^{-6}$	0	1.1	0.93	1.4	$2.2x10^{-1}$
rs2720720	8	24682890	+	T	G	G	0.19	-0.26	0.060	0.77	0.69	0.87	18.63	$1.6x10^{-5}$	0	0.65	0.51	0.83	$4.9x10^{-4}$
rs2720723	8	24684354	+	A	G	A	0.19	-0.26	0.060	0.77	0.69	0.87	18.47	$1.7x10^{-5}$	0	0.65	0.51	0.83	$5.0x10^{-4}$
rs2607622	8	24684955	+	A	G	A	0.19	-0.26	0.060	0.77	0.69	0.87	18.57	$1.6x10^{-5}$	0	0.65	0.51	0.83	$5.1x10^{-4}$
rs10465099	9	8729061	+	T	C	C	0.44	-0.20	0.050	0.82	0.74	0.90	15.95	$6.5x10^{-5}$	1	0.77	0.65	0.91	$2.7x10^{-3}$
rs4742537	9	8755099	+	T	C	C	0.44	-0.19	0.048	0.83	0.75	0.91	15.15	$9.9x10^{-5}$	0	0.77	0.65	0.92	$3.8x10^{-3}$
rs7034778	9	8761327	+	G	C	G	0.47	-0.20	0.048	0.82	0.74	0.90	17.76	$2.5x10^{-5}$	0	0.77	0.64	0.91	$2.4x10^{-3}$
rs2117326	9	8762606	+	A	G	G	0.45	-0.20	0.047	0.82	0.75	0.90	18.15	$2.0x10^{-5}$	0	0.77	0.65	0.92	$3.5x10^{-3}$
rs12350639	9	8765023	+	T	C	C	0.43	-0.20	0.049	0.82	0.75	0.90	16.37	$5.2x10^{-5}$	1	0.77	0.64	0.91	$2.7x10^{-3}$
rs10815939	9	8767234	+	T	C	C	0.44	-0.20	0.049	0.81	0.74	0.90	17.53	$2.8x10^{-5}$	0	0.76	0.64	0.91	$3.4x10^{-3}$
rs10815941	9	8767533	+	G	C	G	0.41	-0.20	0.050	0.82	0.74	0.90	15.72	$7.4x10^{-5}$	0	0.74	0.62	0.90	$1.9x10^{-3}$
rs9299072	9	8767779	+	T	G	T	0.17	-0.25	0.063	0.78	0.68	0.88	16.20	$5.7x10^{-5}$	0	0.70	0.54	0.91	$8.6x10^{-3}$
rs10511509	9	8769297	+	G	C	C	0.17	-0.26	0.064	0.77	0.68	0.87	17.00	$3.7x10^{-5}$	1	0.72	0.56	0.92	$9.3x10^{-3}$
rs1549997	9	8771034	+	A	C	A	0.17	-0.28	0.068	0.76	0.66	0.86	16.97	$3.8x10^{-5}$	0	0.72	0.56	0.92	$8.5x10^{-3}$
rs1549999	9	8771457	+	A	G	G	0.17	-0.28	0.068	0.76	0.66	0.86	16.88	$4.0x10^{-5}$	1	0.72	0.56	0.92	$8.7x10^{-3}$
rs1550000	9	8771871	+	T	C	C	0.17	-0.32	0.075	0.73	0.63	0.85	17.67	$2.6x10^{-5}$	1	0.72	0.56	0.92	$8.8x10^{-3}$
rs1417685	9	18392664	+	T	G	G	0.18	0.25	0.058	1.3	1.1	1.4	17.71	$2.6x10^{-5}$	0	1.3	0.98	1.6	$7.3x10^{-2}$
rs10818118	9	119965781	+	T	C	T	0.40	-0.19	0.047	0.83	0.76	0.91	15.64	$7.7x10^{-5}$	1	0.85	0.71	1.0	$5.7x10^{-2}$
rs7074221	10	403440	+	T	C	C	0.44	-0.20	0.048	0.82	0.74	0.90	17.17	$3.4x10^{-5}$	0	0.76	0.63	0.92	$4.6x10^{-3}$

name	genotyped CHS	hazard ratio CHS	lower bound CHS	upper bound CHS	p-value CHS	genotyped FHS	hazard ratio FHS	lower bound FHS	upper bound FHS	p-value FHS	genotyped RS	hazard ratio RS	lower bound RS	upper bound RS	p-value RS	z-score N-weighting meta-analysis	p-value N-weighting meta-analysis	closest gene	distance from closest gene (kb)	second closest gene	distance from second closest gene (kb)
rs760601	0	1.2	1.0	1.5	$4.4x10^{-2}$	0	1.2	0.93	1.5	$1.6x10^{-1}$	0	1.1	0.95	1.3	$2.1x10^{-1}$	-4.17	$3.0x10^{-5}$	MAN1C1	within gene	SEPN1	25.7
rs760600	0	1.2	1.0	1.5	$4.4x10^{-2}$	0	1.2	0.93	1.5	$1.6x10^{-1}$	0	1.1	0.95	1.3	$2.1x10^{-1}$	-4.18	$3.0x10^{-5}$	MAN1C1	within gene	SEPN1	25.5
rs760599	1	1.2	1.0	1.5	$3.1x10^{-2}$	0	1.2	0.91	1.5	$2.2x10^{-1}$	1	1.1	0.95	1.3	$2.2x10^{-1}$	4.28	$1.9x10^{-5}$	MAN1C1	within gene	SEPN1	20.4
rs11247752	0	0.87	0.59	1.3	$4.7x10^{-1}$	0	1.1	0.79	1.6	$5.6x10^{-1}$	1	1.2	1.0	1.4	$1.5x10^{-2}$	3.80	$1.4x10^{-4}$	EYA3	10.9	PTAFR	49.9
rs12743340	0	1.1	0.75	1.6	$6.7x10^{-1}$	0	1.6	1.1	2.4	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.0x10^{-1}$	4.28	$1.9x10^{-5}$	CTPS	within gene	SLFNL1	25.2
rs12047657	0	1.1	0.76	1.6	$6.0x10^{-1}$	0	1.6	1.1	2.4	$8.0x10^{-3}$	0	1.1	0.89	1.4	$3.0x10^{-1}$	-4.31	$1.6x10^{-5}$	CTPS	within gene	SLFNL1	19.8
rs12023079	0	1.1	0.76	1.6	$5.8x10^{-1}$	0	1.6	1.1	2.4	$7.1x10^{-3}$	0	1.1	0.89	1.4	$3.3x10^{-1}$	4.35	$1.4x10^{-5}$	CTPS	within gene	SLFNL1	11.2
rs11209363	0	1.1	0.77	1.6	$5.6x10^{-1}$	0	1.6	1.1	2.3	$8.9x10^{-3}$	0	1.1	0.89	1.4	$3.4x10^{-1}$	4.26	$2.1x10^{-5}$	SLFNL1	within gene	CTPS	6.8
rs3738369	0	1.1	0.77	1.6	$5.6x10^{-1}$	0	1.6	1.1	2.4	$6.9x10^{-3}$	0	1.1	0.89	1.4	$3.3x10^{-1}$	4.35	$1.4x10^{-5}$	SLFNL1	within gene	SCMH1	6.5
rs12031277	0	1.1	0.81	1.6	$4.8x10^{-1}$	0	1.6	1.1	2.3	$8.3x10^{-3}$	0	1.1	0.89	1.4	$3.4x10^{-1}$	4.29	$1.8x10^{-5}$	SCMH1	1.1	SLFNL1	4.4
rs16911	0	1.1	0.82	1.5	$5.1x10^{-1}$	0	1.6	1.1	2.3	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.5x10^{-1}$	4.27	$1.9x10^{-5}$	SCMH1	within gene	SLFNL1	10.6
rs2300658	1	1.1	0.84	1.4	$5.2x10^{-1}$	0	1.6	1.1	2.3	$8.2x10^{-3}$	1	1.1	0.89	1.4	$3.5x10^{-1}$	4.26	$2.0x10^{-5}$	SCMH1	within gene	SLFNL1	17.6
rs10489521	0	1.1	0.82	1.5	$5.3x10^{-1}$	0	1.8	1.2	2.6	$3.3x10^{-3}$	0	1.1	0.87	1.4	$3.9x10^{-1}$	4.40	$1.1x10^{-5}$	SCMH1	within gene	SLFNL1	21.1
rs12729448	0	1.1	0.83	1.4	$5.3x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.5x10^{-1}$	4.25	$2.1x10^{-5}$	SCMH1	within gene	SLFNL1	22.4
rs2268678	0	1.1	0.83	1.4	$5.3x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.1x10^{-5}$	SCMH1	within gene	SLFNL1	23.7
rs10489520	0	1.1	0.83	1.4	$5.3x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.2x10^{-5}$	SCMH1	within gene	SLFNL1	24.4
rs12406620	0	1.1	0.83	1.4	$5.3x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.2x10^{-5}$	SCMH1	within gene	SLFNL1	25.3
rs12729586	0	1.1	0.83	1.5	$5.0x10^{-1}$	0	1.7	1.1	2.4	$7.2x10^{-3}$	0	1.1	0.90	1.4	$2.7x10^{-1}$	4.41	$1.0x10^{-5}$	SCMH1	within gene	SLFNL1	35.0
rs12742379	0	1.1	0.83	1.5	$4.9x10^{-1}$	0	1.7	1.1	2.4	$7.2x10^{-3}$	0	1.1	0.90	1.4	$2.8x10^{-1}$	4.42	$10.x10^{-6}$	SCMH1	within gene	SLFNL1	39.0
rs12045171	0	1.1	0.84	1.4	$5.2x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.1x10^{-5}$	SCMH1	within gene	SLFNL1	41.4
rs16827876	0	1.1	0.84	1.4	$5.2x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.7x10^{-1}$	4.25	$2.2x10^{-5}$	SCMH1	within gene	SLFNL1	52.1
rs12022978	0	1.1	0.83	1.5	$5.1x10^{-1}$	0	1.6	1.1	2.2	$8.2x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.1x10^{-5}$	SCMH1	within gene	SLFNL1	66.7
rs2300649	0	1.1	0.82	1.5	$5.4x10^{-1}$	0	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.24	$2.2x10^{-5}$	SCMH1	within gene	SLFNL1	81.8
rs11209531	0	1.1	0.82	1.5	$5.4x10^{-1}$	1	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.2x10^{-5}$	SCMH1	within gene	SLFNL1	83.6
rs11209576	0	1.1	0.82	1.5	$5.3x10^{-1}$	0	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.25	$2.1x10^{-5}$	SCMH1	within gene	SLFNL1	98.6
rs12759023	0	1.1	0.81	1.5	$5.9x10^{-1}$	0	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.22	$2.4x10^{-5}$	SCMH1	within gene	SLFNL1	116.6
rs12744845	0	1.1	0.84	1.4	$5.1x10^{-1}$	0	1.6	1.1	2.2	$8.0x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	-4.26	$2.0x10^{-5}$	SCMH1	within gene	SLFNL1	155.3
rs12408956	1	1.1	0.84	1.4	$5.1x10^{-1}$	0	1.6	1.1	2.2	$8.0x10^{-3}$	1	1.1	0.89	1.4	$3.6x10^{-1}$	4.26	$2.0x10^{-5}$	SCMH1	within gene	SLFNL1	164.6
rs12044539	0	1.1	0.84	1.4	$5.0x10^{-1}$	0	1.6	1.1	2.2	$8.0x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.27	$2.0x10^{-5}$	SCMH1	within gene	SLFNL1	174.3
rs11209734	0	1.1	0.82	1.5	$4.8x10^{-1}$	0	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.28	$1.9x10^{-5}$	SCMH1	within gene	SLFNL1	210.7
rs12037037	0	1.1	0.82	1.5	$4.8x10^{-1}$	0	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.28	$1.9x10^{-5}$	SCMH1	within gene	SLFNL1	210.9
rs8179465	0	1.1	0.82	1.5	$4.8x10^{-1}$	1	1.6	1.1	2.2	$8.1x10^{-3}$	0	1.1	0.89	1.4	$3.6x10^{-1}$	4.28	$1.9x10^{-5}$	SCMH1	within gene	SLFNL1	214.4
rs4131949	0	1.2	0.81	1.6	$4.3x10^{-1}$	0	1.6	1.1	2.2	$8.6x10^{-3}$	0	1.1	0.88	1.4	$4.0x10^{-1}$	4.23	$2.3x10^{-5}$	SCMH1	30.8	EDN2	205.8
rs16828019	0	1.2	0.81	1.6	$4.4x10^{-1}$	0	1.6	1.1	2.2	$8.7x10^{-3}$	0	1.1	0.88	1.4	$4.0x10^{-1}$	4.23	$2.4x10^{-5}$	SCMH1	37.2	EDN2	199.4
rs595662	1	1.4	1.0	2.0	$3.6x10^{-2}$	0	1.4	0.86	2.3	$1.7x10^{-1}$	1	1.5	1.2	1.9	$8.6x10^{-4}$	3.65	$2.7x10^{-4}$	LRRC40	within gene	LRRC7	22.2
rs2182325	0	1.3	1.0	1.8	$4.9x10^{-2}$	0	1.4	0.99	1.9	$5.8x10^{-2}$	0	1.3	1.1	1.6	$7.0x10^{-3}$	3.78	$1.6x10^{-4}$	PTGER3	within gene	ZRANB2	157.6
rs2275254	1	1.2	1.0	1.4	$1.8x10^{-2}$	1	1.3	1.0	1.6	$4.7x10^{-2}$	1	1.3	1.1	1.5	$5.3x10^{-4}$	3.67	$2.4x10^{-4}$	CHIA	within gene	C1orf88	27.3
rs342105	0	0.78	0.60	1.0	$5.1x10^{-2}$	0	1.0	0.77	1.3	$9.1x10^{-1}$	0	0.80	0.68	0.94	$6.2x10^{-3}$	-3.71	$2.1x10^{-4}$	RHOB	5.6	PUM2	127.6
rs342109	0	0.78	0.61	1.0	$5.5x10^{-2}$	0	1.0	0.77	1.3	$9.1x10^{-1}$	0	0.80	0.68	0.94	$5.8x10^{-3}$	-3.71	$2.1x10^{-4}$	RHOB	10.7	PUM2	132.7
rs342125	0	0.80	0.64	1.00	$4.8x10^{-2}$	0	1.0	0.77	1.4	$8.9x10^{-1}$	0	0.80	0.68	0.94	$6.3x10^{-3}$	-3.74	$1.9x10^{-4}$	RHOB	22.1	PUM2	144.1
rs10191091	0	1.2	0.99	1.5	$6.2x10^{-2}$	1	1.3	1.0	1.7	$3.3x10^{-2}$	0	1.3	1.1	1.5	$5.9x10^{-4}$	3.75	$1.8x10^{-4}$	EPAS1	within gene	PRKCE	158.1
rs4953356	0	1.2	1.00	1.4	$5.6x10^{-2}$	0	1.4	1.1	1.8	$9.0x10^{-3}$	0	1.3	1.1	1.5	$2.3x10^{-3}$	3.95	$7.7x10^{-5}$	EPAS1	within gene	ATP6V1E2	160.1
rs6756667	0	0.84	0.70	1.0	$5.5x10^{-2}$	0	0.72	0.56	0.92	$9.2x10^{-3}$	1	0.79	0.69	0.92	$2.3x10^{-3}$	-3.93	$8.6x10^{-5}$	EPAS1	within gene	ATP6V1E2	159.6
rs1562452	0	1.2	1.0	1.5	$3.7x10^{-2}$	0	1.3	0.99	1.6	$6.6x10^{-2}$	1	1.3	1.1	1.5	$6.7x10^{-4}$	3.66	$2.5x10^{-4}$	EPAS1	within gene	ATP6V1E2	158.5
rs1562453	0	0.83	0.69	0.99	$4.3x10^{-2}$	0	0.72	0.56	0.93	$1.0x10^{-2}$	0	0.80	0.69	0.93	$3.2x10^{-3}$	-3.88	$1.0x10^{-4}$	EPAS1	within gene	ATP6V1E2	158.5
rs6735812	0	0.83	0.69	0.99	$4.0x10^{-2}$	0	0.72	0.57	0.93	$10.x10^{-3}$	0	0.80	0.69	0.92	$2.6x10^{-3}$	3.93	$8.3x10^{-5}$	EPAS1	within gene	ATP6V1E2	157.9
rs4953358	0	0.83	0.69	0.99	$4.0x10^{-2}$	0	0.72	0.57	0.93	$1.0x10^{-2}$	0	0.80	0.69	0.92	$2.6x10^{-3}$	3.93	$8.4x10^{-5}$	EPAS1	within gene	ATP6V1E2	157.5
rs4953359	0	0.83	0.69	0.99	$3.8x10^{-2}$	0	0.72	0.57	0.93	$1.0x10^{-2}$	0	0.80	0.69	0.92	$2.7x10^{-3}$	-3.93	$8.4x10^{-5}$	EPAS1	within gene	ATP6V1E2	157.3
rs6743991	0	0.83	0.69	0.99	$4.0x10^{-2}$	0	0.73	0.57	0.93	$1.2x10^{-2}$	0	0.79	0.69	0.92	$2.2x10^{-3}$	-3.91	$9.4x10^{-5}$	EPAS1	within gene	ATP6V1E2	155.8
rs6707241	0	0.83	0.70	0.99	$3.9x10^{-2}$	1	0.73	0.57	0.93	$1.0x10^{-2}$	0	0.80	0.69	0.93	$2.8x10^{-3}$	-3.86	$1.2x10^{-4}$	EPAS1	within gene	ATP6V1E2	154.1
rs6740096	0	0.83	0.70	0.99	$3.9x10^{-2}$	0	0.73	0.57	0.93	$1.0x10^{-2}$	0	0.80	0.69	0.93	$2.8x10^{-3}$	-3.86	$1.2x10^{-4}$	EPAS1	within gene	ATP6V1E2	153.1
rs350795	0	2.0	1.4	2.8	$1.2x10^{-4}$	1	1.2	0.86	1.7	$2.6x10^{-1}$	0	1.2	1.0	1.5	$3.6x10^{-2}$	3.80	$1.5x10^{-4}$	ASB3	985.5	CHAC2	1083.3
rs350796	0	1.7	1.2	2.5	$3.7x10^{-3}$	1	1.2	0.88	1.7	$2.3x10^{-1}$	0	1.2	1.0	1.5	$4.3x10^{-2}$	3.98	$6.9x10^{-5}$	ASB3	984.9	CHAC2	1082.7
rs12467772	0	1.4	1.1	1.8	$7.9x10^{-3}$	0	1.3	0.86	1.9	$2.3x10^{-1}$	0	1.4	1.1	1.6	$1.5x10^{-3}$	3.35	$8.0x10^{-4}$	ASB3	584.1	CHAC2	681.9
rs4664033	0	0.84	0.63	1.1	$2.2x10^{-1}$	0	0.87	0.59	1.3	$4.7x10^{-1}$	0	0.78	0.65	0.95	$1.1x10^{-2}$	4.07	$4.7x10^{-5}$	TANK	90.9	PSMD14	262.4
rs4347769	0	1.8	1.1	2.7	$9.6x10^{-3}$	0	1.6	0.93	2.6	$9.5x10^{-2}$	0	1.1	0.79	1.6	$5.5x10^{-1}$	3.95	$7.7x10^{-5}$	CXCR7	2.6	IQCA	77.5
rs13002508	0	1.5	1.0	2.2	$4.4x10^{-2}$	0	1.6	0.93	2.7	$9.2x10^{-2}$	1	1.1	0.81	1.6	$4.5x10^{-1}$	3.84	$1.2x10^{-4}$	CXCR7	6.9	IQCA	81.8
rs17693202	0	0.87	0.64	1.2	$3.9x10^{-1}$	0	1.4	1.1	1.9	$1.8x10^{-2}$	0	1.3	1.1	1.5	$9.4x10^{-3}$	4.03	$5.5x10^{-5}$	ARPP-21	397.2	STAC	1135.5
rs17744129	0	0.87	0.64	1.2	$3.9x10^{-1}$	0	1.4	1.1	1.9	$1.8x10^{-2}$	0	1.3	1.1	1.5	$9.4x10^{-3}$	4.04	$5.4x10^{-5}$	ARPP-21	397.2	STAC	1135.5
rs17693703	0	0.95	0.68	1.3	$7.9x10^{-1}$	0	1.5	1.2	2.0	$2.7x10^{-3}$	0	1.2	1.0	1.5	$4.5x10^{-2}$	4.09	$4.3x10^{-5}$	ARPP-21	349.5	STAC	1087.7
rs12492172	0	0.98	0.72	1.3	$8.9x10^{-1}$	0	1.5	1.1	2.0	$2.8x10^{-3}$	0	1.2	1.0	1.5	$4.6x10^{-2}$	4.13	$3.6x10^{-5}$	ARPP-21	338.8	STAC	1077.0
rs7615446	0	0.98	0.72	1.3	$8.7x10^{-1}$	0	1.5	1.2	2.0	$2.7x10^{-3}$	0	1.2	1.0	1.5	$4.7x10^{-2}$	-4.12	$3.8x10^{-5}$	ARPP-21	328.6	STAC	1066.8
rs697331	1	1.2	0.88	1.7	$2.4x10^{-1}$	0	1.3	0.78	2.1	$3.3x10^{-1}$	1	1.5	1.2	2.0	$3.2x10^{-3}$	3.83	$1.3x10^{-4}$	SLC22A14	0.7	SLC22A13	27.0
rs11712040	0	0.73	0.61	0.87	$6.0x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.2x10^{-1}$	-3.82	$1.3x10^{-4}$	ZNF621	46.1	ZNF620	68.1
rs11708971	0	0.73	0.61	0.87	$6.0x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.1x10^{-1}$	-3.85	$1.2x10^{-4}$	ZNF621	46.8	ZNF620	68.8
rs9844961	0	0.75	0.63	0.90	$1.4x10^{-3}$	0	0.81	0.62	1.1	$1.3x10^{-1}$	0	0.96	0.82	1.1	$5.8x10^{-1}$	-3.85	$1.2x10^{-4}$	ZNF621	47.0	ZNF620	69.0
rs11709108	0	0.73	0.61	0.87	$5.9x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.1x10^{-1}$	3.88	$1.1x10^{-4}$	ZNF621	47.2	ZNF620	69.2
rs12496162	0	0.73	0.61	0.87	$5.9x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.1x10^{-1}$	-3.89	$1.0x10^{-4}$	ZNF621	48.6	ZNF620	70.7
rs7612798	0	0.73	0.61	0.87	$5.9x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.1x10^{-1}$	-3.87	$1.1x10^{-4}$	ZNF621	49.6	ZNF620	71.7
rs6599111	1	0.73	0.61	0.87	$6.2x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	1	0.96	0.82	1.1	$6.1x10^{-1}$	-3.86	$1.1x10^{-4}$	ZNF621	50.3	ZNF620	72.3
rs7645790	0	0.73	0.61	0.87	$5.9x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.1x10^{-1}$	-3.86	$1.1x10^{-4}$	ZNF621	50.5	ZNF620	72.5
rs4256101	0	0.73	0.61	0.87	$5.9x10^{-4}$	0	0.76	0.57	1.0	$5.2x10^{-2}$	0	0.96	0.82	1.1	$6.1x10^{-1}$	-3.84	$1.2x10^{-4}$	ZNF621	52.9	ZNF620	74.9
rs11717510	0	0.72	0.60	0.87	$7.5x10^{-4}$	0	0.77	0.59	1.0	$5.5x10^{-2}$	0	0.97	0.83	1.1	$6.8x10^{-1}$	4.07	$4.7x10^{-5}$	ZNF621	60.0	ZNF620	82.0
rs6599113	0	0.73	0.60	0.89	$1.4x10^{-3}$	0	0.81	0.62	1.1	$1.2x10^{-1}$	0	0.95	0.81	1.1	$5.0x10^{-1}$	4.02	$5.9x10^{-5}$	ZNF621	68.7	ZNF620	90.7
rs4626072	0	0.70	0.57	0.86	$6.5x10^{-4}$	1	0.77	0.59	1.0	$5.2x10^{-2}$	0	0.97	0.82	1.2	$7.2x10^{-1}$	-3.99	$6.7x10^{-5}$	ZNF621	80.6	ZNF620	102.6
rs6790549	0	1.4	0.85	2.4	$1.8x10^{-1}$	0	1.5	0.93	2.5	$9.3x10^{-2}$	0	1.5	1.1	2.0	$3.0x10^{-3}$	4.03	$5.7x10^{-5}$	FHIT	within gene	FLJ42117	904.4
rs13088412	0	1.1	0.94	1.4	$1.8x10^{-1}$	1	0.98	0.78	1.2	$8.9x10^{-1}$	0	1.3	1.1	1.5	$6.2x10^{-4}$	3.89	$1.0x10^{-4}$	CLRN1	29.8	MED12L	84.1
rs9840169	1	1.1	0.94	1.4	$1.9x10^{-1}$	0	0.98	0.78	1.2	$9.0x10^{-1}$	1	1.3	1.1	1.5	$6.3x10^{-4}$	3.88	$1.0x10^{-4}$	CLRN1	30.6	MED12L	83.3
rs2121720	0	1.2	1.00	1.5	$5.1x10^{-2}$	0	1.5	1.1	1.9	$9.3x10^{-3}$	0	1.2	1.0	1.4	$4.6x10^{-2}$	4.46	$8.3x10^{-6}$	PPM1L	within gene	ARL14	183.6
rs1965186	1	1.2	1.00	1.4	$5.3x10^{-2}$	0	1.3	0.97	1.7	$7.7x10^{-2}$	1	1.2	1.0	1.4	$1.9x10^{-2}$	4.05	$5.1x10^{-5}$	PPM1L	within gene	ARL14	183.9
rs1001190	0	0.84	0.67	1.0	$1.1x10^{-1}$	1	0.67	0.51	0.87	$2.7x10^{-3}$	0	0.82	0.69	0.99	$3.8x10^{-2}$	-3.97	$7.3x10^{-5}$	KLHL6	within gene	MCF2L2	65.1
rs1979983	0	0.84	0.67	1.0	$1.1x10^{-1}$	1	0.67	0.51	0.87	$2.7x10^{-3}$	0	0.82	0.69	0.99	$3.8x10^{-2}$	-3.97	$7.3x10^{-5}$	KLHL6	within gene	MCF2L2	65.1
rs13097268	0	0.84	0.67	1.0	$1.1x10^{-1}$	0	0.67	0.51	0.87	$2.8x10^{-3}$	1	0.82	0.69	0.99	$3.7x10^{-2}$	-3.97	$7.3x10^{-5}$	KLHL6	within gene	MCF2L2	65.7
rs3821514	0	0.84	0.67	1.0	$1.1x10^{-1}$	1	0.67	0.51	0.87	$2.8x10^{-3}$	0	0.82	0.69	0.99	$3.7x10^{-2}$	3.98	$7.0x10^{-5}$	KLHL6	within gene	MCF2L2	65.8
rs7626216	1	0.86	0.69	1.1	$1.9x10^{-1}$	0	0.52	0.37	0.73	$1.6x10^{-4}$	1	0.80	0.66	0.97	$2.5x10^{-2}$	-4.73	$2.3x10^{-6}$	KLHL6	within gene	MCF2L2	81.8
rs10513838	1	1.2	0.84	1.6	$3.6x10^{-1}$	1	1.9	1.2	2.9	$8.3x10^{-3}$	1	1.6	1.2	2.1	$5.6x10^{-4}$	4.57	$4.9x10^{-6}$	TP63	116.6	FAM79B	191.4
rs1364595	0	1.2	0.82	1.7	$3.6x10^{-1}$	0	2.0	1.2	3.3	$5.4x10^{-3}$	0	1.5	1.1	2.0	$1.2x10^{-2}$	-4.06	$4.9x10^{-5}$	TP63	116.4	FAM79B	191.6
rs1813739	0	1.2	0.81	1.9	$3.3x10^{-1}$	0	2.0	1.2	3.3	$5.1x10^{-3}$	0	1.5	1.1	2.0	$1.1x10^{-2}$	4.11	$4x10^{-5}$	TP63	109.5	FAM79B	198.4
rs17429019	0	1.2	0.82	1.8	$3.2x10^{-1}$	0	1.9	1.2	3.0	$6.2x10^{-3}$	0	1.6	1.2	2.1	$5.3x10^{-4}$	4.63	$3.6x10^{-6}$	TP63	104.1	FAM79B	203.9
rs16864503	0	1.4	0.71	2.9	$3.1x10^{-1}$	0	2.0	1.2	3.2	$5.4x10^{-3}$	0	1.5	1.1	2.1	$4.2x10^{-3}$	4.05	$5.0x10^{-5}$	TP63	103.9	FAM79B	204.1
rs9814173	0	1.3	1.0	1.6	$5.0x10^{-2}$	1	1.5	1.1	2.0	$3.5x10^{-3}$	0	1.1	0.95	1.3	$1.6x10^{-1}$	4.35	$1.4x10^{-5}$	C3orf59	123.5	HRASLS	199.5
rs11934728	0	0.93	0.43	2.0	$8.5x10^{-1}$	0	1.6	0.87	3.0	$1.3x10^{-1}$	0	1.5	1.2	1.9	$1.0x10^{-3}$	3.67	$2.5x10^{-4}$	LCORL	123.8	NCAPG	300.7
rs7681205	0	0.93	0.43	2.0	$8.6x10^{-1}$	0	1.6	0.88	3.0	$1.2x10^{-1}$	0	1.5	1.2	1.9	$9.9x10^{-4}$	3.67	$2.4x10^{-4}$	LCORL	125.1	NCAPG	302.0
rs10939767	0	0.93	0.43	2.0	$8.6x10^{-1}$	0	1.7	0.91	3.0	$9.8x10^{-2}$	0	1.5	1.2	1.9	$9.8x10^{-4}$	-3.72	$2.0x10^{-4}$	LCORL	128.0	NCAPG	304.9
rs7698465	0	0.93	0.42	2.0	$8.6x10^{-1}$	0	1.7	0.91	3.1	$9.7x10^{-2}$	1	1.5	1.2	1.9	$9.5x10^{-4}$	3.73	$1.9x10^{-4}$	LCORL	132.9	NCAPG	309.8
rs17660253	0	1.2	0.97	1.4	$1.1x10^{-1}$	0	1.5	1.1	1.9	$3.7x10^{-3}$	0	1.2	0.99	1.4	$6.2x10^{-2}$	4.75	$2.1x10^{-6}$	LNX1	within gene	FIP1L1	88.5
rs6820391	0	1.2	0.97	1.4	$1.1x10^{-1}$	0	1.5	1.1	1.9	$3.7x10^{-3}$	1	1.2	0.99	1.4	$6.2x10^{-2}$	4.75	$2.0x10^{-6}$	LNX1	within gene	FIP1L1	88.9
rs2280119	0	1.2	0.97	1.4	$1.1x10^{-1}$	0	1.5	1.1	1.9	$3.7x10^{-3}$	0	1.2	0.99	1.4	$6.2x10^{-2}$	4.74	$2.2x10^{-6}$	LNX1	within gene	FIP1L1	89.6
rs4864801	0	1.2	0.99	1.5	$6.3x10^{-2}$	0	1.5	1.2	2.0	$2.2x10^{-3}$	0	1.1	0.94	1.3	$2.2x10^{-1}$	4.19	$2.8x10^{-5}$	LNX1	17.8	FIP1L1	116.3
rs10016971	0	1.2	0.99	1.5	$6.1x10^{-2}$	0	1.5	1.2	2.0	$2.2x10^{-3}$	0	1.1	0.94	1.3	$2.3x10^{-1}$	-4.15	$3.3x10^{-5}$	LNX1	20.4	FIP1L1	119.0
rs6826933	1	1.2	0.99	1.4	$5.8x10^{-2}$	1	1.5	1.2	2.0	$2.3x10^{-3}$	1	1.1	0.94	1.3	$2.3x10^{-1}$	4.14	$3.4x10^{-5}$	LNX1	21.3	FIP1L1	119.9
rs1002824	0	1.2	0.99	1.5	$6.0x10^{-2}$	1	1.5	1.2	2.0	$2.3x10^{-3}$	0	1.1	0.94	1.3	$2.2x10^{-1}$	4.14	$3.4x10^{-5}$	LNX1	21.6	FIP1L1	120.1
rs4418038	0	1.2	1.00	1.5	$5.1x10^{-2}$	0	1.5	1.2	2.0	$2.3x10^{-3}$	0	1.1	0.94	1.3	$2.2x10^{-1}$	4.17	$3.0x10^{-5}$	LNX1	21.9	FIP1L1	120.5
rs1369355	0	1.2	1.0	1.5	$4.8x10^{-2}$	0	1.5	1.2	2.0	$2.3x10^{-3}$	1	1.1	0.94	1.3	$2.2x10^{-1}$	4.18	$2.9x10^{-5}$	LNX1	22.5	FIP1L1	121.0
rs1369354	0	1.2	1.0	1.5	$4.6x10^{-2}$	0	1.5	1.2	2.0	$2.3x10^{-3}$	0	1.1	0.94	1.3	$2.2x10^{-1}$	4.18	$2.9x10^{-5}$	LNX1	23.6	FIP1L1	122.1
rs1567654	0	1.2	1.0	1.5	$5.0x10^{-2}$	0	1.5	1.2	2.0	$2.3x10^{-3}$	0	1.1	0.94	1.3	$2.2x10^{-1}$	4.17	$3.0x10^{-5}$	LNX1	23.8	FIP1L1	122.3
rs4867131	0	2.4	1.3	4.3	$3.4x10^{-3}$	0	1.7	1.1	2.6	$1.2x10^{-2}$	0	1.4	1.1	1.8	$5.7x10^{-3}$	4.99	$6x10^{-7}$	C5orf23	220.2	NPR3	224.7
rs11743048	0	1.1	0.88	1.5	$3.3x10^{-1}$	0	1.6	1.1	2.3	$1.7x10^{-2}$	0	1.4	1.1	1.7	$1.3x10^{-3}$	4.17	$3.1x10^{-5}$	ISCA1L	465.1	IPO11	613.8
rs7714581	0	1.2	0.97	1.5	$9.1x10^{-2}$	0	1.2	0.90	1.7	$1.9x10^{-1}$	0	1.2	1.0	1.5	$1.5x10^{-2}$	-3.83	$1.3x10^{-4}$	ISCA1L	546.6	HTR1A	636.5
rs4958347	0	0.98	0.63	1.5	$9.2x10^{-1}$	0	1.6	1.2	2.3	$3.9x10^{-3}$	0	1.5	1.2	1.9	$4.4x10^{-5}$	3.81	$1.4x10^{-4}$	GRIA1	within gene	C5orf3	413.1
rs778816	0	1.0	0.66	1.5	$10.x10^{-1}$	1	1.6	1.2	2.2	$4.9x10^{-3}$	1	1.5	1.2	1.9	$5.8x10^{-5}$	3.98	$6.9x10^{-5}$	GRIA1	within gene	C5orf3	403.1
rs17624906	0	1.1	0.88	1.4	$3.9x10^{-1}$	0	1.4	1.1	1.8	$3.5x10^{-3}$	0	1.2	1.1	1.5	$6.6x10^{-3}$	4.01	$6.2x10^{-5}$	C6orf142	18.2	LRRC1	76.6
rs4540322	0	1.1	0.60	2.2	$6.9x10^{-1}$	0	1.3	0.75	2.3	$3.3x10^{-1}$	0	1.6	1.1	2.3	$9.3x10^{-3}$	3.90	$9.7x10^{-5}$	GPR141	45.0	TXNDC3	62.2
rs9639775	0	1.1	0.60	2.2	$6.9x10^{-1}$	0	1.1	0.40	3.0	$8.6x10^{-1}$	0	1.8	1.2	2.8	$8.7x10^{-3}$	3.54	$4.1x10^{-4}$	GPR141	48.0	TXNDC3	59.2
rs6467098	0	1.4	0.76	2.6	$2.7x10^{-1}$	0	1.7	1.1	2.6	$9.4x10^{-3}$	0	1.4	1.1	1.8	$1.3x10^{-2}$	4.09	$4.4x10^{-5}$	GRM8	within gene	ZNF800	583.7
rs10503266	0	2.0	1.2	3.6	$1.3x10^{-2}$	0	1.1	0.66	1.7	$8.2x10^{-1}$	1	1.5	1.2	1.9	$4.1x10^{-4}$	3.72	$2.0x10^{-4}$	CSMD1	within gene	MCPH1	1776.1
rs713536	1	1.4	1.2	1.7	$2.6x10^{-4}$	0	1.2	0.89	1.7	$2.1x10^{-1}$	1	1.2	1.1	1.4	$5.8x10^{-3}$	4.07	$4.7x10^{-5}$	C8orf79	11.5	DLC1	42.1
rs2720720	0	0.77	0.61	0.96	$2.3x10^{-2}$	0	0.93	0.67	1.3	$6.6x10^{-1}$	0	0.81	0.67	0.98	$3.1x10^{-2}$	-4.44	$9.1x10^{-6}$	NEFM	144.3	NEFL	181.5
rs2720723	1	0.77	0.61	0.97	$2.5x10^{-2}$	0	0.93	0.67	1.3	$6.7x10^{-1}$	1	0.81	0.67	0.98	$3.1x10^{-2}$	-4.42	$9.7x10^{-6}$	NEFM	142.8	NEFL	180.0
rs2607622	0	0.77	0.61	0.96	$2.3x10^{-2}$	0	0.93	0.67	1.3	$6.7x10^{-1}$	0	0.81	0.67	0.98	$3.1x10^{-2}$	-4.43	$9.5x10^{-6}$	NEFM	142.2	NEFL	179.4
rs10465099	0	0.76	0.59	0.98	$3.2x10^{-2}$	1	0.90	0.68	1.2	$4.9x10^{-1}$	0	0.86	0.74	1.0	$5.7x10^{-2}$	-3.98	$7.0x10^{-5}$	PTPRD	within gene	C9orf123	939.3
rs4742537	0	0.82	0.66	1.0	$6.0x10^{-2}$	0	0.93	0.70	1.2	$5.9x10^{-1}$	0	0.85	0.73	0.99	$3.8x10^{-2}$	-3.84	$1.2x10^{-4}$	PTPRD	within gene	C9orf123	965.3
rs7034778	0	0.80	0.64	0.99	$3.8x10^{-2}$	0	0.93	0.70	1.2	$6.1x10^{-1}$	0	0.84	0.72	0.97	$1.9x10^{-2}$	4.12	$3.8x10^{-5}$	PTPRD	within gene	C9orf123	971.5
rs2117326	0	0.81	0.66	0.99	$3.6x10^{-2}$	0	0.93	0.71	1.2	$6.3x10^{-1}$	0	0.83	0.71	0.96	$1.2x10^{-2}$	-4.14	$3.5x10^{-5}$	PTPRD	within gene	C9orf123	972.8
rs12350639	0	0.80	0.65	0.99	$3.7x10^{-2}$	0	0.93	0.70	1.2	$6.1x10^{-1}$	0	0.85	0.73	0.99	$3.8x10^{-2}$	-3.97	$7.2x10^{-5}$	PTPRD	within gene	C9orf123	975.2
rs10815939	0	0.79	0.64	0.97	$2.4x10^{-2}$	0	0.96	0.72	1.3	$7.9x10^{-1}$	1	0.83	0.71	0.97	$1.6x10^{-2}$	-4.04	$5.4x10^{-5}$	PTPRD	within gene	C9orf123	977.4
rs10815941	0	0.78	0.63	0.97	$2.4x10^{-2}$	0	0.95	0.71	1.3	$7.1x10^{-1}$	0	0.86	0.74	1.0	$6.3x10^{-2}$	3.91	$9.3x10^{-5}$	PTPRD	within gene	C9orf123	977.7
rs9299072	1	0.75	0.60	0.94	$1.1x10^{-2}$	0	0.95	0.68	1.3	$7.8x10^{-1}$	1	0.78	0.63	0.97	$2.8x10^{-2}$	-3.89	$1.0x10^{-4}$	PTPRD	within gene	C9orf123	978.0
rs10511509	0	0.72	0.57	0.91	$6.4x10^{-3}$	0	0.95	0.68	1.3	$7.9x10^{-1}$	0	0.78	0.63	0.97	$2.7x10^{-2}$	3.94	$8.2x10^{-5}$	PTPRD	within gene	C9orf123	979.5
rs1549997	0	0.62	0.45	0.84	$2.2x10^{-3}$	0	0.97	0.70	1.3	$8.5x10^{-1}$	1	0.79	0.63	0.98	$2.9x10^{-2}$	-4.02	$5.9x10^{-5}$	PTPRD	within gene	C9orf123	981.2
rs1549999	0	0.61	0.44	0.84	$2.1x10^{-3}$	1	0.97	0.70	1.3	$8.5x10^{-1}$	0	0.78	0.63	0.98	$2.9x10^{-2}$	-4.01	$6.0x10^{-5}$	PTPRD	within gene	C9orf123	981.7
rs1550000	0	0.53	0.36	0.78	$1.3x10^{-3}$	0	0.93	0.64	1.4	$7.1x10^{-1}$	0	0.76	0.59	0.97	$3.0x10^{-2}$	-4.13	$3.6x10^{-5}$	PTPRD	within gene	C9orf123	982.1
rs1417685	0	1.3	1.0	1.6	$2.3x10^{-2}$	0	1.1	0.69	1.8	$6.6x10^{-1}$	0	1.3	1.1	1.6	$2.0x10^{-3}$	3.74	$1.8x10^{-4}$	ADAMTSL1	71.4	C9orf138	525.2
rs10818118	0	0.71	0.58	0.87	$8.1x10^{-4}$	0	0.92	0.68	1.2	$5.7x10^{-1}$	1	0.87	0.75	1.0	$5.9x10^{-2}$	-3.61	$3.1x10^{-4}$	TLR4	446.2	ASTN2	748.6
rs7074221	1	0.85	0.71	1.0	$9.0x10^{-2}$	0	0.76	0.55	1.0	$7.7x10^{-2}$	1	0.85	0.73	0.99	$3.6x10^{-2}$	-4.33	$1.5x10^{-5}$	DIP2C	within gene	ZMYND11	112.9

name	chromosome	position	strand	allele1	allele2	minor allele (coded allele)	minor allele frequency	meta-beta inverse variance	meta-se inverse variance	hazard ratio inverse variance	lower bound	upper bound	chi2 statistic inverse variance	p-value inverse variance	genotyped ARIC	hazard ratio ARIC	lower bound ARIC	upper bound ARIC	p-value ARIC	genotyped CHS	hazard ratio CHS	lower bound CHS	upper bound CHS	p-value CHS	genotyped FHS	hazard ratio FHS	lower bound FHS	upper bound FHS	p-value FHS	genotyped RS	hazard ratio RS	lower bound RS	upper bound RS	p-value RS	z-score N-weighting meta-analysis	p-value N-weighting meta-analysis	closest gene	distance from closest gene (kb)	second closest gene	distance from second closest gene (kb)
rs1218366	10	14362674	+	T	C	T	0.47	-0.20	0.052	0.82	0.74	0.90	15.40	8.7×10^{-5}	0	0.86	0.72	1.0	1.1×10^{-1}	0	0.64	0.46	0.90	9.8×10^{-3}	0	1.2	0.88	1.6	2.7×10^{-1}	0	0.74	0.64	0.86	1.1×10^{-4}	-3.47	5.3×10^{-4}	FRMD4A	within gene	FAM107B	237.9
rs11012681	10	21704511	+	A	G	A	0.15	-0.28	0.073	0.75	0.65	0.87	15.39	8.8×10^{-5}	0	0.72	0.55	0.95	2.1×10^{-2}	0	0.64	0.47	0.86	3.3×10^{-3}	0	0.67	0.43	1.0	7.8×10^{-2}	0	0.87	0.70	1.1	2.1×10^{-1}	-3.98	6.9×10^{-5}	C10orf114	118.9	C10orf140	137.9
rs11005650	10	58551611	+	T	C	T	0.23	0.20	0.050	1.2	1.1	1.3	15.15	9.9×10^{-5}	0	1.2	0.99	1.4	6.7×10^{-2}	1	1.2	1.0	1.5	3.0×10^{-2}	0	1.1	0.74	1.5	7.7×10^{-1}	0	1.3	1.1	1.5	5.1×10^{-3}	3.52	4.3×10^{-4}	ZWINT	760.6	IPMK	1074.0
rs16914297	10	61302000	+	T	C	T	0.13	0.25	0.062	1.3	1.1	1.5	16.64	4.5×10^{-5}	0	1.6	1.3	2.0	2.1×10^{-5}	0	1.4	1.0	1.8	2.0×10^{-2}	0	1.0	0.76	1.4	8.5×10^{-1}	0	1.1	0.90	1.4	3.2×10^{-1}	3.94	8.1×10^{-5}	CCDC6	within gene	SLC16A9	136.2
rs4592379	10	61354605	+	T	G	G	0.18	0.26	0.062	1.3	1.1	1.5	16.78	4.2×10^{-5}	0	1.5	1.2	1.9	2.9×10^{-4}	0	1.3	0.99	1.7	5.6×10^{-2}	0	1.1	0.84	1.5	4.2×10^{-1}	0	1.2	0.96	1.5	1.1×10^{-1}	4.09	4.4×10^{-5}	CCDC6	17.8	ANK3	103.6
rs1318644	10	78547619	+	A	G	G	0.20	0.25	0.060	1.3	1.1	1.4	17.71	2.6×10^{-5}	0	1.1	0.88	1.4	4.2×10^{-1}	0	1.3	0.83	1.9	2.8×10^{-1}	0	1.5	1.1	2.0	3.8×10^{-3}	0	1.3	1.1	1.6	7.7×10^{-4}	4.04	5.4×10^{-5}	KCNMA1	within gene	C10orf11	560.5
rs2505777	10	86457113	+	T	C	T	0.44	-0.19	0.046	0.83	0.75	0.90	17.45	3×10^{-5}	0	0.78	0.65	0.93	5.7×10^{-3}	1	0.80	0.67	0.97	2.2×10^{-2}	0	0.71	0.55	0.91	6.5×10^{-3}	1	0.92	0.80	1.1	2.7×10^{-1}	-4.39	1.1×10^{-5}	KIAA1128	188.9	RGR	448.2
rs2505776	10	86457277	+	T	C	C	0.44	-0.19	0.046	0.83	0.76	0.90	17.28	3.2×10^{-5}	0	0.78	0.66	0.93	5.9×10^{-3}	0	0.81	0.67	0.97	2.3×10^{-2}	0	0.71	0.55	0.91	6.5×10^{-3}	0	0.92	0.80	1.1	2.7×10^{-1}	-4.37	1.2×10^{-5}	KIAA1128	189.0	RGR	448.4
rs2153669	10	124599273	+	T	C	T	0.45	0.18	0.044	1.2	1.1	1.3	17.34	3.1×10^{-5}	0	1.3	1.1	1.5	5.4×10^{-3}	0	1.1	0.91	1.3	3.6×10^{-1}	0	1.3	1.0	1.7	2.4×10^{-2}	0	1.2	1.0	1.4	1.5×10^{-2}	4.44	9.2×10^{-6}	FAM24B	within gene	CUZD1	3.6
rs1891110	10	124600017	+	A	G	G	0.45	0.18	0.044	1.2	1.1	1.3	17.74	2.5×10^{-5}	1	1.3	1.1	1.5	5.5×10^{-3}	1	1.1	0.91	1.3	3.6×10^{-1}	1	1.3	1.0	1.7	2.4×10^{-2}	1	1.2	1.0	1.4	1.2×10^{-2}	4.48	7.5×10^{-6}	FAM24B	within gene	CUZD1	4.3
rs12263072	10	124632001	+	A	T	T	0.47	0.17	0.045	1.2	1.1	1.3	15.17	9.8×10^{-5}	0	1.2	1.0	1.5	1.2×10^{-2}	0	1.1	0.90	1.3	3.9×10^{-1}	0	1.4	1.1	1.7	1.9×10^{-2}	0	1.2	1.0	1.4	2.6×10^{-2}	4.17	3.0×10^{-5}	FAM24B	2.9	FAM24A	28.2
rs2994807	10	124637031	+	A	G	A	0.45	0.19	0.044	1.2	1.1	1.3	17.94	2.3×10^{-5}	0	1.3	1.1	1.5	7.7×10^{-3}	0	1.1	0.92	1.3	3.1×10^{-1}	0	1.3	1.0	1.6	4.6×10^{-2}	0	1.2	1.1	1.4	6.8×10^{-3}	4.42	9.9×10^{-6}	FAM24B	7.9	FAM24A	23.2
rs10902839	10	124638275	+	A	G	G	0.47	0.18	0.045	1.2	1.1	1.3	15.32	9.1×10^{-5}	0	1.2	1.0	1.5	1.2×10^{-2}	0	1.1	0.90	1.3	3.8×10^{-1}	0	1.4	1.0	1.7	2.0×10^{-2}	1	1.2	1.0	1.4	2.7×10^{-2}	4.18	3.0×10^{-5}	FAM24B	9.1	FAM24A	21.9
rs2901352	10	124640067	+	G	C	C	0.47	0.18	0.045	1.2	1.1	1.3	15.29	9.2×10^{-5}	0	1.2	1.0	1.5	1.2×10^{-2}	0	1.1	0.90	1.3	3.9×10^{-1}	0	1.4	1.0	1.7	2.0×10^{-2}	0	1.2	1.0	1.4	2.6×10^{-2}	-4.17	3.1×10^{-5}	FAM24B	10.9	FAM24A	20.1
rs7078864	10	124640528	+	A	C	A	0.47	0.18	0.045	1.2	1.1	1.3	15.28	9.3×10^{-5}	0	1.2	1.0	1.5	1.2×10^{-2}	0	1.1	0.90	1.3	3.9×10^{-1}	0	1.4	1.0	1.7	2.0×10^{-2}	0	1.2	1.0	1.4	2.6×10^{-2}	4.17	3.1×10^{-5}	FAM24B	11.4	FAM24A	19.7
rs7088051	10	124645716	+	A	T	A	0.45	0.19	0.045	1.2	1.1	1.3	18.31	1.9×10^{-5}	0	1.3	1.1	1.5	7.8×10^{-3}	0	1.1	0.92	1.3	2.7×10^{-1}	0	1.3	1.0	1.6	4.7×10^{-2}	0	1.2	1.1	1.4	6.5×10^{-3}	4.44	8.9×10^{-6}	FAM24A	14.5	FAM24B	16.6
rs7902274	10	124647799	+	T	G	G	0.45	0.19	0.045	1.2	1.1	1.3	18.39	1.8×10^{-5}	0	1.3	1.1	1.5	7.9×10^{-3}	0	1.1	0.93	1.3	2.6×10^{-1}	0	1.3	1.0	1.6	4.7×10^{-2}	0	1.2	1.1	1.4	6.4×10^{-3}	4.45	8.5×10^{-6}	FAM24A	12.4	FAM24B	18.7
rs7915165	10	124650448	+	A	G	G	0.47	0.18	0.045	1.2	1.1	1.3	15.71	7.4×10^{-5}	0	1.2	1.0	1.4	1.9×10^{-2}	0	1.1	0.91	1.3	3.2×10^{-1}	0	1.3	1.0	1.7	2.2×10^{-2}	0	1.2	1.0	1.4	1.8×10^{-2}	4.16	3.1×10^{-5}	FAM24A	9.8	FAM24B	21.3
rs10902840	10	124652552	+	A	G	G	0.46	0.19	0.045	1.2	1.1	1.3	18.42	1.8×10^{-5}	0	1.2	1.0	1.5	1.3×10^{-2}	0	1.1	0.93	1.3	2.5×10^{-1}	0	1.3	1.00	1.6	5.1×10^{-2}	0	1.2	1.1	1.4	4.2×10^{-3}	4.41	1.0×10^{-5}	FAM24A	7.7	FAM24B	23.4
rs10794578	10	124656846	+	T	C	T	0.47	0.18	0.045	1.2	1.1	1.3	15.68	7.5×10^{-5}	0	1.2	1.0	1.4	2.0×10^{-2}	0	1.1	0.91	1.3	3.2×10^{-1}	0	1.3	1.0	1.7	2.2×10^{-2}	0	1.2	1.0	1.4	1.8×10^{-2}	4.16	3.2×10^{-5}	FAM24A	3.4	C10orf88	23.6
rs2293435	10	124660259	+	A	G	G	0.47	0.18	0.045	1.2	1.1	1.3	15.60	7.8×10^{-5}	0	1.2	1.0	1.4	2.0×10^{-2}	0	1.1	0.91	1.3	3.4×10^{-1}	0	1.3	1.0	1.7	2.2×10^{-2}	0	1.2	1.0	1.4	1.7×10^{-2}	4.15	3.4×10^{-5}	FAM24A	within gene	C10orf88	20.1
rs7921647	10	124661645	+	T	C	C	0.45	0.19	0.045	1.2	1.1	1.3	18.28	1.9×10^{-5}	1	1.2	1.0	1.5	1.4×10^{-2}	0	1.1	0.93	1.3	2.5×10^{-1}	0	1.3	1.00	1.6	5.2×10^{-2}	0	1.2	1.1	1.4	4.0×10^{-3}	4.40	1.1×10^{-5}	FAM24A	within gene	C10orf88	18.8
rs10902842	10	124665198	+	T	C	T	0.47	0.18	0.045	1.2	1.1	1.3	15.32	9.1×10^{-5}	1	1.2	1.0	1.4	2.4×10^{-2}	0	1.1	0.91	1.3	3.3×10^{-1}	0	1.3	1.0	1.7	2.3×10^{-2}	0	1.2	1.0	1.4	1.7×10^{-2}	4.11	4.0×10^{-5}	FAM24A	2.6	C10orf88	15.2
rs10902843	10	124665243	+	A	G	A	0.46	0.19	0.045	1.2	1.1	1.3	18.07	2.1×10^{-5}	0	1.2	1.0	1.4	1.6×10^{-2}	0	1.1	0.93	1.3	2.5×10^{-1}	0	1.3	1.00	1.6	5.2×10^{-2}	0	1.2	1.1	1.4	3.9×10^{-3}	4.37	1.3×10^{-5}	FAM24A	2.6	C10orf88	15.2
rs4311998	10	124665291	+	A	C	A	0.46	0.19	0.045	1.2	1.1	1.3	18.09	2.1×10^{-5}	0	1.2	1.0	1.4	1.6×10^{-2}	0	1.1	0.93	1.3	2.5×10^{-1}	0	1.3	1.00	1.6	5.2×10^{-2}	0	1.2	1.1	1.4	3.9×10^{-3}	4.37	1.2×10^{-5}	FAM24A	2.7	C10orf88	15.1
rs11248332	10	124666325	+	T	C	T	0.47	0.18	0.045	1.2	1.1	1.3	15.44	8.5×10^{-5}	1	1.2	1.0	1.4	2.3×10^{-2}	0	1.1	0.91	1.3	3.2×10^{-1}	1	1.3	1.0	1.7	2.3×10^{-2}	0	1.2	1.0	1.4	1.6×10^{-2}	4.12	3.7×10^{-5}	FAM24A	3.7	C10orf88	14.1
rs2421162	10	124670919	+	A	C	C	0.47	0.18	0.045	1.2	1.1	1.3	15.48	8.3×10^{-5}	0	1.2	1.0	1.4	2.3×10^{-2}	0	1.1	0.91	1.3	3.2×10^{-1}	0	1.3	1.0	1.7	2.3×10^{-2}	0	1.2	1.0	1.4	1.6×10^{-2}	4.13	3.7×10^{-5}	FAM24A	8.3	C10orf88	9.5
rs7091776	10	124672473	+	T	C	C	0.47	0.18	0.045	1.2	1.1	1.3	15.46	8.5×10^{-5}	0	1.2	1.0	1.4	2.3×10^{-2}	0	1.1	0.91	1.3	3.2×10^{-1}	0	1.3	1.0	1.7	2.3×10^{-2}	0	1.2	1.0	1.4	1.6×10^{-2}	4.13	3.7×10^{-5}	C10orf88	7.9	FAM24A	9.9
rs11248338	10	124675953	+	A	C	C	0.47	-0.20	0.047	0.82	0.75	0.90	17.58	2.8×10^{-5}	0	0.76	0.64	0.92	3.9×10^{-3}	0	0.88	0.73	1.1	1.9×10^{-1}	1	0.79	0.61	1.0	8.7×10^{-2}	0	0.83	0.72	0.97	1.5×10^{-2}	-4.38	1.2×10^{-5}	C10orf88	4.5	FAM24A	13.3
rs10794579	10	124676646	+	T	C	T	0.43	0.21	0.045	1.2	1.1	1.3	22.51	2.1×10^{-6}	0	1.3	1.1	1.5	1.2×10^{-2}	1	1.1	0.96	1.4	1.3×10^{-1}	0	1.3	1.0	1.7	5.0×10^{-2}	1	1.3	1.1	1.5	8.1×10^{-4}	4.82	1.4×10^{-6}	C10orf88	3.8	FAM24A	14.0
rs4980169	10	124682576	+	A	G	A	0.43	0.21	0.045	1.2	1.1	1.3	22.46	2.1×10^{-6}	0	1.3	1.1	1.5	1.2×10^{-2}	0	1.1	0.96	1.4	1.3×10^{-1}	0	1.3	1.0	1.7	5.0×10^{-2}	1	1.3	1.1	1.5	8.1×10^{-4}	4.82	1.5×10^{-6}	C10orf88	within gene	FAM24A	20.0
rs2901360	10	124684400	+	A	C	A	0.47	-0.20	0.047	0.82	0.75	0.90	17.61	2.7×10^{-5}	0	0.76	0.63	0.92	3.8×10^{-3}	0	0.88	0.73	1.1	1.9×10^{-1}	0	0.79	0.60	1.0	8.5×10^{-2}	0	0.83	0.72	0.97	1.5×10^{-2}	-4.39	1.2×10^{-5}	C10orf88	within gene	FAM24A	21.8
rs7904130	10	124684943	+	T	G	G	0.47	-0.20	0.047	0.82	0.75	0.90	17.60	2.7×10^{-5}	0	0.76	0.63	0.92	3.8×10^{-3}	0	0.88	0.73	1.1	1.9×10^{-1}	0	0.79	0.60	1.0	8.5×10^{-2}	0	0.83	0.72	0.97	1.5×10^{-2}	-4.39	1.1×10^{-5}	C10orf88	within gene	FAM24A	22.3
rs10794580	10	124687188	+	A	G	A	0.47	-0.20	0.047	0.82	0.75	0.90	17.69	2.6×10^{-5}	0	0.76	0.63	0.91	3.5×10^{-3}	0	0.88	0.73	1.1	1.9×10^{-1}	0	0.79	0.60	1.0	8.5×10^{-2}	1	0.83	0.72	0.97	1.5×10^{-2}	-4.40	1.1×10^{-5}	C10orf88	within gene	FAM24A	24.6
rs4145321	10	124689075	+	T	C	C	0.47	-0.20	0.047	0.82	0.75	0.90	17.75	2.5×10^{-5}	0	0.76	0.63	0.91	3.5×10^{-3}	0	0.88	0.73	1.1	1.8×10^{-1}	0	0.79	0.60	1.0	8.5×10^{-2}	0	0.83	0.72	0.97	1.5×10^{-2}	-4.41	1.0×10^{-5}	C10orf88	within gene	FAM24A	26.5
rs6599638	10	124694139	+	A	G	A	0.49	-0.21	0.046	0.81	0.74	0.89	20.46	6.1×10^{-6}	0	0.75	0.62	0.90	2.1×10^{-3}	1	0.87	0.73	1.0	1.3×10^{-1}	0	0.83	0.64	1.1	1.7×10^{-1}	1	0.81	0.70	0.93	4.0×10^{-3}	-4.64	3.5×10^{-6}	C10orf88	within gene	FAM24A	31.5
rs9423291	10	124699346	+	T	G	T	0.49	-0.21	0.046	0.81	0.74	0.89	20.43	6.2×10^{-6}	0	0.75	0.62	0.90	2.1×10^{-3}	0	0.87	0.73	1.0	1.4×10^{-1}	0	0.83	0.64	1.1	1.7×10^{-1}	0	0.81	0.70	0.93	4.0×10^{-3}	-4.64	3.5×10^{-6}	C10orf88	within gene	PSTK	30.2
rs1348735	11	25076561	+	A	G	G	0.31	0.20	0.050	1.2	1.1	1.3	15.45	8.5×10^{-5}	0	1.1	0.93	1.3	2.5×10^{-1}	0	1.4	1.1	1.7	1.3×10^{-2}	0	1.5	1.1	2.0	1.2×10^{-2}	0	1.2	1.0	1.4	2.5×10^{-2}	3.94	8.1×10^{-5}	LUZP2	15.8	TMEM16C	1233.7
rs10837576	11	41103075	+	A	G	A	0.29	-0.25	0.053	0.78	0.70	0.86	22.51	2.1×10^{-6}	0	0.85	0.70	1.0	1.1×10^{-1}	0	0.71	0.57	0.88	1.7×10^{-3}	0	0.82	0.62	1.1	1.5×10^{-1}	0	0.75	0.63	0.90	1.7×10^{-3}	-4.45	8.6×10^{-6}	LRRC4C	830.8	API5	2187.0
rs2035628	11	41157340	+	T	G	T	0.44	0.18	0.044	1.2	1.1	1.3	16.16	5.8×10^{-5}	1	1.0	0.88	1.2	6.9×10^{-1}	1	1.4	1.2	1.7	2.7×10^{-4}	1	1.2	0.98	1.5	7.9×10^{-2}	1	1.2	1.0	1.4	1.9×10^{-2}	3.56	3.8×10^{-4}	LRRC4C	885.1	API5	2132.8
rs7928155	11	41168678	+	A	G	A	0.43	-0.18	0.046	0.83	0.76	0.91	15.59	7.9×10^{-5}	1	0.98	0.83	1.2	8.1×10^{-1}	0	0.74	0.61	0.89	1.8×10^{-3}	1	0.87	0.67	1.1	2.9×10^{-1}	0	0.78	0.67	0.90	1.1×10^{-3}	-3.45	5.6×10^{-4}	LRRC4C	896.4	API5	2121.4
rs10768670	11	41176740	+	A	G	A	0.28	-0.21	0.053	0.81	0.73	0.90	16.03	6.2×10^{-5}	0	0.93	0.77	1.1	4.4×10^{-1}	0	0.71	0.56	0.89	3.3×10^{-3}	0	0.83	0.62	1.1	2.1×10^{-1}	0	0.77	0.65	0.91	2.8×10^{-3}	-3.67	2.4×10^{-4}	LRRC4C	904.5	API5	2113.4
rs990199	11	41177814	+	A	T	T	0.28	-0.21	0.052	0.81	0.73	0.90	16.33	5.3×10^{-5}	0	0.93	0.77	1.1	4.5×10^{-1}	0	0.72	0.58	0.90	3.3×10^{-3}	0	0.83	0.62	1.1	2.0×10^{-1}	0	0.77	0.65	0.91	2.8×10^{-3}	-3.68	2.4×10^{-4}	LRRC4C	905.6	API5	2112.3
rs990200	11	41177850	+	T	C	C	0.28	-0.21	0.052	0.81	0.73	0.90	16.19	5.7×10^{-5}	0	0.93	0.77	1.1	4.6×10^{-1}	1	0.73	0.59	0.90	3.5×10^{-3}	0	0.83	0.62	1.1	2.0×10^{-1}	1	0.77	0.65	0.91	2.8×10^{-3}	-3.66	2.6×10^{-4}	LRRC4C	905.6	API5	2112.3
rs10768671	11	41178098	+	T	C	T	0.28	-0.21	0.052	0.81	0.73	0.90	16.30	5.4×10^{-5}	1	0.93	0.77	1.1	4.6×10^{-1}	0	0.72	0.58	0.90	3.1×10^{-3}	0	0.83	0.62	1.1	2.0×10^{-1}	0	0.77	0.65	0.91	2.8×10^{-3}	-3.67	2.5×10^{-4}	LRRC4C	905.9	API5	2112.0
rs12786242	11	41181650	+	A	G	G	0.44	-0.19	0.045	0.83	0.76	0.91	16.84	4.1×10^{-5}	0	1.0	0.86	1.2	7.9×10^{-1}	0	0.78	0.66	0.94	6.8×10^{-3}	0	0.82	0.64	1.1	1.3×10^{-1}	0	0.74	0.64	0.86	7.5×10^{-5}	-3.60	3.2×10^{-4}	LRRC4C	909.4	API5	2108.5
rs2902115	11	41182434	+	T	C	C	0.44	-0.18	0.045	0.84	0.76	0.91	15.93	6.6×10^{-5}	1	1.0	0.88	1.2	6.5×10^{-1}	0	0.79	0.66	0.94	6.9×10^{-3}	0	0.82	0.64	1.1	1.3×10^{-1}	1	0.74	0.64	0.86	8.1×10^{-5}	-3.47	5.2×10^{-4}	LRRC4C	910.2	API5	2107.7
rs1487081	11	41183210	+	T	C	C	0.44	-0.18	0.045	0.83	0.76	0.91	16.01	6.3×10^{-5}	0	1.0	0.88	1.2	6.5×10^{-1}	0	0.78	0.65	0.93	6.1×10^{-3}	0	0.82	0.63	1.1	1.2×10^{-1}	0	0.74	0.64	0.86	8.7×10^{-5}	-3.48	5.0×10^{-4}	LRRC4C	911.0	API5	2106.9
rs4627063	11	41183928	+	A	C	C	0.44	-0.18	0.045	0.83	0.76	0.91	15.99	6.4×10^{-5}	0	1.0	0.88	1.2	6.5×10^{-1}	0	0.78	0.65	0.93	6.1×10^{-3}	0	0.82	0.63	1.1	1.2×10^{-1}	0	0.74	0.64	0.86	8.8×10^{-5}	-3.48	5.1×10^{-4}	LRRC4C	911.7	API5	2106.2
rs1021271	11	41184031	+	T	C	C	0.44	-0.18	0.045	0.83	0.76	0.91	15.99	6.4×10^{-5}	0	1.0	0.88	1.2	6.5×10^{-1}	0	0.78	0.65	0.93	6.1×10^{-3}	0	0.82	0.63	1.1	1.2×10^{-1}	0	0.74	0.64	0.86	8.9×10^{-5}	-3.48	5.1×10^{-4}	LRRC4C	911.8	API5	2106.1
rs4325297	11	41191720	+	A	G	A	0.42	-0.18	0.045	0.83	0.76	0.91	16.21	5.7×10^{-5}	1	1.0	0.86	1.2	8.1×10^{-1}	1	0.78	0.66	0.93	5.9×10^{-3}	0	0.80	0.62	1.0	9.4×10^{-2}	1	0.75	0.65	0.87	2.2×10^{-4}	-3.55	3.9×10^{-4}	LRRC4C	919.5	API5	2098.4
rs7934599	11	131662082	+	T	C	T	0.17	0.24	0.056	1.3	1.1	1.4	17.88	2.4×10^{-5}	0	1.4	1.1	1.7	4.2×10^{-3}	1	1.1	0.89	1.4	3.4×10^{-1}	1	0.96	0.66	1.4	8.3×10^{-1}	1	1.4	1.2	1.7	2.3×10^{-4}	3.97	7.3×10^{-5}	HNT	within gene	OPCML	128.0
rs11600871	11	131664954	+	A	G	A	0.17	0.24	0.057	1.3	1.1	1.4	18.20	2.0×10^{-5}	0	1.4	1.1	1.7	4.2×10^{-3}	0	1.1	0.88	1.4	3.8×10^{-1}	0	0.96	0.66	1.4	8.3×10^{-1}	0	1.4	1.2	1.7	1.6×10^{-4}	3.99	6.6×10^{-5}	HNT	within gene	OPCML	125.1
rs12808059	11	131666425	+	A	G	G	0.17	0.25	0.057	1.3	1.1	1.4	18.78	1.5×10^{-5}	1	1.4	1.1	1.7	3.9×10^{-3}	0	1.1	0.87	1.4	3.9×10^{-1}	0	0.96	0.66	1.4	8.2×10^{-1}	0	1.4	1.2	1.7	1.3×10^{-4}	4.03	5.7×10^{-5}	HNT	within gene	OPCML	123.7
rs12786704	11	131684538	+	A	G	G	0.16	0.31	0.068	1.4	1.2	1.6	20.50	6.0×10^{-6}	0	1.4	1.1	1.8	8.0×10^{-3}	0	1.1	0.76	1.5	7.2×10^{-1}	0	0.92	0.60	1.4	6.9×10^{-1}	0	1.6	1.3	1.9	4.8×10^{-6}	4.04	5.5×10^{-5}	HNT	within gene	OPCML	105.5
rs11833579	12	645460	+	A	G	A	0.23	0.34	0.054	1.4	1.3	1.6	40.17	2.3×10^{-10}	0	1.2	1.0	1.5	2.6×10^{-2}	0	1.5	1.1	2.0	2.8×10^{-3}	0	1.9	1.4	2.5	2.7×10^{-6}	0	1.3	1.1	1.6	8.8×10^{-4}	6.37	2×10^{-10}	NINJ2	2.4	WNK1	87.0
rs7297967	12	646632	+	A	G	G	0.44	0.22	0.045	1.2	1.1	1.4	23.24	1.4×10^{-6}	1	1.2	1.0	1.4	4.2×10^{-2}	0	1.3	1.1	1.5	6.2×10^{-3}	1	1.5	1.1	1.9	4.2×10^{-3}	0	1.2	1.0	1.4	1.8×10^{-2}	4.81	1.5×10^{-6}	NINJ2	3.6	WNK1	85.9
rs7298096	12	646732	+	A	G	G	0.45	0.21	0.045	1.2	1.1	1.3	22.20	2.5×10^{-6}	0	1.2	0.99	1.4	5.9×10^{-2}	1	1.3	1.1	1.5	5.6×10^{-3}	0	1.4	1.1	1.8	5.6×10^{-3}	1	1.2	1.0	1.4	2.0×10^{-2}	4.66	3.1×10^{-6}	NINJ2	3.7	WNK1	85.8
rs12425791	12	653745	+	A	G	A	0.19	0.33	0.055	1.4	1.2	1.5	35.48	2.6×10^{-9}	1	1.2	1.0	1.5	5.0×10^{-2}	0	1.5	1.1	1.9	8.7×10^{-3}	1	1.8	1.4	2.3	2.2×10^{-5}	1	1.3	1.1	1.6	5.8×10^{-4}	5.94	2.9×10^{-9}	NINJ2	10.7	WNK1	78.7
rs11609145	12	3885559	+	G	C	G	0.20	0.28	0.070	1.3	1.1	1.5	15.70	7.4×10^{-5}	0	1.4	1.1	1.8	1.3×10^{-2}	0	1.3	0.91	1.7	1.7×10^{-1}	0	0.93	0.61	1.4	7.2×10^{-1}	0	1.4	1.2	1.8	9.2×10^{-4}	-3.63	2.9×10^{-4}	PARP11	32.7	EFCAB4B	153.0
rs11615969	12	75251067	+	T	C	C	0.09	0.43	0.095	1.5	1.3	1.8	20.10	7.4×10^{-6}	0	1.7	1.2	2.5	6.0×10^{-3}	0	1.4	0.70	2.9	3.2×10^{-1}	0	1.4	0.78	2.4	2.8×10^{-1}	0	1.5	1.2	1.9	$10.\times10^{-4}$	4.29	1.8×10^{-5}	BBS10	11.3	OSBPL8	18.6
rs12430490	13	45309813	+	T	C	T	0.50	0.18	0.045	1.2	1.1	1.3	15.37	8.8×10^{-5}	1	1.2	1.0	1.5	1.2×10^{-2}	0	1.2	0.98	1.4	8.2×10^{-2}	0	1.3	1.0	1.7	3.6×10^{-2}	0	1.1	0.98	1.3	9.0×10^{-2}	4.07	4.8×10^{-5}	LOC283514	within gene	SPERT	123.1
rs9634794	13	45309941	+	G	C	G	0.50	0.18	0.045	1.2	1.1	1.3	15.36	8.9×10^{-5}	0	1.2	1.0	1.5	1.2×10^{-2}	0	1.2	0.98	1.4	8.2×10^{-2}	0	1.3	1.0	1.7	3.6×10^{-2}	0	1.1	0.98	1.3	8.9×10^{-2}	-4.07	4.8×10^{-5}	LOC283514	within gene	SPERT	123.2
rs9318087	13	72073751	+	T	C	C	0.23	0.22	0.053	1.2	1.1	1.4	16.39	5.2×10^{-5}	0	1.3	1.0	1.5	2.3×10^{-2}	0	1.4	1.1	1.7	1.3×10^{-2}	0	1.3	0.96	1.7	9.3×10^{-2}	0	1.2	0.99	1.4	6.9×10^{-2}	4.00	6.3×10^{-5}	LOC440145	106.7	C13orf34	126.3
rs12716717	13	72075257	+	A	G	G	0.23	0.21	0.053	1.2	1.1	1.4	16.51	4.8×10^{-5}	0	1.2	1.0	1.5	2.5×10^{-2}	0	1.4	1.1	1.7	1.2×10^{-2}	0	1.3	0.97	1.7	8.5×10^{-2}	0	1.2	0.99	1.4	7.0×10^{-2}	4.01	6.0×10^{-5}	LOC440145	105.2	C13orf34	124.8
rs12427547	13	72088956	+	T	C	C	0.24	0.21	0.051	1.2	1.1	1.4	17.48	2.9×10^{-5}	0	1.3	1.0	1.5	1.7×10^{-2}	0	1.3	1.1	1.6	9.2×10^{-3}	0	1.3	0.96	1.7	9.9×10^{-2}	0	1.2	0.98	1.4	7.8×10^{-2}	4.07	4.6×10^{-5}	LOC440145	91.5	C13orf34	111.1
rs9599990	13	72089215	+	T	C	T	0.23	0.21	0.050	1.2	1.1	1.4	16.73	4.3×10^{-5}	0	1.2	1.0	1.5	3.0×10^{-2}	1	1.3	1.1	1.6	9.4×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	1	1.2	0.98	1.4	7.8×10^{-2}	3.97	7.3×10^{-5}	LOC440145	91.3	C13orf34	110.8
rs4885019	13	72089991	+	T	C	T	0.23	0.20	0.050	1.2	1.1	1.4	16.52	4.8×10^{-5}	0	1.2	1.0	1.5	4.0×10^{-2}	0	1.3	1.1	1.6	7.7×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	7.9×10^{-2}	3.92	9×10^{-5}	LOC440145	90.5	C13orf34	110.1
rs4885020	13	72090106	+	T	C	C	0.23	0.20	0.050	1.2	1.1	1.4	16.50	4.9×10^{-5}	0	1.2	1.0	1.5	4.1×10^{-2}	0	1.3	1.1	1.6	7.7×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	7.9×10^{-2}	3.92	9.0×10^{-5}	LOC440145	90.4	C13orf34	109.9
rs4885021	13	72090581	+	T	G	G	0.23	0.20	0.050	1.2	1.1	1.4	16.38	5.2×10^{-5}	0	1.2	1.0	1.5	4.2×10^{-2}	0	1.3	1.1	1.6	7.9×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	7.9×10^{-2}	3.90	9.6×10^{-5}	LOC440145	89.9	C13orf34	109.5
rs9592846	13	72091233	+	A	G	G	0.23	0.20	0.050	1.2	1.1	1.4	16.34	5.3×10^{-5}	0	1.2	1.0	1.5	4.3×10^{-2}	0	1.3	1.1	1.6	8.0×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	8.0×10^{-2}	3.89	9.9×10^{-5}	LOC440145	89.3	C13orf34	108.8
rs7329494	13	72092202	+	A	C	C	0.23	0.20	0.050	1.2	1.1	1.4	16.25	5.6×10^{-5}	0	1.2	1.0	1.5	4.4×10^{-2}	0	1.3	1.1	1.6	8.1×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	8.0×10^{-2}	3.88	1.0×10^{-4}	LOC440145	88.3	C13orf34	107.8
rs9599991	13	72092530	+	T	G	T	0.23	0.20	0.050	1.2	1.1	1.4	16.21	5.7×10^{-5}	0	1.2	1.0	1.5	4.5×10^{-2}	0	1.3	1.1	1.6	8.2×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	8.0×10^{-2}	3.88	1.1×10^{-4}	LOC440145	88.0	C13orf34	107.5
rs9592847	13	72092569	+	A	G	A	0.23	0.20	0.050	1.2	1.1	1.4	16.19	5.7×10^{-5}	0	1.2	1.0	1.5	4.6×10^{-2}	0	1.3	1.1	1.6	8.0×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	8.0×10^{-2}	3.88	1.1×10^{-4}	LOC440145	87.9	C13orf34	107.5
rs9592848	13	72092614	+	A	G	A	0.23	0.20	0.050	1.2	1.1	1.3	16.01	6.3×10^{-5}	0	1.2	1.0	1.5	4.6×10^{-2}	0	1.3	1.1	1.6	9.1×10^{-3}	0	1.3	0.97	1.7	8.4×10^{-2}	0	1.2	0.98	1.4	8.1×10^{-2}	3.86	1.1×10^{-4}	LOC440145	87.9	C13orf34	107.4
rs1772579	13	80086174	+	T	C	T	0.29	-0.20	0.052	0.82	0.74	0.90	15.56	8.0×10^{-5}	0	0.81	0.66	1.00	4.9×10^{-2}	1	0.78	0.64	0.95	1.2×10^{-2}	0	0.81	0.59	1.1	1.9×10^{-1}	1	0.84	0.71	1.00	4.4×10^{-2}	-3.80	1.5×10^{-4}	SPRY2	273.1	NDFIP2	1060.0
rs1772577	13	80086369	+	A	T	T	0.34	-0.19	0.049	0.82	0.75	0.91	16.06	6.1×10^{-5}	0	0.83	0.69	1.00	4.5×10^{-2}	0	0.83	0.69	1.00	4.9×10^{-2}	0	0.82	0.62	1.1	1.5×10^{-1}	0	0.82	0.70	0.96	1.3×10^{-2}	-3.94	8.0×10^{-5}	SPRY2	273.3	NDFIP2	1060.1
rs1772576	13	80086677	+	A	C	A	0.34	-0.19	0.049	0.82	0.75	0.91	16.05	6.2×10^{-5}	0	0.83	0.69	1.00	4.5×10^{-2}	0	0.83	0.69	1.00	4.9×10^{-2}	0	0.82	0.62	1.1	1.5×10^{-1}	0	0.82	0.70	0.96	1.3×10^{-2}	-3.94	8.1×10^{-5}	SPRY2	273.6	NDFIP2	1060.5
rs1772574	13	80086824	+	T	G	T	0.34	-0.19	0.049	0.82	0.75	0.91	15.98	6.4×10^{-5}	0	0.83	0.69	1.00	4.5×10^{-2}	0	0.83	0.69	1.00	4.9×10^{-2}	0	0.82	0.62	1.1	1.5×10^{-1}	0	0.82	0.70	0.96	1.4×10^{-2}	-3.94	8.3×10^{-5}	SPRY2	273.7	NDFIP2	1060.6
rs1176311	13	80115583	+	T	C	C	0.34	-0.20	0.049	0.82	0.75	0.90	16.01	6.3×10^{-5}	0	0.83	0.68	1.0	5.1×10^{-2}	0	0.86	0.72	1.0	1.1×10^{-1}	0	0.77	0.58	1.0	6.9×10^{-2}	0	0.81	0.69	0.95	8.5×10^{-3}	-4.05	5.2×10^{-5}	SPRY2	302.5	NDFIP2	1089.4
rs1176321	13	80125244	+	A	G	A	0.34	-0.20	0.050	0.82	0.74	0.90	15.82	7.0×10^{-5}	0	0.82	0.68	1.00	4.9×10^{-2}	0	0.86	0.71	1.0	1.4×10^{-1}	0	0.77	0.58	1.0	6.8×10^{-2}	0	0.81	0.69	0.95	8.4×10^{-3}	-4.03	5.5×10^{-5}	SPRY2	312.2	NDFIP2	1099.0
rs2318307	14	65460674	+	A	G	G	0.30	-0.24	0.058	0.79	0.70	0.88	16.80	4.2×10^{-5}	0	0.88	0.72	1.1	2.3×10^{-1}	0	0.81	0.61	1.1	1.7×10^{-1}	0	0.70	0.50	1.0	5.1×10^{-2}	0	0.74	0.62	0.88	6.3×10^{-4}	-3.98	6.8×10^{-5}	FUT8	181.0	GPHN	583.2
rs2318308	14	65460852	+	A	G	A	0.27	-0.29	0.061	0.75	0.67	0.85	21.84	3.0×10^{-6}	0	0.80	0.64	1.0	5.4×10^{-2}	0	0.77	0.55	1.1	1.3×10^{-1}	0	0.64	0.43	0.96	2.9×10^{-2}	1	0.74	0.62	0.88	5.3×10^{-4}	-4.65	3.4×10^{-6}	FUT8	181.1	GPHN	583.0
rs566792	15	38013787	+	T	C	T	0.14	0.28	0.072	1.3	1.2	1.5	15.39	8.7×10^{-5}	1	1.1	0.83	1.3	6.9×10^{-1}	0	2.0	1.00	4.0	5.1×10^{-2}	1	1.4	1.0	1.8	3.5×10^{-2}	0	1.5	1.2	1.9	2.3×10^{-4}	3.89	1.0×10^{-4}	EIF2AK4	within gene	GPR176	13.4
rs11866791	16	61864415	+	T	C	T	0.29	-0.21	0.053	0.81	0.73	0.90	15.26	9.4×10^{-5}	0	0.67	0.54	0.82	1.5×10^{-4}	0	0.83	0.67	1.0	9.1×10^{-2}	0	0.89	0.68	1.2	3.8×10^{-1}	0	0.88	0.74	1.0	1.6×10^{-1}	-4.22	2.4×10^{-5}	CDH8	1236.9	CDH11	1673.8
rs4491514	16	79083971	+	A	G	A	0.17	-0.26	0.064	0.77	0.68	0.88	16.23	5.6×10^{-5}	1	0.91	0.72	1.1	3.9×10^{-1}	1	0.69	0.54	0.88	2.8×10^{-3}	0	0.70	0.47	1.0	7.4×10^{-2}	1	0.75	0.60	0.94	1.1×10^{-2}	-3.75	1.8×10^{-4}	DYNLRB2	48.4	CDYL2	111.2
rs8079581	17	763866	+	T	C	T	0.21	0.28	0.070	1.3	1.1	1.5	15.57	8.0×10^{-5}	0	2.3	1.3	4.0	2.9×10^{-3}	0	1.7	1.3	2.2	1.1×10^{-4}	0	1.8	1.1	2.8	1.5×10^{-2}	1	1.1	0.88	1.3	5.5×10^{-1}	4.58	4.8×10^{-6}	NXN	within gene	TIMM22	83.2
rs2670636	17	5444603	+	A	G	A	0.46	-0.18	0.046	0.83	0.76	0.91	15.54	8.1×10^{-5}	1	0.92	0.77	1.1	3.1×10^{-1}	0	0.81	0.68	0.97	2.2×10^{-2}	1	0.83	0.63	1.1	1.9×10^{-1}	0	0.80	0.69	0.92	2.5×10^{-3}	-3.65	2.6×10^{-4}	NLRP1	16.0	MIS12	109.8
rs2137719	17	5446169	+	T	C	T	0.46	-0.18	0.046	0.83	0.76	0.91	15.79	7.1×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.80	0.67	0.97	2.0×10^{-2}	0	0.83	0.63	1.1	1.9×10^{-1}	0	0.80	0.69	0.92	2.3×10^{-3}	-3.68	2.3×10^{-4}	NLRP1	17.6	MIS12	111.3
rs925591	17	5451053	+	A	G	A	0.46	-0.18	0.046	0.83	0.76	0.91	15.82	7.0×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.80	0.67	0.97	1.9×10^{-2}	0	0.83	0.63	1.1	1.9×10^{-1}	0	0.80	0.69	0.92	2.3×10^{-3}	-3.68	2.3×10^{-4}	NLRP1	22.5	MIS12	116.2
rs2733375	17	5457949	+	T	C	T	0.46	-0.18	0.046	0.83	0.76	0.91	15.49	8.3×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.2×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.5×10^{-3}	-3.65	2.7×10^{-4}	NLRP1	29.4	MIS12	123.1
rs2716920	17	5457995	+	A	G	A	0.46	-0.18	0.046	0.83	0.76	0.91	15.49	8.3×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.2×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.5×10^{-3}	-3.65	2.7×10^{-4}	NLRP1	29.4	MIS12	123.1
rs2716919	17	5458053	+	T	C	C	0.46	-0.18	0.046	0.83	0.76	0.91	15.48	8.3×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.2×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.6×10^{-3}	-3.65	2.7×10^{-4}	NLRP1	29.5	MIS12	123.2
rs2716918	17	5458378	+	A	C	A	0.46	-0.18	0.046	0.83	0.76	0.91	15.47	8.4×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.2×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.6×10^{-3}	-3.65	2.7×10^{-4}	NLRP1	29.8	MIS12	123.5
rs2670657	17	5458491	+	A	G	G	0.46	-0.18	0.046	0.83	0.76	0.91	15.61	7.8×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.0×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.6×10^{-3}	-3.66	2.5×10^{-4}	NLRP1	29.9	MIS12	123.6
rs2670659	17	5459424	+	A	T	T	0.46	-0.18	0.046	0.83	0.76	0.91	15.58	7.9×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.0×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.6×10^{-3}	-3.66	2.6×10^{-4}	NLRP1	30.9	MIS12	124.6
rs2670661	17	5460531	+	G	C	C	0.46	-0.18	0.046	0.83	0.76	0.91	15.30	9.2×10^{-5}	1	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.4×10^{-2}	1	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.6×10^{-3}	3.63	2.8×10^{-4}	NLRP1	32.0	MIS12	125.7
rs1877659	17	5460550	+	G	C	G	0.46	-0.18	0.046	0.83	0.76	0.91	15.27	9.3×10^{-5}	0	0.91	0.77	1.1	3.1×10^{-1}	0	0.81	0.67	0.97	2.4×10^{-2}	0	0.83	0.63	1.1	2.0×10^{-1}	0	0.80	0.69	0.92	2.6×10^{-3}	3.63	2.8×10^{-4}	NLRP1	32.0	MIS12	125.7
rs2716916	17	5461751	+	T	C	C	0.46	-0.18	0.046	0.83	0.76	0.91	15.18	9.8×10^{-5}	0	0.92	0.77	1.1	3.2×10^{-1}	0	0.81	0.67	0.98	2.9×10^{-2}	0	0.81	0.61	1.1	1.5×10^{-1}	0	0.80	0.69	0.93	2.9×10^{-3}	-3.65	2.6×10^{-4}	NLRP1	33.2	MIS12	126.9
rs2716915	17	5461916	+	T	C	T	0.46	-0.18	0.046	0.83	0.76	0.91	15.14	$10.\times10^{-5}$	0	0.92	0.77	1.1	3.2×10^{-1}	0	0.81	0.67	0.98	2.9×10^{-2}	0	0.81	0.61	1.1	1.5×10^{-1}	0	0.80	0.69	0.93	2.9×10^{-3}	-3.65	2.6×10^{-4}	NLRP1	33.4	MIS12	127.1
rs17806566	17	7292887	+	T	C	C	0.04	0.43	0.11	1.5	1.2	1.9	15.62	7.7×10^{-5}	0	1.8	1.3	2.6	1.4×10^{-3}	0	1.0	0.55	1.9	9.7×10^{-1}	0	1.2	0.65	2.3	5.3×10^{-1}	0	1.6	1.2	2.2	4.2×10^{-3}	3.71	2.1×10^{-4}	CHRNB1	within gene	FGF11	3.9
rs4265880	17	7336991	+	T	C	T	0.04	0.41	0.10	1.5	1.2	1.8	16.28	5.5×10^{-5}	0	1.8	1.2	2.5	1.3×10^{-3}	0	1.0	0.67	1.6	8.5×10^{-1}	0	1.2	0.66	2.2	5.4×10^{-1}	1	1.7	1.2	2.3	1.8×10^{-3}	3.92	9.0×10^{-5}	POLR2A	within gene	ZBTB4	8.8
rs4450459	17	7337341	+	A	G	A	0.04	0.41	0.10	1.5	1.2	1.8	16.25	5.5×10^{-5}	0	1.8	1.2	2.5	1.3×10^{-3}	0	1.0	0.67	1.6	8.5×10^{-1}	0	1.2	0.66	2.2	5.4×10^{-1}	0	1.7	1.2	2.3	1.8×10^{-3}	3.91	9.1×10^{-5}	POLR2A	within gene	ZBTB4	9.1
rs4239258	17	7337767	+	A	G	A	0.04	0.41	0.10	1.5	1.2	1.8	16.24	5.6×10^{-5}	0	1.8	1.2	2.5	1.3×10^{-3}	0	1.0	0.67	1.6	8.5×10^{-1}	0	1.2	0.66	2.2	5.3×10^{-1}	0	1.7	1.2	2.3	1.8×10^{-3}	3.91	9.1×10^{-5}	POLR2A	within gene	ZBTB4	9.5
rs2228130	17	7345715	+	T	C	T	0.04	0.42	0.10	1.5	1.2	1.9	16.89	4.0×10^{-5}	1	1.8	1.2	2.5	1.4×10^{-3}	0	1.0	0.66	1.7	8.4×10^{-1}	0	1.2	0.67	2.3	5.1×10^{-1}	0	1.7	1.2	2.4	1.3×10^{-3}	3.98	7.0×10^{-5}	POLR2A	within gene	ZBTB4	17.5
rs7224988	17	7350605	+	A	G	G	0.04	0.42	0.10	1.5	1.2	1.9	17.09	3.6×10^{-5}	1	1.8	1.2	2.5	1.3×10^{-3}	0	1.0	0.66	1.7	8.4×10^{-1}	1	1.2	0.68	2.3	4.8×10^{-1}	0	1.7	1.2	2.4	1.3×10^{-3}	4.01	6.1×10^{-5}	POLR2A	within gene	ZBTB4	22.4
rs9303219	17	7351649	+	T	C	C	0.03	0.42	0.10	1.5	1.2	1.9	17.12	3.5×10^{-5}	0	1.8	1.3	2.5	1.2×10^{-3}	0	1.0	0.66	1.7	8.4×10^{-1}	0	1.2	0.68	2.3	4.8×10^{-1}	0	1.7	1.2	2.4	1.3×10^{-3}	4.01	6.0×10^{-5}	POLR2A	within gene	ZBTB4	23.4
rs9989479	17	7358833	+	A	G	A	0.03	0.41	0.10	1.5	1.2	1.8	16.11	6.0×10^{-5}	0	1.8	1.3	2.6	1.0×10^{-3}	0	1.0	0.69	1.6	8.4×10^{-1}	0	1.2	0.66	2.3	5.2×10^{-1}	0	1.7	1.2	2.4	1.6×10^{-3}	3.99	6.7×10^{-5}	POLR2A	within gene	ZBTB4	30.6
rs13894	17	7470627	+	A	G	A	0.07	0.30	0.076	1.3	1.2	1.6	15.44	8.5×10^{-5}	0	1.6	1.2	2.1	2.6×10^{-3}	1	1.0	0.78	1.4	8.2×10^{-1}	1	0.99	0.59	1.6	9.7×10^{-1}	1	1.6	1.2	2.0	2.5×10^{-4}	3.84	1.2×10^{-4}	SAT2	within gene	SHBG	3.6
rs8069583	17	40026019	+	T	C	C	0.45	0.18	0.046	1.2	1.1	1.3	15.85	6.9×10^{-5}	0	1.2	1.00	1.4	5.3×10^{-2}	0	1.3	1.1	1.6	1.0×10^{-2}	0	1.3	0.97	1.6	7.8×10^{-2}	0	1.1	0.99	1.3	6.4×10^{-2}	3.90	9.6×10^{-5}	FZD2	33.6	FLJ35848	72.0
rs12944467	17	40026304	+	A	G	A	0.45	0.18	0.046	1.2	1.1	1.3	15.85	6.9×10^{-5}	0	1.2	1.00	1.4	5.3×10^{-2}	0	1.3	1.1	1.6	1.0×10^{-2}	0	1.3	0.97	1.6	7.9×10^{-2}	0	1.1	0.99	1.3	6.3×10^{-2}	3.90	9.7×10^{-5}	FZD2	33.9	FLJ35848	71.7
rs7217227	17	40027765	+	A	G	A	0.45	0.18	0.046	1.2	1.1	1.3	15.83	6.9×10^{-5}	1	1.2	1.00	1.4	5.4×10^{-2}	0	1.3	1.1	1.6	1.0×10^{-2}	0	1.3	0.97	1.6	7.9×10^{-2}	0	1.1	0.99	1.3	6.2×10^{-2}	3.90	9.8×10^{-5}	FZD2	35.3	FLJ35848	70.2
rs7218040	17	40028258	+	A	G	A	0.45	0.18	0.045	1.2	1.1	1.3	15.57	8.0×10^{-5}	0	1.2	1.00	1.4	5.5×10^{-2}	1	1.3	1.1	1.5	1.2×10^{-2}	0	1.3	0.97	1.6	8.0×10^{-2}	1	1.1	0.99	1.3	6.3×10^{-2}	3.86	1.1×10^{-4}	FZD2	35.8	FLJ35848	69.8
rs11659121	17	52910887	+	A	G	A	0.12	-0.45	0.11	0.64	0.52	0.79	17.52	2.8×10^{-5}	0	0.46	0.28	0.74	1.4×10^{-3}	0	0.66	0.39	1.1	1.3×10^{-1}	0	1.1	0.49	2.3	8.6×10^{-1}	1	0.66	0.50	0.87	3.5×10^{-3}	-4.13	3.6×10^{-5}	MSI2	within gene	AKAP1	357.2
rs8183455	20	11141550	+	T	G	G	0.09	0.36	0.090	1.4	1.2	1.7	16.02	6.3×10^{-5}	0	1.7	1.2	2.3	7.5×10^{-4}	0	1.5	0.82	2.7	1.8×10^{-1}	0	1.2	0.71	2.0	5.2×10^{-1}	0	1.3	1.0	1.7	3.6×10^{-2}	3.87	1.1×10^{-4}	JAG1	539.0	C20orf94	589.5
rs370087	20	55960896	+	T	C	T	0.24	0.21	0.052	1.2	1.1	1.4	16.76	4.2×10^{-5}	0	1.4	1.1	1.6	1.8×10^{-3}	0	1.4	1.1	1.7	8.9×10^{-4}	0	1.2	0.83	1.7	3.4×10^{-1}	1	1.1	0.90	1.3	4.9×10^{-1}	3.85	1.2×10^{-4}	C20orf85	198.5	TMEPAI	240.9
rs2839095	21	46300785	+	A	G	A	0.13	0.33	0.080	1.4	1.2	1.6	17.12	3.5×10^{-5}	0	1.2	0.79	1.7	4.6×10^{-1}	0	1.5	1.1	2.0	1.8×10^{-2}	0	0.99	0.39	2.5	9.8×10^{-1}	0	1.5	1.2	1.8	3.6×10^{-4}	3.17	1.5×10^{-3}	COL6A2	41.7	COL6A1	51.4
rs2330334	22	21693882	+	A	G	A	0.31	0.18	0.047	1.2	1.1	1.3	15.25	9.4×10^{-5}	0	1.2	1.0	1.5	2.7×10^{-2}	0	1.3	1.1	1.6	3.9×10^{-3}	0	1.1	0.85	1.4	4.9×10^{-1}	0	1.2	0.99	1.3	6.8×10^{-2}	3.65	2.6×10^{-4}	RTDR1	37.7	GNAZ	48.8
rs5996449	22	21695301	+	A	G	G	0.31	0.18	0.046	1.2	1.1	1.3	15.24	9.5×10^{-5}	0	1.2	1.0	1.5	2.7×10^{-2}	0	1.3	1.1	1.6	3.9×10^{-3}	0	1.1	0.85	1.4	4.9×10^{-1}	0	1.2	0.99	1.3	6.8×10^{-2}	3.65	2.7×10^{-4}	RTDR1	36.3	GNAZ	47.4
rs6003465	22	21695501	+	T	C	C	0.28	0.22	0.055	1.2	1.1	1.4	15.94	6.5×10^{-5}	0	1.2	1.0	1.5	3.8×10^{-2}	0	1.4	1.1	1.8	3.0×10^{-3}	0	1.1	0.79	1.5	6.2×10^{-1}	0	1.2	1.0	1.5	3.3×10^{-2}	3.66	2.5×10^{-4}	RTDR1	36.1	GNAZ	47.2
rs139071	22	42885910	+	G	C	C	0.28	-0.25	0.061	0.78	0.69	0.88	17.02	3.7×10^{-5}	0	0.76	0.61	0.95	1.7×10^{-2}	0	0.89	0.67	1.2	4.5×10^{-1}	0	0.87	0.64	1.2	3.4×10^{-1}	0	0.71	0.58	0.86	4.9×10^{-4}	4.13	3.7×10^{-5}	PARVB	within gene	PARVG	22.3

Table 3: Results of NINJ2 associations with total and ischemic stroke adjusted for age-, sex- and various stroke risk factors

	Rs11833579	**Rs12425791**
Total stroke		
Adjusted for age-,sex	1.26 (1.16-1.37)	1.30 (1.19-1.42)
Adjusted for age-,sex- and systolic blood pressure	1.24 (1.14-1.34)	1.30 (1.20-1.41)
Adjusted for age-,sex- and presence of hypertension (JNC-7 criteria)	1.25 (1.15-1.36)	1.30 (1.19-1.42)
Adjusted for age-,sex- and presence of diabetes	1.25 (1.15-1.36)	1.28 (1.18-1.40)
Adjusted for age-,sex- and current smoking status	1.26 (1.16-1.37)	1.30 (1.19-1.42)
Adjusted for age-,sex- and presence of atrial fibrillation	1.28 (1.18-1.39)	1.33 (1.21-1.45)
Adjusted for age-,sex- and all of the above	1.27 (1.17-1.39)	1.31 (1.20-1.43)
Ischemic Stroke		
Adjusted for age-,sex	1.33 (1.21-1.46)	1.33 (1.21-1.47)
Adjusted for age-,sex- and systolic blood pressure	1.30 (1.19-1.43)	1.36 (1.24-1.50)
Adjusted for age-,sex- and presence of hypertension (JNC-7 criteria)	1.33 (1.21-1.46)	1.36 (1.24-1.51)
Adjusted for age-,sex- and presence of diabetes	1.32 (1.20-1.45)	1.34 (1.21-1.48)
Adjusted for age-,sex- and current smoking status	1.32 (1.20-1.45)	1.35 (1.22-1.49)
Adjusted for age-,sex- and presence of atrial fibrillation	1.32 (1.20-1.45)	1.38 (1.25-1.52)
Adjusted for age-,sex- and all of the above	1.34 (1.21-1.47)	1.35 (1.22-1.50)

*All results are presented as HR (hazard ratio) and 95% CI (confidence interval) per copy of minor allele, these results are based on directly genotyped data for rs11833579 and rs12425791.

Table 4. Characteristics of Participants in Replication Cohorts

STUDY	ARIC African-American cohort	CHS African-American cohort	The Netherlands (White)	
			Cases	Controls
Number in sample*	2430	574	652	3613
Women %	63%	65%	48%	62%
Mean follow-up (yrs)	14.7 (3.6)	9.9 (4.03)	-	-
at DNA draw	53.6 (5.7)	72.5 (5.5)	76.5 (7.0)	74.6 (7.0)
at stroke	63.8 (6.9)	79.97 (5.8)	76.5 (7.0)	74.6 (7.0)
Number of total strokes	214	85	652	-
Number of ischemic strokes	191	68	501	-
Number of atherothrombotic strokes	153	57	400	-

Table 5: Association of rs12425791 and rs11833579 with various stroke related phenotypes in discovery and replication cohorts

	Discovery						Replication								
	Using genotyped and imputed GWAS data			Using only directly genotyped data			ARIC African - American cohort			CHS African-American cohort			Netherlands, white case-control sample		
	n	HR	p	n	HR	p	n	RR	p	n	HR	p	n	HR	p
Rs12425791															
Total stroke	1544	1.31	$1.5x10^{-8}$	1544	1.30	$5.0x10^{-9}$	215	1.35	$3.6x10^{-2}$	85	0.58	ns	652	1.17	$3.5x10^{-2}$
Ischemic stroke	1164	1.39	$2.6x10^{-9}$	1164	1.33	$1.2x10^{-8}$	191	1.42	$1.9x10^{-2}$	68	0.49	ns	501	1.19	$3.7x10^{-2}$
Atherothrombotic	-	-	-	876	1.37	$3.3x10^{-8}$	153	1.41	$4.1x10^{-2}$	57	0.51	ns	400	1.29	$5.2x10^{-3}$
Rs11833579															
Total stroke	1544	1.32	$4.8x10^{-9}$	1544	1.26	$6.1*10^{-8}$	215	1.15	ns	85	0.72	ns	652	1.10	ns
Ischemic stroke	1164	1.41	$2.3x10^{-10}$	1164	1.33	$2.3x10^{-9}$	191	1.20	ns	68	0.65	ns	501	1.11	ns
Atherothrombotic	-	-	-	876	1.35	$4.0x10^{-8}$	153	1.28	ns†	57	0.65	ns	400	1.19	$4.8x10^{-2}$

	Meta-meta analysis					
	All data in whites			All data		
	n	HR	p	n	HR	p
Rs12425791						
Total stroke	2196	1.27	$1.0x10^{-9}$	2496	1.26	$7.9x10^{-10}$
Ischemic stroke	1665	1.29	$2.4x10^{-9}$	1924	1.29	$1.1x10^{-9}$
Atherothrombotic	1029	1.35	$7.2x10^{-10}$	1486	1.33	$5.2x10^{-10}$
Rs11833579						
Total stroke	2196	1.21	$1.2x0^{-7}$	2496	1.19	$4.3x10^{-7}$
Ischemic stroke	1665	1.27	$6.4x10^{-9}$	1924	1.24	$2.3x10^{-8}$
Atherothrombotic	1029	1.30	$1.3x10^{-8}$	1486	1.28	$2.2x10^{-8}$

n= number of strokes in sample

† Two-sided p–values are shown, one-sided p-value for this replication analysis is 0.04 falling below a threshold of $p<0.05$.

Table 6: Associations with Putative Candidate Stroke SNPs in the CHARGE meta-analysis

Chr	Gene Name	Gene Symbol	Candidate SNP	proxy SNP	coded allele	Total stroke		Ischemic stroke	
						Hazard ratio	pvalue	Hazard ratio	pvalue
1	5,10-methylenetetrahydrofolate reductase	MTHFR	C677T = rs1801133		C	0.94 (0.86-1.02)	0.12	0.93 (0.84-1.02)	0.11
1	Factor V leiden	F5	1691G>A = rs6025	NA					
4	intergenic		Rs2200733		C	0.97 (0.86-1.08)	0.55	1.00 (0.88-1.15)	0.95
5	Phosphodiesterase 4D	PDE4D	SNP 39 = rs3887175		T	1.01 (0.91-1.13)	0.81	1.00 (0.88-1.13)	0.96
			SNP 41 = rs12188950		C	0.97 (0.87-1.08)	0.57	0.97 (0.86-1.10)	0.66
			SNP 45 = rs12153798		C	1.02 (0.91-1.13)	0.78	1.03 (0.91-1.16)	0.67
			SNP 56 = rs702553	NA					
			SNP 83 = rs1396476		G	1.03 (0.93-1.14)	0.56	0.99 (0.88-1.12)	0.87
			SNP 87 = rs966221		C	0.98 (0.91-1.06)	0.68	0.96 (0.88-1.06)	0.43
			SNP 89 = rs2910829		G	1.01 (0.94-1.09)	0.80	1.01 (0.93-1.11)	0.76
7	Serpin peptidase inhibitor	SERPINE1	11053G/T = rs7242		G	0.98 (0.91-1.06)	0.63	0.99 (0.91-1.08)	0.86
			-675 G4/G5 = rs1799768	NA					
9	intergenic		Rs1537378		C	1.05 (0.97-1.14)	0.21	1.06 (0.97-1.16)	0.22
11	Prothrombin	F2	20210G>A = rs1799963	NA	See Supplementary Table A rows 206-211 for other SNPs (not in LD with candidate SNP) in this gene at $p<10^{-4}$				
11	Glycoprotein 1 b alpha	GP1BA	HPA-2 (Thr/Met) = rs6065		C	0.92 (0.80-1.05)	0.219	0.93 (0.79-1.09)	0.35
			Kozak sequence –5 C/T = rs2243093	***rs16954257***	***T***	***0.86 (0.76-0.98)***	***0.020***	***0.83 (0.72-0.97)***	***0.02***
13	Arachidonate 5-lipoxygenase-activating	ALOX5AP	SG13S25 = rs17222814	NA					

	protein								
17	Angiotensin converting enzyme	ACE	I/D = rs1799752	*rs4343*	*G*	*1.04 (0.96-1.12)*	*0.32*	*1.03 (0.94-1.12)*	*0.54*
19	Apolipoprotein E	APOE	rs7412, rs429358	NA					

If the reported SNP was not present in our dataset, a proxy SNP was selected using the SNAP program

http://www.broad.mit.edu/mpg/snap/

A proxy SNP was required to have an r^2 >0.8 with the reported SNP. If no such proxy SNP was present in our dataset this is indicated as NA (not available).