ARTICLE

Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations

Santhi K. Ganesh,[1,39,*] Daniel I. Chasman,[2,3,39] Martin G. Larson,[4,5,39] Xiuqing Guo,[6,7,39] Germain Verwoert,[8,9,39] Joshua C. Bis,[10,39] Xiangjun Gu,[11,39] Albert V. Smith,[12,13,39] Min-Lee Yang,[1] Yan Zhang,[14] Georg Ehret,[15,16] Lynda M. Rose,[2] Shih-Jen Hwang,[4,17] George J. Papanicolau,[18] Eric J. Sijbrands,[9] Kenneth Rice,[19] Gudny Eiriksdottir,[12] Vasyl Pihur,[15] Paul M. Ridker,[2,3] Ramachandran S. Vasan,[4,20] Christopher Newton-Cheh,[21] Global Blood Pressure Genetics Consortium, Leslie J. Raffel,[22] Najaf Amin,[8] Jerome I. Rotter,[6,7] Kiang Liu,[23] Lenore J. Launer,[24] Ming Xu,[25] Mark Caulfield,[26,27] Alanna C. Morrison,[28] Andrew D. Johnson,[4,29] Dhananjay Vaidya,[30] Abbas Dehghan,[8] Guo Li,[10] Claude Bouchard,[31] Tamara B. Harris,[24] He Zhang,[1] Eric Boerwinkle,[28] David S. Siscovick,[10,32] Wei Gao,[25] Andre G. Uitterlinden,[8,9,33] Fernando Rivadeneira,[8,9] Albert Hofman,[8] Cristen J. Willer,[1] Oscar H. Franco,[8] Yong Huo,[14] Jacqueline C.M. Witteman,[8] Patricia B. Munroe,[26,27] Vilmundur Gudnason,[12,13,40] Walter Palmas,[34,40] Cornelia van Duijn,[8,33,35,40] Myriam Fornage,[11,36,40] Daniel Levy,[4,17,37,40] Bruce M. Psaty,[10,32,38,40] and Aravinda Chakravarti[15,40,*]

Blood pressure (BP) is a heritable, quantitative trait with intraindividual variability and susceptibility to measurement error. Genetic studies of BP generally use single-visit measurements and thus cannot remove variability occurring over months or years. We leveraged the idea that averaging BP measured across time would improve phenotypic accuracy and thereby increase statistical power to detect genetic associations. We studied systolic BP (SBP), diastolic BP (DBP), mean arterial pressure (MAP), and pulse pressure (PP) averaged over multiple years in 46,629 individuals of European ancestry. We identified 39 trait-variant associations across 19 independent loci ($p < 5 \times 10^{-8}$); five associations (in four loci) uniquely identified by our LTA analyses included those of SBP and MAP at 2p23 (rs1275988, near *KCNK3*), DBP at 2q11.2 (rs7599598, in *FER1L5*), and PP at 6p21 (rs10948071, near *CRIP3*) and 7p13 (rs2949837, near *IGFBP3*). Replication analyses conducted in cohorts with single-visit BP data showed positive replication of associations and a nominal association ($p < 0.05$). We estimated a 20% gain in statistical power with long-term average (LTA) as compared to single-visit BP association studies. Using LTA analysis, we identified genetic loci influencing BP. LTA might be one way of increasing the power of genetic associations for continuous traits in extant samples for other phenotypes that are measured serially over time.

[1]Departments of Internal Medicine and Human Genetics, University of Michigan, Ann Arbor, MI 48109, USA; [2]Division of Preventive Medicine, Brigham and Women's Hospital, Boston, MA 02215, USA; [3]Harvard Medical School, Boston MA, 02115, USA; [4]Framingham Heart Study, National Heart, Lung, and Blood Institute, Framingham, MA 01702, USA; [5]Department of Mathematics, Boston University, Boston, MA 02215, USA; [6]Institute for Translational Genomics and Population Sciences, Los Angeles Biomedical Research Institute, Torrance, CA 90502, USA; [7]Department of Pediatrics, Harbor-UCLA Medical Center, Torrance, CA 90502, USA; [8]Department of Epidemiology, Erasmus University Medical Center, 's-Gravendijkwal 230, 3015 Rotterdam, the Netherlands; [9]Department of Internal Medicine, Erasmus University Medical Center, 's-Gravendijkwal 230, 3015 Rotterdam, the Netherlands; [10]Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, WA 98101, USA; [11]Research Center for Human Genetics, Brown Foundation Institute of Molecular Medicine, University of Texas Health Science Center at Houston, Houston, TX 77030, USA; [12]Icelandic Heart Association, 201 Kopavogur, Iceland; [13]Faculty of Medicine, University of Iceland, 101 Reykjavik, Iceland; [14]Department of Cardiology, Peking University First Hospital, Beijing 100034, China; [15]Center for Complex Disease Genomics, McKusick-Nathans Institute of Genetic Medicine, Johns-Hopkins University School of Medicine, Baltimore, MD 21205, USA; [16]Cardiology, Department of Specialties of Internal Medicine, Geneva University Hospitals, 1211 Geneva, Switzerland; [17]Center for Population Studies, National Heart, Lung, and Blood Institute, Bethesda, MD 20892, USA; [18]Division of Cardiovascular Sciences, National Heart, Lung, and Blood Institute, Bethesda, MD 20892, USA; [19]Department of Biostatistics, University of Washington, Seattle, WA 98195, USA; [20]Divisions of Epidemiology and Cardiology, Department of Medicine, Boston University School for Medicine, Boston, MA 02118, USA; [21]Cardiovascular Research Center and Center for Human Genetic Research, Massachusetts General Hospital, Boston, MA 02114, USA; [22]Medical Genetics Research Institute, Cedars-Sinai Medical Center, Los Angeles, CA 90048, USA; [23]Department of Preventive Medicine, Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA; [24]Laboratory of Epidemiology and Population Science, National Institute on Aging, Bethesda, MD 20892, USA; [25]Department of Cardiology, Peking University Third Hospital, Beijing 100191, China; [26]Clinical Pharmacology and the Genome Centre, William Harvey Research Institute, Barts and The London School of Medicine and Dentistry, Queen Mary University of London, London EC1M 6BQ, UK; [27]NIHR Barts Cardiovascular Biomedical Research Unit, Queen Mary University of London, London EC1M 6BQ, UK; [28]Human Genetics Center, University of Texas Health Sciences Center at Houston, Houston, TX 77030, USA; [29]Cardiovascular Epidemiology and Human Genomics Branch, National Heart, Lung, and Blood Institute, Bethesda, MD 02892, USA; [30]Department of Medicine, Johns Hopkins University, Baltimore, MD 21287, USA; [31]Human Genomics Laboratory, Pennington Biomedical Research Center, Baton Rouge, LA 70808, USA; [32]Department of Epidemiology, University of Washington, Seattle, WA 98101, USA; [33]Netherlands Consortium for Healthy Aging, Netherlands Genomics Initiative, 2593 the Hague, the Netherlands; [34]Department of Medicine, Columbia University, New York, NY 10032, USA; [35]Centre for Medical Systems Biology, Netherlands Genomics Initiative, 2593 the Hague, the Netherlands; [36]Human Genetics Center, School of Public Health, University of Texas Health Science Center at Houston, Houston, TX 77030, USA; [37]Boston University School of Medicine, Boston, MA 02118, USA; [38]Group Health Research Institute, Group Health Cooperative, Seattle, WA 98101, USA

[39]These authors contributed equally to this work

[40]These authors contributed equally to this work

*Correspondence: sganesh@umich.edu (S.K.G.), aravinda@jhmi.edu (A.C.)

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Introduction

Blood pressure (BP) is a quantitative trait that varies both within subjects, according to diurnal patterns and longer-term changes (across weeks or months because of changes in environmental and physiologic influences), and between subjects, according to environmental factors and genetic determinants. Measurement error adds a third source of variability to BP quantification. These sources of variability present a challenge for the detection of genetic associations with BP given that the genetic component is a relatively small portion of overall variability. As it stands, the known genetic determinants of complex quantitative traits, such as BP, are common polymorphisms with small allelic effects that require very large sample sizes for detection. However, if measurement errors could be reduced, the statistical power could be improved. Hypertension is an important major cardiovascular risk factor affecting approximately one-third of the adult population globally and estimated to contribute to 13.5 million deaths yearly.[1] Therefore, further improvements in methods for signal detection in BP genetic association studies are important.

Most epidemiologic and genetic association studies of BP use single-visit, or "visit 1" (V1), measurements of BP.[2–5] The standard protocol is to take multiple measurements at a single point in time, discard the highest (first) value, and average the rest to account for the "white-coat effect."[6] Although these V1 BP traits have proved valuable, they might be unrepresentative of an individual's BP norm as might be assessed from multiple BP measurements for an individual across years. The use of such longitudinal phenotype data, also known as repeated measures, might alleviate some of the effects of measurement error and similar sources underlying continuous traits, such as BP. Simple averaging of repeated measurements presents a straightforward opportunity to reduce phenotypic variability and thereby increase power to detect associations while utilizing existing sample sizes. The utility of such long-term average (LTA) procedures to study BP genetic association has not been assessed. In this investigation, we quantitatively explored the nature and degree of improvement of genetic associations by LTA analyses of BP traits.

We performed genome-wide association studies (GWASs) of LTA BP traits within multiple longitudinal community-based cohorts in which BP traits have been measured at multiple visits over several years of follow-up.[7] For comparison, we also conducted parallel GWASs of V1 BP in these same cohorts. We identified four loci associated with BP traits in the LTA analyses; we also conducted replication analyses by using independent samples with V1 BP measurements and showed definitive replication of two loci and nominal association at a third locus. We compared the results of the LTA discovery analyses to the corresponding V1 findings for the number of loci detected and the characteristics of SNP associations within the detected loci.

Material and Methods

Study Subjects

For the discovery analyses, the phenotype and genotype data of 46,629 individuals from eight participating longitudinal population studies collaborating with the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium,[7] the Age, Gene/Environment Susceptibility (AGES) Reykjavik Study, the Atherosclerosis Risk in Communities (ARIC) Study, the Cardiovascular Health Study (CHS), the Framingham Heart Study (FHS), the Rotterdam Study (RS), the Women's Genome Health Study (WGHS), the Multi-Ethnic Study of Atherosclerosis (MESA), and Coronary Artery Risk Development in Young Adults (CARDIA) were analyzed for LTA BP and V1 BP trait genome-wide associations after adjustment for covariates. Only individuals of European ancestry, as confirmed by principal-component analysis of genetic ancestry, were included in this analysis. For the replication analyses, V1 BP data from 34,433 individuals across 17 cohorts participating in the Global BP Genetics (GBPG) Consortium and 5,056 individuals in the Peking University – University of Michigan Study of Atherosclerosis (PUUMA) were analyzed by identical methods.[5] All participants gave written informed consent for participation in their respective studies and the conduct of genetic research, and the studies in which the subjects were enrolled were approved by their respective institutional review boards. Detailed information on each participating study is provided in the Supplemental Data, available online.

BP Phenotypes

BP in each study was measured according to protocols described in the cohort descriptions in the Supplemental Data. The traits analyzed were systolic BP (SBP), diastolic BP (DBP), mean arterial pressure (MAP), and pulse pressure (PP) as continuous traits. PP was defined as SBP minus DBP, and MAP was defined as two-thirds DBP plus one-third SBP. BP at each visit was corrected for antihypertensive medication use by the addition of 10 mmHg to the observed SBP value and 5 mmHg to the observed DBP value. These adjustments were also implemented prior to the calculation of estimated off-treatment MAP and PP. To obtain the LTA BP traits, we averaged repeated BP measurements for study participants; individuals with two, three, or four repeated BP measures at least 1 year apart and within a 15-year timespan were included in our analyses. For the ARIC cohort, we removed outliers greater than 4 SD units from the mean at each visit, but we did not remove outliers from the other cohorts. Follow-up measurements beyond 15 years were not included in this analysis; individuals with only one BP measurement were also excluded. At each study visit, we performed linear regression, including adjustment for age, age-squared, gender, body mass index, and study-specific corrections for population substructure (based on principal-component analysis) to generate visit-specific BP residuals. These residual values were subsequently averaged over all available visits, and the final averaged residual was the LTA trait analyzed (termed LTA SBP, LTA DBP, LTA MAP, and LTA PP). In the analyses of V1 BP traits, BP values at the earliest visit among those included in this study were analyzed. To facilitate comparisons of the LTA and V1 analyses, we conducted the V1 analyses in the same individuals included in the LTA analyses. We adjusted V1 BP traits for antihypertensive medication use and performed linear regression by using covariate adjustment in a manner identical to what has been done in prior V1 BP association analyses.[4]

Genotyping and Quality Control

Each study in the discovery LTA and V1 analyses genotyped samples by using high-density SNP marker platforms (Affymetrix SNP6.0 in ARIC, CARDIA, and MESA; Affymetrix 500K in the FHS; Illumina 370K in the AGES Reykjavik Study, CHS, and WGHS; and Illumina 550K in the RS). Genotypes were imputed to a set of approximately 2.5 million HapMap SNPs with the use of HapMap Phase II CEU individuals (Utah residents with ancestry from northern and western Europe from the CEPH collection) as a reference and either MACH (ARIC, AGES Reykjavik Study, FHS, MESA, RS, and WGHS), BEAGLE (CARDIA), or BIMBAM (CHS) software. Similar methods were used in the replication cohorts. Further details of SNP genotyping and quality-control measures used for each cohort have been previously published.[2,4,5]

Statistical Association and Meta-analysis

Individual SNP association statistics were calculated for each SNP meeting quality-control criteria via linear regression for LTA and V1 BP traits. In each cohort, except in the FHS, association analysis was performed with PLINK[8] with linear regression under an additive genetic model. In the FHS, family structure was modeled with a linear mixed-effects model implemented in R.[9] Regression coefficients and corresponding SEs for each SNP and trait were meta-analyzed by inverse-variance-weighted meta-analysis to provide the primary findings. Genomic control[10] was applied to individual study results and to the final meta-analysis results to control effects possibly due to population stratification or cryptic relatedness. The statistical-significance threshold was set at the p value of 5.0×10^{-8}. For loci where variants showed significant associations, we examined the linkage-disequilibrium (LD) patterns with SNAP;[11] we assumed that loci with $r^2 < 0.3$ were effectively independent associations.

Replication Analyses Using V1 BP Traits

For replication analyses, we carried forward the five trait-locus associations that we identified in our discovery LTA analyses but that were not found in single-visit BP data in European-ancestry individuals from GBPG and Chinese-ancestry individuals from PUUMA. Details on the cohorts used for reproducibility analyses are provided in the Supplemental Data. There are no sufficiently sized replication cohorts with LTA traits to our knowledge, and we elected to include as many samples as possible in a meta-analysis to increase power for the discovery analysis. Because the follow-up association testing performed in the GBPG Consortium and PUUMA participants was based on V1 data rather than trait averages, as in our LTA discovery analyses, this experiment does not constitute a true statistical "replication analysis" but rather a biological one that might be partly underpowered. We used a Bonferroni correction for the number of SNP-trait associations tested for each of the four BP traits. To assess associations close to a genome-wide significance threshold ($p < 5 \times 10^{-8}$), but not yet meeting this criterion, we used V1 BP traits to test all LTA-analysis SNPs with $p < 5.0 \times 10^{-7}$ in the GBPG Consortium V1 data.

Simulation of Statistical Power

We conducted computer simulations to evaluate the change in statistical power to detect associations by using LTA versus V1 BP traits as a function of sample size and effect size. The genome-wide significance level was set to $p < 5 \times 10^{-8}$. We simulated phenotypic data across four visits, as well as SNP data with different allele frequencies and different effect sizes. Phenotype data were simulated from a multivariate normal distribution with correlation structures based upon those observed in the ARIC Study. Next, we simulated genotype for a single SNP by setting the minor allele frequency to 0.05, 0.1, 0.2, 0.3, or 0.4 and then randomly drawing genotypes as 0, 1, or 2, with probabilities p^2, $2pq$, or q^2, respectively, by assuming Hardy-Weinberg equilibrium. We tested three scenarios in these simulation tests: (1) in V1, we took simulated SBP measurements from V1 only and ignored the following three visits and regressed SBP onto each SNP; (2) in LTA, we averaged the four visits and performed a linear regression of SBP onto each SNP; (3) in a third analysis, using generalized estimating equations (GEEs), we included data from all four visits in a model with an exchangeable correlation structure between the visits. In initial experiments, assuming a sample size of 1,000, we repeated our simulations 10,000 times (with independent sampling of both phenotype and genotype data from their distributions) and computed the proportion of times when a SNP was significantly associated with the trait. To estimate power in a more representative case, such as for the ARIC cohort, we assumed a sample size of 10,000 and repeated the simulations.

Analysis of Signal Enrichment by LTA in Comparison with V1 BP Trait Associations

Using the LTA and V1 association results on the same 46,553 individuals, we used the Kolmogorov-Smirnov (K-S) statistic to compare each region's $-\log_{10}$ p values meeting criteria for genome-wide significance ($p < 5 \times 10^{-8}$) to evaluate whether LTA results showed departure of the association statistics from the distribution of corresponding V1 association statistics. This analysis was performed to compare LTA SBP with V1 SBP and to compare LTA DBP with V1 DBP. Regions with at least one SNP marker with $p < 5 \times 10^{-8}$ in either LTA or V1 analyses were selected for enrichment analysis. Regions were defined by the lead SNP and by the LD-pruned list of SNPs in the region ($r^2 > 0.3$).

Analysis of Expression Quantitative Trait Loci

For the purpose of annotating our findings, we searched for primary SNPs identified in our LTA analyses and LD proxies against a collected database of expression SNP (eSNP) results from several tissues. Using SNAP,[11] we identified alias rsIDs for rs445925. SNAP also helped us identify four further proxy SNPs (rs72654473, rs80125357, rs7412, and rs283810) in LD ($r^2 > 0.5$) in four HapMap builds. SNP rsIDs were searched for primary SNPs and LD proxies against a collected database of eSNP results.[12–60] The collected eSNP results met criteria for statistical thresholds for association with gene transcript levels, as described in the original papers, for several tissues. mRNA quantitative trait loci (QTLs) were also queried for gluteal and abdominal adipose.[12]

Additional expression QTL (eQTL) data were integrated from online sources, including ScanDB, the Broad Institute GTex browser, and the Prichard Lab (see Web Resources). Data on cerebellum, parietal lobe, and liver eQTLs were downloaded from ScanDB; *cis*-eQTLs were limited to those with $p < 1.0 \times 10^{-6}$, and *trans*-eQTLs were limited to those with $p < 5.0 \times 10^{-8}$. The top 1,000 eQTL results were downloaded (on November 26, 2013) from the GTex Browser at the Broad Institute for nine tissues: thyroid, leg skin (sun exposed), tibial nerve, tibial artery, skeletal muscle, lung, heart (left ventricle), whole blood, and subcutaneous adipose.[14] All GTex results had associations with $p < 8.4 \times 10^{-7}$.

Table 1. Summary of Discovery Cohorts, Sample Sizes, and Visits for the LTA Analyses

Cohort	No. of Visits	No. of Individuals	Age at First Visit in Years (SD)	Age at Last Visit in Years (SD)	Mean BMI in kg/m^2 (SD)	Mean SBP in mmHg (SD)	Mean DBP in mmHg (SD)	Antihypertensive Therapy at First Visit	Antihypertensive Therapy at Last Visit
AGES Reykjavik Study	2	526	66.0 (7.0)	78.5 (5.9)	26.2 (3.9)	141.4 (18.8)	82.1 (8.7)	24%	65%
ARIC Study	4	7,310	54.3 (5.7)	63.1 (5.6)	27.0 (4.9)	118.5 (17.0)	71.7 (10.0)	26%	40%
CARDIA	4	1,671	32.6 (3.3)	45.8 (3.4)	25.6 (5.1)	106.3 (11.4)	67.8 (9.5)	0.9%	11%
CHS	4	3,159	72.4 (5.4)	75.3 (5.4)	26.3 (4.5)	138.7 (22.5)	72.2 (11.9)	35%	41%
FHS original cohort	4	660	74.4 (4.5)	85.6 (4.0)	26.7 (4.6)	148.1 (23.5)	72.9 (11.3)	49%	60%
FHS offspring	4	3,235	50.7 (9.8)	61.0 (9.5)	26.8 (4.9)	127.4 (20.0)	79.7 (10.6)	15%	32%
MESA	4	2,414	62.7 (10.2)	66.9 (10.2)	27.7 (5.1)	123.5 (20.5)	70.1 (9.9)	33%	45%
RS 1	4	4,710	67.9 (8.2)	75.5 (6.2)	26.3 (3.6)	140.4 (22.8)	74.9 (11.7)	22%	37%
RS 2	4	1,535	63.7 (2.3)	67.9 (7.2)	27.2 (4.1)	143.4 (21.6)	79.7 (11.1)	21%	30%
WGHS	3	21,409	54.7 (7.0)	65.2 (6.8)	25.9 (4.9)	124.8 (15.4)	77.3 (9.7)	13%	43%

Abbreviations are as follows: AGES, Age, Gene/Environment Susceptibility; ARIC, Atherosclerosis Risk in Communities; BMI, body mass index; CARDIA, Coronary Artery Risk Development in Young Adults; CHS, Cardiovascular Health Study; DBP, diastolic blood pressure; FHS, Framingham Heart Study; MESA, Multi-Ethnic Study of Atherosclerosis; RS, Rotterdam Study; SBP, systolic blood pressure; and WGHS, Women's Genome Health Study.

Results

Longitudinal Analysis of BP

The discovery analyses of LTA BP traits were conducted in a sample size of 46,629 individuals, whose characteristics, including age, sex, and trait summaries, are summarized in Table 1. Our overall study design is shown in Figure S1. By requiring each study participant included in the LTA analyses to have two or more BP measurements, we excluded a total of 8,887 individuals with data at V1 only across the cohorts (Table S1) and consequently analyzed 46,553 individuals for both the LTA and V1 analyses reported. Information on the specific visits included in the LTA analyses is provided in Table S2. Phenotypic correlations were performed in the ARIC cohort on the average LTA and V1 residuals we analyzed (Figure 1) and showed $r > 0.7$ (the V1 measurement was included in the LTA measurement, and thus correlation was expected).

Meta-analysis of GWASs for LTA BP Traits for Discovery of Genetic Associations

When individual cohort results were combined via inverse-variance-weighted meta-analysis, 488 SNP-trait associations at 19 independent loci ($r^2 < 0.3$ between SNPs) reached genome-wide significance ($p < 5 \times 10^{-8}$) (Table 2). Quantile-quantile p value plots are shown in Figure S2, and genomic-control inflation factors (λ_{GC}) ranged from 1.055 to 1.095 for the LTA traits (Table S3) and were comparable for V1 SBP (1.076) and V1 DBP (1.066). The $-\log_{10}$ p value genome-wide association plots for SBP and DBP are shown in Figure 2, and those for MAP and PP are shown in Figure S3. In total, there were 39 trait-locus combinations with at least one genome-wide significant association. We identified 13 loci associated with LTA SBP, ten loci associated with LTA DBP, 11 loci associated with LTA MAP, and five loci associated with LTA PP (all are summarized in Table 2). The complete set of SNPs identified is provided in Table S4. For the purpose of annotating the associations identified in our analyses, index SNPs and proxies were checked for eQTL associations. Some SNPs showed associations with expression levels, including with genes with known BP roles (e.g., *AGT* [MIM 106150] and *NPR3* [MIM 108962]). The loci identified in this analysis, but not previously described, did not show new eQTL associations, suggesting that mechanisms of effect are not mediated through regulation of gene expression. The full results are summarized in Table S5.

Replication Studies

For follow-up, we focused on the five SNP-trait associations that we identified in the LTA analyses but that had not been identified in prior studies of V1 BP (Table 3). We conducted replication analyses of independent samples not studied in the discovery work by using pooled V1 data from 23 GBPG Consortium cohorts—for a total sample size of 34,433 individuals of European ancestry[5]—and 5,605 Han Chinese individuals from PUUMA. Clinical summaries have been previously published for the GBPG Consortium. [5] Clinical summaries for PUUMA are provided in Table S6. We tested the lead SNP from each region identified in our LTA analyses for its association with each corresponding V1 trait and corrected for the number of regions tested (the p value threshold was 0.05 / 1 = 0.05 for LTA SBP, LTA DBP, and LTA MAP and 0.05 / 2 = 0.025 for LTA PP). The GBPG Consortium and PUUMA results were combined in a fixed-effects meta-analysis and demonstrated significant association between chromosomal region 2p23 (*KCNK3* [MIM 603220]) and

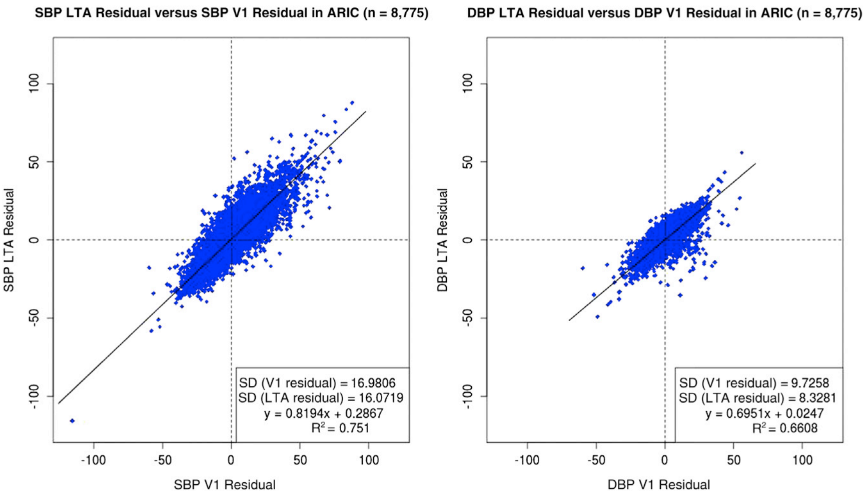

Figure 1. LTA versus V1 SBP and DBP Residuals in the ARIC Cohort
The final averaged residuals for LTA SBP and LTA DBP ($n = 8{,}778$) are plotted on the y axis against the corresponding V1 SBP and V1 DBP residuals on the x axis.

both MAP ($p = 0.0091$) and SBP ($p = 0.0079$) and between chromosomal region 6p21 (*CRIP3*) and PP ($p = 0.0041$), all of which met the Bonferroni-corrected threshold (Table 4). A nominal association ($p < 0.05$) was noted between region 7p13 (*IGFBP3* [MIM 146732]) and PP (Table 4). In the individual replication groups, we observed positive replication for two SNP-trait associations in the GBPG Consortium V1 replication analyses ($p = 0.030$ between chromosomal region 2p23 [*KCNK3*] and SBP and $p = 0.0067$ between region 6p21 [*CRIP3*] and PP). In two of the remaining loci, there was a nonsignificant trend ($p < 0.10$) of association (between 2p23 [*KCNK3*] and MAP and between 7p13 [*IGFBP3*] and PP). In the PUUMA study, replication was observed for the association between chromosome region 2p23 (*KCNK3*) and MAP ($p = 0.0079$). Plots of the –log p value for these regions are shown in Figure S6.

To assess overall rates of replication, including for known signals, in the GBPG Consortium V1 data, we assessed the associations for all SNPs where the LTA association analyses provided $p < 5.0 \times 10^{-7}$ (213 SNPs for LTA SBP, 186 SNPs for LTA DBP, 273 SNPs for LTA MAP, and 225 SNPs for LTA PP). In the analysis of these top SNPs, we reproduced associations ($p < 5 \times 10^{-7}$) in the GBPG Consortium V1 data for 13/16 DBP-associated loci, 14/18 SBP-associated loci, 15/18 MAP-associated loci, and seven PP-associated loci (Table S7). Restricting testing to the loci with genome-wide significant association results in the LTA analyses and association p values $< 5 \times 10^{-8}$ resulted in reproduction of associations at 11/13 SBP-associated loci, 8/10 DBP-associated loci, 9/11 MAP-associated loci, and 4/4 PP-associated loci (Table S7). Thus, the overall replication rates in this analysis were 83% (49/59) and 84% (32/38) for $p < 5 \times 10^{-7}$ and $p < 5 \times 10^{-8}$, respectively.

Comparing LTA and V1 BP Association Patterns to Evaluate the Impact of LTA

Using exactly the same samples and genotypes as in the discovery LTA analyses, we conducted a secondary analysis of V1 BP traits for the purpose of characterizing the difference between LTA BP and V1 BP associations. Overall, we identified more loci meeting genome-wide significance thresholds in the LTA analyses than in the V1 analyses. In the LTA analyses, we observed 488 SNP-trait associations with $p < 5 \times 10^{-8}$ in 19 loci (117 for LTA SBP, 96 for LTA DBP, 155 for LTA MAP, and 120 for LTA PP); in the corresponding V1 analyses, we observed 402 SNP-trait associations with $p < 5 \times 10^{-8}$ (122 for V1 SBP, 126 for V1 DBP, 153 for V1 MAP, and 1 for V1 PP) (Figure S4). At the p value threshold of 5×10^{-7}, we identified 897 SNP-trait associations in the LTA analyses (213 for LTA SBP, 186 for LTA DBP, 273 for LTA MAP, and 225 for LTA PP) and 570 SNP-trait associations in the V1 analyses (163 for V1 SBP, 182 for V1 DBP, 222 for V1 MAP, and 3 for V1 PP) (Table S8). Overall, these data show that the LTA analyses yielded a greater number of significant associations. The V1 results in the same samples as the LTA analyses are shown for the top LTA loci in Table 5; they show a large degree of concordance in both analyses but a greater yield from the LTA analyses.

To further evaluate the impact of LTA, we performed additional comparisons between the LTA and V1 BP association statistics by focusing on SBP and DBP results only. Comparisons of beta estimates, SEs, and chi-square values demonstrated the impact of averaging on the SE of the phenotypic estimate (Figure S5). Correlations between the genome-wide LTA and V1 association statistics were high; the correlations of standardized effect estimates were $r^2 = 0.82$ for SBP and $r^2 = 0.80$ for DBP. When restricted to the sentinel SNP-trait associations for SBP (13 SNPs) and DBP (ten SNPs), the correlations of the beta estimates were higher at $r^2 = 0.99$ for both SBP and DBP.

In comparisons of the LTA and V1 association results, the p values for LTA SBP and LTA DBP summary results were generally lower than the corresponding V1 results (Table 5). However, in some regions, the association p values were lower in the V1 analyses, demonstrating that LTA might not enrich association signals in all genomic regions. We assessed the distribution of the lead LTA-identified SNPs ($p < 5 \times 10^{-8}$) across all loci by comparing the number of SNPs found at the tails of the ranked p value distribution for each trait in the LTA and V1 analyses. In each of the four traits, there was substantial enrichment of signals at the tails of the p value distribution in the LTA analyses (Table S9).

Table 2. Summary of LTA Discovery Analyses for Loci with SNP-Trait Association p Values $< 5 \times 10^{-8}$

SNP ID	Allele	Chr	Position	In Gene	Closest Gene	Genes in LD Block	Beta	SE	p Value
LTA DBP									
rs13306561	a	1	11,788,391	*MTHFR*	*MTHFR*	*NPPA-AS1, CLCN6, MTHFR, NPPA*	0.48	0.07	2.08×10^{-10}
rs2004776	t	1	228,915,325	*AGT*	*AGT*	*AGT*	0.35	0.06	3.20×10^{-8}
rs7599598[a]	a	2	96,715,567	*FER1L5*	*FER1L5*	*FER1L5*	–0.31	0.05	2.91×10^{-8}
rs198823	t	6	26,230,912	NA	*HIST1H2BC*	*HIST1H1T, HIST1H4A, HIST1H2BB, HIST1H3C, HIST1H3A, HIST1H2BC, TRIM38, HFE, HIST1H2AB, HIST1H2AC, HIST1H3B, HIST1H4B, HIST1H4C, HIST1H1A, HIST1H1C*	–0.33	0.06	6.57×10^{-9}
rs12258967	c	10	18,767,965	*CACNB2*	*CACNB2*	*CACNB2*	0.35	0.06	2.48×10^{-9}
rs12244842	t	10	63,109,192	*C10orf107*	*C10orf107*	*C10orf107*	–0.38	0.06	7.05×10^{-9}
rs2681472	a	12	88,533,090	*ATP2B1*	*ATP2B1*	*ATP2B1, LOC338758*	0.52	0.07	4.01×10^{-13}
rs3184504	t	12	110,368,991	*SH2B3*	*SH2B3*	*TRAFD1, PTPN11, RPL6, ALDH2, ATXN2, TMEM116, ERP29, MAPKAPK5, ADAM1, SH2B3, C12orf51, C12orf47, NAA25, ACAD10, BRAP*	0.39	0.05	6.08×10^{-13}
rs1133323	t	15	72,999,278	NA	*COX5A*	*CSK, CPLX3, COX5A, SCAMP2, C15orf17, MPI, ULK3, LMAN1L, MIR4513*	–0.33	0.05	2.66×10^{-9}
rs6092743	a	20	57,133,765	NA	*C20orf174*	NA	0.50	0.08	1.11×10^{-8}
LTA SBP									
rs880315	t	1	10,719,453	*CASZ1*	*CASZ1*	*MTOR, C1orf127, TARDBP, EXOSC10, C1orf187, FBXO2, FBXO6, MAD2L2, MTHFR, FBXO44, SRM, PTCHD2, MASP2, UBIAD1, CASZ1, ANGPTL7, AGTRAP*	–0.71	0.10	7.98×10^{-12}
rs13306561	a	1	11,788,391	*MTHFR*	*MTHFR*	*NPPB, NPPA-AS1, CLCN6, MTHFR, NPPA*	0.88	0.12	6.38×10^{-12}
rs1275988[a]	t	2	26,767,868	NA	*KCNK3*	*KCNK3*	–0.60	0.09	2.61×10^{-10}
rs6712094	a	2	164,751,706	NA	*GRB14*	NA	0.60	0.10	9.89×10^{-9}
rs7733331	t	5	32,864,603	NA	*C5orf23*	*NPR3*	–0.55	0.09	5.38×10^{-9}
rs12705390	a	7	106,198,013	NA	*PIK3CG*	NA	0.63	0.11	3.17×10^{-8}
rs12258967	c	10	18,767,965	*CACNB2*	*CACNB2*	*CACNB2*	0.63	0.10	4.53×10^{-10}
rs7070797	a	10	63,221,779	NA	*C10orf107*	*C10orf107*	–0.74	0.13	4.30×10^{-8}
rs2681472	a	12	88,533,090	*ATP2B1*	*ATP2B1*	*ATP2B1, LOC338758*	0.95	0.12	1.04×10^{-14}
rs4766578	a	12	110,388,754	*ATXN2*	*ATXN2*	*TRAFD1, PTPN11, RPL6, ALDH2, ATXN2, TMEM116, ERP29, MAPKAPK5, ADAM1, SH2B3, C12orf51, C12orf47, NAA25, ACAD10, BRAP*	–0.56	0.09	2.82×10^{-9}
rs35444	a	12	114,036,820	NA	*TBX3*	NA	0.55	0.09	1.47×10^{-8}
rs11072518	t	15	73,021,663	NA	*COX5A*	*CSK, CPLX3, COX5A, SCAMP2, C15orf17, CYP1A2, MPI, ULK3, LMAN1L, MIR4513*	0.57	0.09	6.54×10^{-9}
rs6092743	a	20	57,133,765	NA	*C20orf174*	NA	0.84	0.14	2.25×10^{-8}
LTA MAP									
rs880315	t	1	10,719,453	*CASZ1*	*CASZ1*	*CASZ1*	–0.46	0.07	5.49×10^{-11}
rs13306561	a	1	11,788,391	*MTHFR*	*MTHFR*	*NPPB, NPPA-AS1, CLCN6, MTHFR, NPPA*	0.61	0.08	1.83×10^{-12}
rs2004776	t	1	228,915,325	*AGT*	*AGT*	*AGT*	0.42	0.07	1.18×10^{-8}
rs1275988[a]	t	2	26,767,868	NA	*KCNK3*	*KCNK3*	–0.39	0.06	1.51×10^{-9}
rs12258967	c	10	18,767,965	*CACNB2*	*CACNB2*	*CACNB2*	0.45	0.07	4.98×10^{-11}
rs2166122	t	10	63,193,080	*C10orf107*	*C10orf107*	*C10orf107*	–0.48	0.08	1.88×10^{-9}
rs2681472	a	12	88,533,090	*ATP2B1*	*ATP2B1*	*ATP2B1, LOC338758*	0.69	0.08	1.77×10^{-16}

(*Continued on next page*)

Table 2. ***Continued***

SNP ID	Allele	Chr	Position	In Gene	Closest Gene	Genes in LD Block	Beta	SE	p Value
rs3184504	t	12	110,368,991	*SH2B3*	*SH2B3*	*CUX2, FAM109A, TRAFD1, PTPN11, RPL6, ALDH2, ATXN2, TMEM116, ERP29, MAPKAPK5, ADAM1, SH2B3, C12orf51, C12orf47, NAA25, ACAD10, BRAP*	0.45	0.06	1.68×10^{-12}
rs35444	a	12	114,036,820	NA	*TBX3*	NA	0.36	0.06	3.20×10^{-8}
rs11072518	t	15	73,021,663	NA	*COX5A*	*CSK, CPLX3, COX5A, SCAMP2, C15orf17, CYP1A2, MPI, ULK3, LMAN1L, MIR4513*	0.43	0.06	8.95×10^{-11}
rs6092743	a	20	57,133,765	NA	*C20orf174*	NA	0.64	0.10	3.60×10^{-10}
LTA PP									
rs880315	t	1	10,719,453	*CASZ1*	*CASZ1*	*CASZ1*	−0.42	0.07	5.45×10^{-9}
rs7650227	t	3	41,769,941	*ULK4*	*ULK4*	*ULK4*	0.50	0.08	2.84×10^{-9}
rs10948071[a]	t	6	43,388,691	NA	*CRIP3*	*CRIP3, SLC22A7, ZNF318*	−0.38	0.07	9.06×10^{-9}
rs2949837[a]	a	7	45,960,903	NA	*IGFBP3*	NA	0.40	0.07	2.94×10^{-8}
rs12705390	a	7	106,198,013	NA	*PIK3CG*	NA	0.59	0.08	5.40×10^{-14}

Abbreviations are as follows: Chr, chromosome; DBP, diastolic blood pressure; LTA, long-term average; MAP, mean arterial pressure; NA, not available; PP, pulse pressure; and SBP, systolic blood pressure.

[a] BP-associated loci found in our LTA analyses.

To study the general magnitude of the effect of LTA on the statistical power to detect SNP associations, we carried out a set of simulation experiments. Correlations of SBP and DBP across the four visits included in the ARIC analysis ranged from r = 0.60 to r = 0.73 (Table S10A). Using unstructured correlation structures resulted in similar estimates (data not shown). The simulations showed that LTA increases power by about 20% in most cases (Tables S10B and S10C). It can be a much larger increase if the initial power is very low. GEEs do not improve power over LTA by any significant amount. By comparison, our LTA results are largely consistent with the simulation results.

The simulation results are corroborated by the comparison of our LTA and V1 results: compared with V1 analyses, LTA analyses identified 17 additional trait-locus associations (two with DBP, seven with SBP, three with MAP, and five with PP, for a total of nine additional independent loci).

Enrichment Analysis

To further examine the extent of signal enrichment by LTA and to characterize regions with a lack of enrichment by LTA, we conducted a number of analyses. First, we plotted the V1 and LTA association statistics for all regions identified by either the LTA or the V1 analyses. Chromosomal region 12q21 (*ATP2B1*), which shows the strongest GWAS association signal for BP to date, and region 2p23 (*KCNK3*), which demonstrated enrichment of the association signal in our study, are shown in Figure 3; all other loci are shown in Figure S7. We also aligned LTA and V1 results for each region and calculated the K-S statistic for each region (Figures S8 and S9) and found that evidence of enrichment by the LTA procedure was specific to 21 trait-locus associations and that a significant lack of enrichment, or stronger V1 association signal, was a clear pattern noted at eight other trait-locus associations. One region showed mixed effects: some SNP associations were enriched by LTA, and some were significantly stronger in the V1 analyses (chromosomal region 3p22, *ULK4*). In 15 regions, the results were not significantly enriched in either the LTA or the V1 analyses (Table S11). Specifically, we identified enrichment by LTA in six regions for SBP (chromosome 1 near *MTHFR* [MIM 607093], chromosome 2 near *KCNK3*, chromosome 2 near *GRB14* [MIM 601524], chromosome 5 near *C5orf23*, chromosome 7 near *PIK3CG* [MIM 601232], and chromosome 10 near *C10orf107*); in four regions for DBP (chromosome 1 in *MTHFR*, chromosome 5 near *EBF1* [MIM 164343], chromosome 6 near *HFE* [MIM 613609], and chromosome 12 in *SH2B3* [MIM 605093]); in four regions for MAP (chromosome 1 in *CASZ1* [MIM 609895], chromosome 1 in *MTHFR*, chromosome 2 near *KCNK3*, and chromosome 12 in *ATP2B1* [MIM 108731]); and in three regions for PP (chromosome 6 near *CRIP3*, chromosome 7 near *IGFBP3*, and chromosome 7 near *PIK3CG*).

Discussion

This study was designed to assess the effect of utilizing LTA of BP traits, from longitudinal measures, to detect genetic associations. The motivation for our analyses was to use a procedure that would reduce measurement errors and other variation sources that lower the statistical power of the analysis. In our LTA analyses, we discovered 39 trait-variant associations and uniquely identified four loci (2p23 [near *KCNK3*] for SBP and MAP, 2q11.2 [in *FER1L5*] for DBP, 6p21 [near *CRIP3*] for PP, and 7p13 [near *IGFBP3*] for PP). Replication testing in 34,433

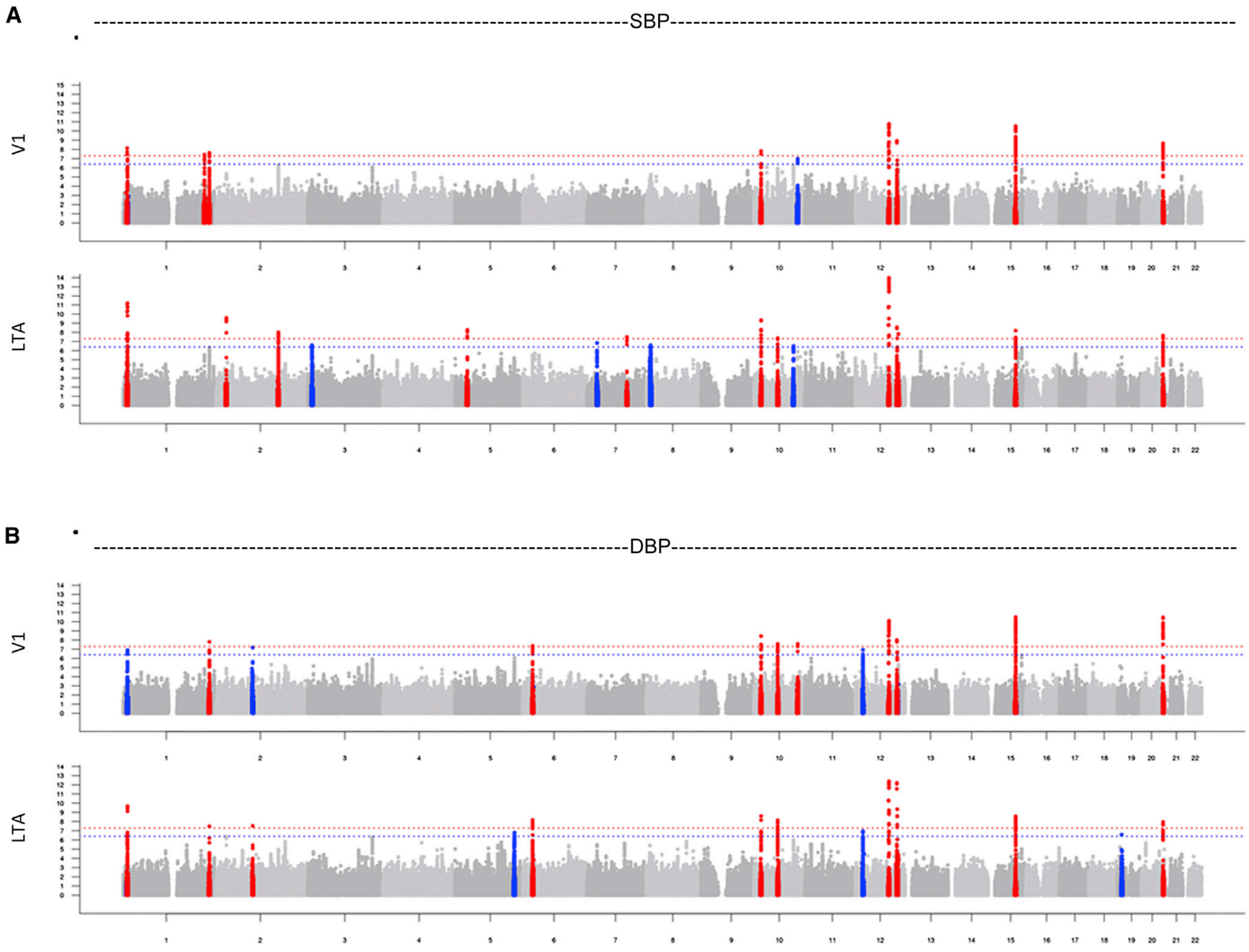

Figure 2. GWASs: –Log p Plots for LTA and V1 SBP and DBP Analyses
GWAS –log p plots compare (A) LTA SBP and V1 SBP and (B) LTA DBP and V1 DBP. Regions containing one or more SNPs with $p < 5 \times 10^{-8}$ are in red, and suggestive associations ($p < 5 \times 10^{-7}$) are shown in blue.

independent European-ancestry samples and 5,600 Chinese-ancestry samples with V1 BP data definitively confirmed these associations at two (*KCNK3* and*CRIP3*) of the four discovered loci, and these were carried forward to replication analyses. At *IGFBP3*, we found a nominal association not meeting statistical significance after adjustment for multiple-hypothesis testing. When we compared LTA and V1 associations in the same group of individuals, we observed that in some loci, the p values of LTA traits were two orders of magnitude lower than the corresponding V1 BP traits. Overall, we demonstrated enrichment of association signals with LTA by detecting a larger number of SNPs and loci. Through computer simulations, we estimated this increase in statistical power by LTA to be ~20%, consistent with the results of our analyses of BP data.

Several sources of variability of BP affect the ability to detect genetic associations. First, there is physiologic, intraindividual variability following both diurnal patterns and longer-term and less predictable patterns as a result of individual-specific factors, such as changes in dietary intake of sodium. Second, there is variation in BP measurement as a result of imprecise measurement techniques and biases such as digit preference.[61] Noise in the measurement of a quantitative trait adversely affects power to detect association signals, essentially by increasing the variance of the trait, and the study of BP in particular has been a notable example in which phenotypic imprecision has hampered our ability to detect alleles.[62] Examples of this impact are also available in clinical pathology, where the variance for analysis measurements can be high for specific analyses, and when up to 20% of the variance derives from intraindividual variation and measurement error, this can result in a 15%–20% loss in power to detect statistical associations.[63] Averaging has been studied in a number of epidemiologic applications, to BP and other continuous traits characterized by variability, where it can improve parameter estimation.[64–67]

We examined the statistical properties of the LTA procedure, and although it is a relatively simple procedure,

Table 3. Loci with SNP-Trait Association p Values $< 5 \times 10^{-8}$ from LTA Discovery Analyses

Trait	SNP ID	Allele	Locus	Position	Closest Gene	Beta	SE	p Value
LTA DBP	rs7599598	a	2q11	96715567	*FER1L5*	−0.31	0.05	2.91×10^{-8}
LTA SBP	rs1275988	t	2p23	26767868	*KCNK3*	−0.60	0.09	2.61×10^{-10}
LTA MAP	rs1275988	t	2p23	26767868	*KCNK3*	−0.39	0.06	1.51×10^{-9}
LTA PP	rs10948071	t	6p21	43388691	*CRIP3*	−0.38	0.07	9.06×10^{-9}
LTA PP	rs2949837	a	7p13	45960903	*IGFBP3*	0.40	0.07	2.94×10^{-8}

Abbreviations are as follows: DBP, diastolic blood pressure; MAP, mean arterial pressure; LTA, long-term average; PP, pulse pressure; and SBP, systolic blood pressure.

there are several important implications of our results. First, LTA is expected to describe a more accurate estimate of an individual's long-term BP value. We averaged two, three, or four visits—not the maximum number of available measurements, which could have been up to 15 visits in some cohorts—in order to keep phenotypic SEs generally comparable across the cohorts we studied. Other age-related trends, such as changes in body mass index (BMI), were accounted for in the visit-specific adjustment of BP traits by BMI at the corresponding visit. In published V1 BP association studies, finding associations for DBP has been more challenging, and there have generally been fewer findings for DBP than for SBP. Our results show a similar trend.

The overall improvement in power with LTA has important implications for study design in genetic association studies. For traits with few extraneous sources of "noise," such as height, weight, or blood analyses measured with standardized clinical assays (such as lipid and hematology traits), GWASs have generally been fruitful in that they yield many positive associations explaining up to ~10% of the phenotypic variance of these continuous traits. In the case of traits with many and varied sources of noise, such as BP, measures to improve phenotypic accuracy help identify additional loci. Typically, increasing sample size is the key strategy to increase statistical power, and this has been done widely in GWASs to detect associations with modest effect sizes. However, in the GWAS and meta-analysis approach, inclusion of additional cohorts to a meta-analysis might increase potential phenotypic and genetic variability, which cannot be adequately corrected for in the analysis. Our results demonstrate that trait averaging is a practical way to increase statistical power for quantitative phenotypes with substantial variability, such as BP, in population cohorts with longitudinal BP data. One surprising finding was that some of the associations identified in the V1 analyses were not detected in the LTA analyses, and in specific regions, the V1 analyses yielded stronger significance. A statistical hypothesis for this finding is regression to the mean, or winner's curse, in the LTA analyses. Biologic hypotheses include possible physiologic intraindividual sources of variation, such as the known circadian pattern of BP, or variation of clinical relevance for which mechanisms are not known.[68] As such, we recommend utilizing LTA to improve the precision of highly variable continuous traits for which measurement error or uncertainty is known. Further, we recommend considering concurrent analysis of LTA and single measurement of traits and an evaluation of any of the differences between the two sets of results for possible insights into the mechanism of the genetic association.

LTA can also capture additional useful information. LTA BP is a clinically relevant phenotype and is associated with cardiovascular disease (CVD) events and target organ damage, an intermediate phenotype for subsequent CVD events.[64,69] Although single "casual" BP measurements in

Table 4. Reproducibility-Analysis Association Results in the GBPG Consortium and PUUMA V1 BP Analyses

			GBPG Consortium V1 BP Association Results			PUUMA V1 BP Association Results			Meta-analysis of GBPG Consortium and PUUMA V1 BP Association Results		
Trait	SNP ID	Closest Gene	Beta	SE	p Value	Beta	SE	p Value	Beta	SE	p Value
V1 DBP	rs7599598	*FER1L5*	−0.04	0.08	6.14×10^{-1}	0.001	0.21	9.95×10^{-1}	−0.03	0.07	6.40×10^{-1}
V1 SBP	rs1275988[a]	*KCNK3*	−0.26	0.12	2.98×10^{-2}	−0.79	0.39	4.54×10^{-2}	−0.30	0.11	7.93×10^{-3}
V1 MAP	rs1275988[a]	*KCNK3*	−0.16	0.08	5.68×10^{-2}	−0.72	0.27	7.85×10^{-3}	−0.21	0.08	9.08×10^{-3}
V1 PP	rs10948071[a]	*CRIP3*	−0.24	0.09	6.69×10^{-3}	−0.25	0.27	3.56×10^{-1}	−0.24	0.08	4.17×10^{-3}
V1 PP	rs2949837	*IGFBP3*	0.15	0.09	9.96×10^{-2}	0.34	0.26	1.94×10^{-1}	0.17	0.09	4.68×10^{-2}

Abbreviations are as follows: BP, blood pressure; DBP, diastolic blood pressure; GBPG, Global Blood Pressure Genetics; MAP, mean arterial pressure; PP, pulse pressure; PUUMA, Peking University – University of Michigan Study of Atherosclerosis; SBP, systolic blood pressure; and V1, visit 1.

[a] Loci meeting a Bonferroni-corrected replication threshold.

Table 5. The LTA Lead SNPs Were Investigated in the V1 Analysis of the Same Cohorts and Study Participants

					LTA BP Results in Discovery Samples				V1 BP Results in LTA Discovery Samples				LTA-V1 Differences	
SNP ID	Allele	Chr	Position	Closest Gene	Trait	Beta	SE	p Value	Trait	Beta	SE	p Value	Δ Beta	Δ p Value
rs880315	t	1	10,719,453	*CASZ1*	LTA SBP	−0.71	0.10	7.98×10^{-12}	V1 SBP	−0.68	0.11	7.20×10^{-9}	3.05×10^{-2}	-7.19×10^{-9}
rs13306561	a	1	11,788,391	*MTHFR*	LTA SBP	0.88	0.12	6.38×10^{-12}	V1 SBP	0.76	0.14	1.11×10^{-7}	-1.21×10^{-1}	-1.11×10^{-7}
rs1275988	t	2	26,767,868	*KCNK3*	LTA SBP	−0.60	0.09	2.61×10^{-10}	V1 SBP	−0.47	0.10	1.38×10^{-5}	1.33×10^{-1}	-1.38×10^{-5}
rs6712094	a	2	164,751,706	*GRB14*	LTA SBP	0.60	0.10	9.89×10^{-9}	V1 SBP	0.58	0.11	5.22×10^{-7}	-1.49×10^{-2}	-5.12×10^{-7}
rs7733331	t	5	32,864,603	*C5orf23*	LTA SBP	−0.55	0.09	5.38×10^{-9}	V1 SBP	−0.41	0.10	1.41×10^{-4}	1.46×10^{-1}	-1.41×10^{-4}
rs12705390	a	7	106,198,013	*PIK3CG*	LTA SBP	0.63	0.11	3.17×10^{-8}	V1 SBP	0.54	0.12	2.63×10^{-5}	-8.91×10^{-2}	-2.62×10^{-5}
rs12258967	c	10	18,767,965	*CACNB2*	LTA SBP	0.63	0.10	4.53×10^{-10}	V1 SBP	0.64	0.11	1.53×10^{-8}	1.04×10^{-2}	-1.48×10^{-8}
rs7070797	a	10	63,221,779	*C10orf107*	LTA SBP	−0.74	0.13	4.30×10^{-8}	V1 SBP	−0.73	0.14	1.17×10^{-6}	1.58×10^{-2}	-1.12×10^{-6}
rs2681472	a	12	88,533,090	*ATP2B1*	LTA SBP	0.95	0.12	1.04×10^{-14}	V1 SBP	0.93	0.13	1.69×10^{-11}	-1.65×10^{-2}	-1.69×10^{-11}
rs4766578	a	12	110,388,754	*ATXN2*	LTA SBP	−0.56	0.09	2.82×10^{-9}	V1 SBP	−0.65	0.10	1.18×10^{-9}	-9.01×10^{-2}	1.64×10^{-9}
rs35444	a	12	114,036,820	*TBX3*	LTA SBP	0.55	0.09	1.47×10^{-8}	V1 SBP	0.51	0.11	2.63×10^{-6}	-3.03×10^{-2}	-2.61×10^{-6}
rs11072518	t	15	73,021,663	*COX5A*	LTA SBP	0.57	0.09	6.54×10^{-9}	V1 SBP	0.73	0.11	2.93×10^{-11}	1.61×10^{-1}	6.52×10^{-9}
rs6092743	a	20	57,133,765	*C20orf174*	LTA SBP	0.84	0.14	2.25×10^{-8}	V1 SBP	1.01	0.16	2.18×10^{-9}	1.66×10^{-1}	2.03×10^{-8}
rs13306561	a	1	11,788,391	*MTHFR*	LTA DBP	0.48	0.07	2.08×10^{-10}	V1 DBP	0.48	0.09	1.28×10^{-7}	2.50×10^{-3}	-1.28×10^{-7}
rs2004776	t	1	228,915,325	*AGT*	LTA DBP	0.35	0.06	3.20×10^{-8}	V1 DBP	0.44	0.07	1.53×10^{-8}	8.31×10^{-2}	1.67×10^{-8}
rs7599598	a	2	96,715,567	*FER1L5*	LTA DBP	−0.31	0.05	2.91×10^{-8}	V1 DBP	−0.37	0.07	6.54×10^{-8}	-5.75×10^{-2}	-3.63×10^{-8}
rs198823	t	6	26,230,912	*HFE*	LTA DBP	−0.33	0.06	6.57×10^{-9}	V1 DBP	−0.32	0.07	4.52×10^{-6}	1.51×10^{-2}	-4.51×10^{-6}
rs12258967	c	10	18,767,965	*CACNB2*	LTA DBP	0.35	0.06	2.48×10^{-9}	V1 DBP	0.43	0.07	3.71×10^{-9}	7.05×10^{-2}	-1.23×10^{-9}
rs12244842	t	10	63,109,192	*C10orf107*	LTA DBP	−0.38	0.06	7.05×10^{-9}	V1 DBP	−0.43	0.08	6.15×10^{-8}	-4.89×10^{-2}	-5.45×10^{-8}
rs2681472	a	12	88,533,090	*ATP2B1*	LTA DBP	0.52	0.07	4.01×10^{-13}	V1 DBP	0.58	0.09	8.68×10^{-11}	5.52×10^{-2}	-8.64×10^{-11}
rs3184504	t	12	110,368,991	*SH2B3*	LTA DBP	0.39	0.05	6.08×10^{-13}	V1 DBP	0.39	0.07	1.26×10^{-8}	-7.50×10^{-3}	-1.26×10^{-8}
rs1133323	t	15	72,999,278	*COX5A*	LTA DBP	−0.33	0.05	2.66×10^{-9}	V1 DBP	−0.42	0.07	4.89×10^{-10}	-9.57×10^{-2}	2.17×10^{-9}
rs6092743	a	20	57,133,765	*C20orf174*	LTA DBP	0.50	0.08	1.11×10^{-8}	V1 DBP	0.71	0.10	3.37×10^{-11}	2.04×10^{-1}	1.11×10^{-8}
rs880315	t	1	10,719,453	*CASZ1*	LTA MAP	−0.46	0.07	5.49×10^{-11}	V1 MAP	−0.43	0.08	1.47×10^{-7}	2.86×10^{-2}	-1.47×10^{-7}
rs13306561	a	1	11,788,391	*MTHFR*	LTA MAP	0.61	0.08	1.83×10^{-12}	V1 MAP	0.57	0.10	1.48×10^{-8}	-3.94×10^{-2}	-1.48×10^{-8}
rs2004776	t	1	228,915,325	*AGT*	LTA MAP	0.42	0.07	1.18×10^{-8}	V1 MAP	0.51	0.08	2.45×10^{-9}	8.91×10^{-2}	9.33×10^{-9}
rs1275988	t	2	26,767,868	*KCNK3*	LTA MAP	−0.39	0.06	1.51×10^{-9}	V1 MAP	−0.34	0.07	7.06×10^{-6}	4.63×10^{-2}	-7.06×10^{-6}
rs12258967	c	10	18,767,965	*CACNB2*	LTA MAP	0.45	0.07	4.98×10^{-11}	V1 MAP	0.50	0.08	5.57×10^{-10}	4.52×10^{-2}	-5.07×10^{-10}

(*Continued on next page*)

Table 5. *Continued*

SNP ID	Allele	Chr	Position	Closest Gene	LTA BP Results in Discovery Samples				V1 BP Results in LTA Discovery Samples				LTA-V1 Differences	
					Trait	Beta	SE	p Value	Trait	Beta	SE	p Value	Δ Beta	Δ p Value
rs2166122	t	10	63,193,080	*C10orf107*	LTA MAP	−0.48	0.08	1.88×10^{-9}	V1 MAP	−0.50	0.09	4.76×10^{-8}	-2.38×10^{-2}	-4.57×10^{-8}
rs2681472	a	12	88,533,090	*ATP2B1*	LTA MAP	0.69	0.08	1.77×10^{-16}	V1 MAP	0.70	0.09	1.70×10^{-12}	9.17×10^{-3}	-1.70×10^{-12}
rs3184504	t	12	110,368,991	*SH2B3*	LTA MAP	0.45	0.06	1.68×10^{-12}	V1 MAP	0.47	0.07	3.71×10^{-10}	2.50×10^{-2}	-3.69×10^{-10}
rs35444	a	12	114,036,820	*TBX3*	LTA MAP	0.36	0.06	3.20×10^{-8}	V1 MAP	0.38	0.08	8.38×10^{-7}	2.16×10^{-2}	-8.06×10^{-7}
rs11072518	t	15	73,021,663	*COX5A*	LTA MAP	0.43	0.06	8.95×10^{-11}	V1 MAP	0.55	0.07	1.86×10^{-12}	1.15×10^{-1}	8.76×10^{-11}
rs6092743	a	20	57,133,765	*C20orf174*	LTA MAP	0.64	0.10	3.60×10^{-10}	V1 MAP	0.81	0.11	1.12×10^{-11}	1.69×10^{-1}	3.49×10^{-10}
rs880315	t	1	10,719,453	*CASZ1*	LTA PP	−0.42	0.07	5.45×10^{-9}	V1 PP	−0.38	0.08	3.31×10^{-6}	4.46×10^{-2}	-3.31×10^{-6}
rs7650227	t	3	41,769,941	*ULK4*	LTA PP	0.50	0.08	2.84×10^{-9}	V1 PP	0.43	0.09	4.38×10^{-6}	-6.71×10^{-2}	-4.38×10^{-6}
rs10948071	t	6	43,388,691	*CRIP3*	LTA PP	−0.38	0.07	9.06×10^{-9}	V1 PP	−0.29	0.07	1.11×10^{-4}	9.49×10^{-2}	-1.11×10^{-4}
rs2949837	a	7	45,960,903	*IGFBP3*	LTA PP	0.40	0.07	2.94×10^{-8}	V1 PP	0.36	0.08	6.88×10^{-6}	-3.79×10^{-2}	-6.85×10^{-6}
rs12705390	a	7	106,198,013	*PIK3CG*	LTA PP	0.59	0.08	5.40×10^{-14}	V1 PP	0.43	0.09	1.20×10^{-6}	-1.59×10^{-1}	-1.20×10^{-6}

Abbreviations are as follows: BP, blood pressure; Chr, chromosome; DBP, diastolic blood pressure; MAP, mean arterial pressure; LTA, long-term average; PP, pulse pressure; SBP, systolic blood pressure; and V1, visit 1.

a population predict CVD,[70] LTA BP, also referred to as "usual" BP, has been shown to be an important predictor of risk for future CVD events beyond single-measurement BP levels.[71] In the clinical setting, treatment for high BP is typically recommended on the basis of repeated observations of elevated BP rather than a single elevated BP measurement, given the known variability and the finding that casual BP measurements might not reliably predict hypertension.[61,72–75] Although precision of the BP estimate is improved, as we have demonstrated here, LTA has the potential to discard information and thus diminish signals by averaging as well. BP variability is also associated with CVD risk, and the finding of decreased association of signals previously linked to CVD risk (such as the 10p12 locus[2]) in the LTA analyses suggests that the relationship between our findings and CVD risk might be imparted through different mechanisms. This hypothesis would need to be formally tested through further hypothesis-driven laboratory experiments.

For the purposes of testing replication of our LTA findings, we conducted follow-up analyses in a set of GBPG Consortium and PUUMA cohorts not analyzed in the LTA analyses. However, these analyses were conducted with V1 BP results rather than LTA BP phenotypes. Also, the GBPG Consortium included a larger number of cohorts (17) in the replication testing than in the LTA discovery phase, increasing the potential variation in effect size across samples. Regardless, we confirmed association with V1 BP traits in three of our four regions tested for replication in samples of diverse ethnicity. The traits we report are highly correlated, and we take the set of associations we identified as determinants of BP traits in the general population. We compared the results of the analyses of LTA SBP and LTA DBP to the published findings of the International Consortium for Blood Pressure (ICBP), which is currently the largest GWAS and meta-analysis in individuals of European ancestry ($n = 69{,}395$).[2] At a significance threshold of $p < 5 \times 10^{-8}$ in the analyses of LTA SBP and LTA DBP, we found 19 loci uniquely identified in the ICBP analysis (but not in our LTA analyses), ten loci identified by both the ICBP and LTA BP analyses, and six loci uniquely identified in the LTA BP analyses. Because the ICBP analysis also included the majority of the cohorts in our LTA analyses, concordance of many loci was expected.

We identified four loci in the LTA discovery analyses. We found an intergenic variant in high LD with SNPs extending into *KCNK3* (also known as *TASK1*), which encodes a potassium channel, to be associated with LTA SBP and LTA MAP. Exome sequencing studies have shown that rare missense alleles in *KCNK3* cause familial forms of pulmonary hypertension.[76] Mice null for *Task1* show lower SBP and have a defect in adrenal gland depolarization and fail to suppress aldosterone in response to increased dietary sodium load.[77] We analyzed the data presented in a previously published report of MAP measured invasively in four *Task1*-null mice and six wild-type littermate mice[78]

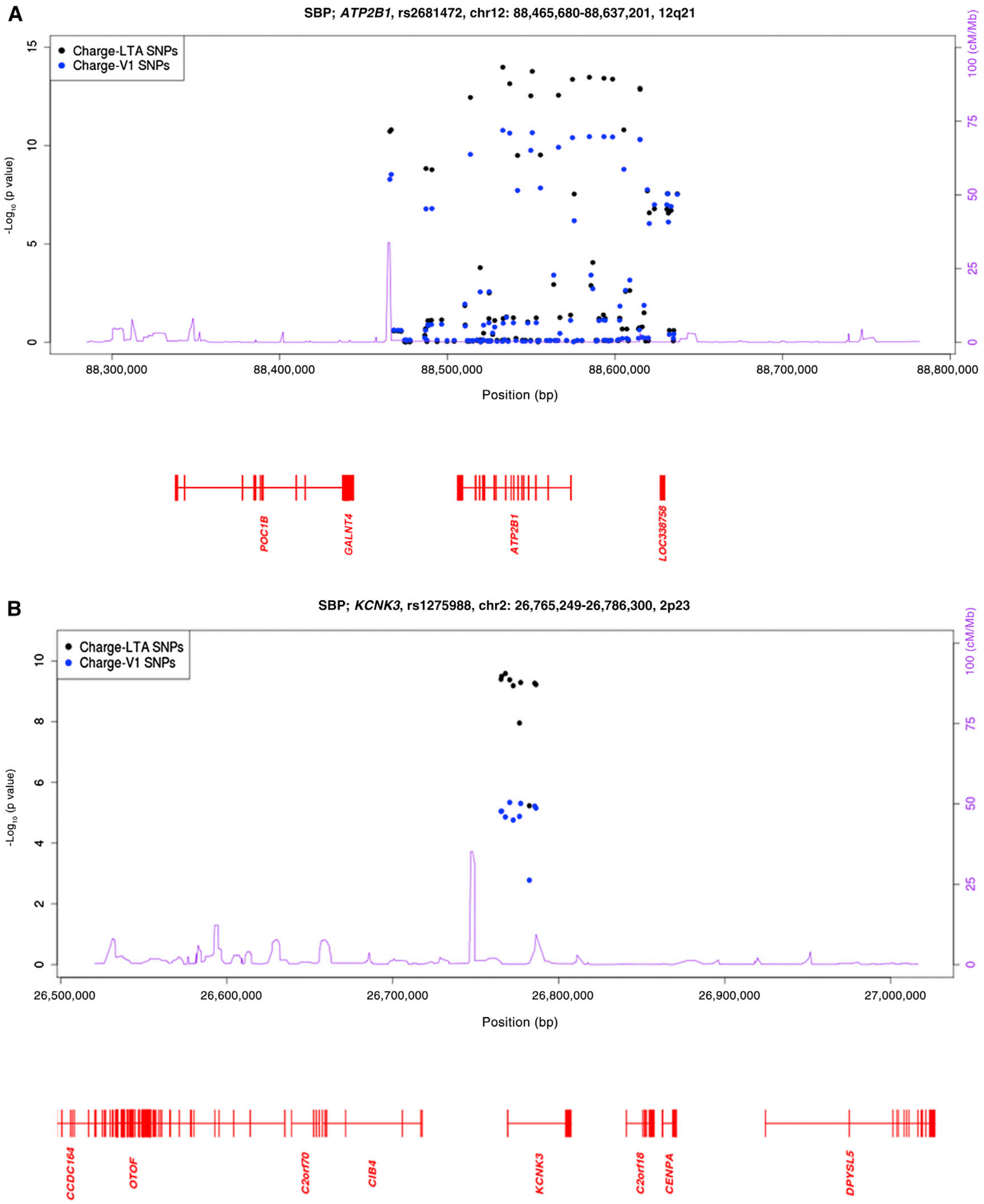

Figure 3. –Log p Values of Association Tests for *ATP2B1* in Chromosomal Region 12q21 Demonstrate Enrichment by LTA
Plots of –log p values of association tests for LTA SBP are shown for (A) the 12q21 *ATP2B1* region, known to be robustly associated with BP, and (B) the 2p23 *KCNK3* region, which was identified in this study. Both regions demonstrated enrichment of the association signal by LTA. The results of the LTA SBP analysis are plotted in black, and the results of the corresponding V1 SBP analysis of the same individuals are plotted in blue.

in an unpaired t test (unequal variance was assumed) and found $p = 0.0034$. MAP in the *Task1*-null mice was approximately 9 mmHg lower (SD ± 2.4 mmHg). In *FER1L5*, which was associated with LTA DBP, we identified a nonsynonymous SNP (exon 21: c.2044A>G [p.Thr682Ala]) in our GWAS analysis. *FER1L5* encodes Fer-1-like 5, identified in *C. elegans*, and its function has not been defined. Two loci, near *CRIP3* (chromosomal region 6p21) and *IGFBP3* (chromosomal region 7p13), were associated with LTA PP. The index SNP associated with LTA PP in the *CRIP3* region was highly correlated with a nonsynonymous SNP (exon 8: c.563T>C [p.Ile188Thr]) in cysteine-rich protein 3 (*CRIP3*), whose vascular function has not been defined. The insulin-like growth factors (IGFs) and their binding proteins, of which IGFBP3 is one, regulate cellular proliferation and apoptosis, and IGF1 stimulates aortic elastin production during development.[79] The lead SNP associated with LTA PP was in LD with SNPs extending across the gene, suggesting a possible functional variant within the gene or gene regulatory region, although a lack of an eQTL finding makes the latter less likely. *IGFBP3* is expressed in the endothelium, and mice null for this gene show decreased retinal vessel growth.[80] Serum levels of *IGFBP3* are associated with measures of aortic stiffness, of which PP is an indicator,[81] and a GWAS of circulating IGFBP3 amounts in plasma showed an association with *IGFBP3* SNPs we identified.[82] Circulating amounts of IGFBP3 are also related to SBP.[83] Consequently, these genes identified by LTA analysis are highly plausible biological candidates for BP regulation.

The limitations of this study include loss of sample size due to the exclusion of individuals with data at only one visit. In the longitudinal cohorts studied here, the proportion lost to follow-up was low. However, bias might have also been introduced through studying only those individuals willing or able to participate at multiple exam cycles. In the discovery analyses, we used European-ancestry samples. Ethnic differences in interindividual variability in BP across years have not been not well defined, and we did not have an opportunity to evaluate this in our study. Although we gained phenotypic precision with LTA, we might have also lost information. BP tracking over time could be more precisely estimated with the use of more sophisticated statistical approaches rather than a crude average.[66,67,84–90] As we demonstrated in our LTA and V1 direct comparisons, there is overall enrichment with LTA. However, in some specific regions, V1 analysis yields stronger results, as assessed by lower p values. The proportion of individuals treated with antihypertensive medication increased between the first and last visits in each cohort by varying amounts, potentially adding to the LTA analyses variability that we did not completely account for, although we did employ a standard correction method for antihypertensive medication use at each visit to attempt to correct for this. Finally, although we adjusted for age and age-squared, there might have been other age-dependent effects, particularly the known change in DBP that typically occurs in the fifth decade of life[91] and across which our averages were obtained in many cases, which might explain the lower yield with LTA for DBP than for SBP. Consequently, there might be value in conducting parallel V1 and LTA analyses to identify BP-associated loci that are subsequently followed up and validated by independent biological studies.

In summary, we have evaluated the utility of averaging repeated BP measurements for the purposes of detecting genetic association. Alternate approaches to the study of BP phenotypes are needed, and we have demonstrated that LTA is useful for improving signal detection. Using LTA of BP traits, we identified and validated common variants at several known loci and at loci not previously known to be associated with BP, and we have shown that trait-averaging methods have important implications for study design of genetic analyses of quantitative traits and ultimately for improved hypothesis generation from GWASs.

Supplemental Data

Supplemental Data include 9 figures, 11 tables, cohort descriptions, and Supplemental Acknowledgments and can be found with this article online at http://dx.doi.org/10.1016/j.ajhg.2014.06.002.

Consortia

The members of the Global Blood Pressure Genetics Consortium are Christopher Newton-Cheh, Toby Johnson, Vesela Gateva, Martin D. Tobin, Murielle Bochud, Lachlan Coin, Samer S. Najjar, Jing Hua Zhao, Simon C. Heath, Susana Eyheramendy, Konstantinos Papadakis, Benjamin F. Voight, Laura J. Scott, Feng Zhang, Martin Farrall, Toshiko Tanaka, Chris Wallace, John C. Chambers, Kay-Tee Khaw, Peter Nilsson, Pim van der Harst, Silvia Polidoro, Diederick E. Grobbee, N. Charlotte Onland-Moret, Michiel L. Bots, Louise V. Wain, Katherine S. Elliott, Alexander Teumer, Jian'an Luan, Gavin Lucas, Johanna Kuusisto, Paul R. Burton, David Hadley, Wendy L. McArdle, Morris Brown, Anna Dominiczak, Stephen J. Newhouse, Nilesh J. Samani, John Webster, Eleftheria Zeggini, Jacques S. Beckmann, Sven Bergmann, Noha Lim, Kijoung Song, Peter Vollenweider, Gerard Waeber, Dawn M. Waterworth, Xin Yuan, Leif Groop, Marju Orho-Melander, Alessandra Allione, Alessandra Di Gregorio, Simonetta Guarrera, Salvatore Panico, Fulvio Ricceri, Valeria Romanazzi, Carlotta Sacerdote, Paolo Vineis, Inês Barroso, Manjinder S. Sandhu, Robert N. Luben, Gabriel J. Crawford, Pekka Jousilahti, Markus Perola, Michael Boehnke, Lori L. Bonnycastle, Francis S. Collins, Anne U. Jackson, Karen L. Mohlke, Heather M. Stringham, Timo T. Valle, Cristen J. Willer, Richard N. Bergman, Mario A. Morken, Angela Döring, Christian Gieger, Thomas Illig, Thomas Meitinger, Elin Org, Arne Pfeufer, H. Erich Wichmann, Sekar Kathiresan, Jaume Marrugat, Christopher J. O'Donnell, Stephen M. Schwartz, David S. Siscovick, Isaac Subirana, Nelson B. Freimer, Anna-Liisa Hartikainen, Mark I. McCarthy, Paul F. O'Reilly, Leena Peltonen, Anneli Pouta, Paul E. de Jong, Harold Snieder, Wiek H. van Gilst, Robert Clarke, Anuj Goel, Anders Hamsten, John F. Peden, Udo Seedorf, Ann-Christine Syvänen, Giovanni Tognoni, Edward G. Lakatta, Serena Sanna, Paul Scheet, David Schlessinger, Angelo Scuteri, Marcus Dörr, Florian Ernst, Stephan B. Felix, Georg Homuth, Roberto Lorbeer, Thorsten Reffelmann, Rainer Rettig, Uwe Völker, Pilar Galan, Ivo G. Gut, Serge Hercberg, G. Mark Lathrop, Diana Zeleneka, Panos Deloukas, Nicole Soranzo, Frances M. Williams, Guangju Zhai, Veikko Salomaa, Markku Laakso, Roberto Elosua, Nita G. Forouhi, Henry Völzke, Cuno S. Uiterwaal, Yvonne T van der Schouw, Mattijs E. Numans, Giuseppe Matullo, Gerjan Navis, Göran Berglund, Sheila A. Bingham, Jaspal S. Kooner, Andrew D. Paterson, John M. Connell, Stefania Bandinelli, Luigi Ferrucci, Hugh Watkins, Tim D. Spector, Jaakko Tuomilehto, David Altshuler, David P. Strachan, Maris Laan, Pierre Meneton, Nicholas J. Wareham, Manuela Uda, Marjo-Riitta Jarvelin, Vincent Mooser, Olle Melander, Ruth J.F. Loos, Paul Elliott, Gonçalo R. Abecasis, Mark Caulfield, and Patricia B. Munroe.

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Web Resources

The URLs for data presented herein are as follows:

eQTL resources from the Pritchard lab, http://eqtl.uchicago.edu/Home.html

Framingham SNP Health Association Resource (SHARe), http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000007.v2.p1

Online Mendelian Inheritance in Man (OMIM), http://www.omim.org

References

1. Lewington, S., Clarke, R., Qizilbash, N., Peto, R., and Collins, R.; Prospective Studies Collaboration (2002). Age-specific relevance of usual blood pressure to vascular mortality: a meta-analysis of individual data for one million adults in 61 prospective studies. Lancet *360*, 1903–1913.
2. Ehret, G.B., Munroe, P.B., Rice, K.M., Bochud, M., Johnson, A.D., Chasman, D.I., Smith, A.V., Tobin, M.D., Verwoert, G.C., Hwang, S.J., et al.; International Consortium for Blood Pressure Genome-Wide Association Studies; CARDIoGRAM consortium; CKDGen Consortium; KidneyGen Consortium; EchoGen consortium; CHARGE-HF consortium (2011). Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature *478*, 103–109.
3. Ganesh, S.K., Tragante, V., Guo, W., Guo, Y., Lanktree, M.B., Smith, E.N., Johnson, T., Castillo, B.A., Barnard, J., Baumert, J., et al.; CARDIOGRAM, METASTROKE; LifeLines Cohort Study (2013). Loci influencing blood pressure identified using a cardiovascular gene-centric array. Hum. Mol. Genet. *22*, 1663–1678.
4. Levy, D., Ehret, G.B., Rice, K., Verwoert, G.C., Launer, L.J., Dehghan, A., Glazer, N.L., Morrison, A.C., Johnson, A.D., Aspelund, T., et al. (2009). Genome-wide association study of blood pressure and hypertension. Nat. Genet. *41*, 677–687.
5. Newton-Cheh, C., Johnson, T., Gateva, V., Tobin, M.D., Bochud, M., Coin, L., Najjar, S.S., Zhao, J.H., Heath, S.C., Eyheramendy, S., et al.; Wellcome Trust Case Control Consortium (2009). Genome-wide association study identifies eight loci associated with blood pressure. Nat. Genet. *41*, 666–676.
6. Chobanian, A.V., Bakris, G.L., Black, H.R., Cushman, W.C., Green, L.A., Izzo, J.L., Jr., Jones, D.W., Materson, B.J., Oparil, S., Wright, J.T., Jr., and Roccella, E.J.; National Heart, Lung, and Blood Institute Joint National Committee on Prevention, Detection, Evaluation, and Treatment of High Blood Pressure; National High Blood Pressure Education Program Coordinating Committee (2003). The Seventh Report of the Joint National Committee on Prevention, Detection, Evaluation, and Treatment of High Blood Pressure: the JNC 7 report. J. Am. Med. Assoc. *289*, 2560–2572.
7. Psaty, B.M., O'Donnell, C.J., Gudnason, V., Lunetta, K.L., Folsom, A.R., Rotter, J.I., Uitterlinden, A.G., Harris, T.B., Witteman, J.C., and Boerwinkle, E.; CHARGE Consortium (2009). Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: Design of prospective meta-analyses of genome-wide association studies from 5 cohorts. Circ Cardiovasc Genet *2*, 73–80.
8. Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A., Bender, D., Maller, J., Sklar, P., de Bakker, P.I., Daly, M.J., and Sham, P.C. (2007). PLINK: a tool set for whole-genome association and population-based linkage analyses. Am. J. Hum. Genet. *81*, 559–575.
9. Chen, M.H., and Yang, Q. (2010). GWAF: an R package for genome-wide association analyses with family data. Bioinformatics *26*, 580–581.
10. Devlin, B., and Roeder, K. (1999). Genomic control for association studies. Biometrics *55*, 997–1004.
11. Johnson, A.D., Handsaker, R.E., Pulit, S.L., Nizzari, M.M., O'Donnell, C.J., and de Bakker, P.I. (2008). SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. Bioinformatics *24*, 2938–2939.
12. Rantalainen, M., Herrera, B.M., Nicholson, G., Bowden, R., Wills, Q.F., Min, J.L., Neville, M.J., Barrett, A., Allen, M., Rayner, N.W., et al. (2011). MicroRNA expression in abdominal and gluteal adipose tissue is associated with mRNA expression levels and partly genetically driven. PLoS ONE *6*, e27338.
13. Lin, H., Dolmatova, E.V., Morley, M.P., Lunetta, K.L., McManus, D.D., Magnani, J.W., Margulies, K.B., Hakonarson, H., del Monte, F., Benjamin, E.J., et al. (2014). Gene expression and genetic variation in human atria. Heart Rhythm *11*, 266–271.
14. Consortium, G.T.; GTEx Consortium (2013). The Genotype-Tissue Expression (GTEx) project. Nat. Genet. *45*, 580–585.
15. Qiu, W., Cho, M.H., Riley, J.H., Anderson, W.H., Singh, D., Bakke, P., Gulsvik, A., Litonjua, A.A., Lomas, D.A., Crapo, J.D., et al.; ECLIPSE Investigators (2011). Genetics of sputum gene expression in chronic obstructive pulmonary disease. PLoS ONE *6*, e24395.
16. Gutierrez-Arcelus, M., Lappalainen, T., Montgomery, S.B., Buil, A., Ongen, H., Yurovsky, A., Bryois, J., Giger, T., Romano, L., Planchon, A., et al. (2013). Passive and active DNA methylation and the interplay with genetic variation in gene regulation. Elife *2*, e00523.
17. Dimas, A.S., Deutsch, S., Stranger, B.E., Montgomery, S.B., Borel, C., Attar-Cohen, H., Ingle, C., Beazley, C., Gutierrez Arcelus, M., Sekowska, M., et al. (2009). Common regulatory variation impacts gene expression in a cell type-dependent manner. Science *325*, 1246–1250.
18. Grundberg, E., Small, K.S., Hedman, A.K., Nica, A.C., Buil, A., Keildson, S., Bell, J.T., Yang, T.P., Meduri, E., Barrett, A., et al.; Multiple Tissue Human Expression Resource (MuTHER) Consortium (2012). Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nat. Genet. *44*, 1084–1089.
19. Ding, J., Gudjonsson, J.E., Liang, L., Stuart, P.E., Li, Y., Chen, W., Weichenthal, M., Ellinghaus, E., Franke, A., Cookson, W., et al. (2010). Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. Am. J. Hum. Genet. *87*, 779–789.
20. Gao, C., Tignor, N.L., Salit, J., Strulovici-Barel, Y., Hackett, N.R., Crystal, R.G., and Mezey, J.G. (2014). HEFT: eQTL analysis of many thousands of expressed genes while simultaneously controlling for hidden factors. Bioinformatics *30*, 369–376.

21. Hao, K., Bossé, Y., Nickle, D.C., Paré, P.D., Postma, D.S., Laviolette, M., Sandford, A., Hackett, T.L., Daley, D., Hogg, J.C., et al. (2012). Lung eQTLs to help reveal the molecular underpinnings of asthma. PLoS Genet. *8*, e1003029.
22. Quigley, D.A., Fiorito, E., Nord, S., Van Loo, P., Alnæs, G.G., Fleischer, T., Tost, J., Moen Vollan, H.K., Tramm, T., Overgaard, J., et al. (2014). The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogen-receptor positive tumors. Mol. Oncol. *8*, 273–284.
23. Keildson, S., Fadista, J., Ladenvall, C., Hedman, A.K., Elgzyri, T., Small, K.S., Grundberg, E., Nica, A.C., Glass, D., Richards, J.B., et al.; MAGIC Consortium; DIAGRAM Consortium; MuTHER Consortium (2014). Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. Diabetes *63*, 1154–1165.
24. Kabakchiev, B., and Silverberg, M.S. (2013). Expression quantitative trait loci analysis identifies associations between genotype and gene expression in human intestine. Gastroenterology *144*, 1488–1496.e1–e3.
25. Grundberg, E., Kwan, T., Ge, B., Lam, K.C., Koka, V., Kindmark, A., Mallmin, H., Dias, J., Verlaan, D.J., Ouimet, M., et al. (2009). Population genomics in a disease targeted primary cell model. Genome Res. *19*, 1942–1952.
26. Schröder, A., Klein, K., Winter, S., Schwab, M., Bonin, M., Zell, A., and Zanger, U.M. (2013). Genomics of ADME gene expression: mapping expression quantitative trait loci relevant for absorption, distribution, metabolism and excretion of drugs in human liver. Pharmacogenomics J. *13*, 12–20.
27. Innocenti, F., Cooper, G.M., Stanaway, I.B., Gamazon, E.R., Smith, J.D., Mirkov, S., Ramirez, J., Liu, W., Lin, Y.S., Moloney, C., et al. (2011). Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. PLoS Genet. *7*, e1002078.
28. Greenawalt, D.M., Dobrin, R., Chudin, E., Hatoum, I.J., Suver, C., Beaulaurier, J., Zhang, B., Castro, V., Zhu, J., Sieberts, S.K., et al. (2011). A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. Genome Res. *21*, 1008–1016.
29. Schadt, E.E., Molony, C., Chudin, E., Hao, K., Yang, X., Lum, P.Y., Kasarskis, A., Zhang, B., Wang, S., Suver, C., et al. (2008). Mapping the genetic architecture of gene expression in human liver. PLoS Biol. *6*, e107.
30. Zhang, B., Gaiteri, C., Bodea, L.G., Wang, Z., McElwee, J., Podtelezhnikov, A.A., Zhang, C., Xie, T., Tran, L., Dobrin, R., et al. (2013). Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. Cell *153*, 707–720.
31. Gamazon, E.R., Badner, J.A., Cheng, L., Zhang, C., Zhang, D., Cox, N.J., Gershon, E.S., Kelsoe, J.R., Greenwood, T.A., Nievergelt, C.M., et al. (2013). Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. Mol. Psychiatry *18*, 340–346.
32. Zou, F., Chai, H.S., Younkin, C.S., Allen, M., Crook, J., Pankratz, V.S., Carrasquillo, M.M., Rowley, C.N., Nair, A.A., Middha, S., et al.; Alzheimer's Disease Genetics Consortium (2012). Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. PLoS Genet. *8*, e1002707.
33. Kim, S., Cho, H., Lee, D., and Webster, M.J. (2012). Association between SNPs and gene expression in multiple regions of the human brain. Transcult. Psychiatry *2*, e113.
34. Gibbs, J.R., van der Brug, M.P., Hernandez, D.G., Traynor, B.J., Nalls, M.A., Lai, S.L., Arepalli, S., Dillman, A., Rafferty, I.P., Troncoso, J., et al. (2010). Abundant quantitative trait loci exist for DNA methylation and gene expression in human brain. PLoS Genet. *6*, e1000952.
35. Liu, C., Cheng, L., Badner, J.A., Zhang, D., Craig, D.W., Redman, M., and Gershon, E.S. (2010). Whole-genome association mapping of gene expression in the human prefrontal cortex. Mol. Psychiatry *15*, 779–784.
36. Colantuoni, C., Lipska, B.K., Ye, T., Hyde, T.M., Tao, R., Leek, J.T., Colantuoni, E.A., Elkahloun, A.G., Herman, M.M., Weinberger, D.R., and Kleinman, J.E. (2011). Temporal dynamics and genetic control of transcription in the human prefrontal cortex. Nature *478*, 519–523.
37. Webster, J.A., Gibbs, J.R., Clarke, J., Ray, M., Zhang, W., Holmans, P., Rohrer, K., Zhao, A., Marlowe, L., Kaleem, M., et al.; NACC-Neuropathology Group (2009). Genetic control of human brain transcript expression in Alzheimer disease. Am. J. Hum. Genet. *84*, 445–458.
38. Heinzen, E.L., Ge, D., Cronin, K.D., Maia, J.M., Shianna, K.V., Gabriel, W.N., Welsh-Bohmer, K.A., Hulette, C.M., Denny, T.N., and Goldstein, D.B. (2008). Tissue-specific genetic control of splicing: implications for the study of complex traits. PLoS Biol. *6*, e1.
39. Li, Q., Seo, J.H., Stranger, B., McKenna, A., Pe'er, I., Laframboise, T., Brown, M., Tyekucheva, S., and Freedman, M.L. (2013). Integrative eQTL-based analyses reveal the biology of breast cancer risk loci. Cell *152*, 633–641.
40. Kompass, K.S., and Witte, J.S. (2011). Co-regulatory expression quantitative trait loci mapping: method and application to endometrial cancer. BMC Med. Genomics *4*, 6.
41. Emilsson, V., Thorleifsson, G., Zhang, B., Leonardson, A.S., Zink, F., Zhu, J., Carlson, S., Helgason, A., Walters, G.B., Gunnarsdottir, S., et al. (2008). Genetics of gene expression and its effect on disease. Nature *452*, 423–428.
42. Zhernakova, D.V., de Klerk, E., Westra, H.J., Mastrokolias, A., Amini, S., Ariyurek, Y., Jansen, R., Penninx, B.W., Hottenga, J.J., Willemsen, G., et al. (2013). DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and non-coding transcripts. PLoS Genet. *9*, e1003594.
43. Westra, H.J., Peters, M.J., Esko, T., Yaghootkar, H., Schurmann, C., Kettunen, J., Christiansen, M.W., Fairfax, B.P., Schramm, K., Powell, J.E., et al. (2013). Systematic identification of trans eQTLs as putative drivers of known disease associations. Nat. Genet. *45*, 1238–1243.
44. Sasayama, D., Hori, H., Nakamura, S., Miyata, R., Teraishi, T., Hattori, K., Ota, M., Yamamoto, N., Higuchi, T., Amano, N., and Kunugi, H. (2013). Identification of single nucleotide polymorphisms regulating peripheral blood mRNA expression with genome-wide significance: an eQTL study in the Japanese population. PLoS ONE *8*, e54967.
45. Mehta, D., Heim, K., Herder, C., Carstensen, M., Eckstein, G., Schurmann, C., Homuth, G., Nauck, M., Völker, U., Roden, M., et al. (2013). Impact of common regulatory single-nucleotide variants on gene expression profiles in whole blood. Eur. J. Hum. Genet. *21*, 48–54.
46. Liang, L., Morar, N., Dixon, A.L., Lathrop, G.M., Abecasis, G.R., Moffatt, M.F., and Cookson, W.O. (2013). A cross-platform analysis of 14,177 expression quantitative trait loci derived from lymphoblastoid cell lines. Genome Res. *23*, 716–726.

47. Landmark-Høyvik, H., Dumeaux, V., Nebdal, D., Lund, E., Tost, J., Kamatani, Y., Renault, V., Børresen-Dale, A.L., Kristensen, V., and Edvardsen, H. (2013). Genome-wide association study in breast cancer survivors reveals SNPs associated with gene expression of genes belonging to MHC class I and II. Genomics *102*, 278–287.
48. Kwan, T., Benovoy, D., Dias, C., Gurd, S., Provencher, C., Beaulieu, P., Hudson, T.J., Sladek, R., and Majewski, J. (2008). Genome-wide analysis of transcript isoform variation in humans. Nat. Genet. *40*, 225–231.
49. Idaghdour, Y., Czika, W., Shianna, K.V., Lee, S.H., Visscher, P.M., Martin, H.C., Miclaus, K., Jadallah, S.J., Goldstein, D.B., Wolfinger, R.D., and Gibson, G. (2010). Geographical genomics of human leukocyte gene expression variation in southern Morocco. Nat. Genet. *42*, 62–67.
50. Heap, G.A., Trynka, G., Jansen, R.C., Bruinenberg, M., Swertz, M.A., Dinesen, L.C., Hunt, K.A., Wijmenga, C., Vanheel, D.A., and Franke, L. (2009). Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Med. Genomics *2*, 1.
51. Göring, H.H., Curran, J.E., Johnson, M.P., Dyer, T.D., Charlesworth, J., Cole, S.A., Jowett, J.B., Abraham, L.J., Rainwater, D.L., Comuzzie, A.G., et al. (2007). Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. Nat. Genet. *39*, 1208–1216.
52. Fehrmann, R.S., Jansen, R.C., Veldink, J.H., Westra, H.J., Arends, D., Bonder, M.J., Fu, J., Deelen, P., Groen, H.J., Smolonska, A., et al. (2011). Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. PLoS Genet. *7*, e1002197.
53. Dixon, A.L., Liang, L., Moffatt, M.F., Chen, W., Heath, S., Wong, K.C., Taylor, J., Burnett, E., Gut, I., Farrall, M., et al. (2007). A genome-wide association study of global gene expression. Nat. Genet. *39*, 1202–1207.
54. Cusanovich, D.A., Billstrand, C., Zhou, X., Chavarria, C., De Leon, S., Michelini, K., Pai, A.A., Ober, C., and Gilad, Y. (2012). The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. Hum. Mol. Genet. *21*, 2111–2123.
55. Benton, M.C., Lea, R.A., Macartney-Coxson, D., Carless, M.A., Göring, H.H., Bellis, C., Hanna, M., Eccles, D., Chambers, G.K., Curran, J.E., et al. (2013). Mapping eQTLs in the Norfolk Island genetic isolate identifies candidate genes for CVD risk traits. Am. J. Hum. Genet. *93*, 1087–1099.
56. Battle, A., Mostafavi, S., Zhu, X., Potash, J.B., Weissman, M.M., McCormick, C., Haudenschild, C.D., Beckman, K.B., Shi, J., Mei, R., et al. (2014). Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. Genome Res. *24*, 14–24.
57. Zeller, T., Wild, P., Szymczak, S., Rotival, M., Schillert, A., Castagne, R., Maouche, S., Germain, M., Lackner, K., Rossmann, H., et al. (2010). Genetics and beyond—the transcriptome of human monocytes and disease susceptibility. PLoS ONE *5*, e10693.
58. van Eijk, K.R., de Jong, S., Boks, M.P., Langeveld, T., Colas, F., Veldink, J.H., de Kovel, C.G., Janson, E., Strengman, E., Langfelder, P., et al. (2012). Genetic analysis of DNA methylation and gene expression levels in whole blood of healthy human subjects. BMC Genomics *13*, 636.
59. Stranger, B.E., Nica, A.C., Forrest, M.S., Dimas, A., Bird, C.P., Beazley, C., Ingle, C.E., Dunning, M., Flicek, P., Koller, D., et al. (2007). Population genomics of human gene expression. Nat. Genet. *39*, 1217–1224.
60. Murphy, A., Chu, J.H., Xu, M., Carey, V.J., Lazarus, R., Liu, A., Szefler, S.J., Strunk, R., Demuth, K., Castro, M., et al. (2010). Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. Hum. Mol. Genet. *19*, 4745–4757.
61. (1978). Variability of blood pressure and the results of screening in the hypertension detection and follow-up program. J. Chronic Dis. *31*, 651–667.
62. Wellcome Trust Case Control Consortium (2007). Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature *447*, 661–678.
63. Chasman, D.I., Paré, G., and Ridker, P.M. (2009). Population-based genomewide genetic analysis of common clinical chemistry analytes. Clin. Chem. *55*, 39–51.
64. Wang, T.D., and Sheu, W.H. (2011). From casual blood pressure measurement to long-term blood pressure burden: better elucidation of the association between versatile blood pressures and cardiovascular events. Hypertens. Res. *34*, 49–51.
65. Rosner, B., Willett, W.C., and Spiegelman, D. (1989). Correction of logistic regression relative risk estimates and confidence intervals for systematic within-person measurement error. Stat. Med. *8*, 1051–1069, discussion 1071–1073.
66. Gillman, M.W., Rosner, B., Evans, D.A., Keough, M.E., Smith, L.A., Taylor, J.O., and Hennekens, C.H. (1991). Use of multiple visits to increase blood pressure tracking correlations in childhood. Pediatrics *87*, 708–711.
67. Zinner, S.H., Margolius, H.S., Rosner, B., and Kass, E.H. (1978). Stability of blood pressure rank and urinary kallikrein concentration in childhood: an eight-year follow-up. Circulation *58*, 908–915.
68. Rossignol, P., Cridlig, J., Lehert, P., Kessler, M., and Zannad, F. (2012). Visit-to-visit blood pressure variability is a strong predictor of cardiovascular events in hemodialysis: insights from FOSIDIAL. Hypertension *60*, 339–346.
69. Wilson, P.W., Hoeg, J.M., D'Agostino, R.B., Silbershatz, H., Belanger, A.M., Poehlmann, H., O'Leary, D., and Wolf, P.A. (1997). Cumulative effects of high cholesterol levels, high blood pressure, and cigarette smoking on carotid stenosis. N. Engl. J. Med. *337*, 516–522.
70. Kannel, W.B., Gordon, T., and Schwartz, M.J. (1971). Systolic versus diastolic blood pressure and risk of coronary heart disease. The Framingham study. Am. J. Cardiol. *27*, 335–346.
71. Vasan, R.S., Massaro, J.M., Wilson, P.W., Seshadri, S., Wolf, P.A., Levy, D., and D'Agostino, R.B.; Framingham Heart Study (2002). Antecedent blood pressure and risk of cardiovascular disease: the Framingham Heart Study. Circulation *105*, 48–53.
72. Carey, R.M., Reid, R.A., Ayers, C.R., Lynch, S.S., McLain, W.L., 3rd, and Vaughan, E.D., Jr. (1976). The Charlottesville Blood-Pressure Survey. Value of repeated blood-pressure measurements. J. Am. Med. Assoc. *236*, 847–851.
73. (1977). Blood pressure studies in 14 communities. A two-stage screen for hypertension. J. Am. Med. Assoc. *237*, 2385–2391.
74. Rosner, B., and Polk, B.F. (1979). The implications of blood pressure variability for clinical and screening purposes. J. Chronic Dis. *32*, 451–461.
75. Rosner, B., and Polk, B.F. (1981). The instability of blood pressure variability over time. J. Chronic Dis. *34*, 135–139.

76. Ma, L., Roman-Campos, D., Austin, E.D., Eyries, M., Sampson, K.S., Soubrier, F., Germain, M., Trégouët, D.A., Borczuk, A., Rosenzweig, E.B., et al. (2013). A novel channelopathy in pulmonary arterial hypertension. N. Engl. J. Med. *369*, 351–361.
77. Davies, L.A., Hu, C., Guagliardo, N.A., Sen, N., Chen, X., Talley, E.M., Carey, R.M., Bayliss, D.A., and Barrett, P.Q. (2008). TASK channel deletion in mice causes primary hyperaldosteronism. Proc. Natl. Acad. Sci. USA *105*, 2203–2208.
78. Muhammad, S., Aller, M.I., Maser-Gluth, C., Schwaninger, M., and Wisden, W. (2010). Expression of the kcnk3 potassium channel gene lessens the injury from cerebral ischemia, most likely by a general influence on blood pressure. Neuroscience *167*, 758–764.
79. Wolfe, B.L., Rich, C.B., Goud, H.D., Terpstra, A.J., Bashir, M., Rosenbloom, J., Sonenshein, G.E., and Foster, J.A. (1993). Insulin-like growth factor-I regulates transcription of the elastin gene. J. Biol. Chem. *268*, 12418–12426.
80. Lofqvist, C., Chen, J., Connor, K.M., Smith, A.C., Aderman, C.M., Liu, N., Pintar, J.E., Ludwig, T., Hellstrom, A., and Smith, L.E. (2007). IGFBP3 suppresses retinopathy through suppression of oxygen-induced vessel loss and promotion of vascular regrowth. Proc. Natl. Acad. Sci. USA *104*, 10589–10594.
81. Zachariah, J.P., Xanthakis, V., Larson, M.G., Vita, J.A., Sullivan, L.M., Smith, H.M., Safa, R., Peng, X., Hamburg, N., Levy, D., et al. (2012). Circulating vascular growth factors and central hemodynamic load in the community. Hypertension *59*, 773–779.
82. Kaplan, R.C., Petersen, A.K., Chen, M.H., Teumer, A., Glazer, N.L., Döring, A., Lam, C.S., Friedrich, N., Newman, A., Müller, M., et al. (2011). A genome-wide association study identifies novel loci associated with circulating IGF-I and IGFBP-3. Hum. Mol. Genet. *20*, 1241–1251.
83. Lam, C.S., Chen, M.H., Lacey, S.M., Yang, Q., Sullivan, L.M., Xanthakis, V., Safa, R., Smith, H.M., Peng, X., Sawyer, D.B., and Vasan, R.S. (2010). Circulating insulin-like growth factor-1 and its binding protein-3: metabolic and genetic correlates in the community. Arterioscler. Thromb. Vasc. Biol. *30*, 1479–1484.
84. Beckett, L.A., Rosner, B., Roche, A.F., and Guo, S. (1992). Serial changes in blood pressure from adolescence into adulthood. Am. J. Epidemiol. *135*, 1166–1177.
85. Chen, X., and Wang, Y. (2008). Tracking of blood pressure from childhood to adulthood: a systematic review and metaregression analysis. Circulation *117*, 3171–3180.
86. Chen, X., Wang, Y., Appel, L.J., and Mi, J. (2008). Impacts of measurement protocols on blood pressure tracking from childhood into adulthood: a metaregression analysis. Hypertension *51*, 642–649.
87. Cook, N.R., Rosner, B.A., Chen, W., Srinivasan, S.R., and Berenson, G.S. (2004). Using the area under the curve to reduce measurement error in predicting young adult blood pressure from childhood measures. Stat. Med. *23*, 3421–3435.
88. Gillman, M.W., Cook, N.R., Rosner, B., Evans, D.A., Keough, M.E., Taylor, J.O., and Hennekens, C.H. (1992). Assessing the validity of childhood blood pressure screening: unbiased estimates of sensitivity, specificity, and predictive values. Epidemiology *3*, 40–46.
89. Kollias, A., Pantsiotou, K., Karpettas, N., Roussias, L., and Stergiou, G.S. (2012). Tracking of blood pressure from childhood to adolescence in a Greek cohort. Eur. J. Public Health *22*, 389–393.
90. Sundström, J., Sullivan, L., D'Agostino, R.B., Levy, D., Kannel, W.B., and Vasan, R.S. (2005). Relations of serum uric acid to longitudinal blood pressure tracking and hypertension incidence. Hypertension *45*, 28–33.
91. Franklin, S.S., Gustin, W., 4th, Wong, N.D., Larson, M.G., Weber, M.A., Kannel, W.B., and Levy, D. (1997). Hemodynamic patterns of age-related changes in blood pressure. The Framingham Heart Study. Circulation *96*, 308–315.

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Supplemental Data

Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations

Santhi K. Ganesh, Daniel I. Chasman, Martin G. Larson, Xiuqing Guo, Germain Verwoert, Joshua C. Bis, Xiangjun Gu, Albert V. Smith, Min-Lee Yang, Yan Zhang, Georg Ehret, Lynda M. Rose, Shih-Jen Hwang, George J. Papanicolau, Eric J. Sijbrands, Kenneth Rice, Gudny Eiriksdottir, Vasyl Pihur, Paul M. Ridker, Ramachandran S. Vasan, Christopher Newton-Cheh, Global Blood Pressure Genetics Consortium, Leslie J. Raffel, Najaf Amin, Jerome I. Rotter, Kiang Liu, Lenore J. Launer, Ming Xu, Mark Caulfield, Alanna C. Morrison, Andrew D. Johnson, Dhananjay Vaidya, Abbas Dehghan, Guo Li, Claude Bouchard, Tamara B. Harris, He Zhang, Eric Boerwinkle, David S. Siscovick, Wei Gao, Andre G. Uitterlinden, Fernando Rivadeneira, Albert Hofman, Cristen J. Willer, Oscar H. Franco, Yong Huo, Jacqueline C.M. Witteman, Patricia B. Munroe, Vilmundur Gudnason, Walter Palmas, Cornelia van Duijn, Myriam Fornage, Daniel Levy, Bruce M. Psaty, and Aravinda Chakravarti

FIGURE S1: Study design summary.

The study design of the long-term averaged (LTA) analysis is summarized to accomplish the goals of firstly, identifying novel BP associations, which were replicated in an independent sample, and secondly characterizing the impact of LTA on genetic associations as compared to single-visit (V1) BP associations.

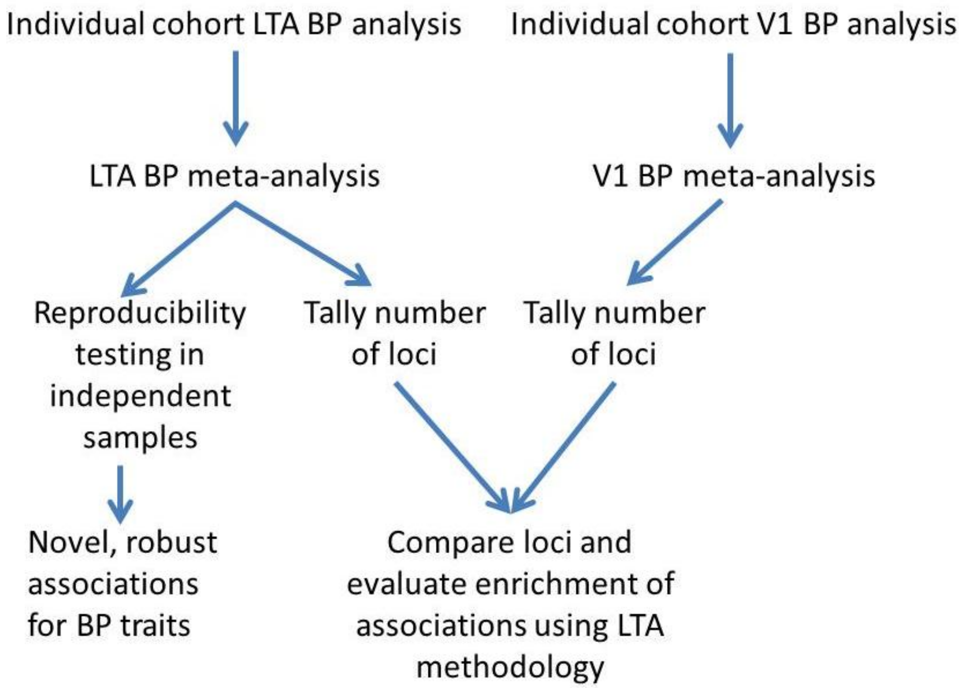
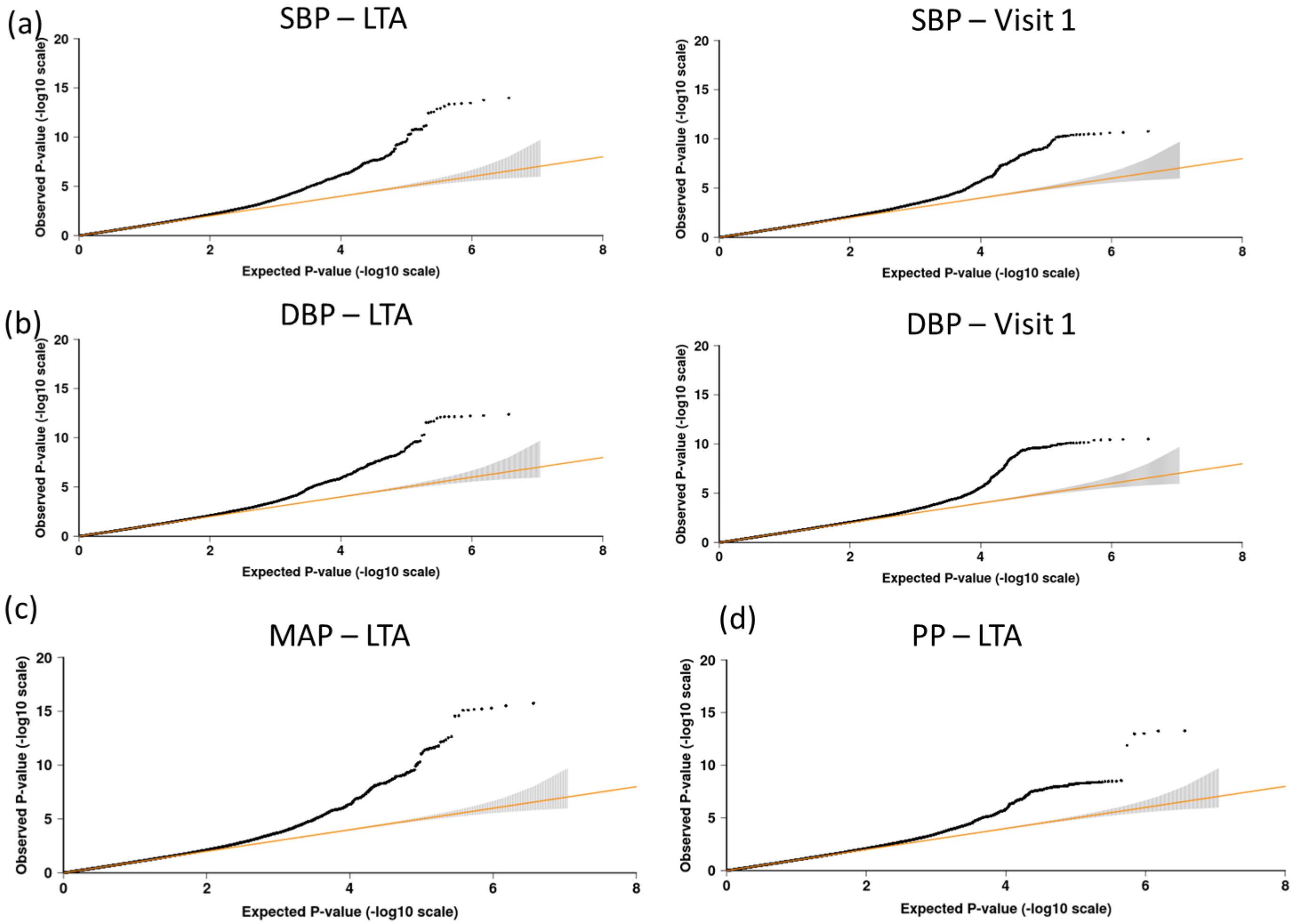


FIGURE S2. QQ plots for LTA BP traits and single visit (V1) SBP and DBP.

Quantile-quantile (QQ) plots are shown for (a) LTA and V1 SBP traits, (b) LTA and V1 DBP traits, (c) LTA-MAP and (d) LTA-PP. The null hypothesis is shown as the orange line. The 95% confidence interval around the null is shown in gray.



(a) SBP – LTA

SBP – Visit 1

(b) DBP – LTA

DBP – Visit 1

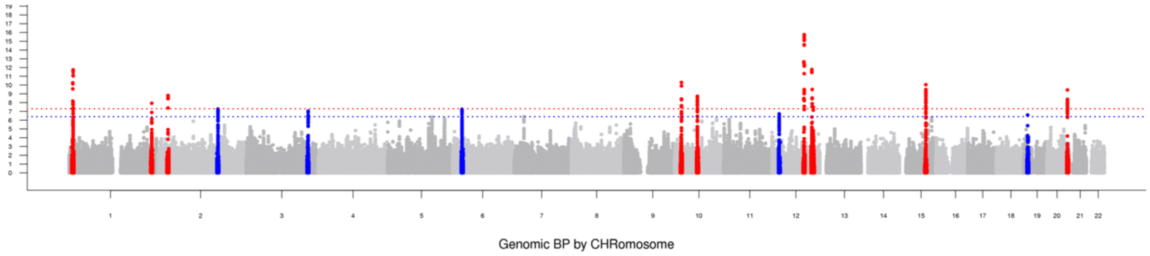
(c) MAP – LTA

(d) PP – LTA

FIGURE S3. Genome-wide association studies: –log*P* values for (a) LTA-MAP and (b) LTA-PP.

Genome wide association studies' –log*P* plots are shown for LTA-MAP and LTA-PP traits. Regions with SNP associations reaching *P* value < 5 x 10^{-8} are shown in red, and regions reaching *P* value < 5×10^{-7} are shown in blue.

(a) LTA-MAP



(b) LTA-PP

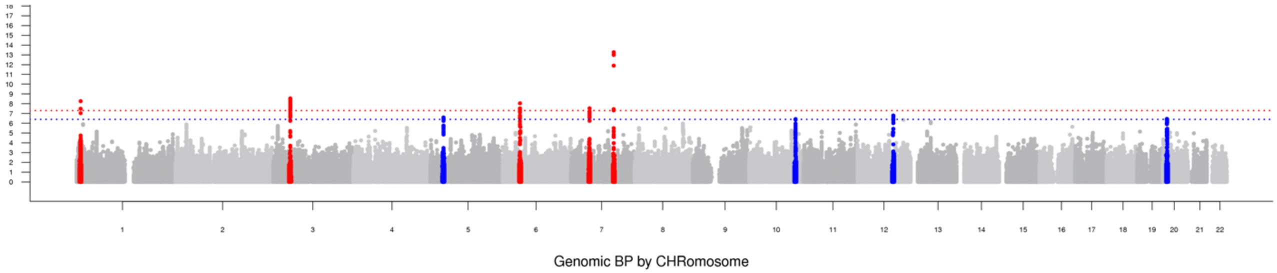
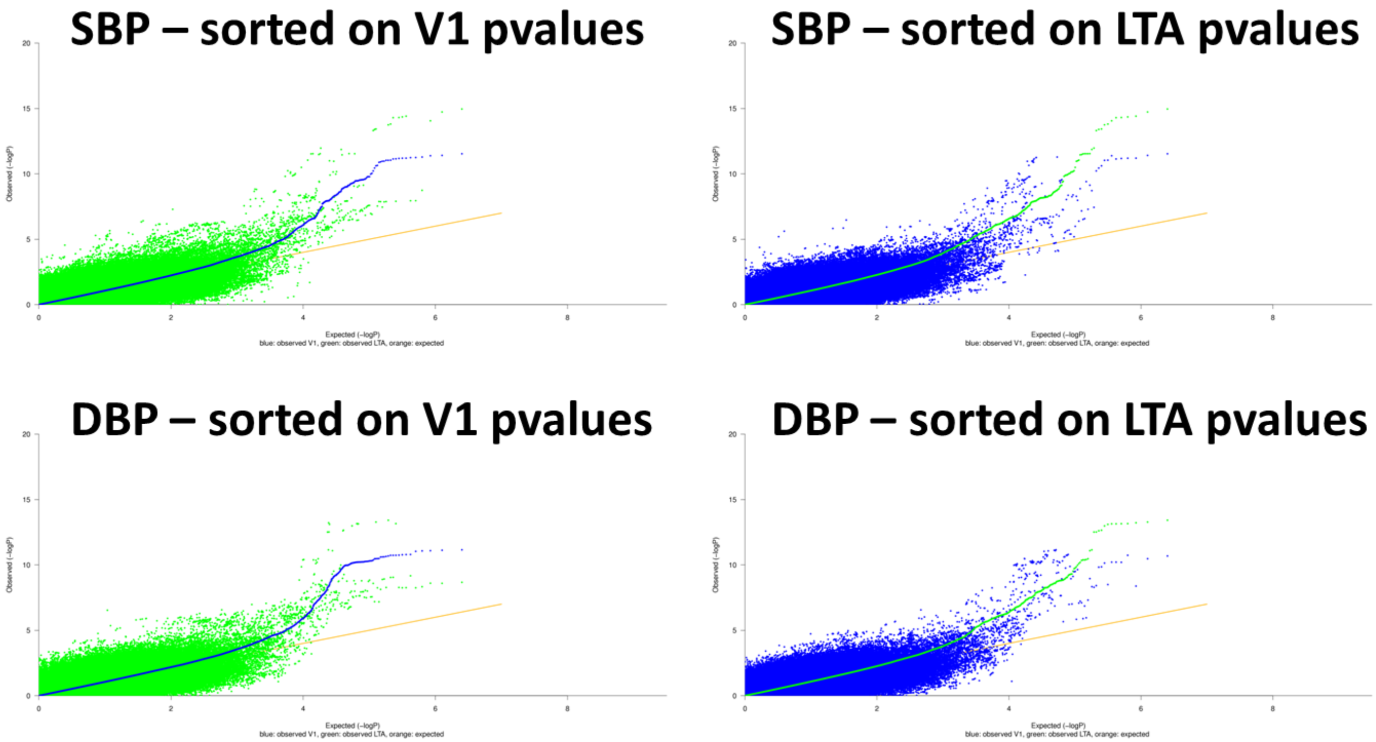


FIGURE S4. QQ plots for SBP and DBP traits showing associations statistics for both LTA and V1 traits.

Genome-wide association statistics for SBP and DBP analyses using LTA versus V1 only in quantile-quantile plots of LTA-SBP and LTA-DBP, with corresponding V1-SBP and V1-DBP results. The distribution of *P* values is shown with SNPs plotted in blue corresponding to V1 results, and SNPs plotted in green corresponding to LTA analysis results.



SBP – sorted on V1 pvalues

SBP – sorted on LTA pvalues

DBP – sorted on V1 pvalues

DBP – sorted on LTA pvalues

FIGURE S5. Genome-wide association statistics for SBP and DBP analyses using LTA versus V1.

Genome-wide association statistics for SBP and DBP analyses using LTA versus V1, with LTA values plotted on the X-axis and V1 on the Y-axis, for the effect size (beta, regression) estimate, standard error, chi-squared values and the normalized regression estimate (beta recalculated as the raw beta divided by the standard deviation of the phenotype).

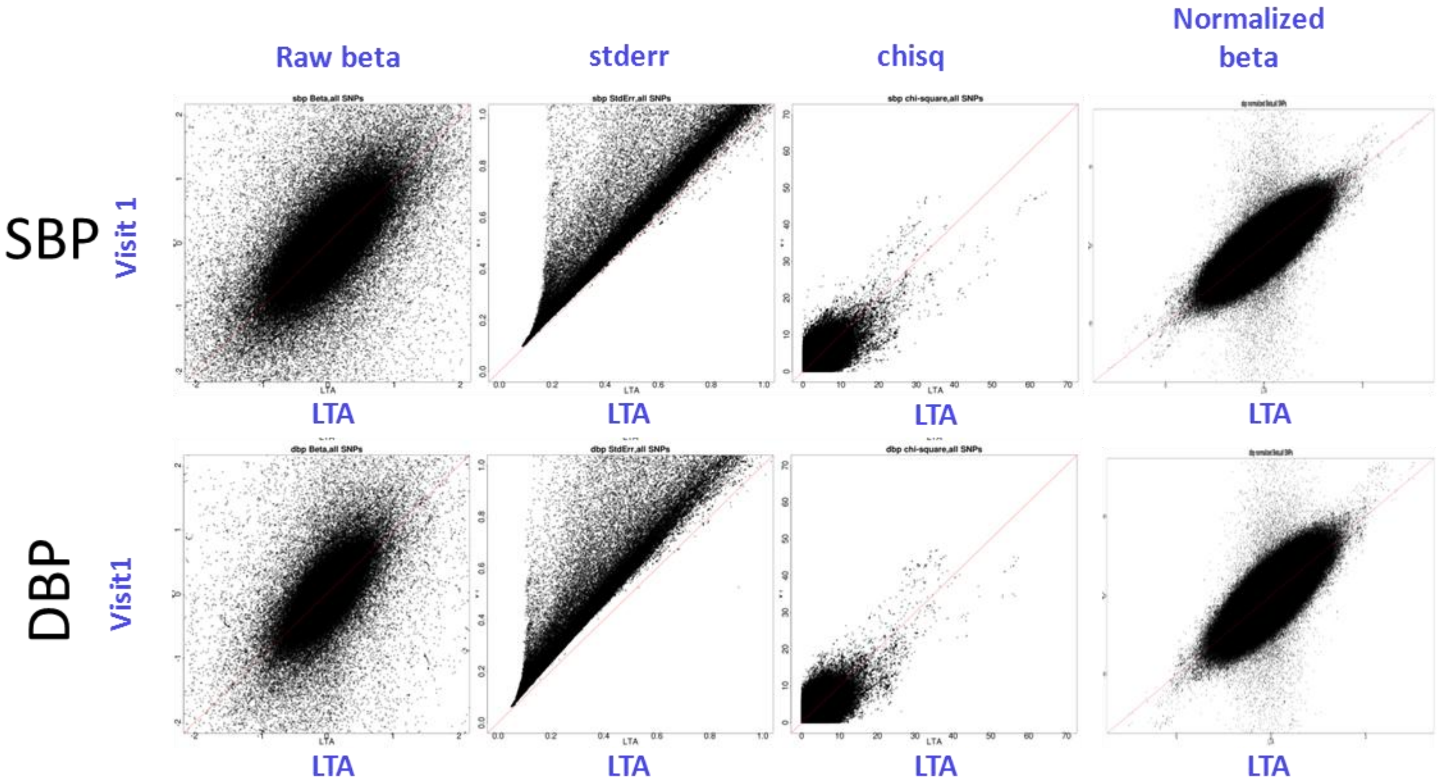
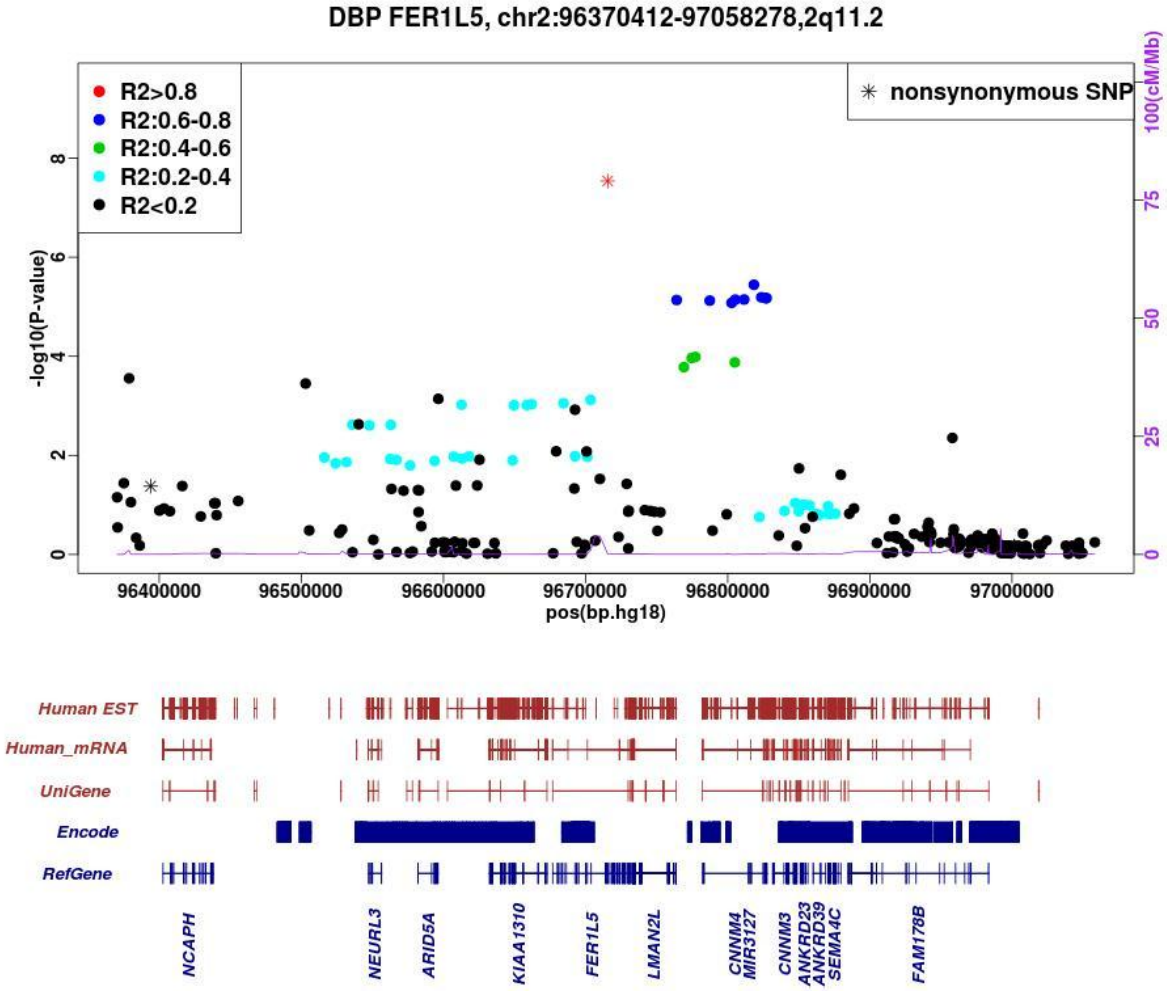
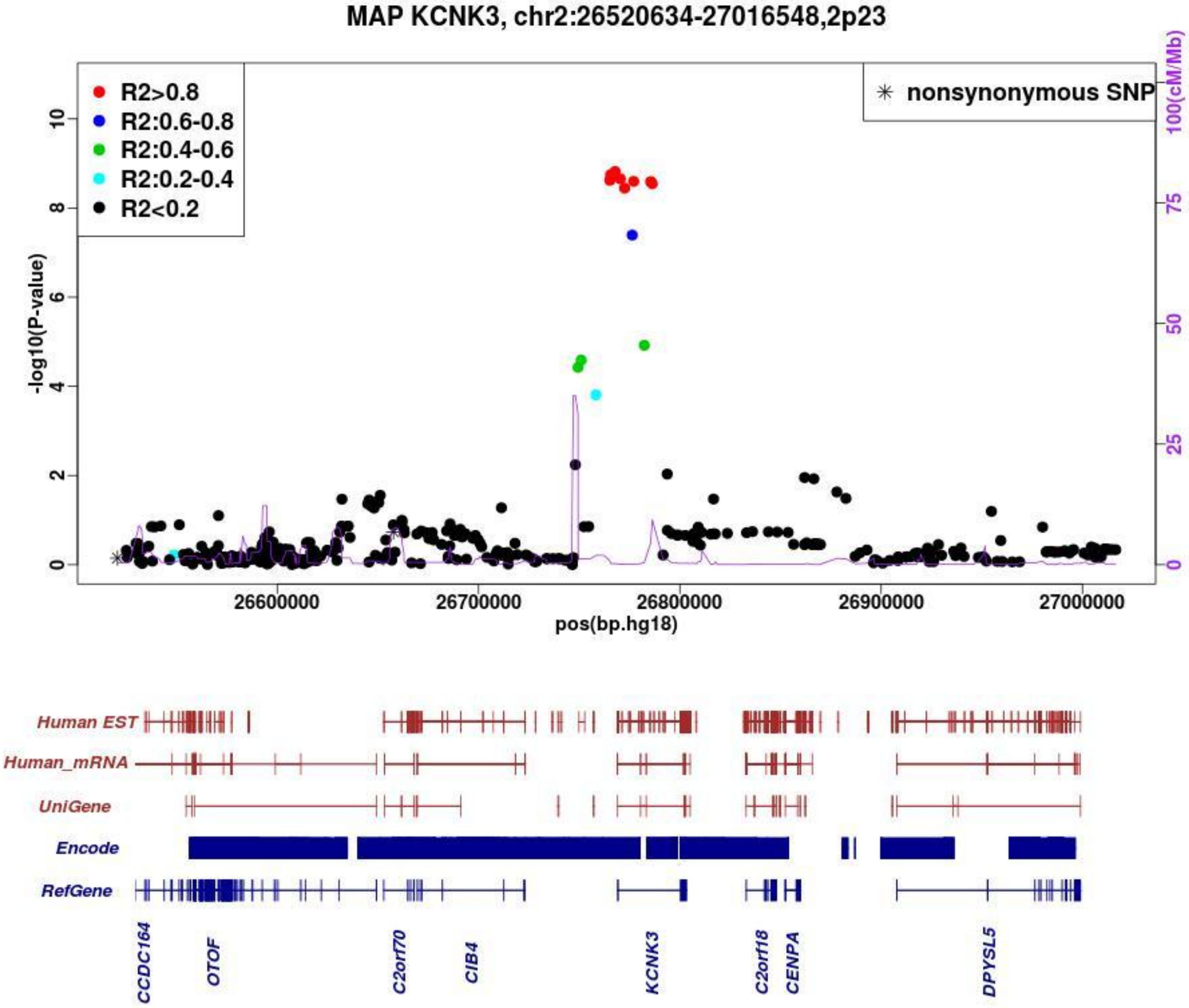


FIGURE S6. -log*P* value plots for regions identified in the LTA analysis incorporating LD estimates and annotation of nonsynonymous SNPs for each of the new 5 SNP-trait associations we identified in the LTA analysis (a-e).

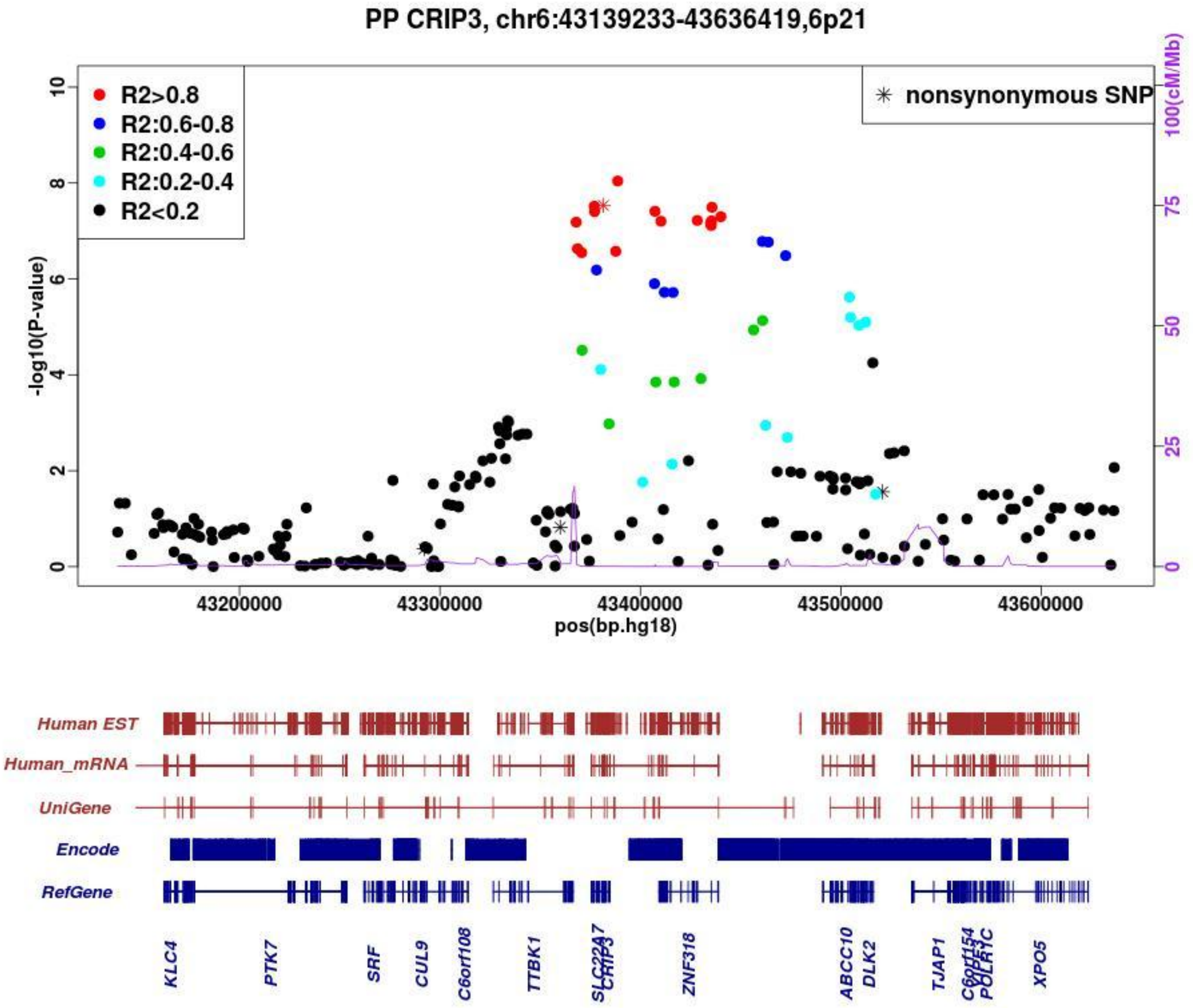
(a)



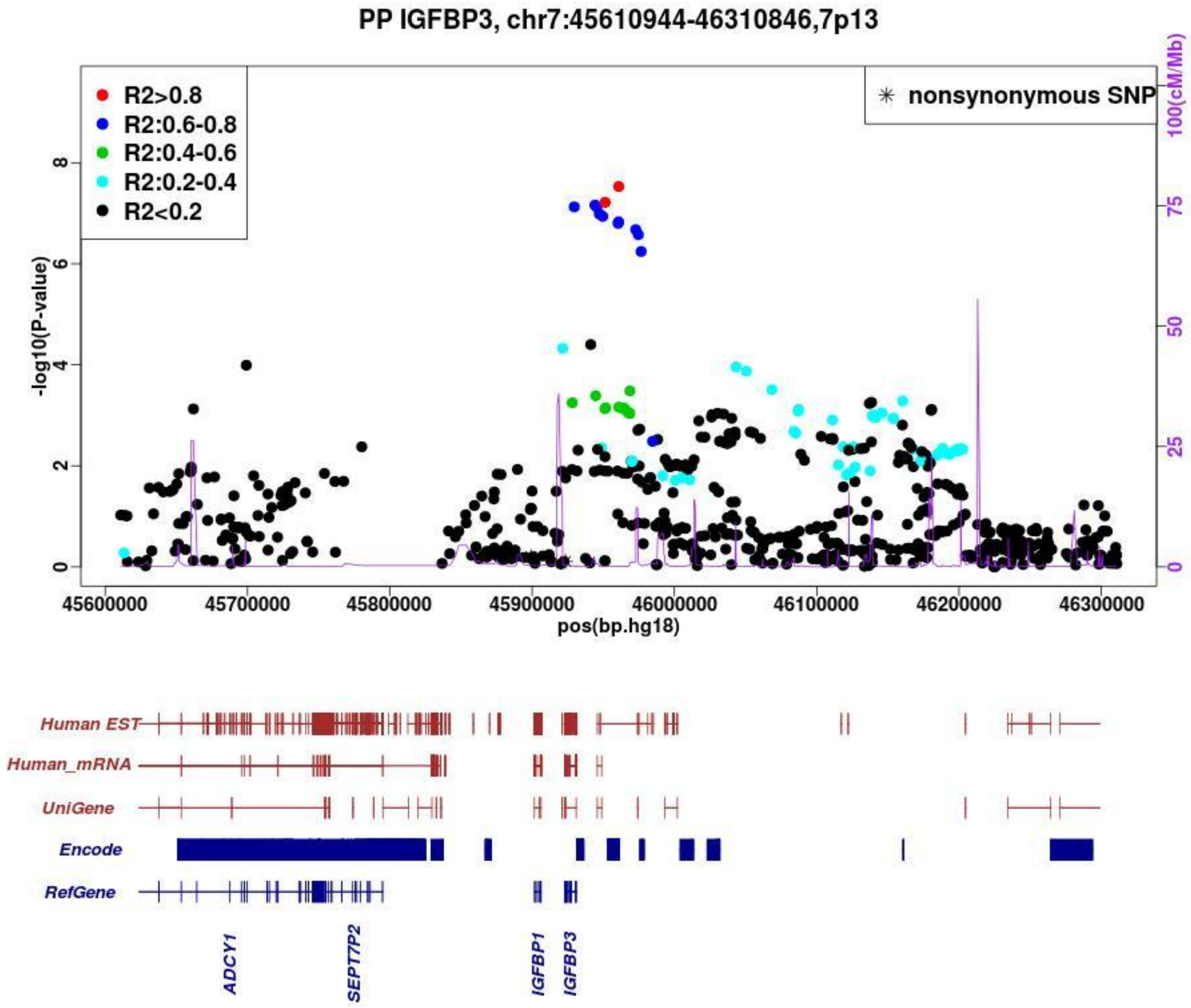
(b)


MAP KCNK3, chr2:26520634-27016548,2p23
● R2>0.8
● R2:0.6-0.8
● R2:0.4-0.6
● R2:0.2-0.4
● R2<0.2
* nonsynonymous SNP
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
26600000
26700000
26800000
26900000
27000000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
CCDC164
OTOF
C2orf70
CIB4
KCNK3
C2orf18
CENPA
DPYSL5

(c)


PP CRIP3, chr6:43139233-43636419,6p21
R2>0.8
R2:0.6-0.8
R2:0.4-0.6
R2:0.2-0.4
R2<0.2
nonsynonymous SNP
-log10(P-value)
100(cM/Mb)
0
2
4
6
8
10
0
25
50
75
43200000
43300000
43400000
43500000
43600000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
KLC4
PTK7
SRF
CUL9
C6orf108
TTBK1
SLC22A7
CRIP3
ZNF318
ABCC10
DLK2
TJAP1
C6orf154
YIPF3
POLR1C
XPO5

(d)


PP IGFBP3, chr7:45610944-46310846,7p13
● R2>0.8
● R2:0.6-0.8
● R2:0.4-0.6
● R2:0.2-0.4
● R2<0.2
✳ nonsynonymous SNP
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
45600000
45700000
45800000
45900000
46000000
46100000
46200000
46300000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
ADCY1
SEPT7P2
IGFBP1
IGFBP3

(e)

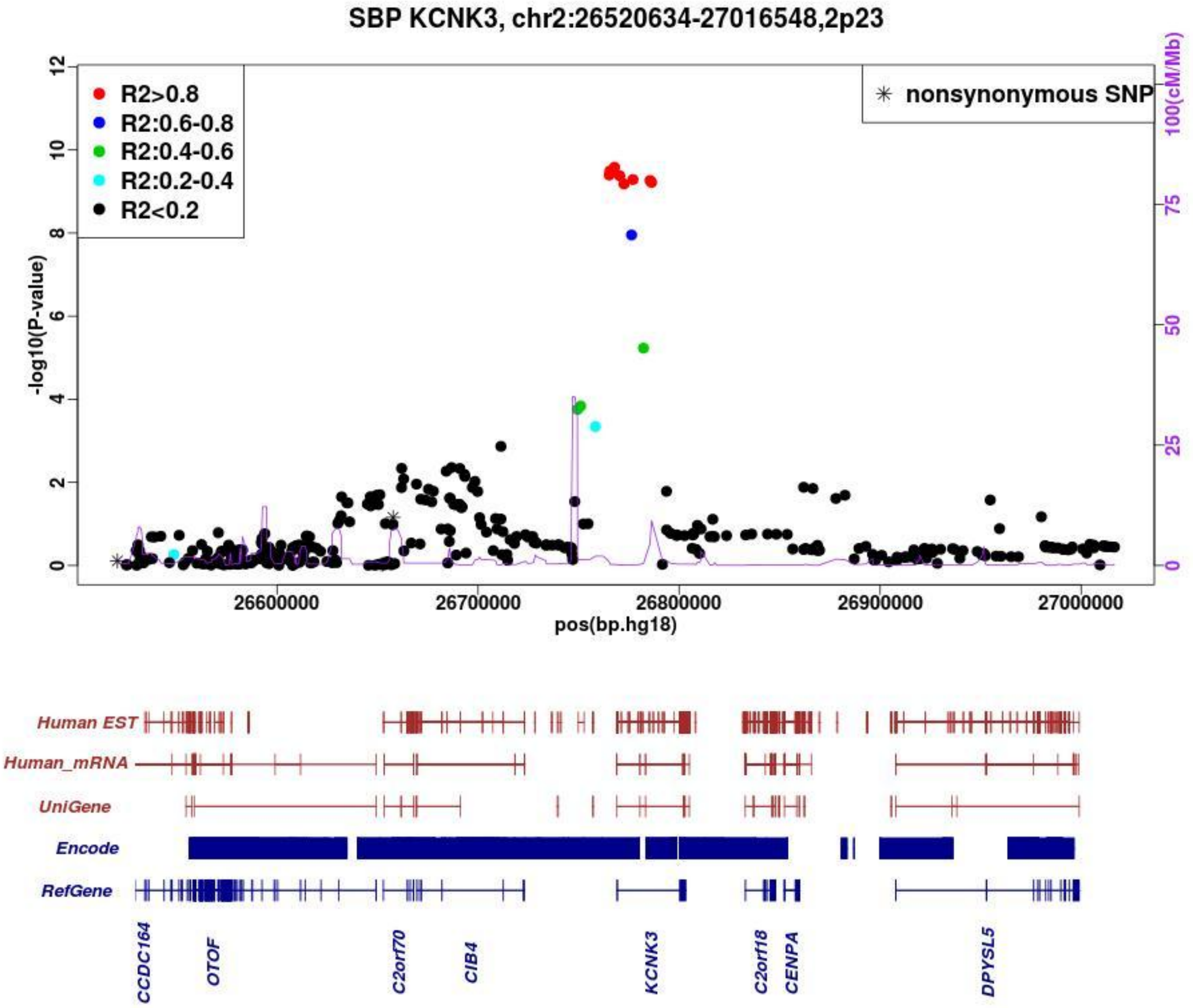
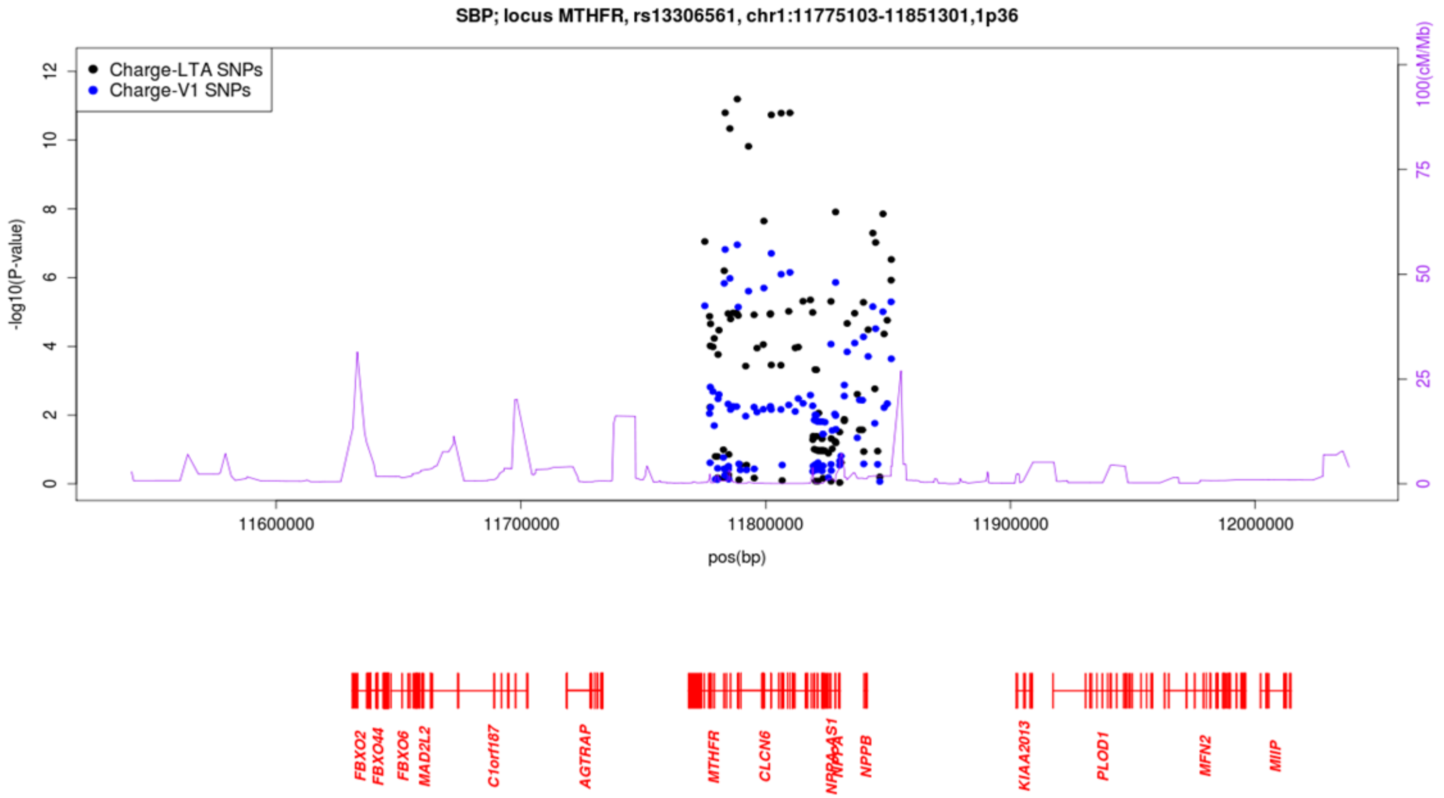

SBP KCNK3, chr2:26520634-27016548,2p23
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
R2>0.8
R2:0.6-0.8
R2:0.4-0.6
R2:0.2-0.4
R2<0.2
nonsynonymous SNP
26600000
26700000
26800000
26900000
27000000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
CCDC164
OTOF
C2orf70
CIB4
KCNK3
C2orf18
CENPA
DPYSL5

FIGURE S7. -log*P* value plots for regions identified in the LTA analysis.

–log*P* values of association tests are shown for all regions identified in the LTA analyses for (a) regions with enrichment in the LTA analysis compared to the corresponding V1 analyses (rank test *P* value < 0.001), (b) regions with enrichment in the V1 analysis compared to the corresponding LTA analyses (rank test *P* value < 0.001), (c) one region with enrichment of some SNP by LTA and other SNPs by V1 (*P* Value < 0.001) and (d) regions without enrichment by either LTA or V1 within the locus. The results of the LTA-SBP analysis are plotted in black and the results of the corresponding V1-SBP analysis of the same individuals are plotted in blue.

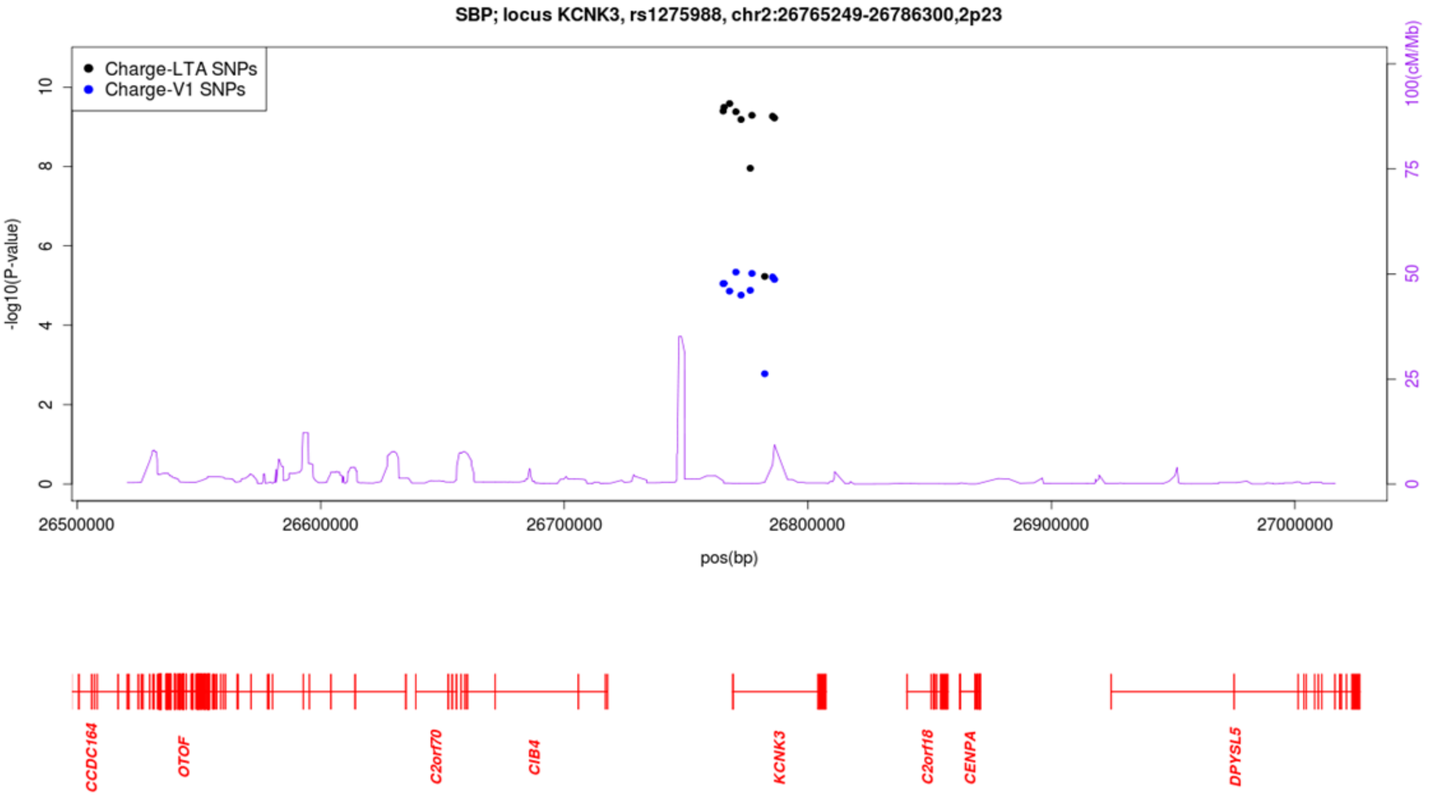
(a1)

SBP, MTHFR, 1p36



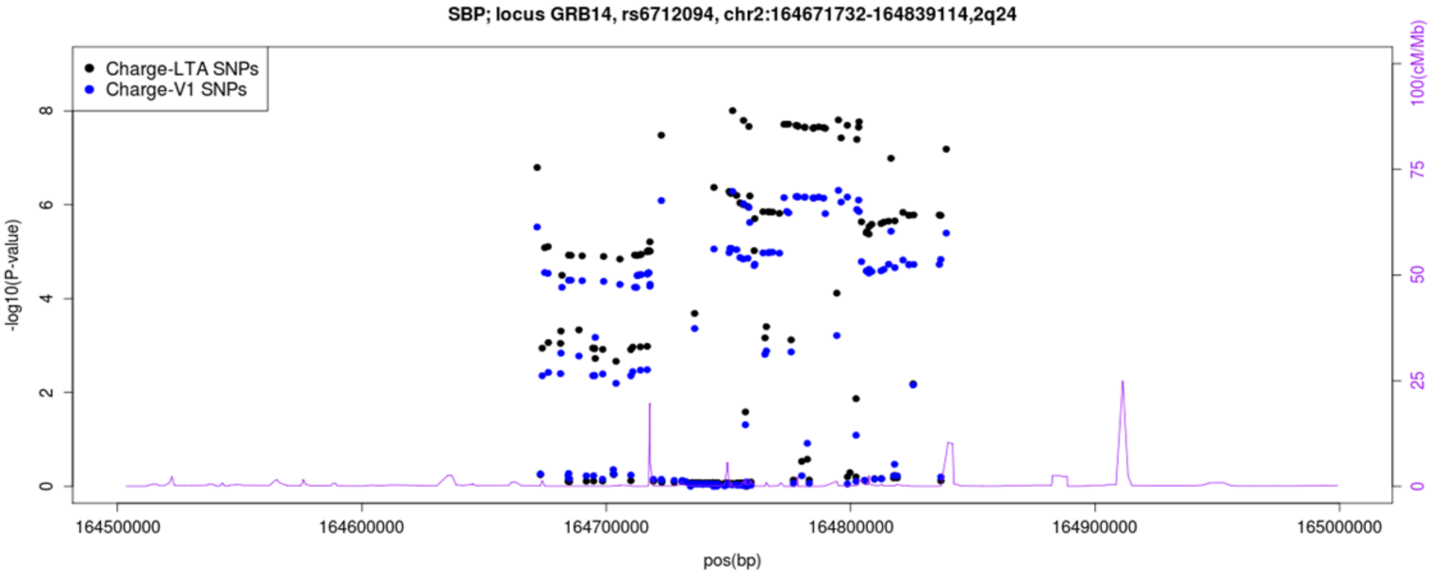
(a2)

SBP, KCNK3, 2p23



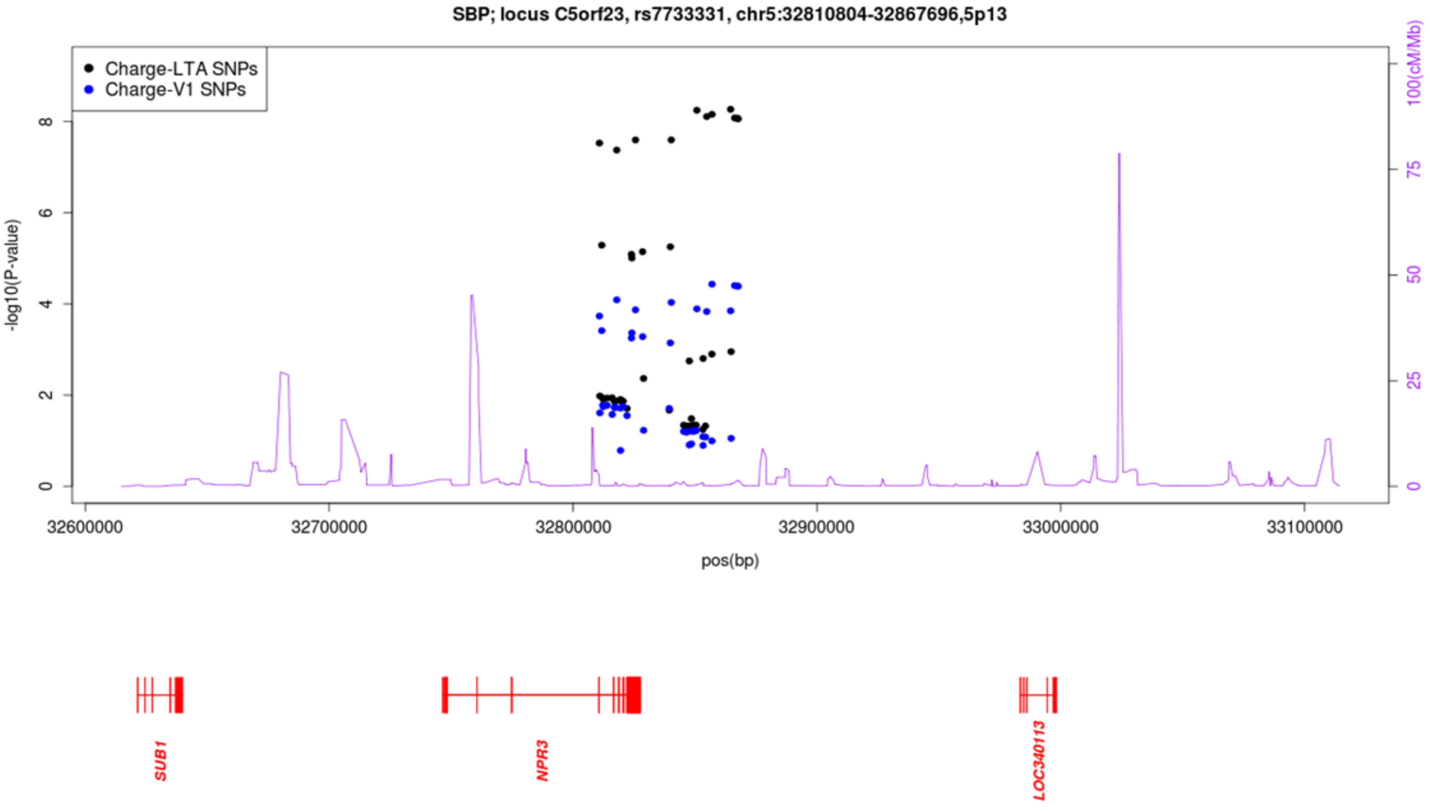
(a3)

SBP, GRB14,2q24



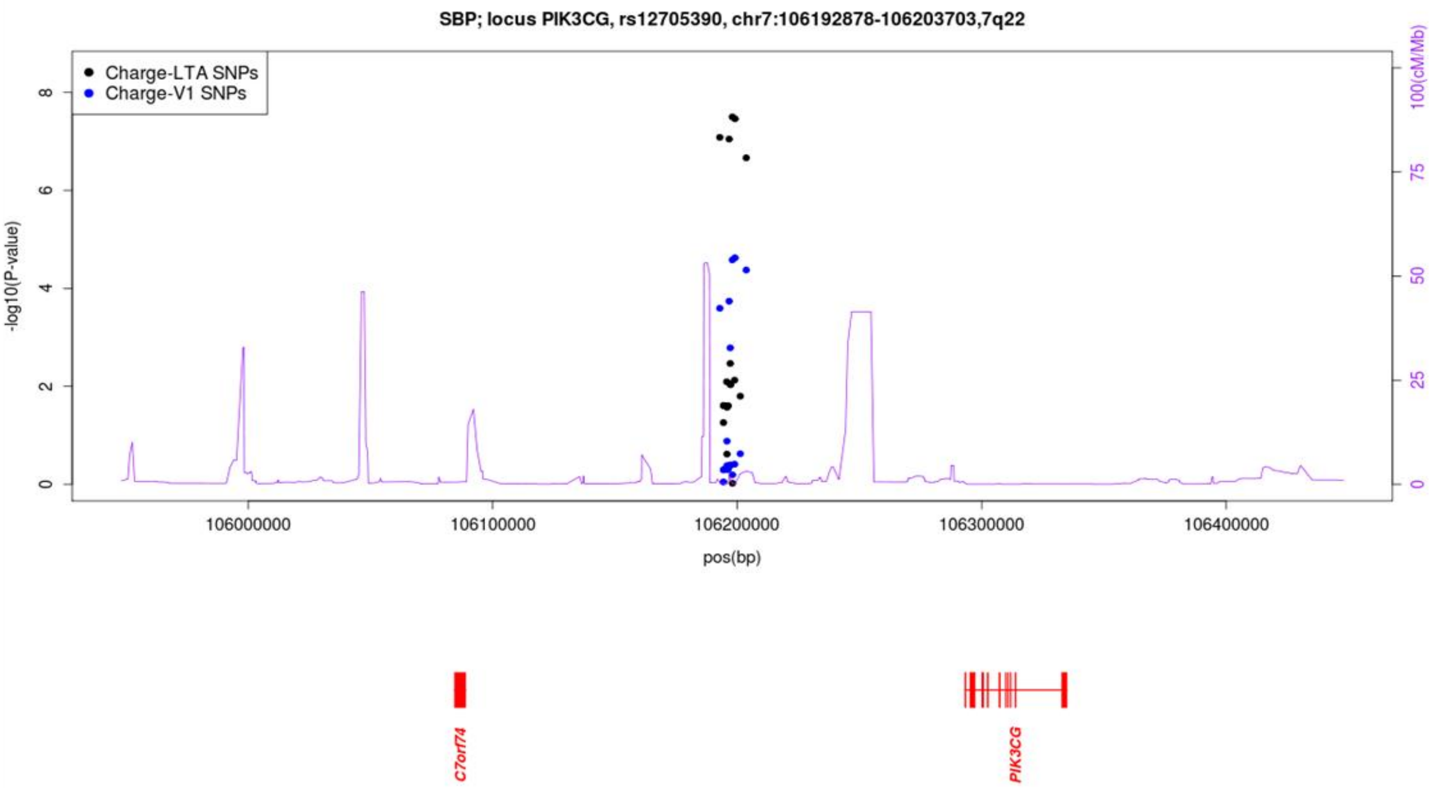
(a4)

SBP, C5orf23,5p13



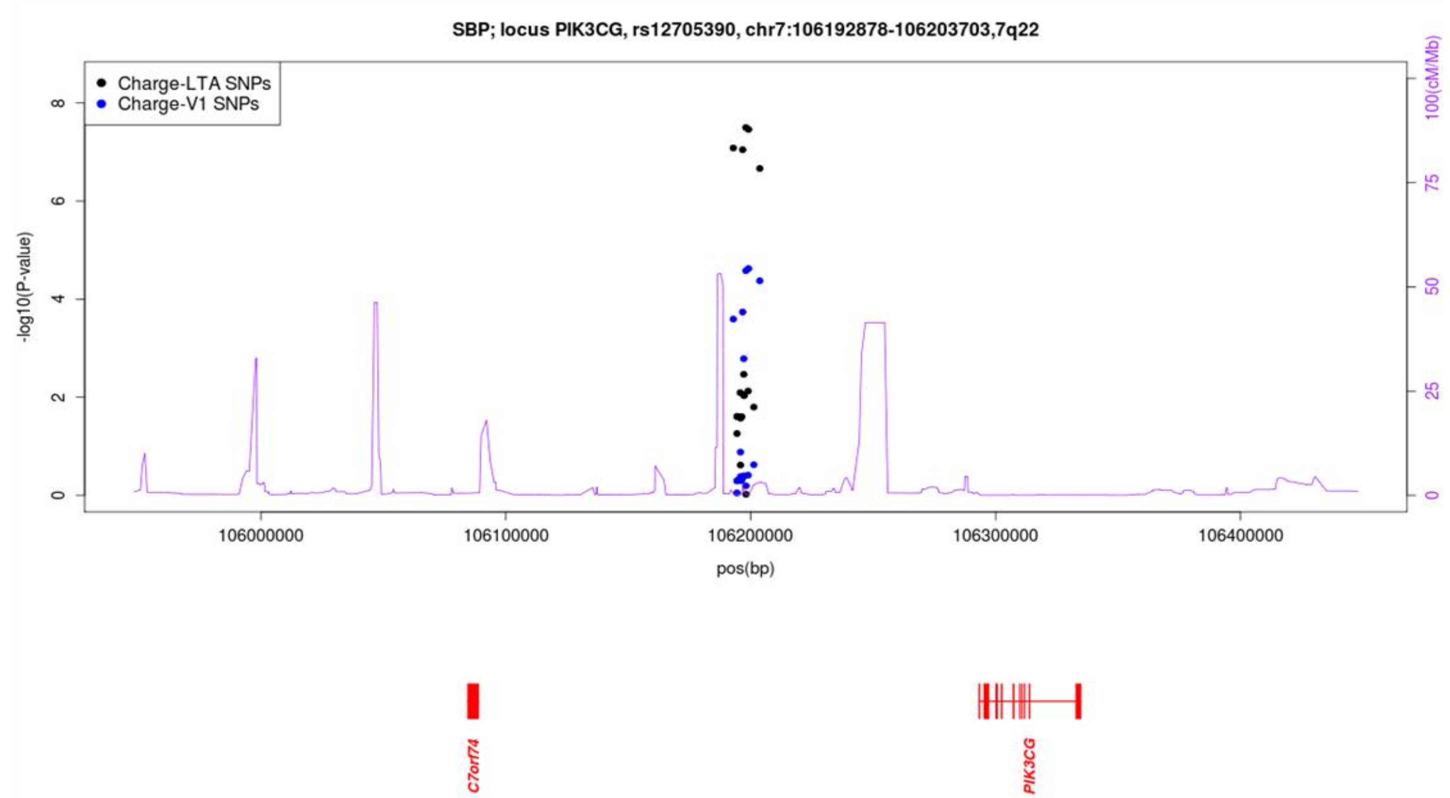
(a5)

SBP, PIK3CG,7q22



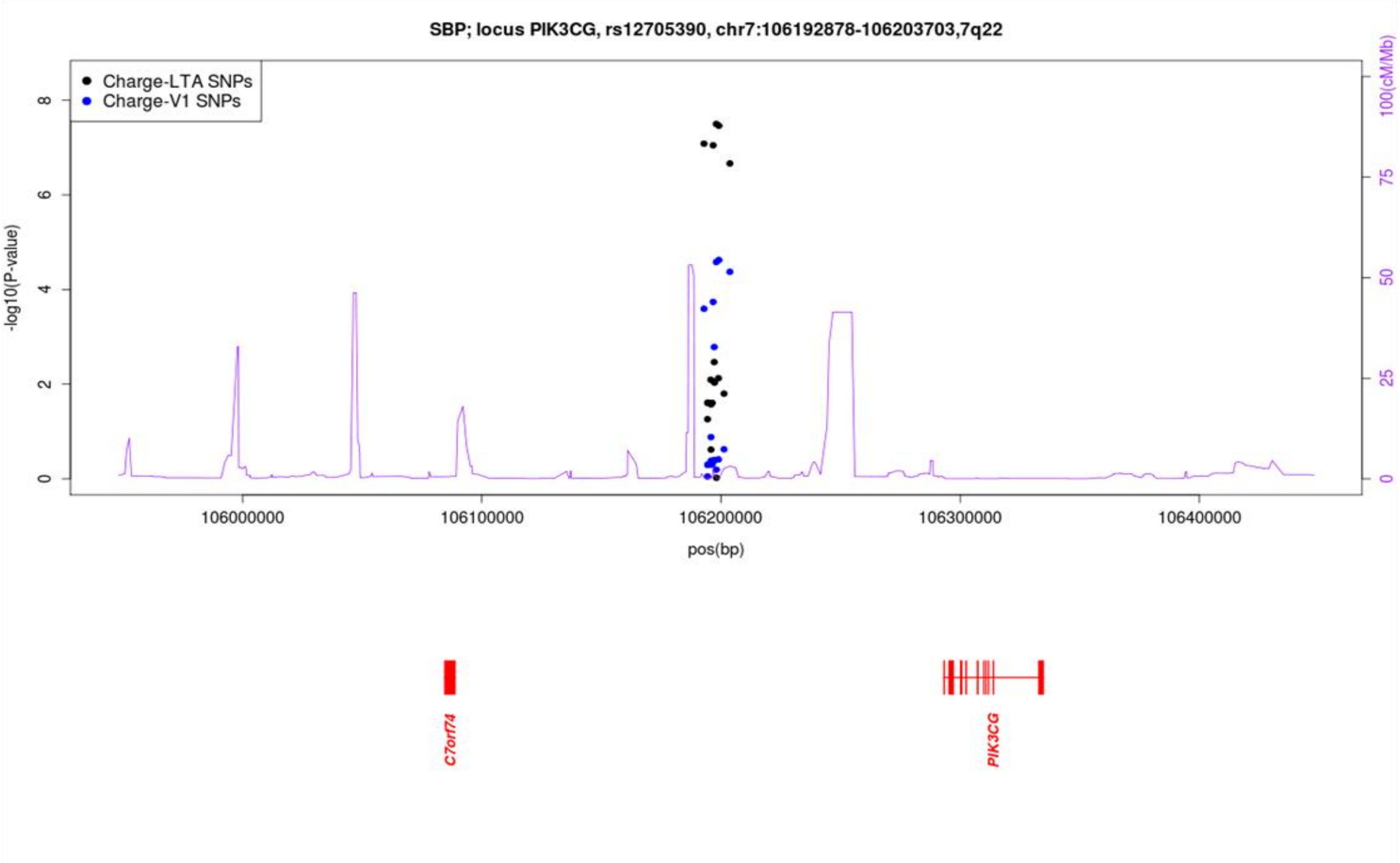
(a6)

SBP, PIK3CG,7q22



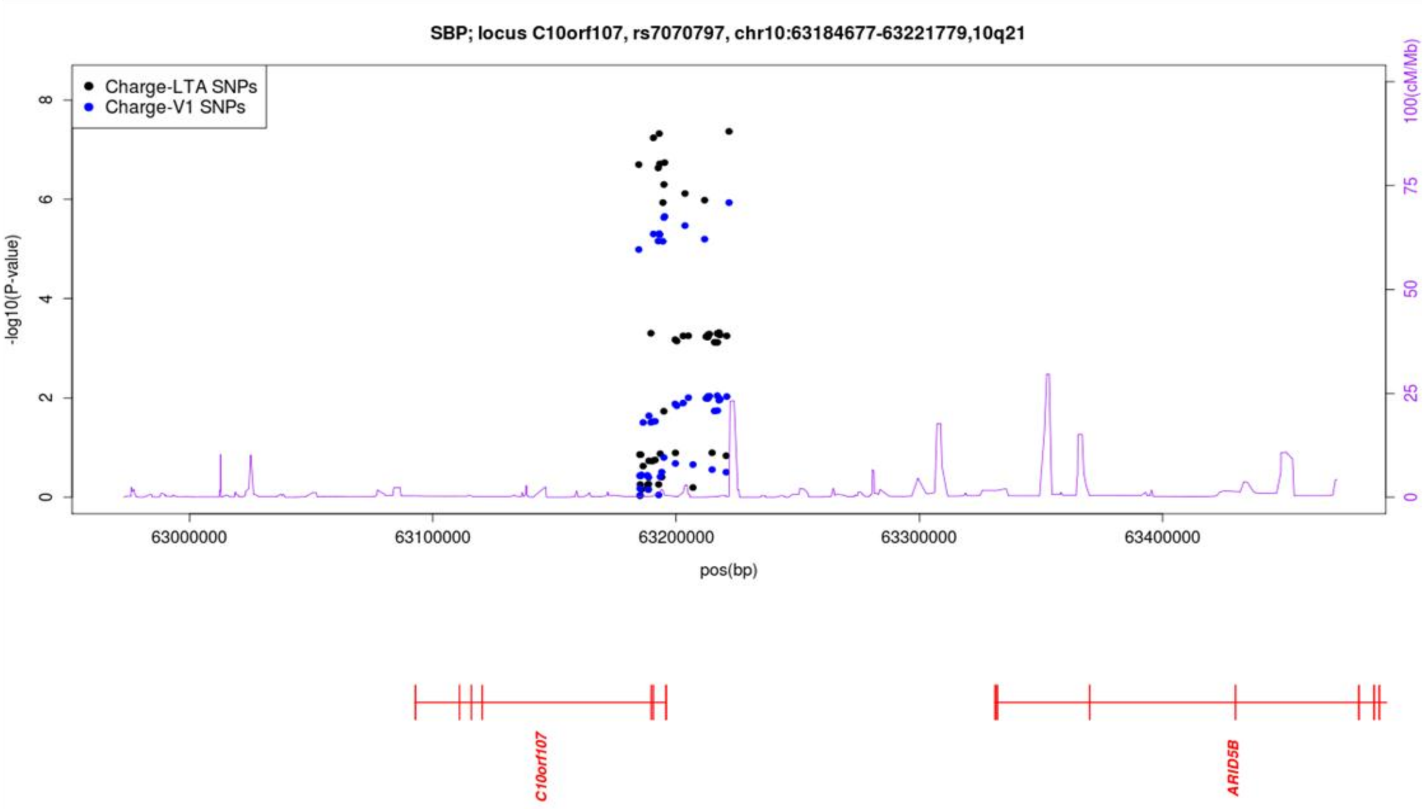
(a7)

SBP, PIK3CG,7q22



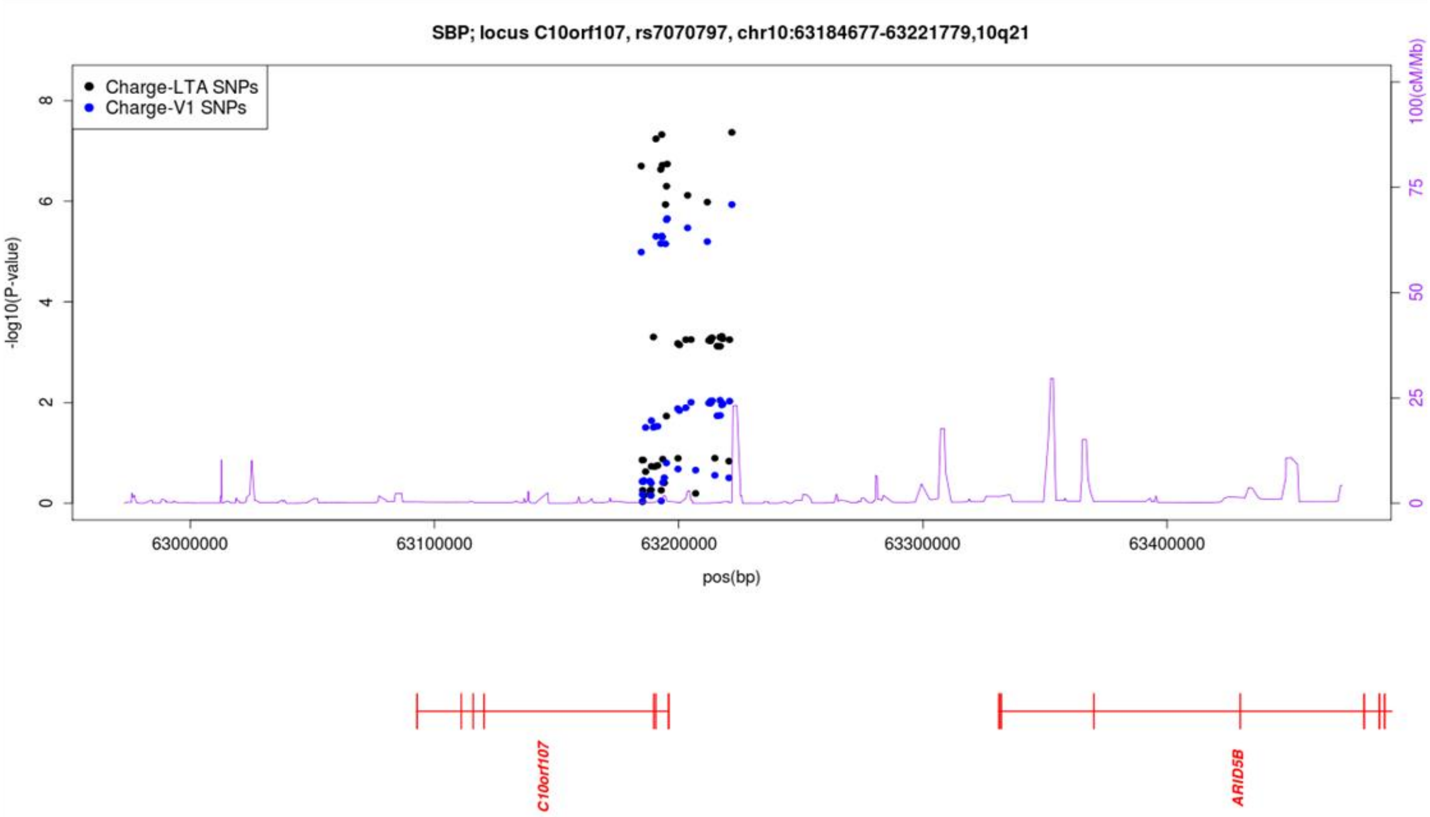
(a8)

SBP, C10orf107, 10q21



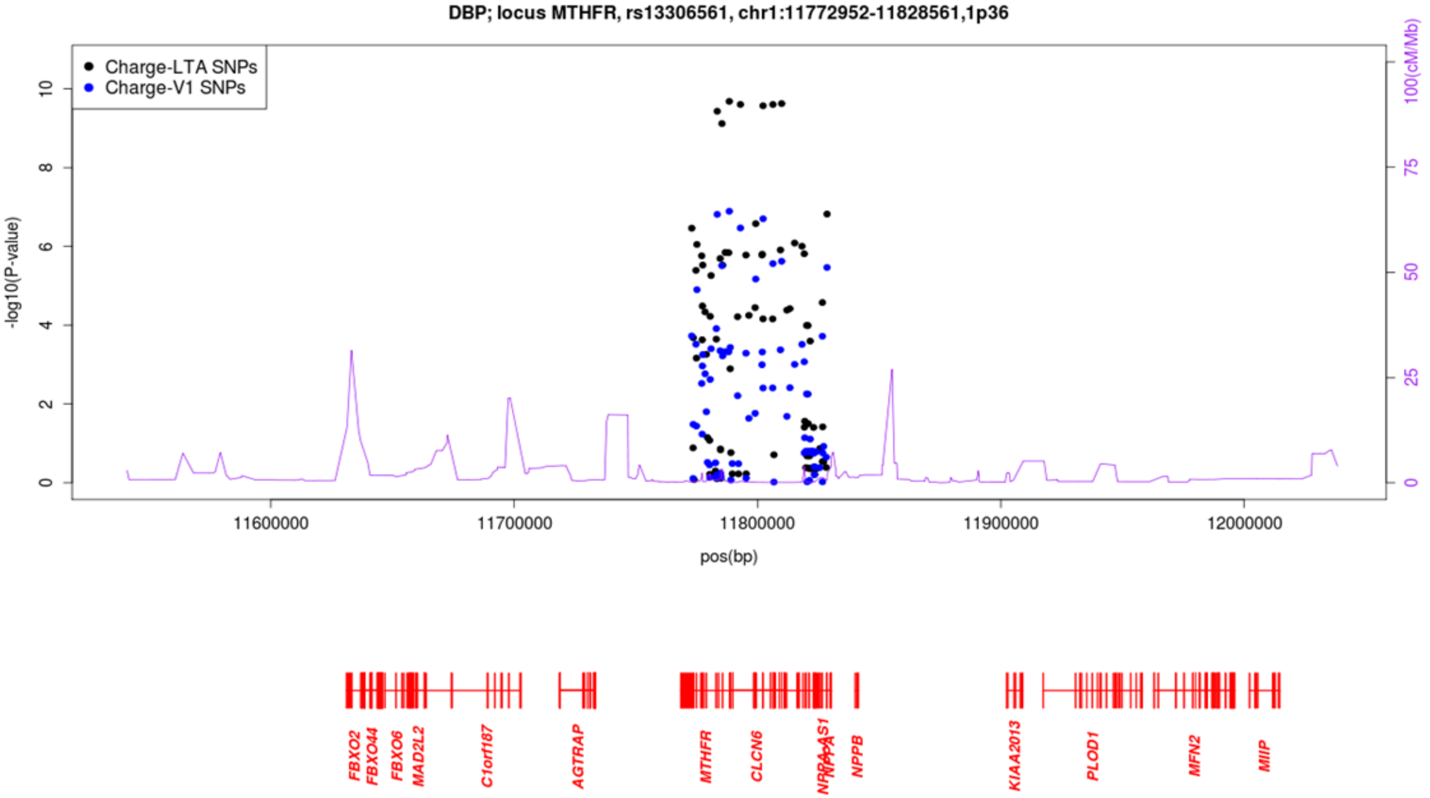
(a9)

SBP, C10orf107, 10q21



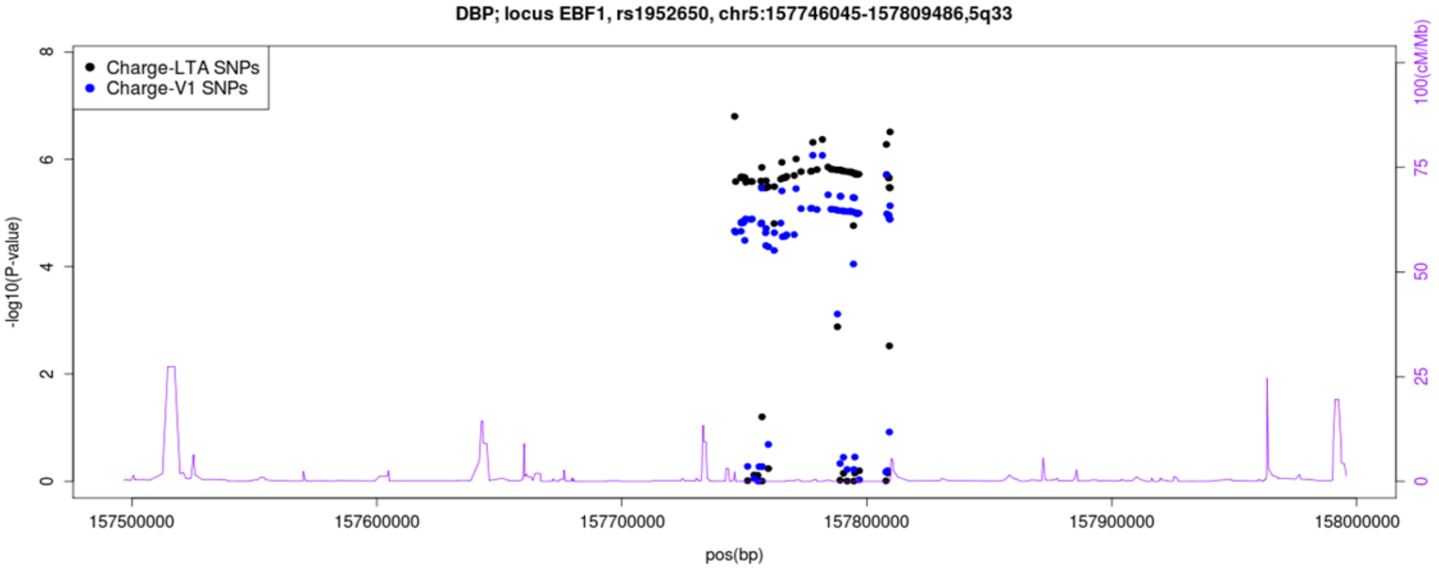
(a10)

DBP, MTHFR,1p36



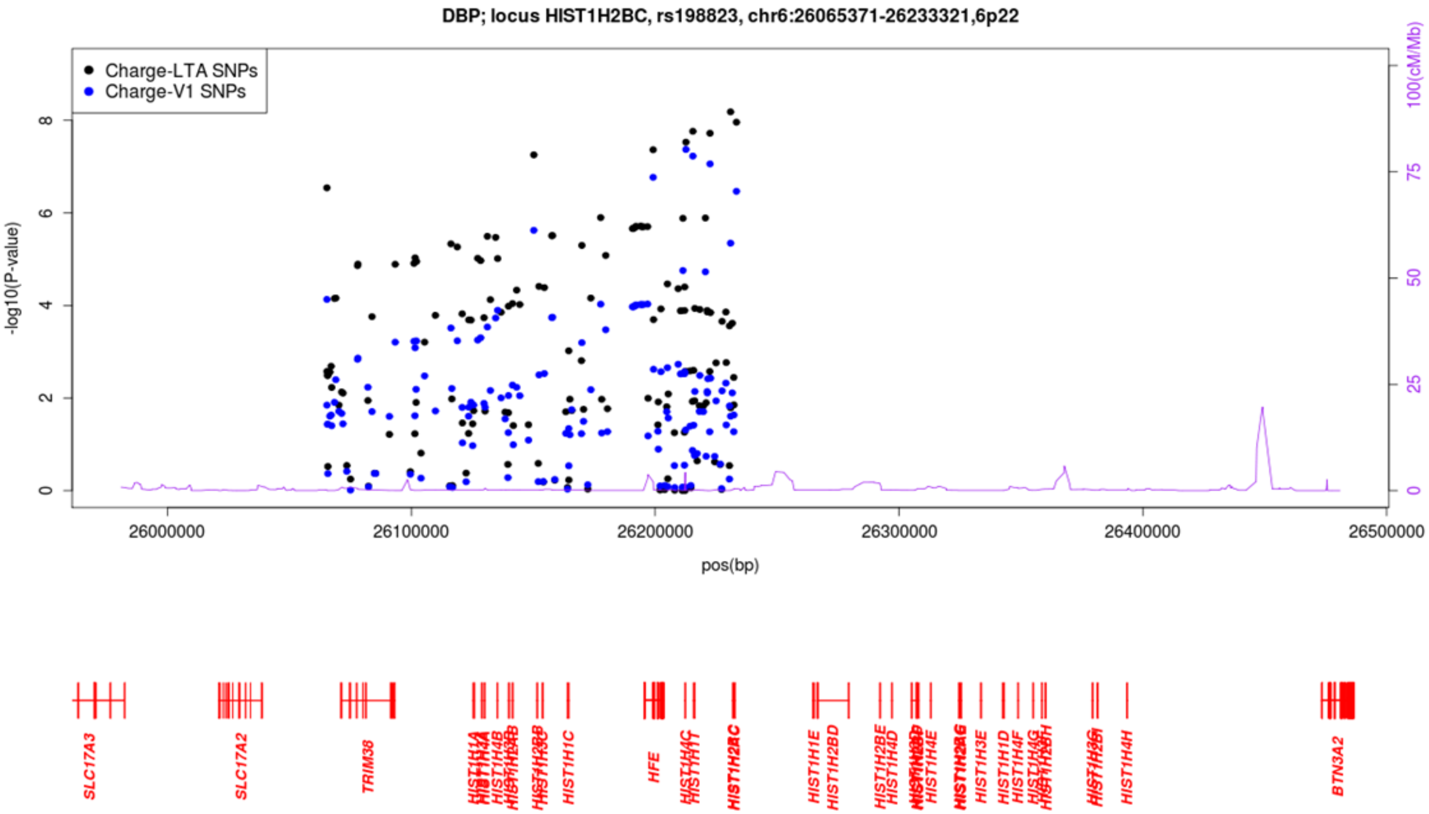
(a11)

DBP,EBF1,5q33



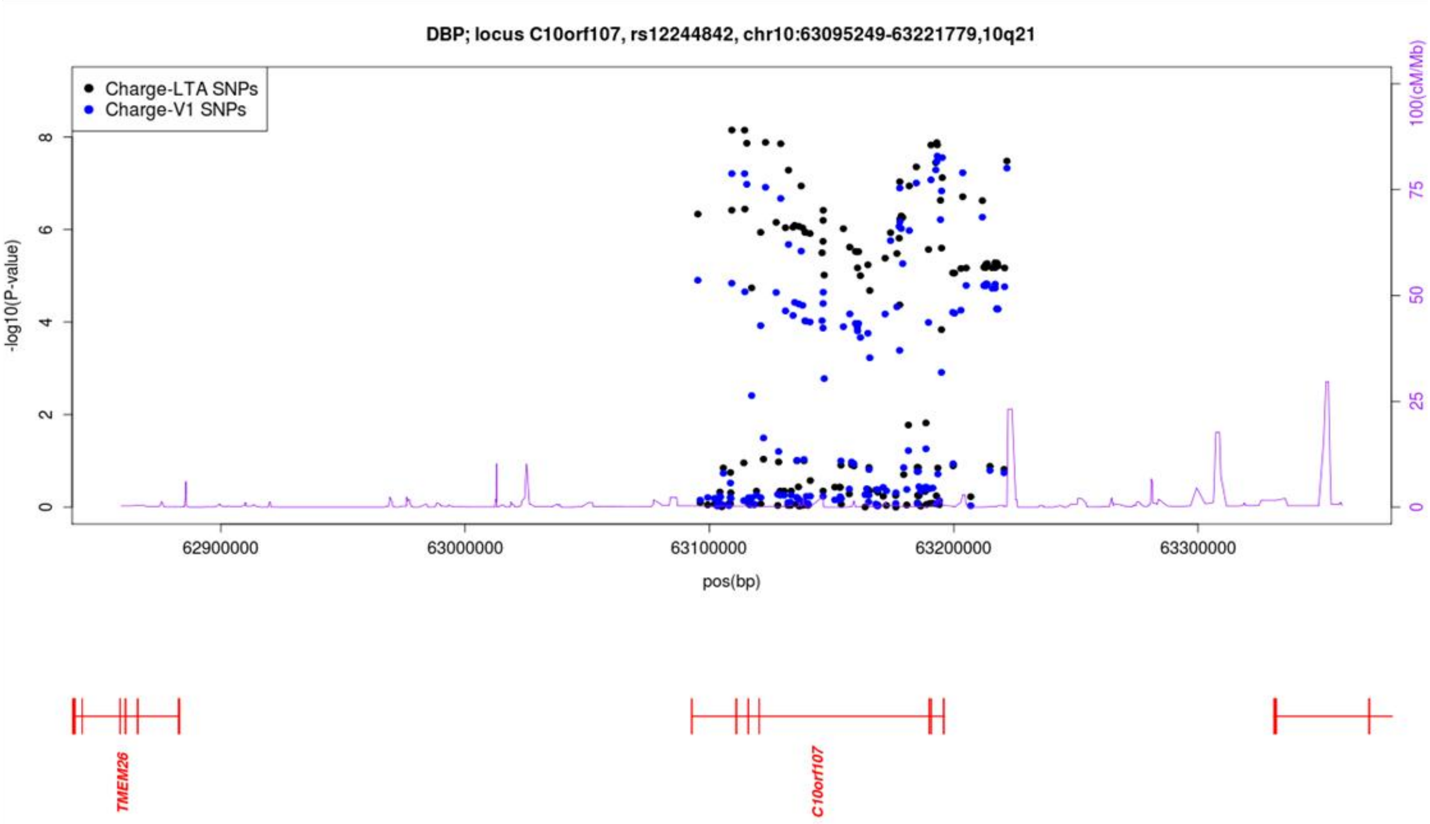
(a12)

DBP, HIST1H2BC,6p22



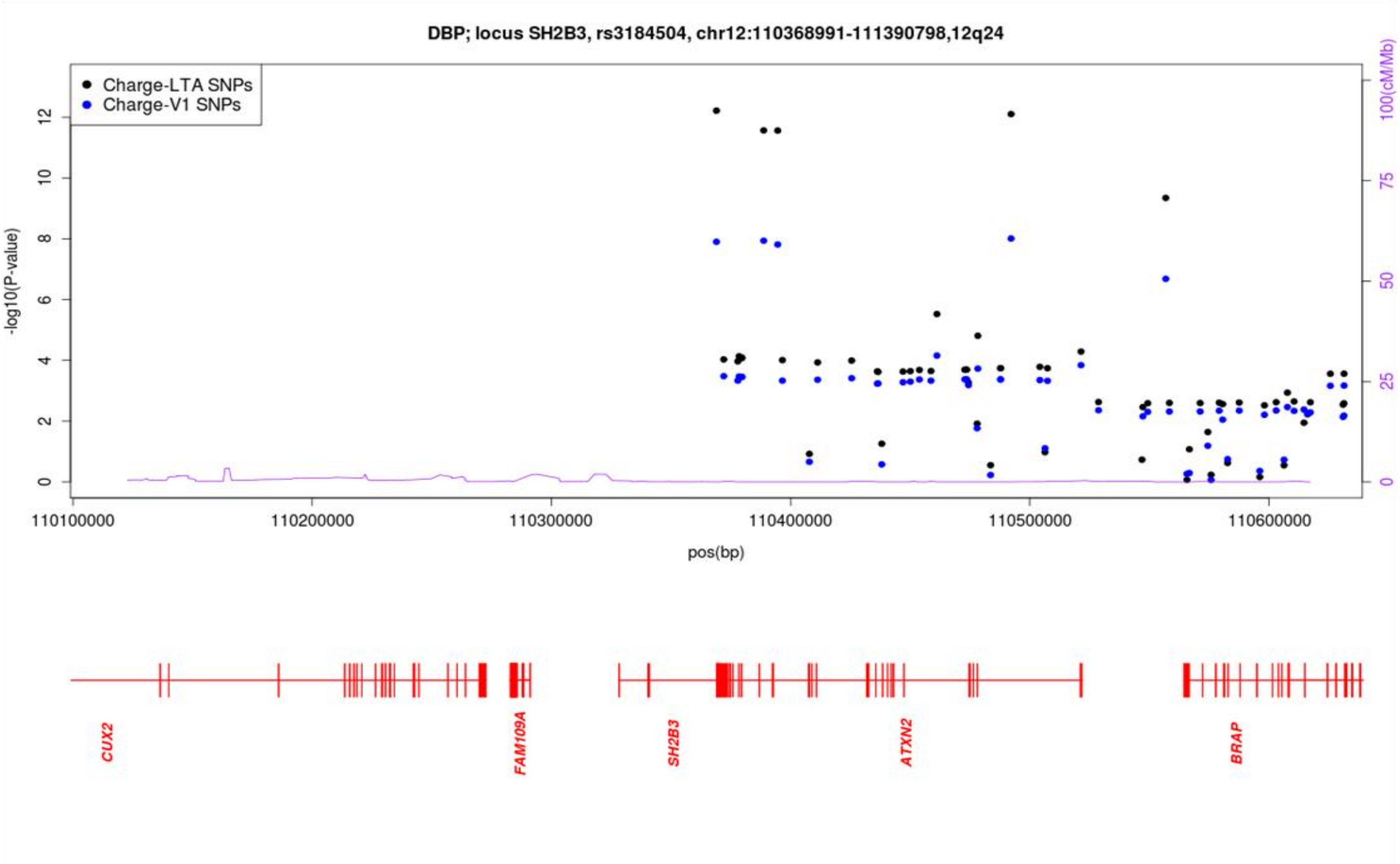
(a13)

DBP,C10orf107



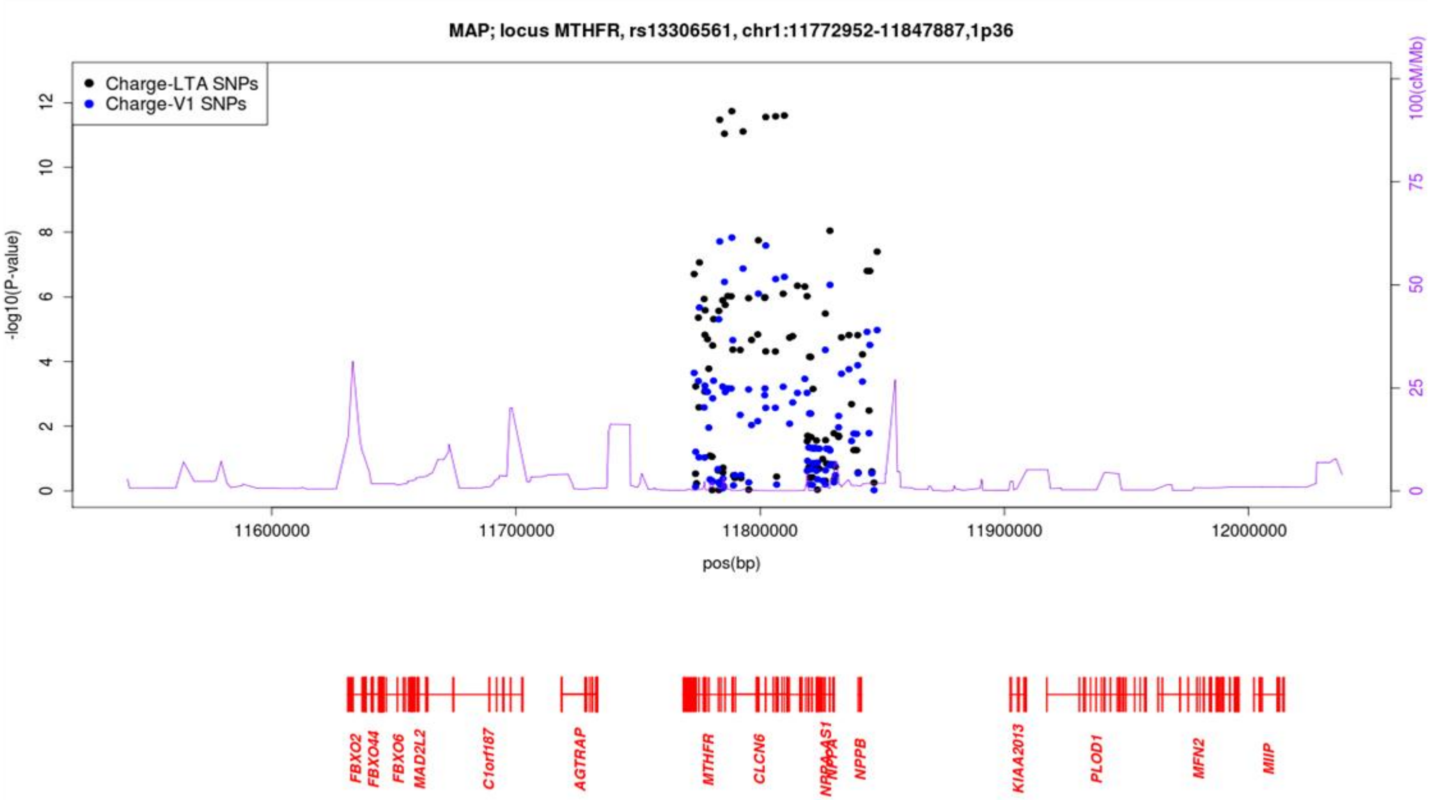
(a14)

DBP, SH2B3,12q24



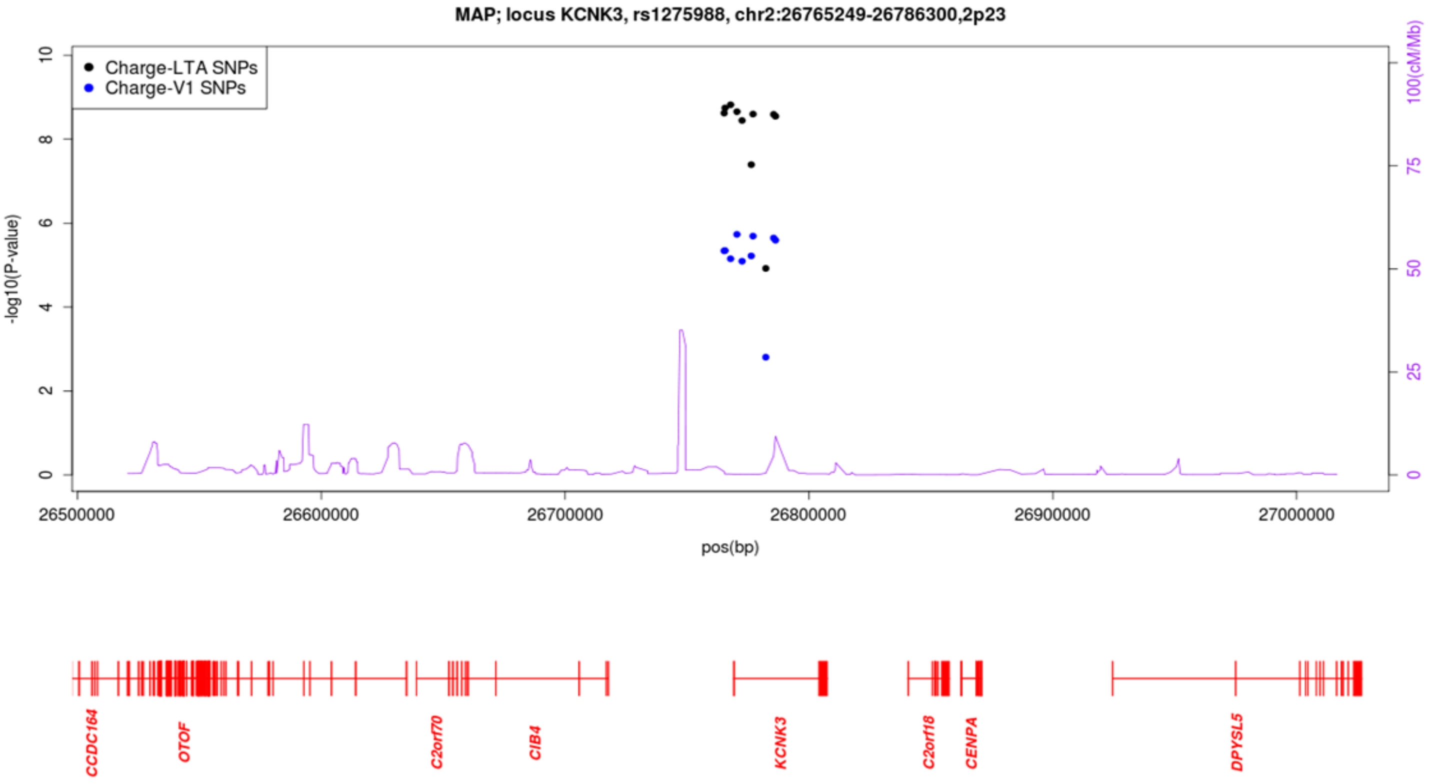
(a15)

MAP, MTHFR,1p36



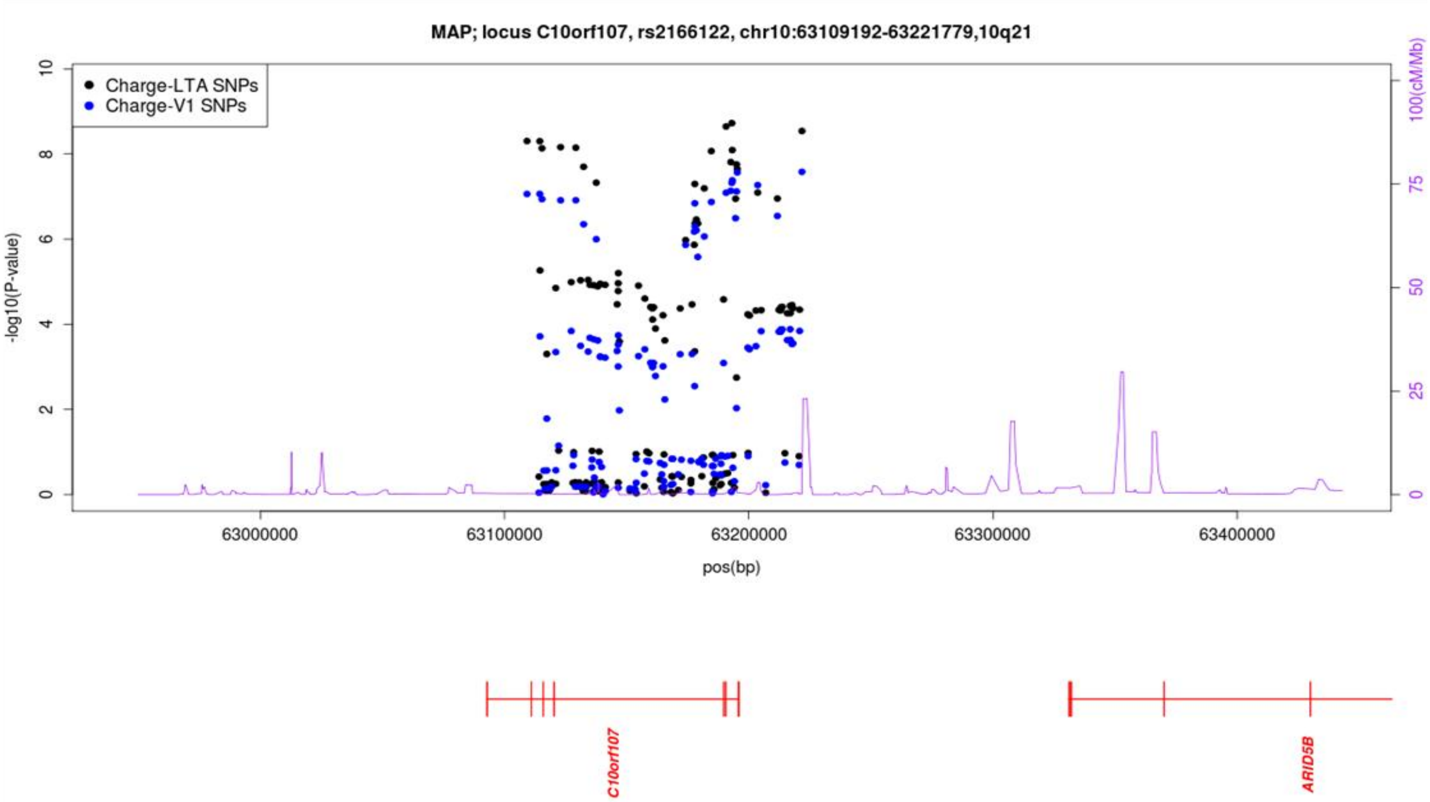
(a16)

MAP, KCNK3,2p23



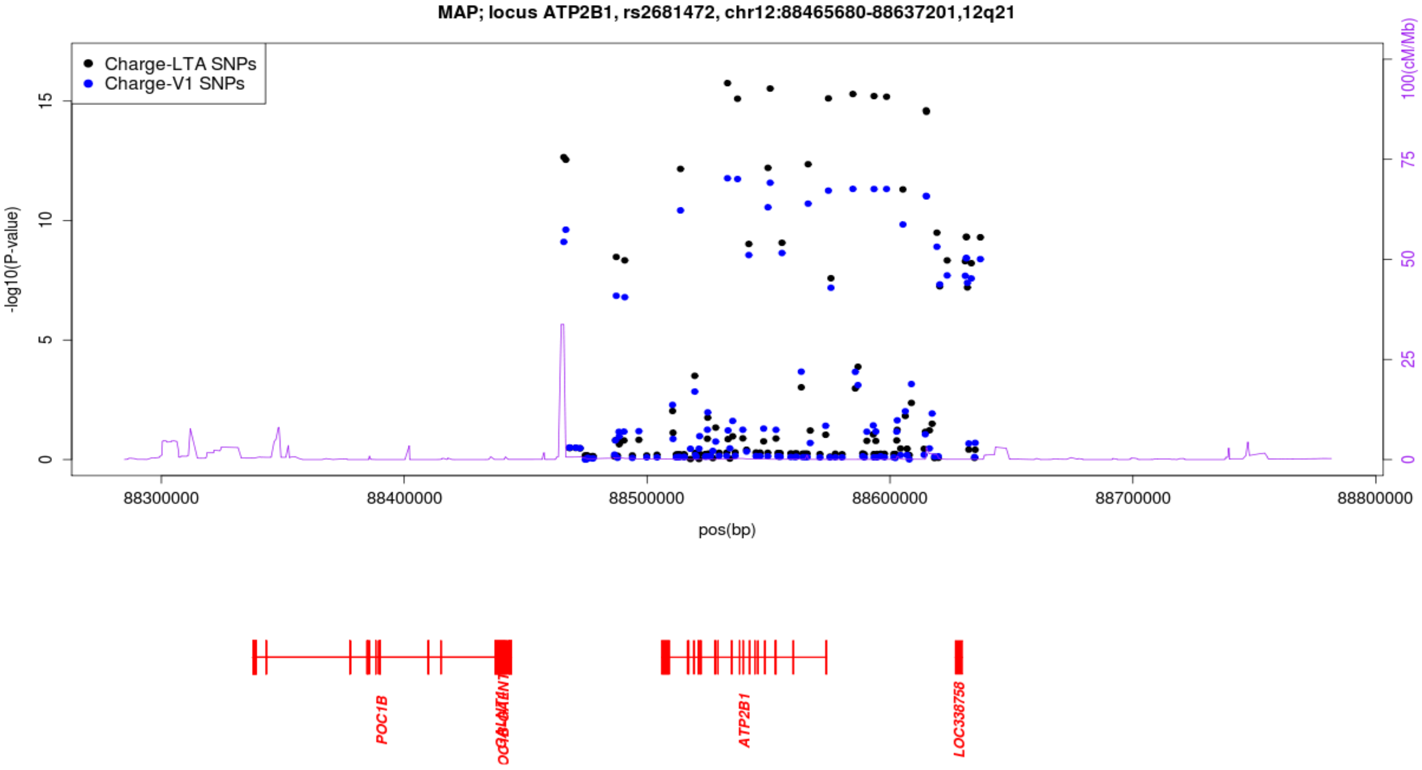
(a17)

MAP, C10orf107,10q21



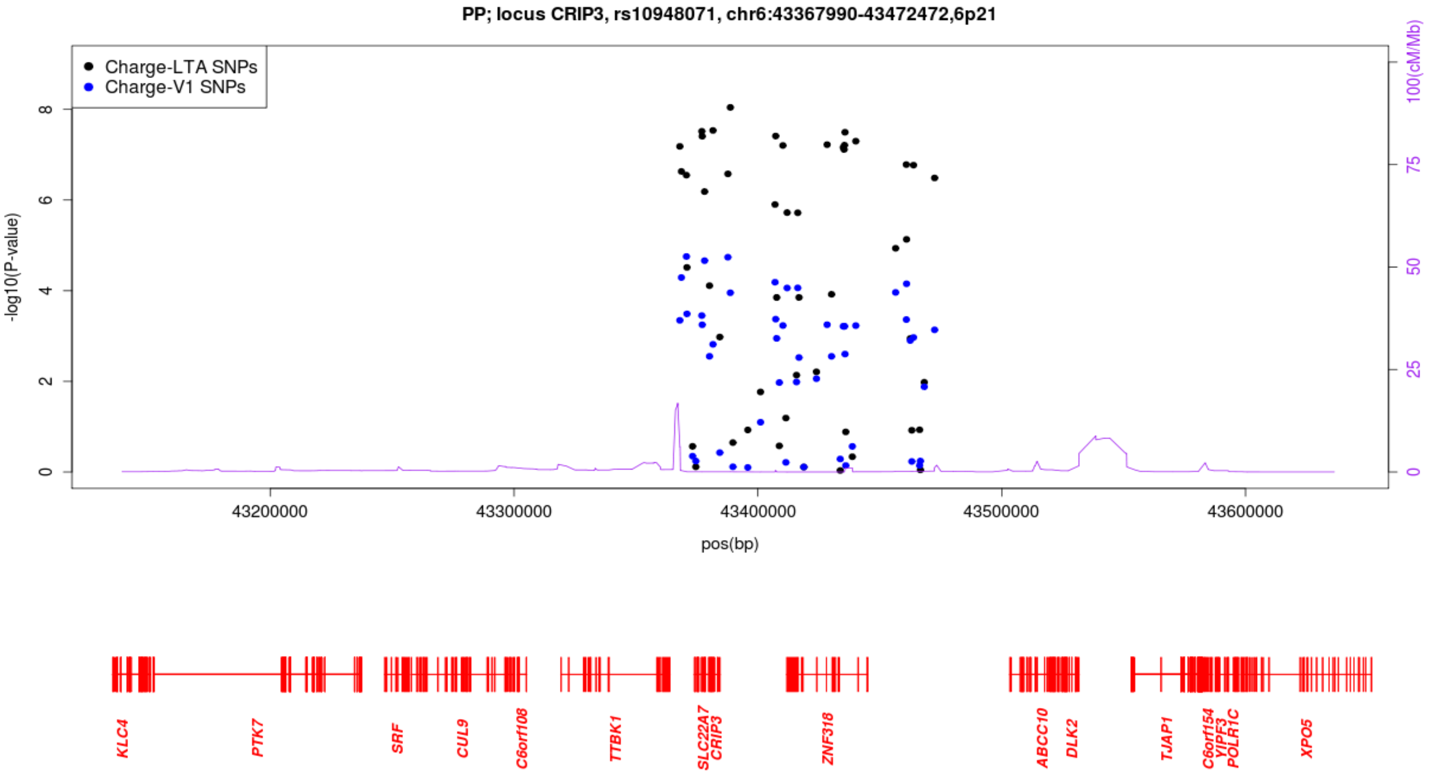
(a18)

MAP, ATP2B1,12q21



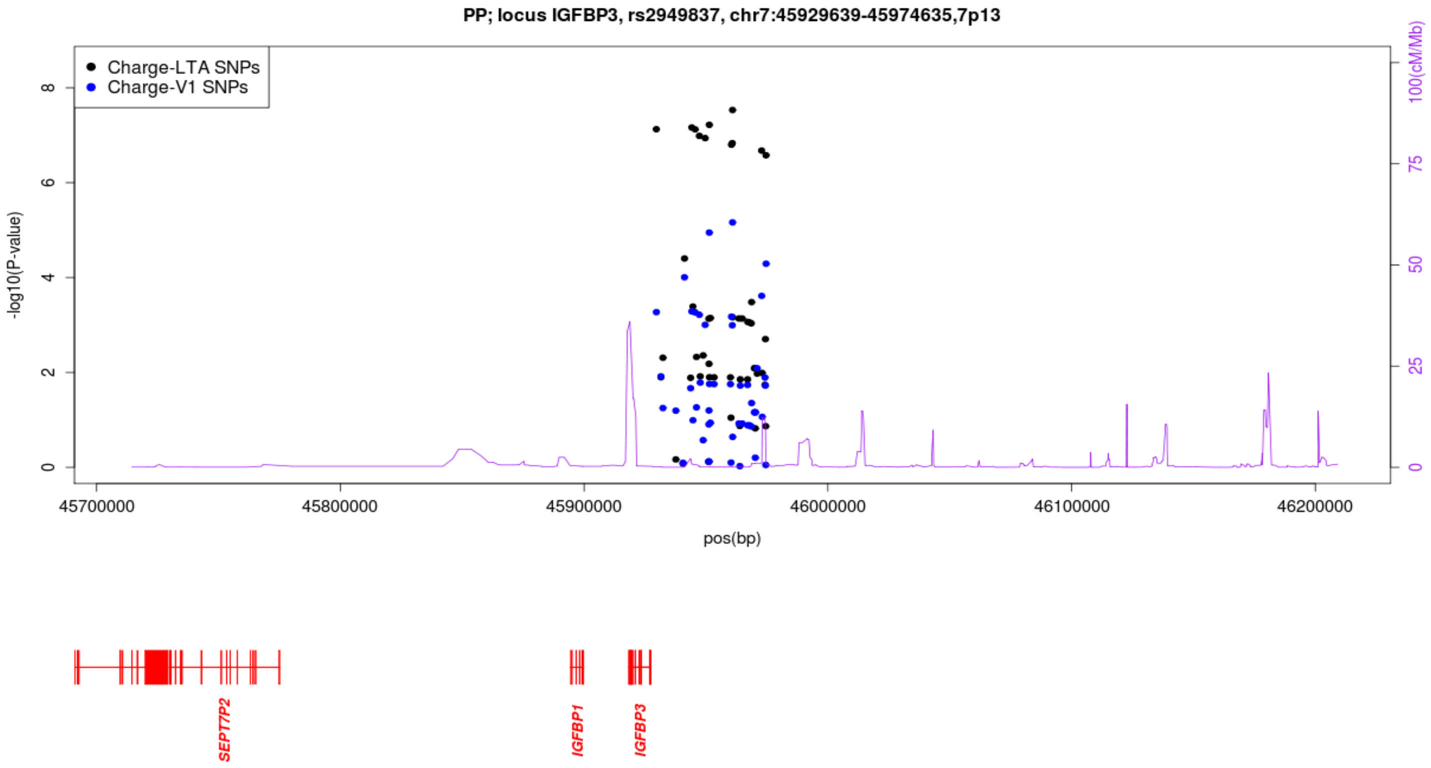
(a19)

PP, CRIP3,6p21



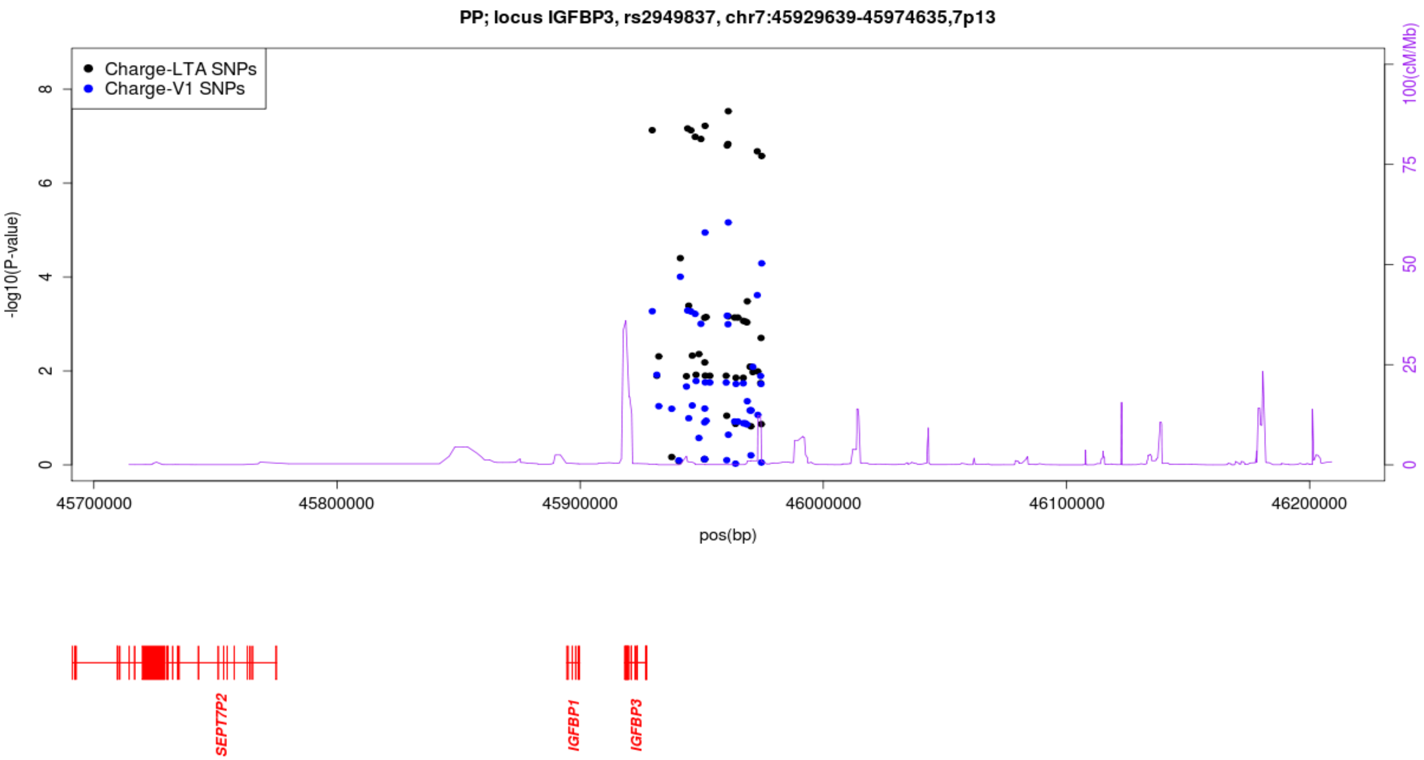
(a20)

PP, IGFBP3,7p13



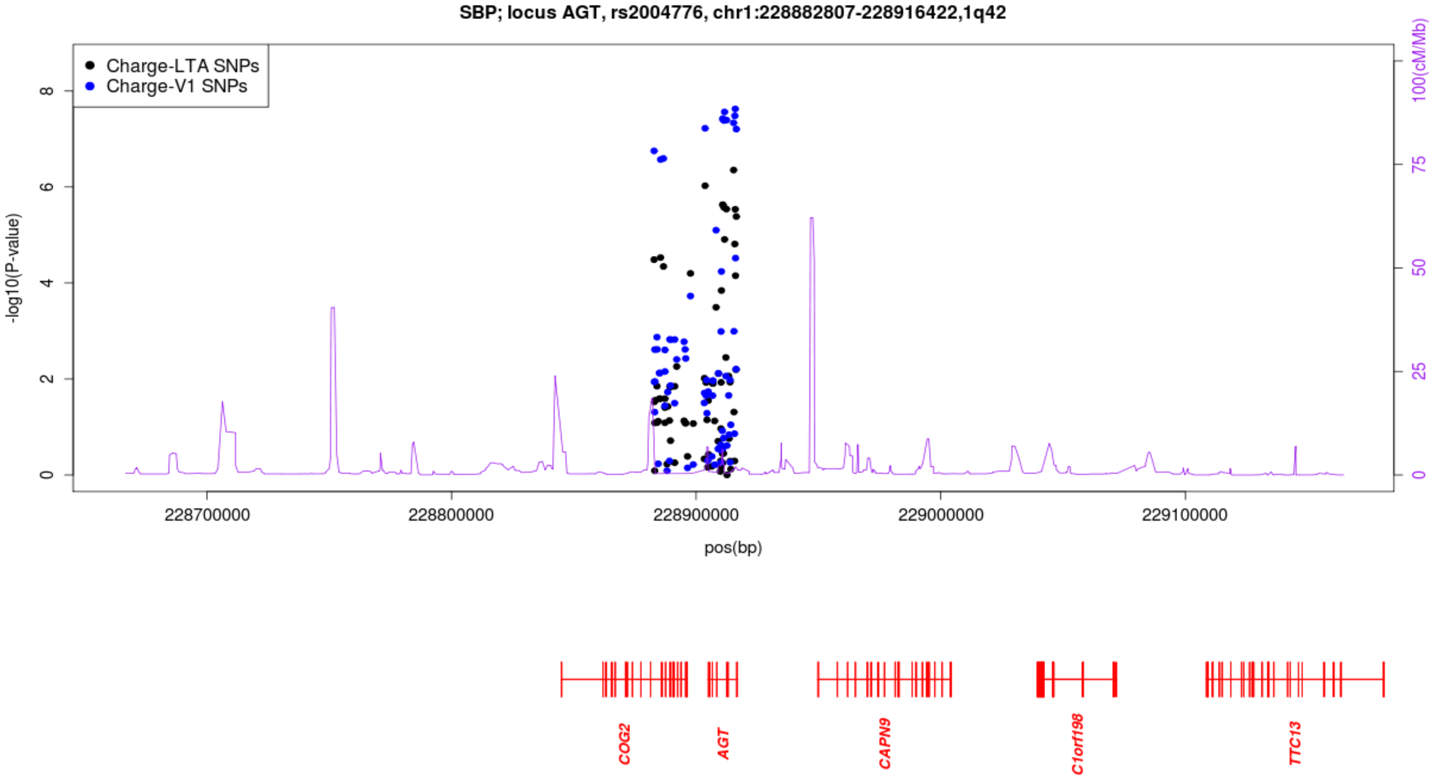
(a21)

PP, IGFBP3,7p13



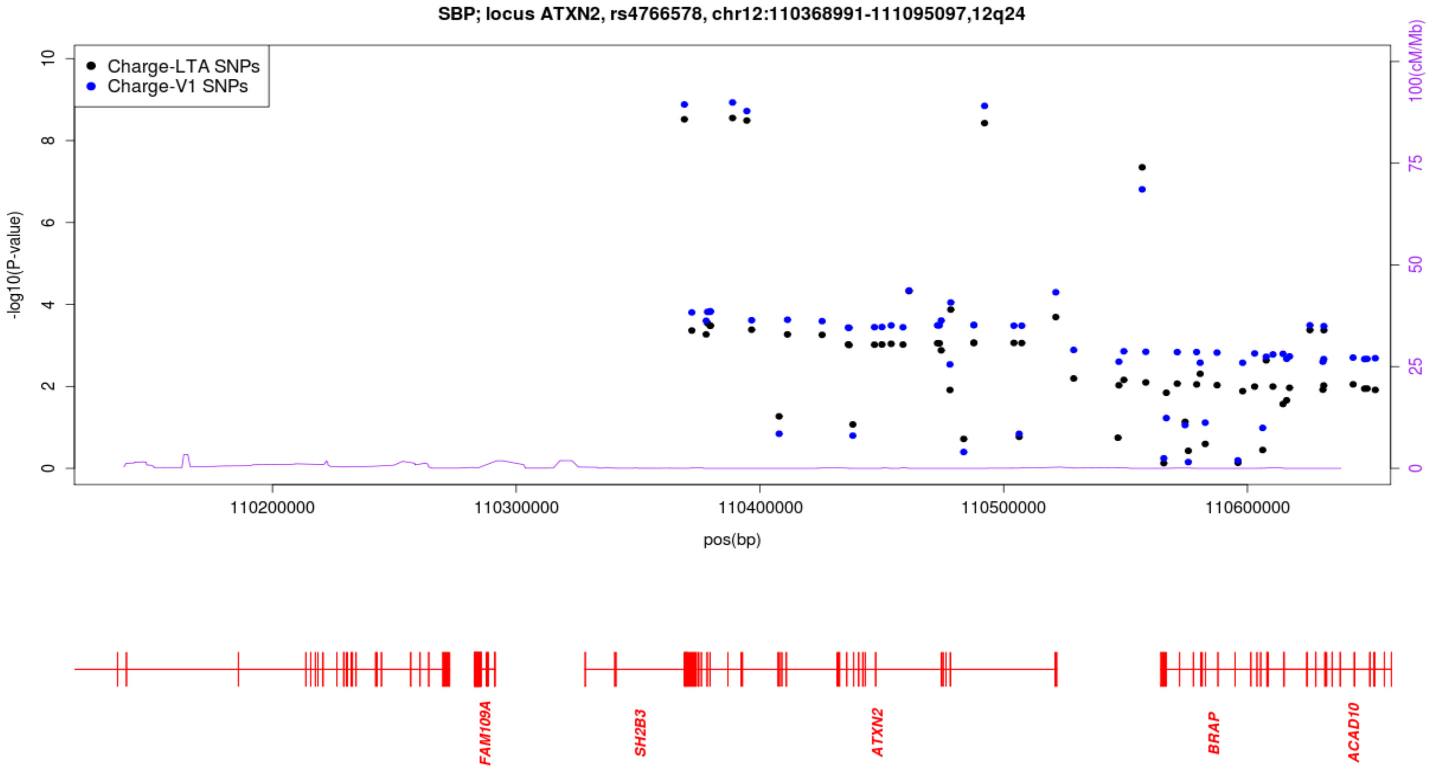
(b1)

SBP,AGT,1q42



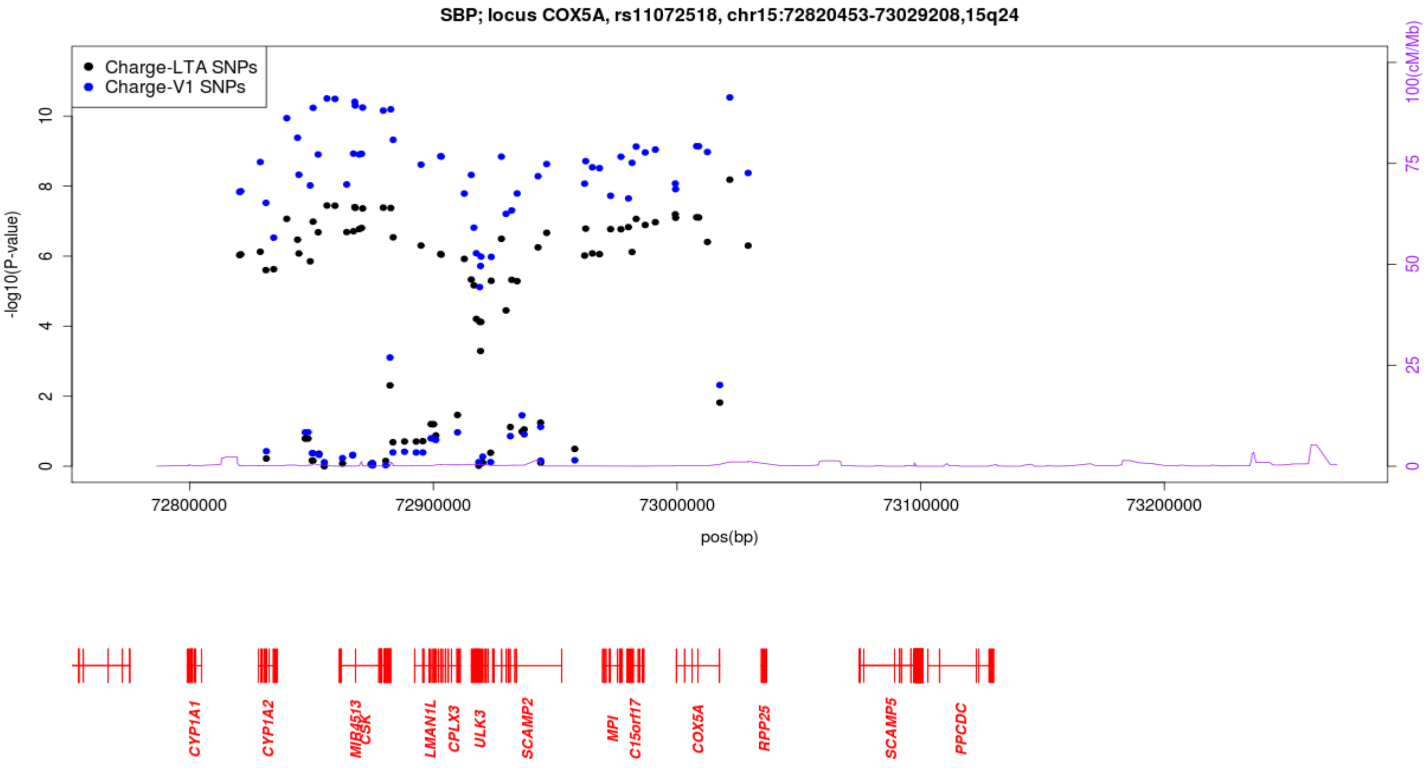
(b2)

SBP,ATXN2,12q24



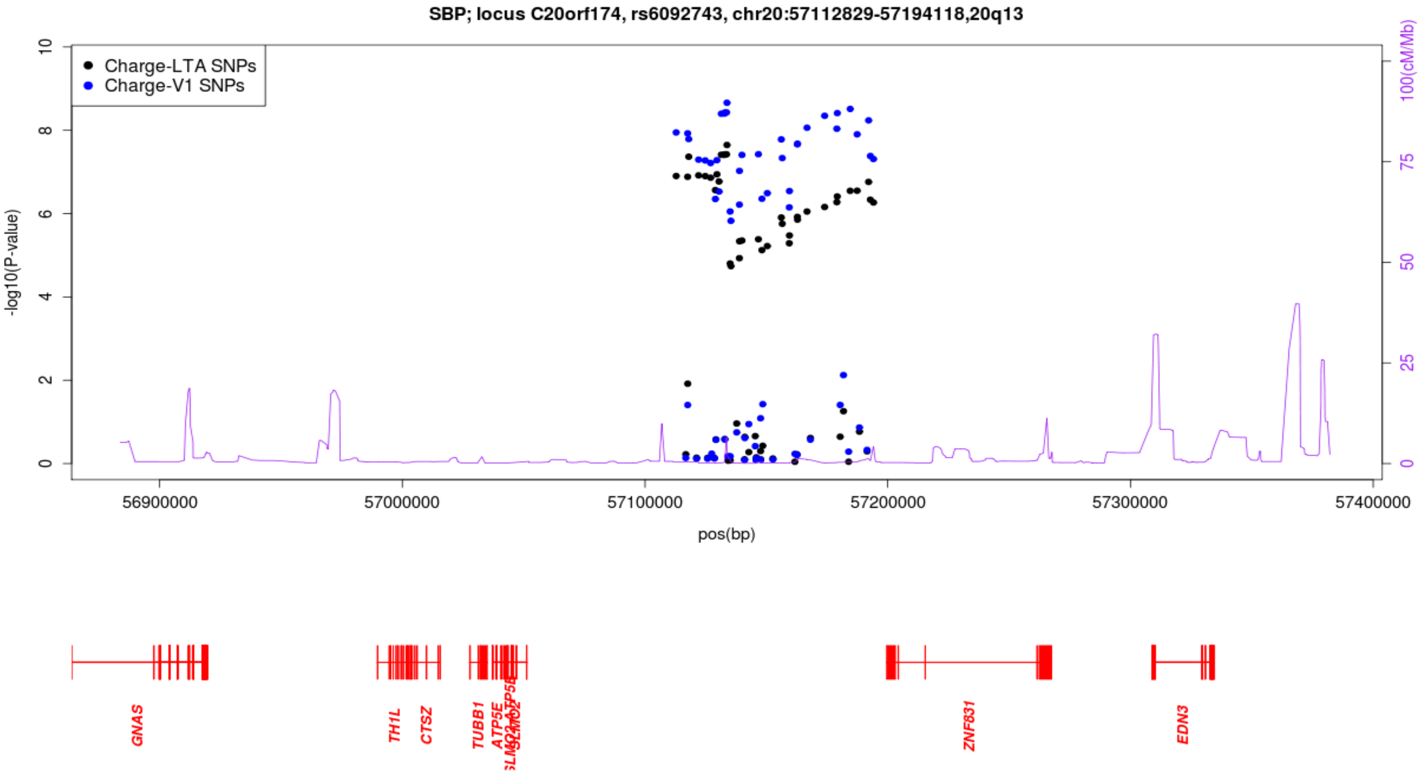
(b3)

SBP,COX5A,15q24



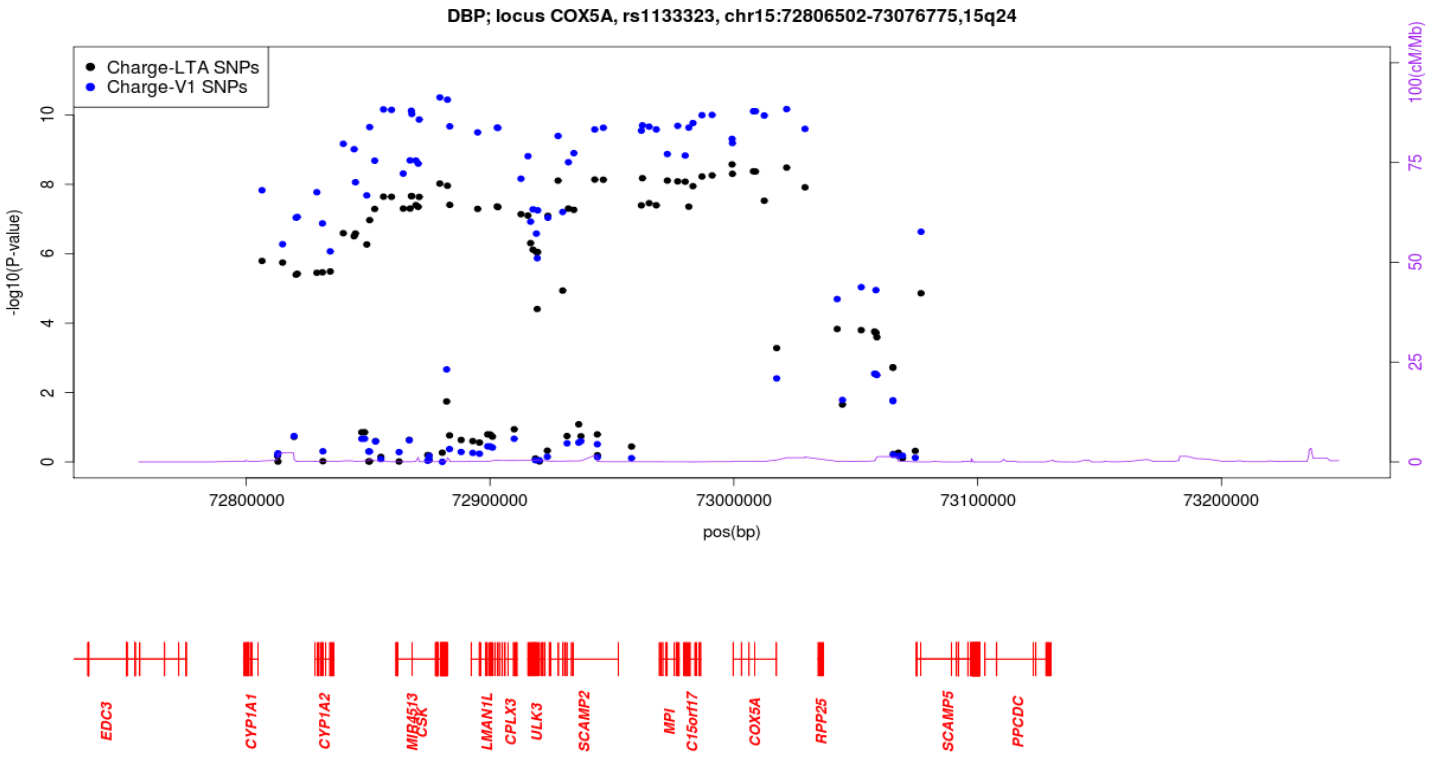
(b4)

SBP, C20orf174,20q13



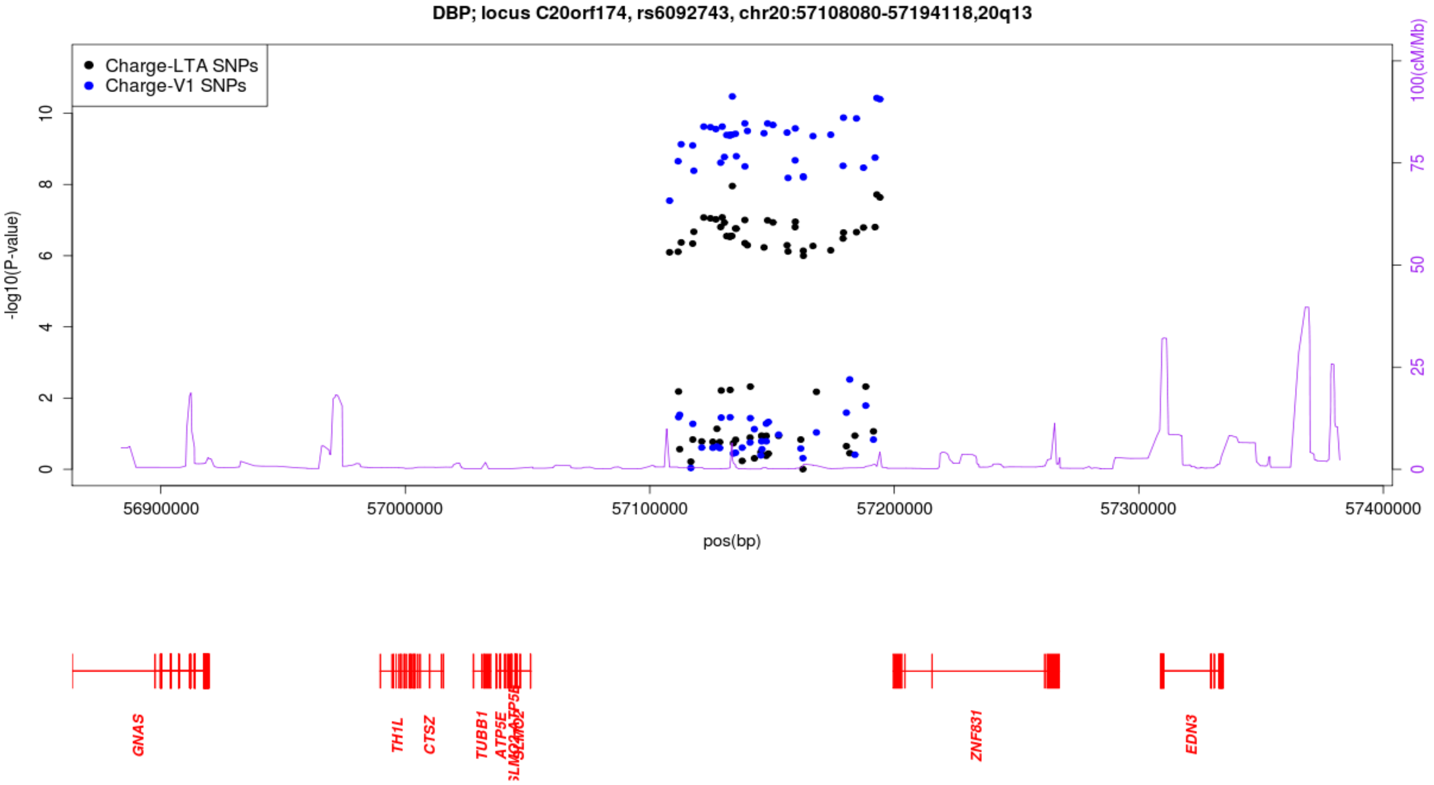
(b5)

DBP, COX5A,15q24



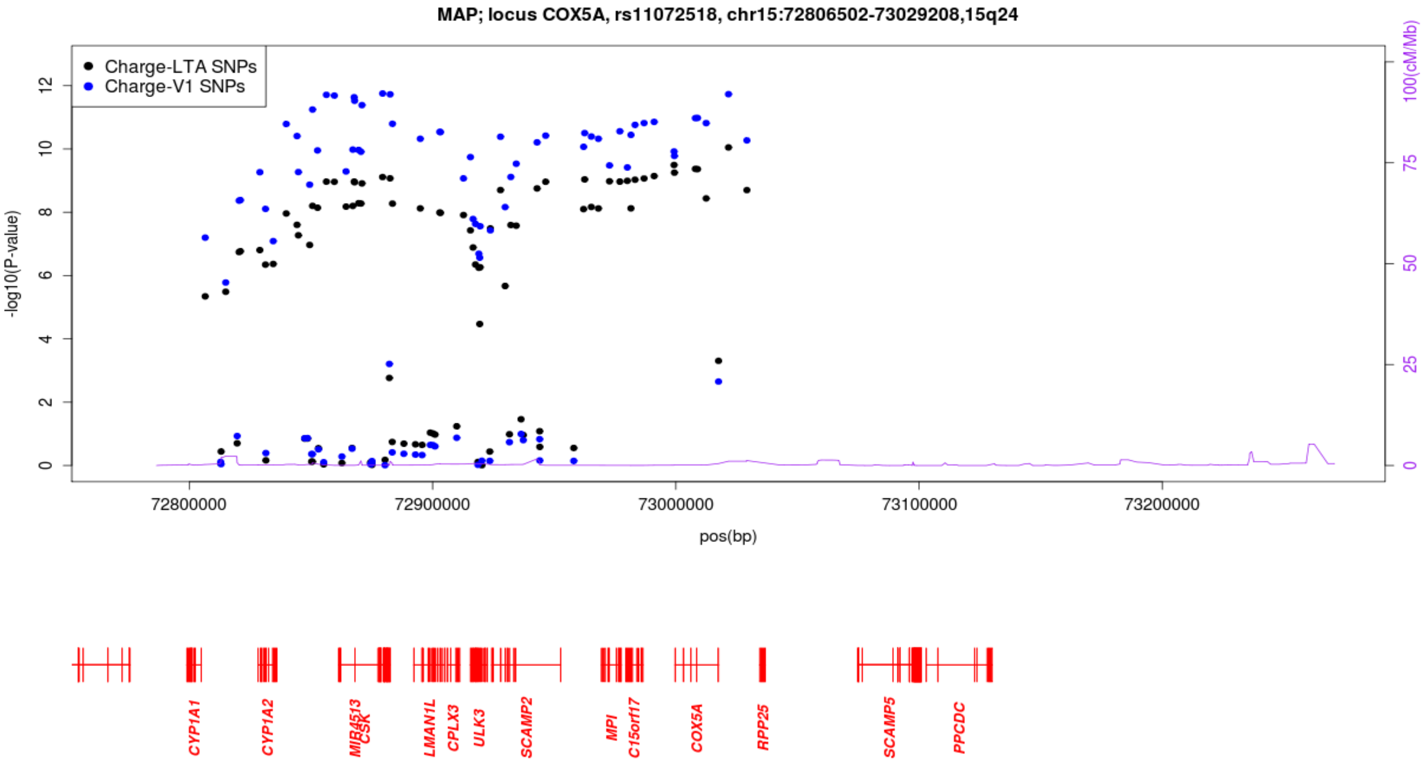
(b6)

DBP, C20orf174,20q13



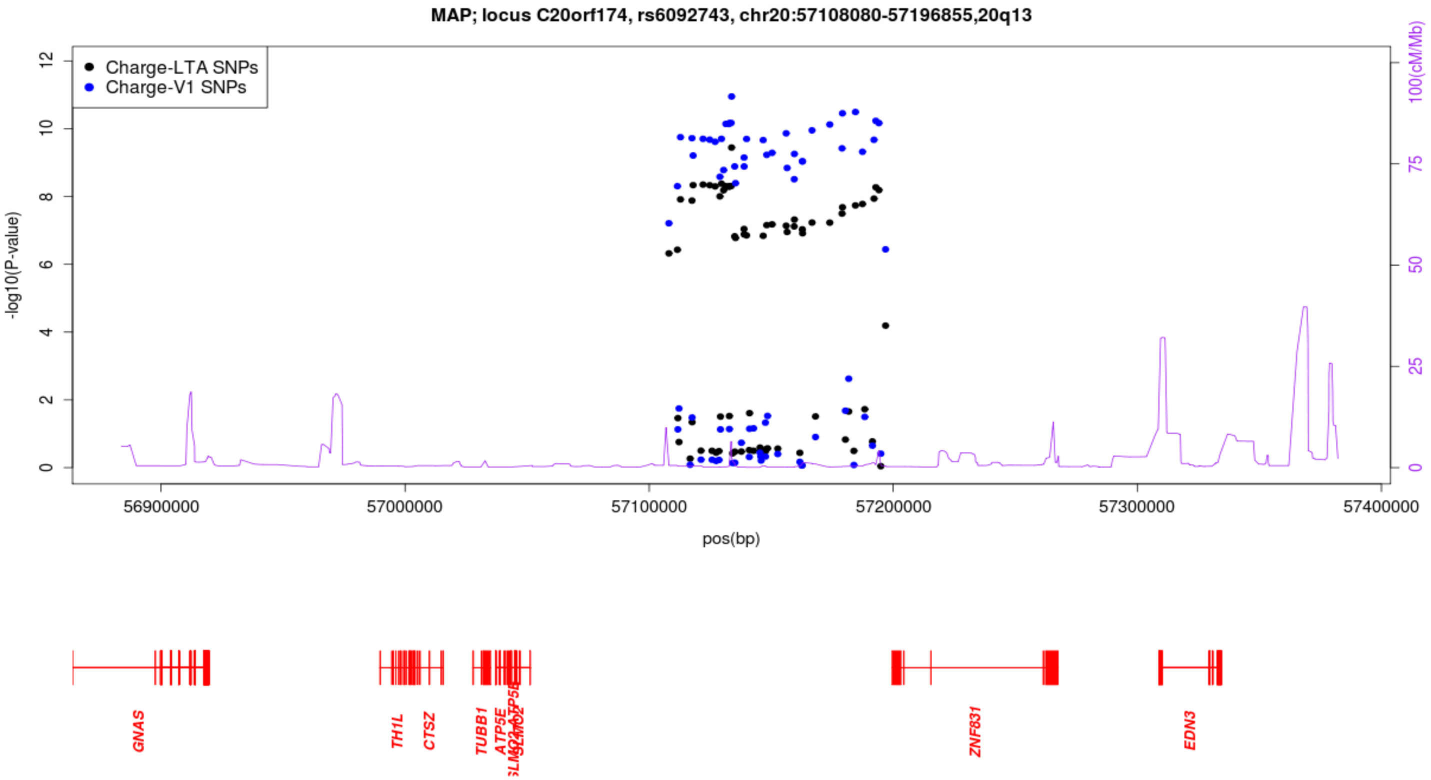
(b7)

MAP, COX5A,15q24



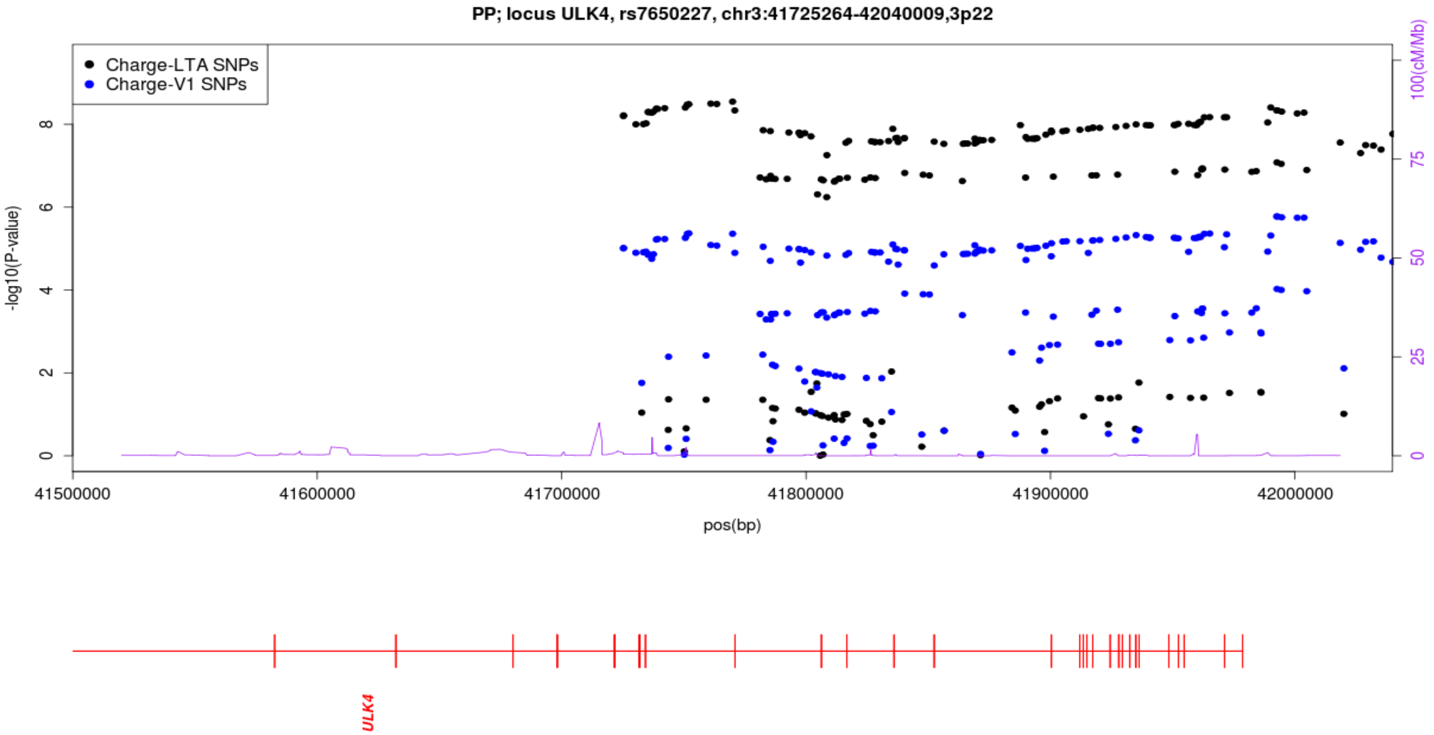
(b8)

MAP, C20orf174,20q13



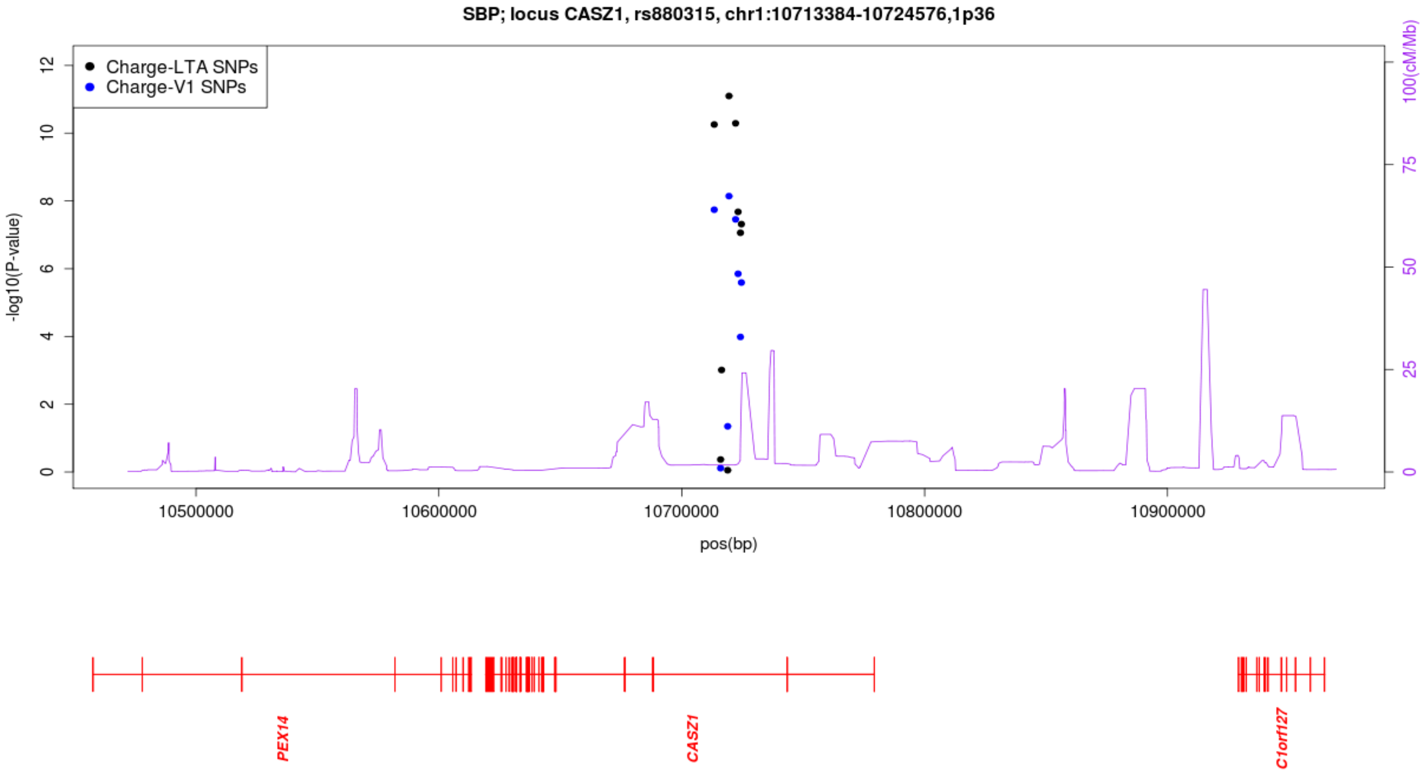
(c1)

PP,ULK4,3p22



(d1)

SBP, CASZ1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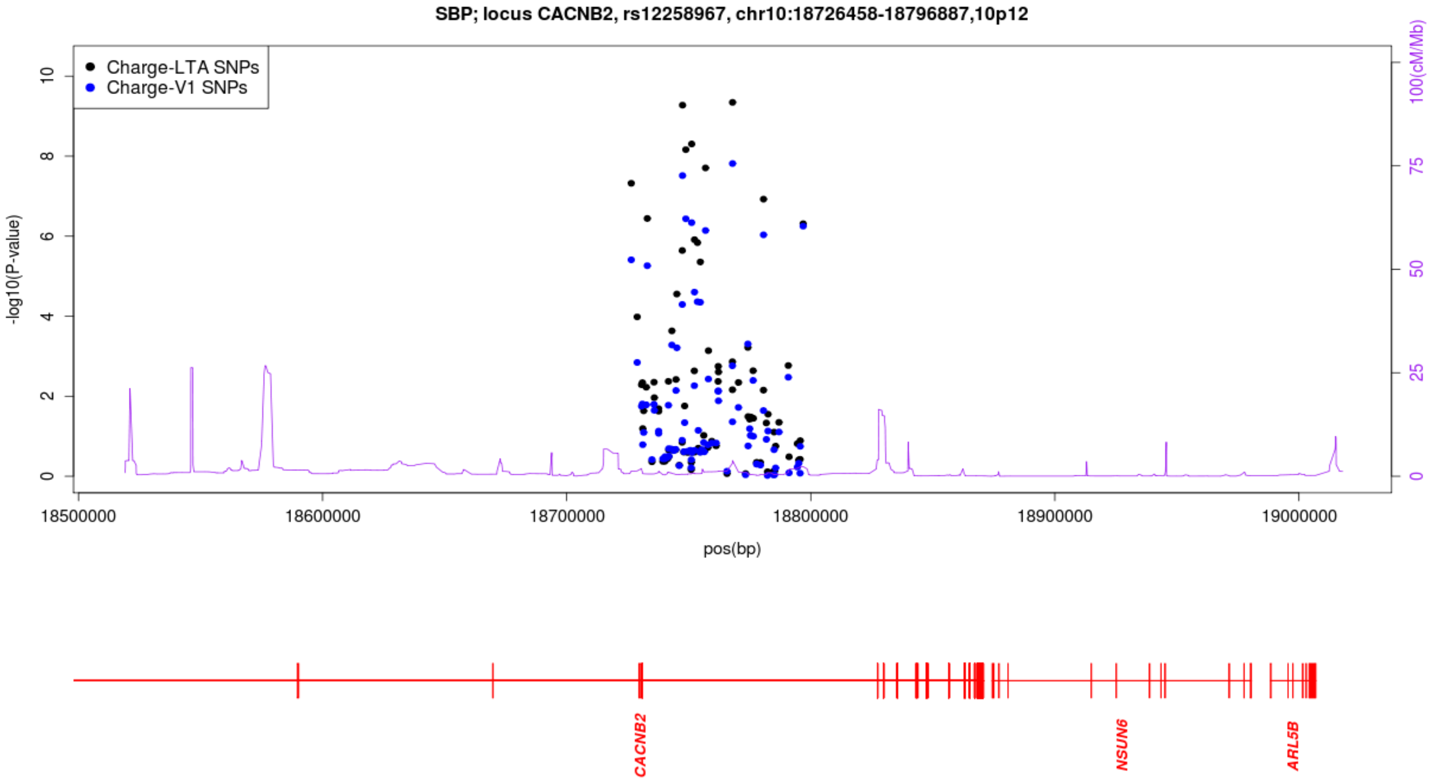
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
10500000
10600000
10700000
10800000
10900000
pos(bp)
PEX14
CASZ1
C1orf127

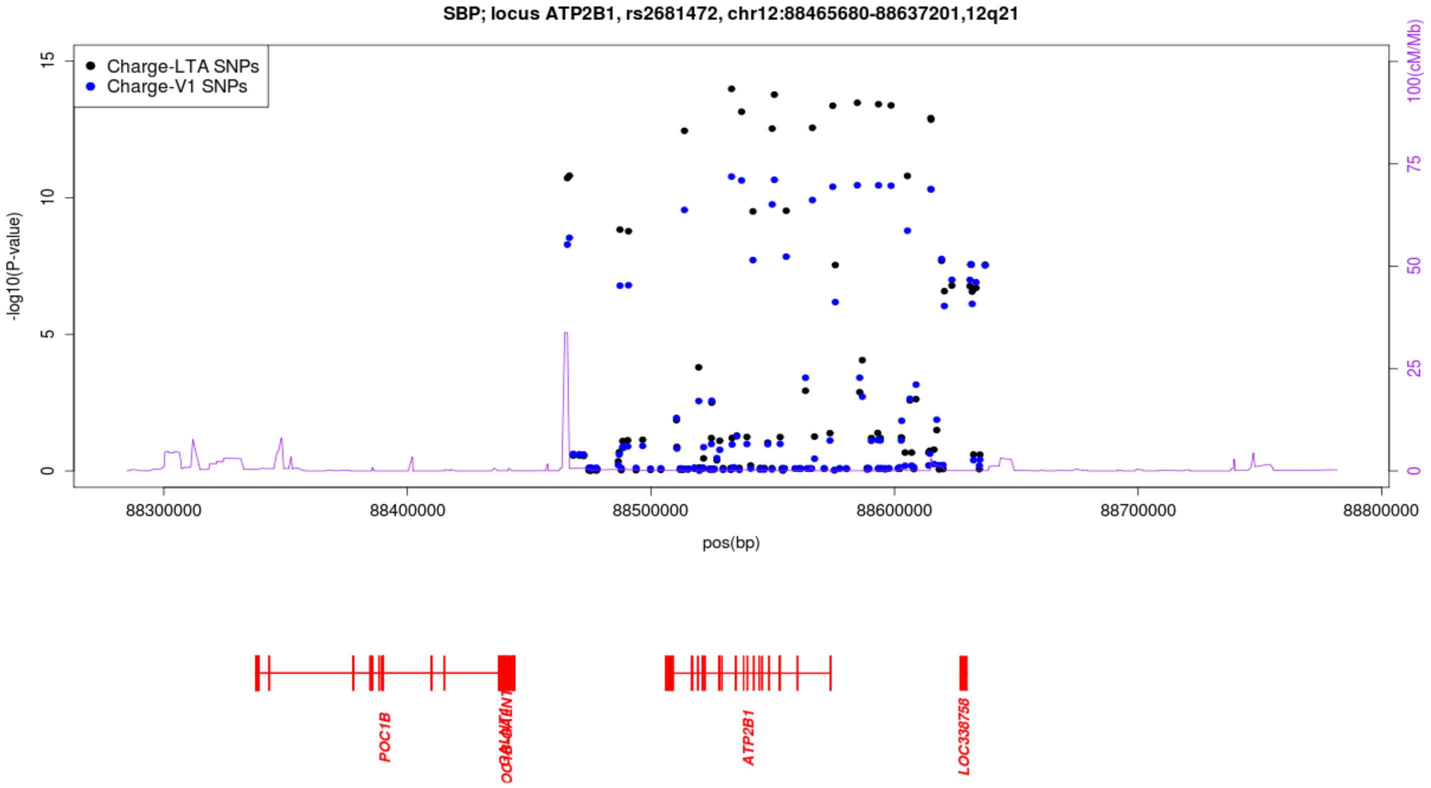
(d2)

SBP, CACNB2



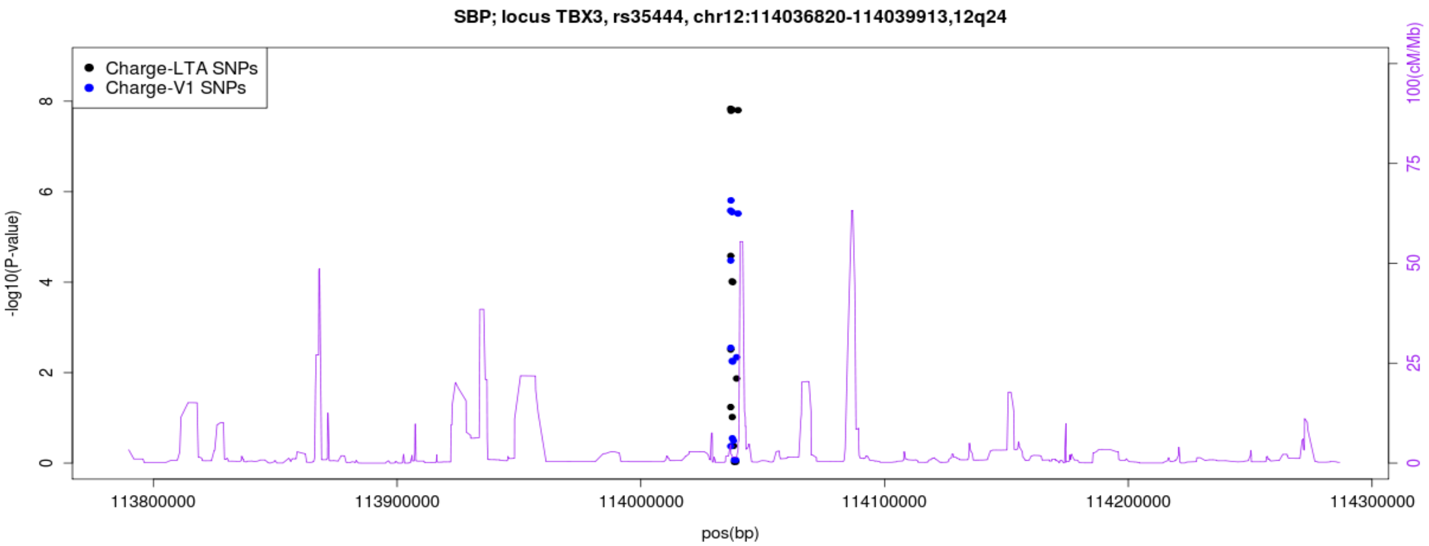
(d3)

SBP, ATP2B1



(d4)

SBP, TBX3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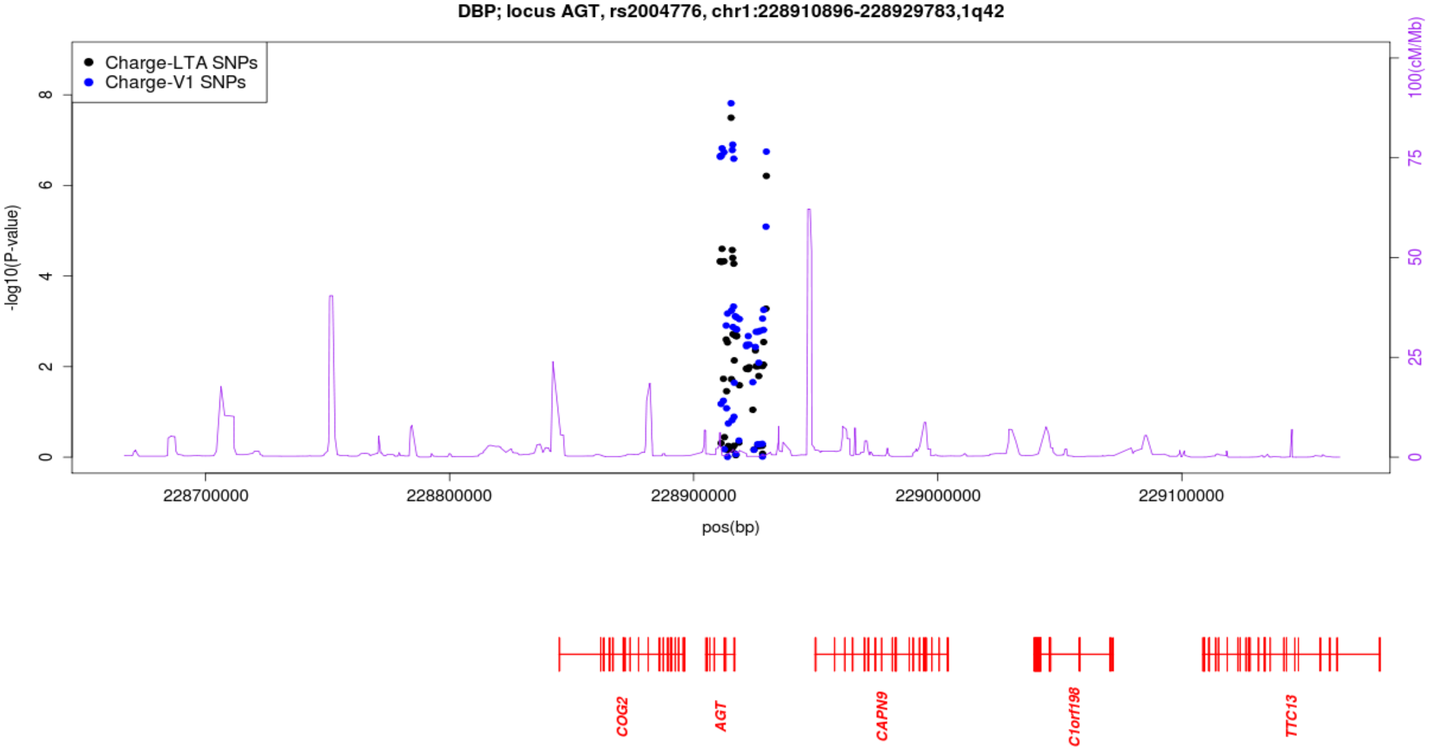
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
113800000
113900000
114000000
114100000
114200000
114300000
pos(bp)

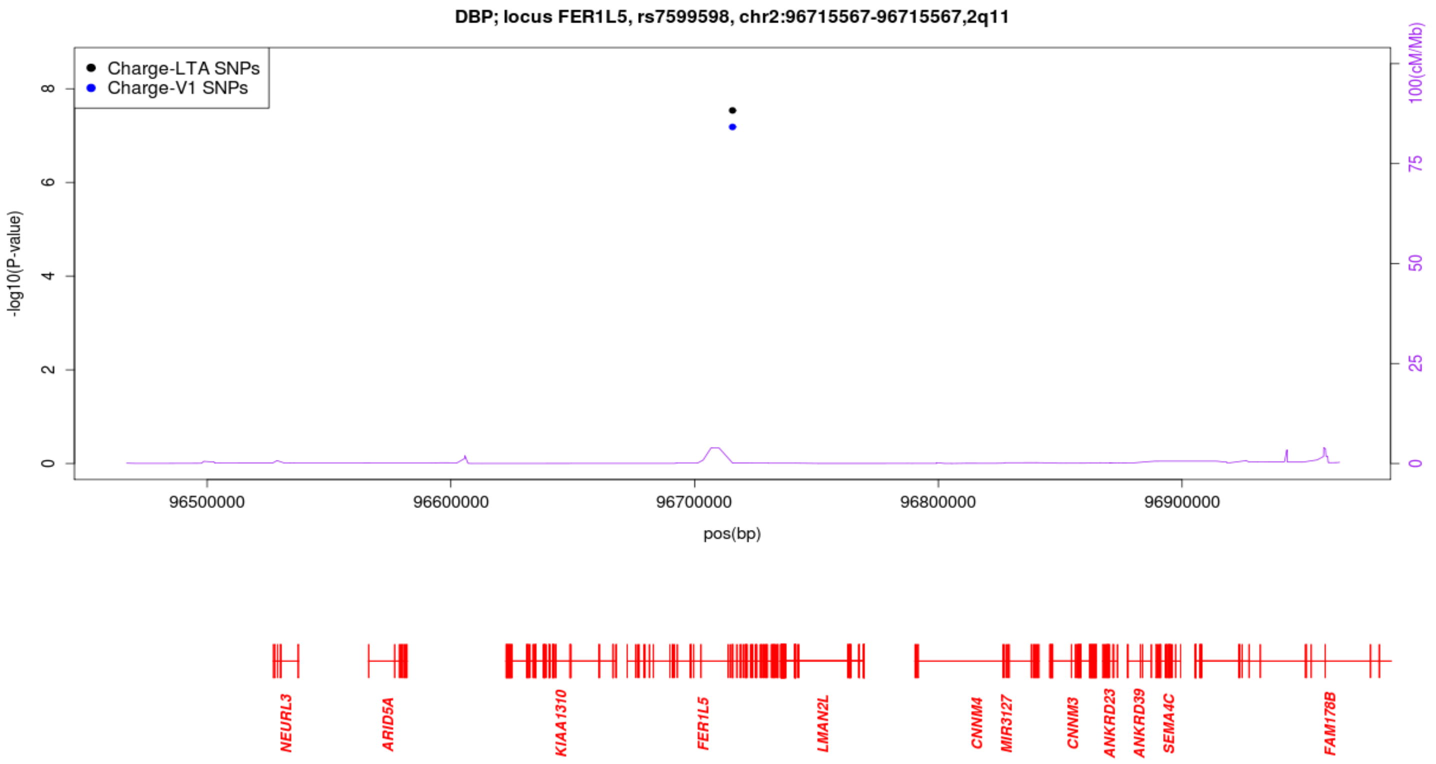
(d5)

DBP, AGT


DBP; locus AGT, rs2004776, chr1:228910896-228929783,1q42
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
228700000
228800000
228900000
229000000
229100000
pos(bp)
COG2
AGT
CAPN9
C1orf198
TTC13

(d6)

DBP, FER1L5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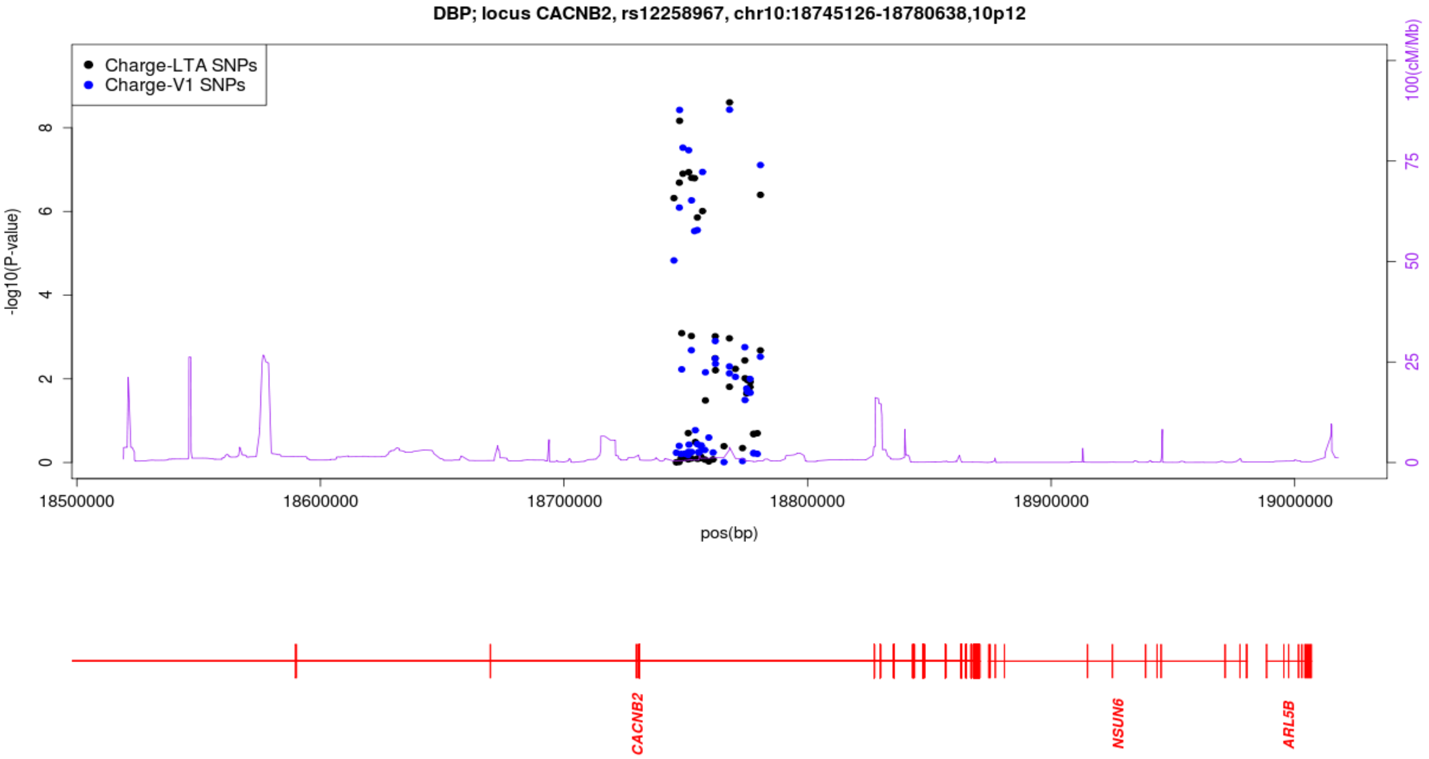
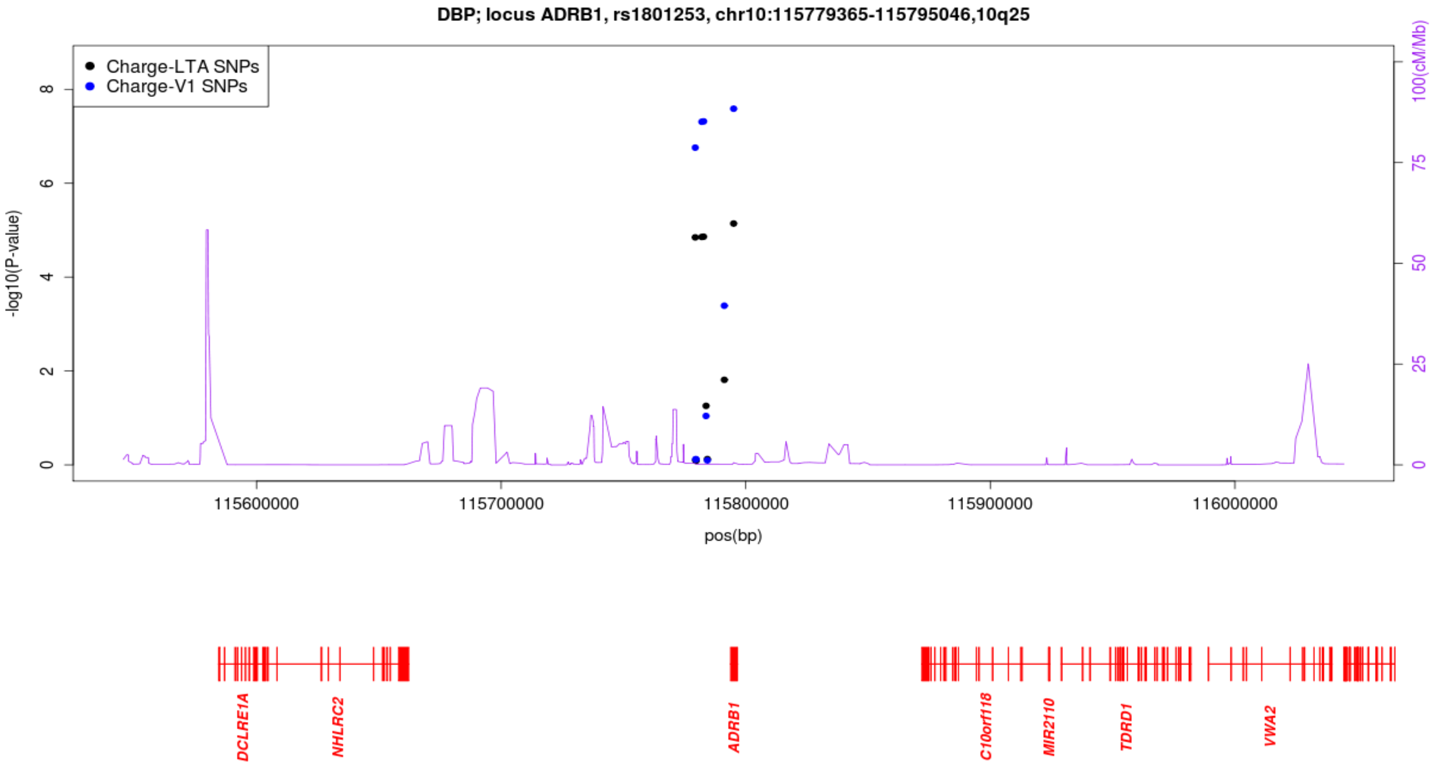
(d7)

DBP, CACNB2



(d8)

DBP, ADRB1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● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
115600000
115700000
115800000
115900000
116000000
pos(bp)
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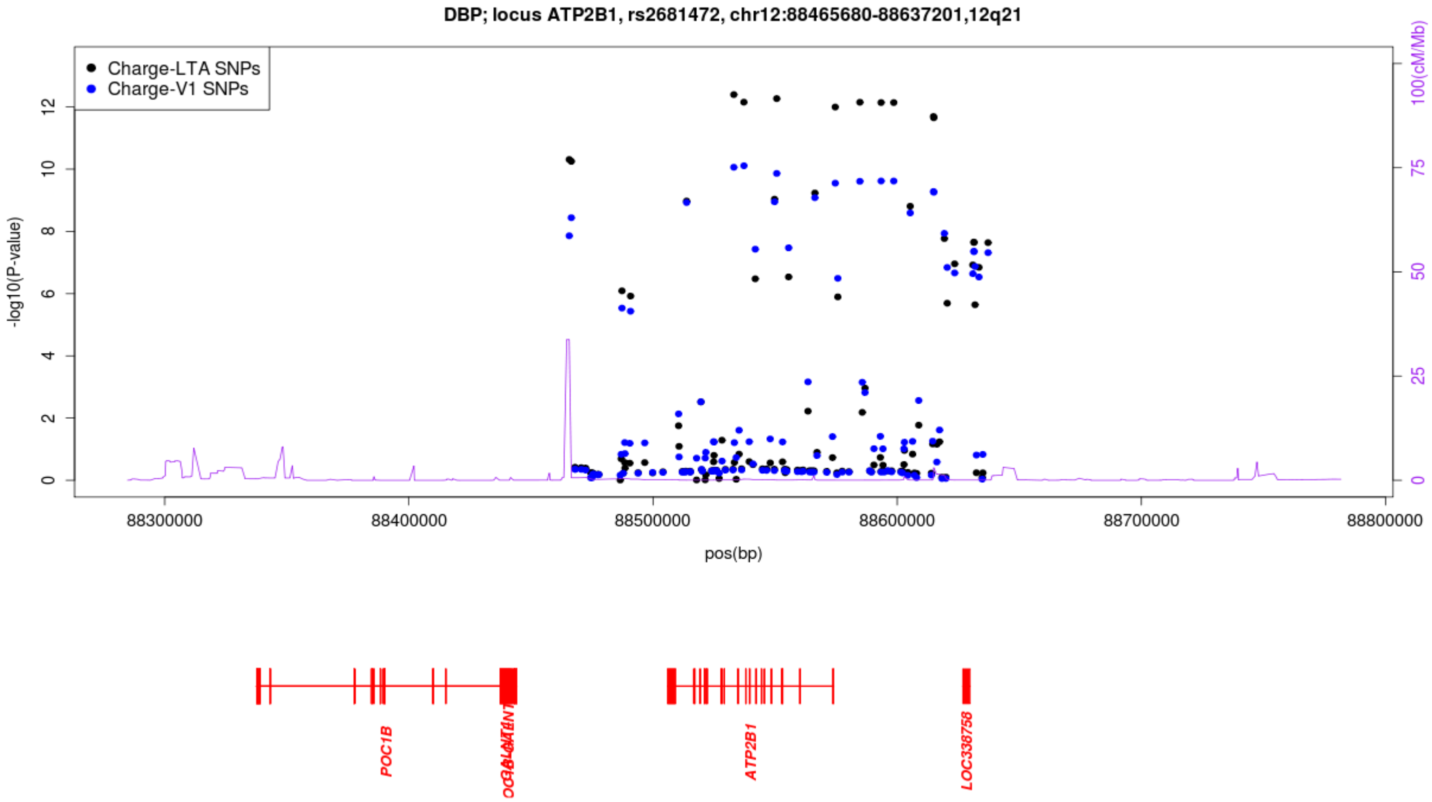
NHLRC2
ADRB1
C10orf118
MIR2110
TDRD1
VWA2

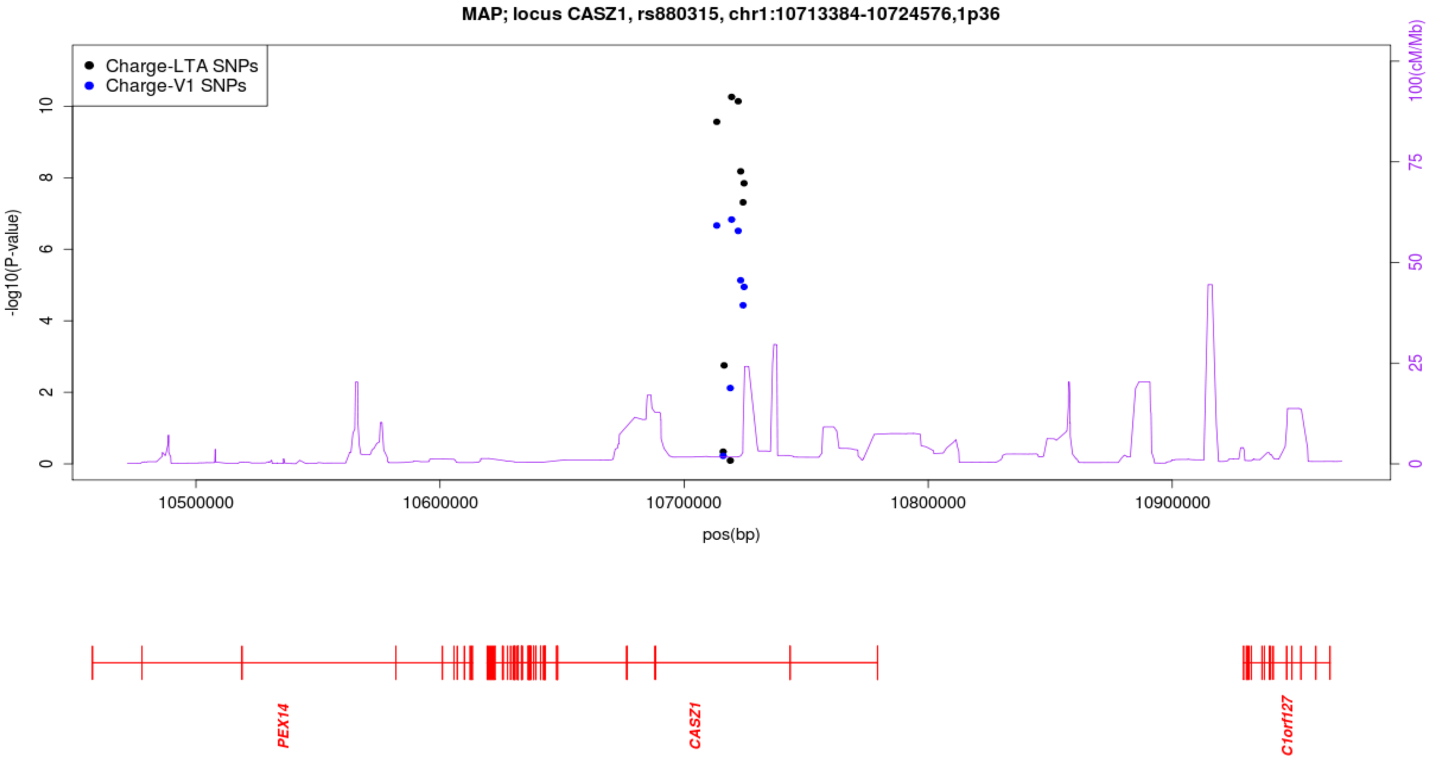
(d9)

DBP, ATP2B1



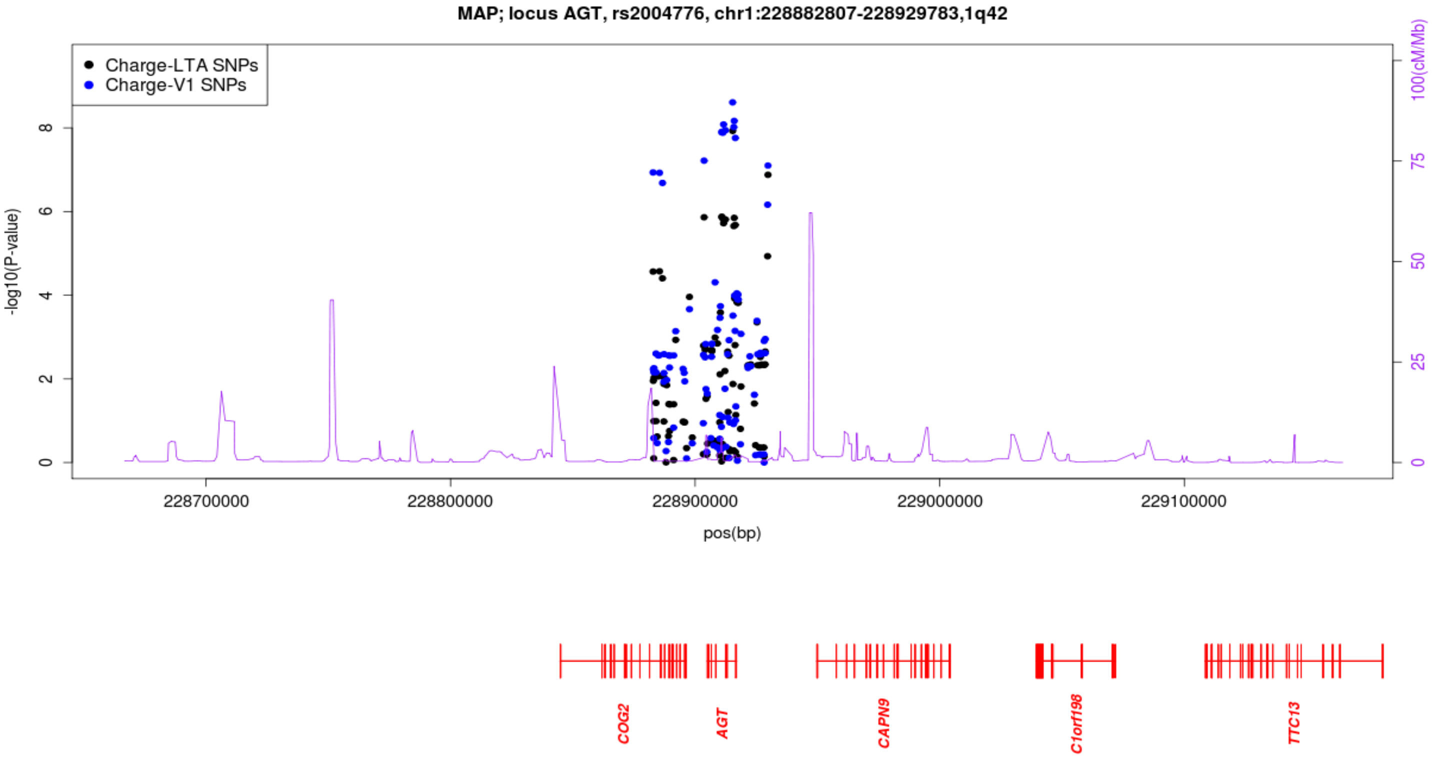
(d10)

MAP, CASZ1



(d11)

MAP, AGT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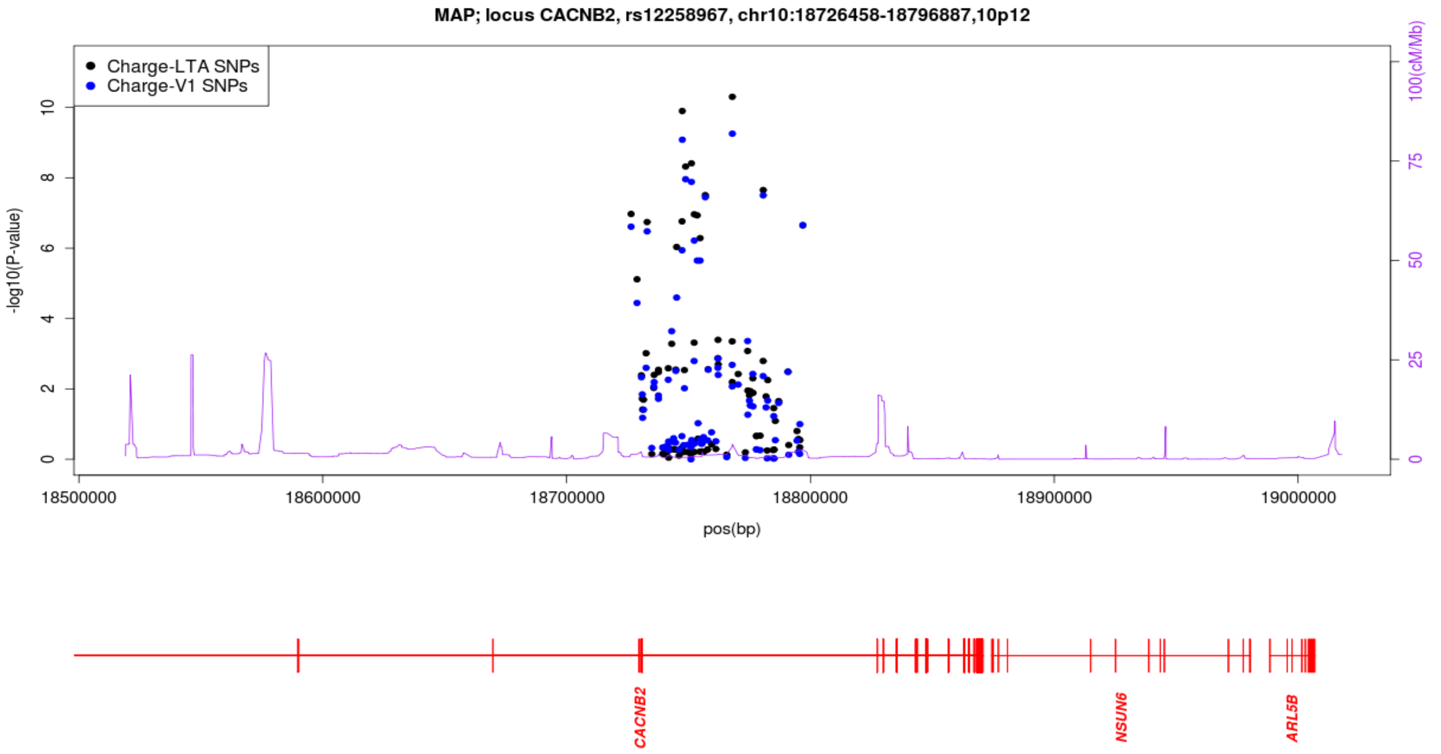
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
228700000
228800000
228900000
229000000
229100000
pos(bp)
COG2
AGT
CAPN9
C1orf198
TTC13

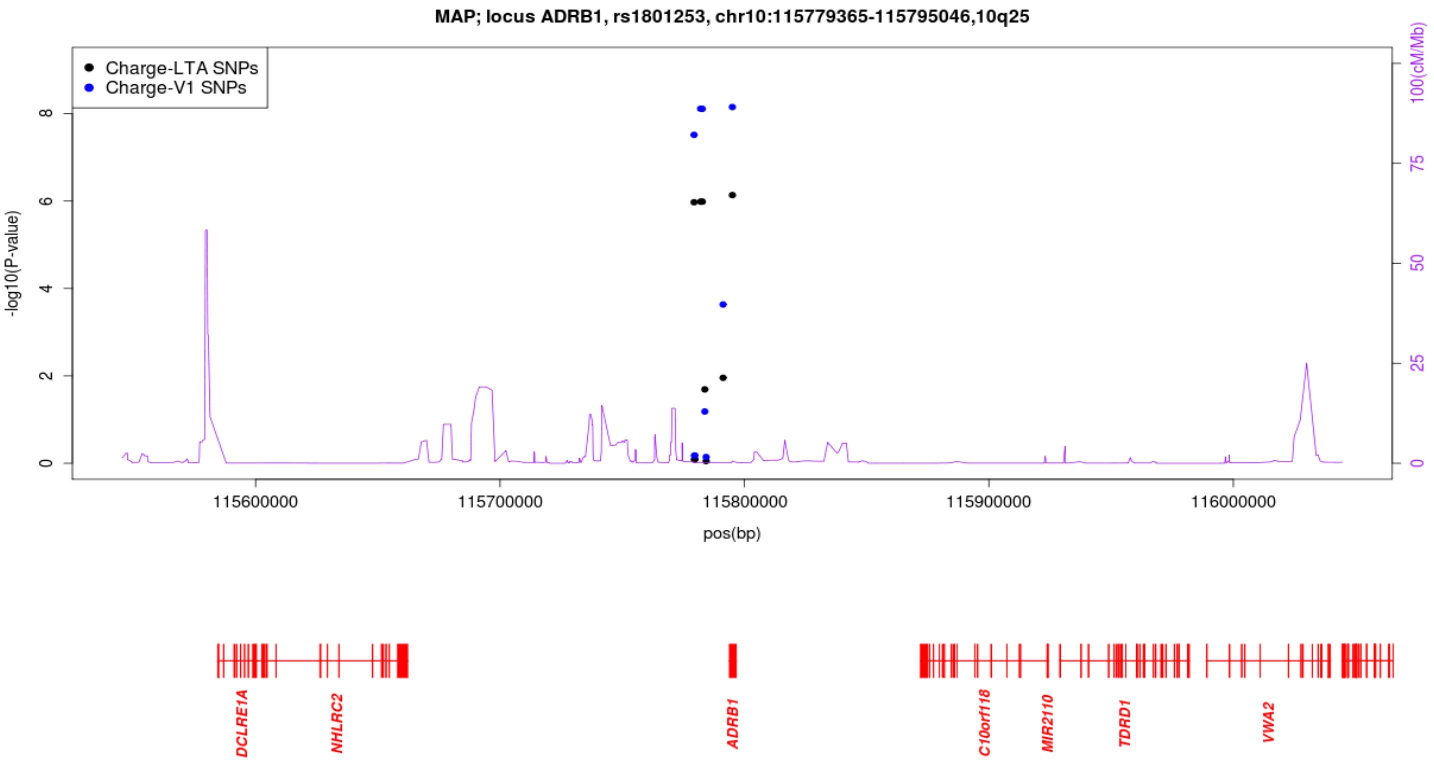
(d12)

MAP, CACNB2



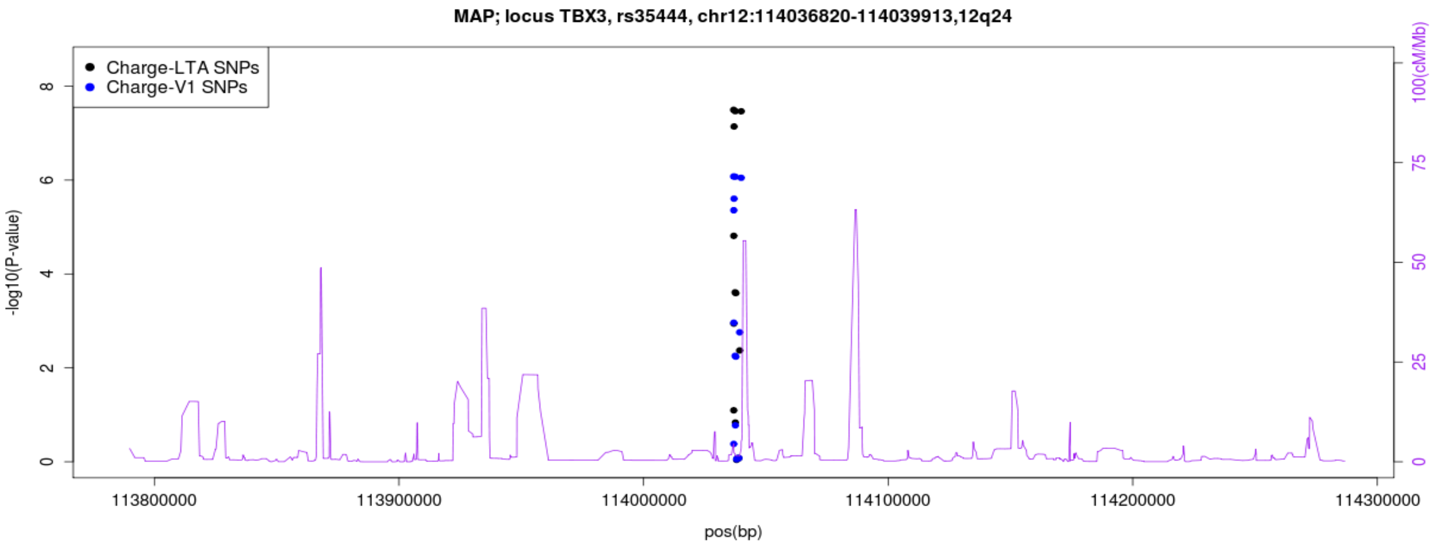
(d13)

MAP, ADRB1



(d14)

MAP, TBX3


MAP; locus TBX3, rs35444, chr12:114036820-114039913,12q24
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
113800000
113900000
114000000
114100000
114200000
114300000
pos(bp)

(d15)

PP,CASZ1

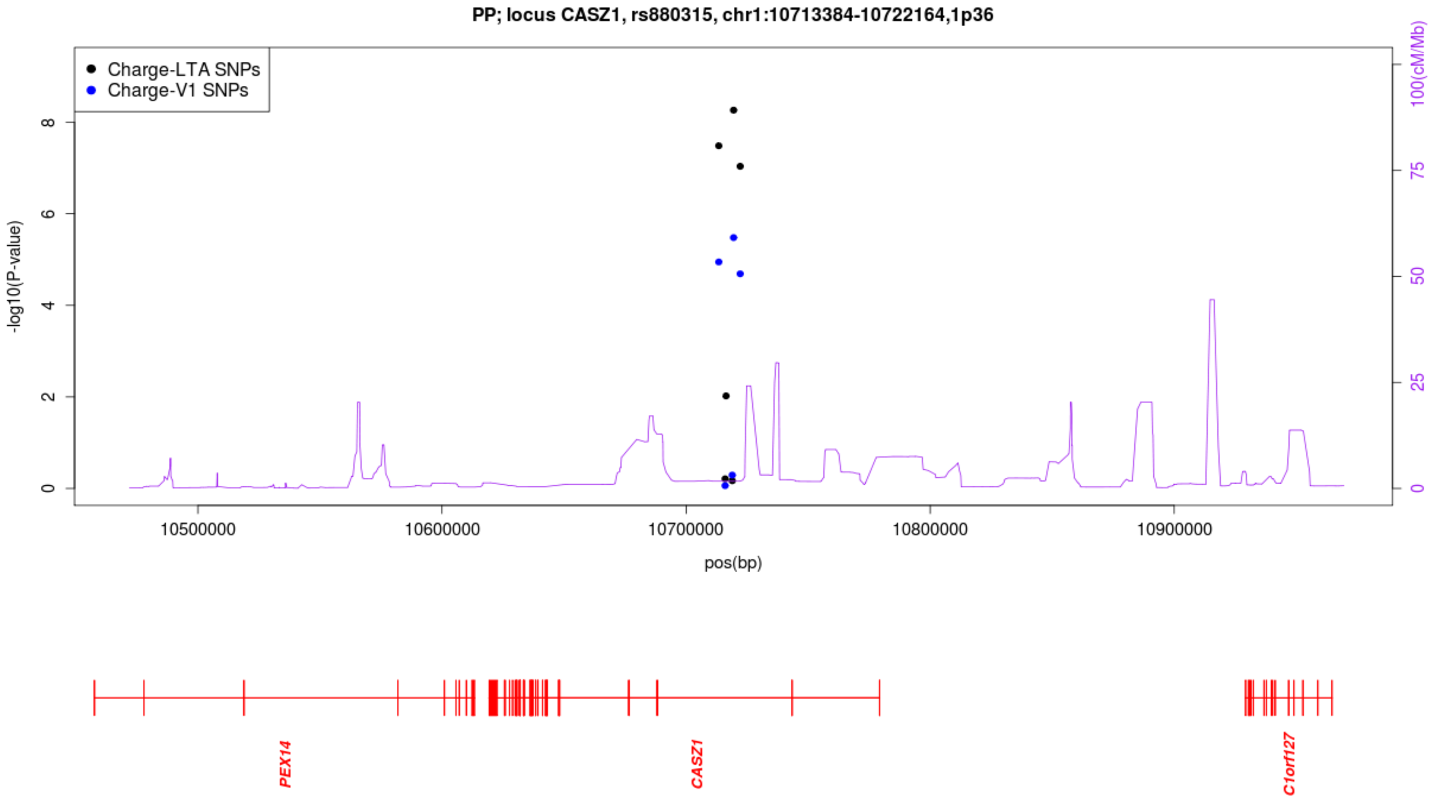
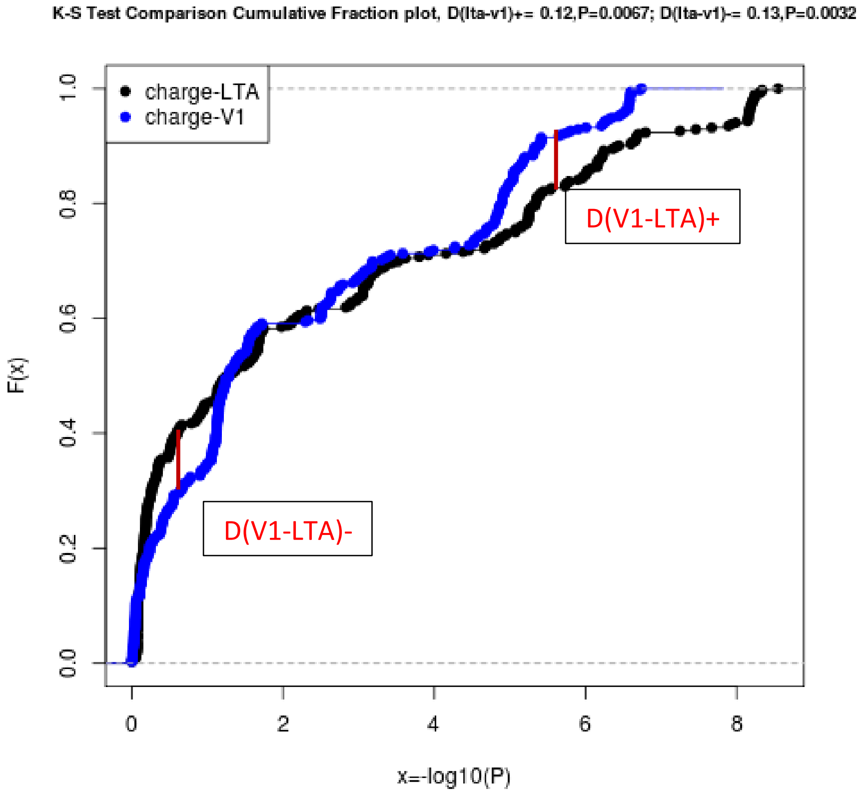

PP; locus CASZ1, rs880315, chr1:10713384-10722164,1p36
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
10500000
10600000
10700000
10800000
10900000
pos(bp)
PEX14
CASZ1
C1orf127

Figure S8. K-S test comparison cumulative fraction plot, where x-axis is the –log10(*P*) values and y-axis is the cumulative fraction.



To identify regions in which the enrichment of V1 is larger than LTA or LTA larger than V1 significantly, we used the Kolmogorov-Smirnov (K-S) statistics to compare the –log10(*P* values) within each region meeting criteria for genome-wide significance (*P* value < $5x10^{-8}$). Regions with at least one marker with *P* value<$5x10^{-8}$ in either LTA or V1 analysis were selected for enrichment analysis. Regions were defined as the lead SNP and by the LD-pruned list of SNPs in the region (r^2 >0.3). Since the KS-test uses the maximum vertical deviation between the two cumulative fraction curves as the statistic D, we used a one-tailed hypothesis test to test whether the positive vertical deviation derived from D(cdf(V1(X))-cdf(LTA(X)))+ was significant or whether the negative vertical deviation derived from D(cdf(V1(X))-cdf(LTA(X)))- was significant, where X is the –log10(P value).

Since the statistics based on different test directions are independent, for each region, two tests were conducted, one testing whether the LTA analysis yielded smaller *P* values than the V1 analysis, and vice versa. To test the structure and the strength of the K-S statistics, for each of the two tests, 10000 times permutation test was conducted by randomly shuffling the attributes of V1 and LTA and calculating new statistics repeatedly. From 10000 iterations, the permutation p-value was obtained by calculating the percentage of times when the original p-value from our data was smaller than the p-value of the new re-sampling data. Since the number of markers which selected for each region may influence the power of the K-S non-parametric test, regions with more markers may have a greater likelihood of being detected compared to regions with fewer markers. To overcome this issue, bootstrapping was used by randomly selecting *n* markers from the N=2.5 million whole-genome markers to do the K-S test of LTA and V1 10000 times, where *n* corresponds to the original number of markers we used for test in each region before. These 10000 test statistics were used as the baseline distribution, to test against whether regions with lower P values of association in the LTA or V1 analyses were truly significant compared to the distribution of the whole-genome-level baseline test statistics. Regions with true enrichment differences between LTA and V1 were identified as those with larger test statistics compared to the whole-genome-level distribution.

Two sample K-S statistics, where x is –log10(Pvalue):

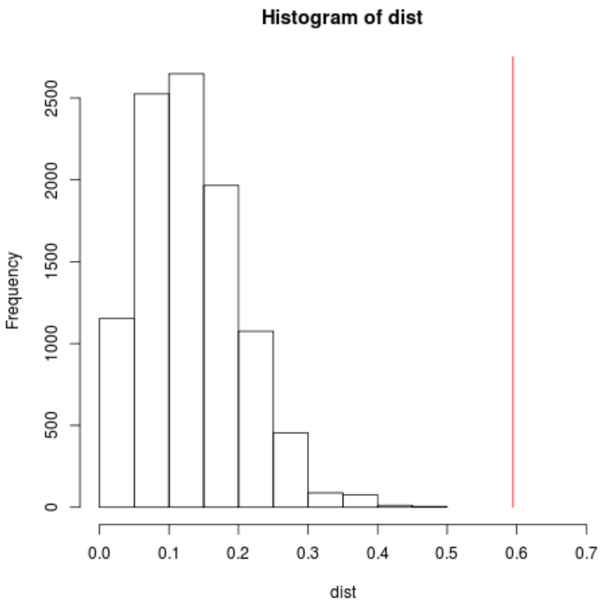
Dv1,LTA + = sup x (F1,v1(x) − F2,LTA(x)) +:

The maximum vertical positive deviation between the cdf of V1 and LTA. Deviation at each point X will be taken into account only if cdf(V1(X))-cdf(LTA(X)) is positive. This statistics means to test whether LTA has larger P-value than V1 in general.

Dv1,LTA - = sup x (F1,v1(x) − F2,LTA(x)) - :

The maximum vertical negative deviation between the cdf of V1 and LTA. Deviation at each point X will be taken into account only if cdf(V1(X))-cdf(LTA(X)) is negative. This statistics means to test whether V1 has larger P-value than LTA in general.

Figure S9. Distribution of the K-S test statistics (D-, H1: V1 analysis is more enriched) from 10000 times boot-strapping of the whole-genome markers, where the number of markers selected each time is correspondence to the number used for test in CYP1A2 region in DBP analysis. The red line is the original K-S test statistics (D-) in this CYP1A2 region.



For the Bootstrapping computing method:

1. For each selected region, we identified the number of markers (n) we used in our previous K-S test.

2. From the overall N=2.5 million genome-wide markers in our LTA or V1 data, we will (i) randomly select n markers from the N complete marker pool as our test samples, or (ii) considered the 'region' to be markers in near side instead of from different far-away sites, thus we could also randomly select one marker as the position start and then select the following n markers around this one marker as our test samples.

3. Used the sample we selected in 2 to do the K-S test. Then report the test statistics.

4. Repeated step2 to step3 many times(at least 100 times, depend on the computing speed)

5. Calculated the percentage when the simulated statistics is larger than the original K-S statistics.

Suppose the genome-wide markers are the baseline, when we randomly selected the markers from them to do the test, the test statistics should be not large (in other words, should be not significant) compared to the test statistics we got from the selected region we identified as the potential change region. Therefore, the percentage when the simulated test statistics is larger than our original K-S test statistics can be seen as the bootstrapping *P* value. If the *P* value was small enough, then we can say the region we identified is truly the one with enrichment change.

Table S1:Sample sizes available for the LTA analyses and Visit 1 analyses.

Cohort	LTA Sample Size	Visit1 Sample Size Available
AGES	526	3,219
ARIC	7,310	8,778
CARDIA	1,671	1,595
CHS	3,159	3,295
FHS	3,895	8,096
MESA	2,414	2,414
RS1	4,710	4,838
RS2	1,535	1,535
WGHS	21,409	21,670
Total	**46,629**	**55,440**

Table S2: Cohort summaries across all visit included in the analyses

		Year	*N*	Age, years (sd)	BMI, kg/m2 (sd)	SBP, mmHg (sd)	DBP, mmHg (sd)	Anti-hypertensive therapy (%)
AGES	Visit 1 (Reykjavik Study)	1987-1995	530	66.01 (7.0)	26.2 (3.9)	141.4 (18.8)	82.1 (8.7)	24%
AGES	Visit 2 (AGES)	2002-2005	530	78.49 (5.9)	26.5 (4.3)	143.4 (21.2)	73.1 (9.8)	65%
ARIC	Visit 1	1986-1990	8,778	54.3 (5.7)	27.0 (4.9)	118.5 (17.0)	71.7 (10.0)	26%
ARIC	Visit 2	1990-1993	7,844	57.2 (5.7)	27.4 (5.0)	119.9 (17.8)	71.3 (9.9)	28%
ARIC	Visit 3	1993-1996	7,214	60.3 (5.6)	28.0 (5.3)	122.9 (18.0)	70.8 (10.0)	33%
ARIC	Visit 4	1996-1999	6,582	63.1 (5.6)	28.4 (5.3)	126.1 (18.4)	70.0 (9.9)	40%
CARDIA	Visit 4	1993-1994	1,595	32.6 (3.3)	25.6 (5.1)	106.3 (11.4)	67.8 (9.5)	0.88%
CARDIA	Visit 5	1996-1997	1,571	35.6 (3.4)	26.1 (5.4)	107.2 (11.3)	70.4 (9.4)	1.34%
CARDIA	Visit 6	2001-2002	1,601	40.7 (3.4)	27.2 (5.9)	110.2 (13.4)	72.5 (10.3)	4.06%
CARDIA	Visit 7	2006-2007	1,563	45.8 (3.4)	27.9 (5.9)	113.4 (13.6)	69.9 (10.6)	11.34%
CHS	Visit 0	1989-90	3,153	72.2 (5.2)	26.3 (4.4)	134.9 (20.9)	70.3 (11.4)	35%
CHS	Visit 1	1990-91	3,056	73.1 (5.2)	-	132.2 (20.4)	69.3 (10.3)	37%
CHS	Visit 2	1992-93	2,991	74.1 (5.2)	-	133.4 (20.2)	69.5 (10.4)	39%
CHS	Visit 3	1993-94	2,838	75.0 (5.1)	26.4 (4.5)	135.3 (20.9)	70.8 (10.9)	41%
FHS-offspring	Visit 23	1992-1996	579	80.0 (4.4)	26.7 (4.6)	148.1 (23.5)	72.9 (11.3)	49%
FHS-offspring	Visit 24	1995-1998	525	82.0 (4.2)	26.4 (4.5)	146.8 (21.7)	73.2 (10.7)	51%
FHS-offspring	Visit 25	1997-1999	486	83.8 (4.1)	26.2 (4.6)	146.9 (21.9)	71.8 (11.7)	55%
FHS-offspring	Visit 26	2000-2001	389	85.6 (4.0)	26.2 (4.7)	146.6 (22.6)	71.2 (11.2)	60%
FHS-offspring	Visit 20	1986-1990	598	74.4 (4.5)	26.8 (4.6)	150.3 (22.6)	78.8 (10.7)	43%
FHS-offspring	Visit 21	1988-1992	606	76.4 (4.6)	27.1 (4.5)	149.8 (22.3)	77.1 (10.7)	48%
FHS-offspring	Visit 22	1990-1994	588	78.2 (4.4)	26.9 (4.7)	147.8 (21.3)	74.6 (11.1)	47%
FHS	Visit 4	1987-1991	3,108	50.7 (9.8)	26.8 (4.9)	127.4 (20.0)	79.7 (10.6)	15%
FHS	Visit 5	1991-1995	3,104	54.4 (9.8)	27.4 (4.9)	127.4 (20.0)	75.4 (10.3)	17%
FHS	Visit 6	1995-1998	2,975	58.3 (9.7)	27.9 (5.1)	130.6 (20.4)	76.8 (10.0)	26%
FHS	Visit 7	1998-2001	2,954	61.0 (9.5)	28.1 (5.3)	130.1 (20.4)	75.7 (10.1)	32%
MESA	Exam 1	2000-2002	2,414	62.7	27.7 (5.0)	123.5 (20.5)	70.2 (10.0)	33%
MESA	Exam 2	2002-2004	2,383	64.2	27.1 (5.1)	121.1 (19.2)	68.8 (9.6)	39%
MESA	Exam 3	2004-2005	2,302	65.5	27.7 (5.2)	120.0 (19.6)	68 (10.9)	42%
MESA	Exam 4	2005-2007	2,219	66.9	27.8 (5.2)	120.5 (19.3)	68.02 (9.7)	45%
RS1	Visit 1	1990-1993	4,838	67.9	26.3 (3.6)	140.4 (22.8)	74.9 (11.7)	22%
RS1	Visit 2	1994-1995	4,678	70.0	26.4 (3.7)	144.1 (23.4)	78.3 (12.3)	30%
RS1	Visit 3	1997-1999	3,562	72.6	26.8 (3.9)	146.0 (22.4)	76.4 (11.7)	26%
RS1	Visit 4	2002-2004	2,691	75.5	27.4 (4.1)	156.7 (23.2)	81.2 (11.7)	37%
RS2	Visit 1	2001-2001	1,535	63.7	27.2 (4.1)	143.4 (21.6)	79.7 (11.1)	21%
RS2	Visit 2	2004-2006	1,535	67.9	27.8 (4.1)	148.1 (21.4)	81.2 (11.2)	30%
WGHS	Visit 1	1992-1994	21,670	54.7	25.9 (4.9)	124.8 (15.4)	77.3 (9.7)	13%
WGHS	Visit 2	1996-1998	19,410	58.2	26.5 (5.1)	127.3 (16.7)	76.8 (9.8)	23%
WGHS	Visit 3	2003-2005	18,625	65.2	26.9 (5.4)	128.4 (14.7)	76.1 (8.9)	43%

Table S3: Genomic control inflation factors (λ_{GC}).

LTA

LTA- SBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.014	1.052	1.009	1.061	1.034	1.002	1.093	0.996	1.015	1.074

LTA - DBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.005	1.046	1.034	1.051	1.036	1.014	1.065	1.006	1.012	1.088

LTA - PP

ARIC	CHS	FHS	RS1	RS2	AGES	WGHS	MESA	CARDIA	Meta-analysis
1.041	1.023	1.026	1.037	1.017	1.015	1.071	0.996	1.031	1.055

LTA - MAP

ARIC	CHS	FHS	RS1	RS2	AGES	WGHS	MESA	CARDIA	Meta-analysis
1.048	1.031	1.022	1.039	1.006	1.019	1.101	0.996	1.008	1.095

Visit 1

Visit 1 - SBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.014	1.052	1.009	1.061	1.034	1.002	1.093	0.996	1.025	1.076

Visit 1 - DBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.005	1.046	1.034	1.051	1.036	1.014	1.065	1.006	1.025	1.066

Table S4: All trait-SNPs with *P* value < 5x10-8 in the LTA analyses (LTA *P* value <5x10-8, Total 488 SNPs, 117 SBP, 96 DBP, 155 MAP, and 120 PP SNPs).

Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-SBP	rs1275986	2p23	26765583	a	c	-0.5974	0.0917	3.22E-10	-----+--+	NA	KCNK3;CIB4	KCNK3	3539
LTA-SBP	rs10858914	12q21	88555526	t	c	0.5902	0.0904	3.02E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	18449
LTA-SBP	rs7537765	1p36	11809890	a	g	0.8523	0.1221	1.60E-11	+++++++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA-SBP	rs1275979	2p23	26777072	t	c	0.5921	0.0919	5.15E-10	+++++-++-	KCNK3	KCNK3;CIB4	KCNK3	7950
LTA-SBP	rs10858911	12q21	88487272	a	g	-0.5607	0.0895	1.48E-09	----+----	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	18686
LTA-SBP	rs7085	15q24	72882536	t	c	0.5665	0.0997	4.22E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-SBP	rs5068	1p36	11828561	a	g	1.1766	0.1994	1.23E-08	+++++++++	NPPA	MTHFR;NPPA;CLCN6;NPPB	NPPA	199
LTA-SBP	rs11105354	12q21	88550654	a	g	0.9429	0.1186	1.69E-14	++++-++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-SBP	rs13031603	2q24	164803435	t	c	-0.582	0.0996	1.71E-08	----+----	NA	NA	GRB14	254143
LTA-SBP	rs10774625	12q24	110394602	a	g	0.5575	0.0909	3.25E-09	+++++-+++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LTA-SBP	rs882384	20q13	57132808	t	c	0.7241	0.1271	3.80E-08	+++++-+++	NA	NA	C20orf174	66661
LTA-SBP	rs6092743	20q13	57133765	a	g	0.8396	0.1449	2.25E-08	+++++++++	NA	NA	C20orf174	65704
LTA-SBP	rs1173770	5p13	32856968	t	c	-0.5468	0.0911	6.93E-09	----+----	NA	C5orf23;NPR3	C5orf23	29392
LTA-SBP	rs6712094	2q24	164751706	a	g	0.598	0.1007	9.89E-09	++++-++++	NA	NA	GRB14	305872
LTA-SBP	rs35444	12q24	114036820	a	g	0.5452	0.0929	1.47E-08	+++++-+-+	NA	NA	TBX3	430468
LTA-SBP	rs4842666	12q21	88465680	t	c	0.8816	0.1267	1.92E-11	++++-++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-SBP	rs1173727	5p13	32866278	t	c	-0.5439	0.0911	8.32E-09	----+----	NA	C5orf23;NPR3	C5orf23	38702
LTA-SBP	rs17367504	1p36	11785365	a	g	0.8355	0.1225	4.60E-11	+++++++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	3337
LTA-SBP	rs13035163	2q24	164781173	a	g	0.5775	0.0996	2.22E-08	++++-++++	NA	NA	GRB14	276405
LTA-SBP	rs13035934	2q24	164781318	a	g	-0.5772	0.0996	2.25E-08	----+----	NA	NA	GRB14	276260
LTA-SBP	rs12995749	2q24	164777689	t	c	-0.5795	0.0997	2.03E-08	----+----	NA	NA	GRB14	279889
LTA-SBP	rs1173747	5p13	32817909	a	c	0.512	0.0901	4.21E-08	++++-++++	NPR3	C5orf23;NPR3	NPR3	5100
LTA-SBP	rs7136259	12q21	88605319	t	c	-0.6301	0.0902	1.60E-11	----+----	NA	ATP2B1	ATP2B1	31344
LTA-SBP	rs2681485	12q21	88549753	a	g	0.687	0.0909	2.97E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-SBP	rs1275923	2p23	26786300	t	c	-0.6048	0.0943	6.02E-10	-----+--+	KCNK3	KCNK3;C2orf18	KCNK3	17178
LTA-SBP	rs13154066	5p13	32867427	t	c	-0.5436	0.0911	8.41E-09	----+----	NA	C5orf23;NPR3	C5orf23	39851
LTA-SBP	rs979223	2q24	164803267	a	c	-0.577	0.0995	2.23E-08	----+----	NA	NA	GRB14	254311
LTA-SBP	rs1173743	5p13	32810804	t	g	0.5212	0.0907	2.95E-08	++++-++++	NPR3	C5orf23;NPR3	NPR3	12205
LTA-SBP	rs12258967	10p12	18767965	c	g	0.6307	0.0976	4.53E-10	+++++++++	CACNB2	CACNB2	CACNB2	38447
LTA-SBP	rs13004226	2q24	164788924	c	g	-0.5763	0.0995	2.28E-08	----+----	NA	NA	GRB14	268654
LTA-SBP	rs6100343	20q13	57133607	a	g	0.725	0.1272	3.76E-08	+++++-+++	NA	NA	C20orf174	65862
LTA-SBP	rs13030081	2q24	164796086	t	c	0.5731	0.1005	3.77E-08	++++-++++	NA	NA	GRB14	261492
LTA-SBP	rs12705390	7q22	106198013	a	g	0.6307	0.11	3.17E-08	++++--++-	NA	NA	PIK3CG	95146
LTA-SBP	rs2586886	2p23	26785535	t	c	-0.6016	0.0936	5.43E-10	-----+--+	KCNK3	C2orf18;KCNK3	KCNK3	16413
LTA-SBP	rs12230074	12q21	88614998	a	g	0.934	0.1219	1.39E-13	++++-++++	NA	ATP2B1	ATP2B1	41023
LTA-SBP	rs4441488	2q24	164773873	t	c	0.5809	0.0998	1.92E-08	++++-++++	NA	NA	GRB14	283705
LTA-SBP	rs11065987	12q24	110556807	a	g	-0.5274	0.0931	4.50E-08	---------	NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-SBP	rs936226	15q24	72856335	t	c	-0.5733	0.1004	3.58E-08	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-SBP	rs6707357	2q24	164722539	t	c	-0.5232	0.0914	3.29E-08	-----+---	NA	NA	GRB14	335039
LTA-SBP	rs880315	1p36	10719453	t	c	-0.7125	0.1005	7.98E-12	--------?	CASZ1	CASZ1	CASZ1	59841
LTA-SBP	rs2166122	10q21	63193080	t	c	-0.6435	0.1137	4.75E-08	-+-------	C10orf107	C10orf107	C10orf107	3015
LTA-SBP	rs653178	12q24	110492139	t	c	-0.5508	0.0902	3.76E-09	-----+---	ATXN2	ATXN2	ATXN2	29724
LTA-SBP	rs13034053	2q24	164784645	a	t	-0.5762	0.0996	2.34E-08	----+----	NA	NA	GRB14	272933
LTA-SBP	rs4842667	12q21	88490785	a	g	0.5579	0.0894	1.69E-09	++++-++++	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	15173
LTA-SBP	rs284277	1p36	10713384	a	c	-0.7091	0.1044	5.54E-11	--------?	CASZ1	CASZ1	CASZ1	65910
LTA-SBP	rs1275982	2p23	26772593	t	c	-0.5881	0.0919	6.56E-10	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	3471
LTA-SBP	rs6100342	20q13	57132656	a	c	-0.7232	0.127	3.89E-08	-----+---	NA	NA	C20orf174	66813
LTA-SBP	rs11072518	15q24	73021663	t	c	0.5692	0.0947	6.54E-09	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
LTA-SBP	rs1401982	12q21	88513730	a	g	0.6828	0.0906	3.59E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	7772
LTA-SBP	rs998981	20q13	57133036	t	c	0.7246	0.1271	3.78E-08	+++++-+++	NA	NA	C20orf174	66433
LTA-SBP	rs2070759	12q21	88541867	t	g	0.5881	0.0902	3.19E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	32108
LTA-SBP	rs12442901	15q24	72870965	a	g	0.5675	0.1	4.34E-08	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	9198
LTA-SBP	rs11014049	10p12	18726458	a	g	-0.5453	0.0964	4.77E-08	---------	CACNB2	CACNB2	CACNB2	3060
LTA-SBP	rs13306561	1p36	11788391	a	g	0.8795	0.1235	6.38E-12	+++++++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	311
LTA-SBP	rs1439214	2q24	164778248	t	c	-0.5791	0.0997	2.07E-08	----+----	NA	NA	GRB14	279330
LTA-SBP	rs2681492	12q21	88537220	t	c	0.8967	0.1156	7.18E-14	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-SBP	rs2168519	15q24	72867925	t	c	0.5679	0.0999	4.18E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
LTA-SBP	rs1275977	2p23	26776359	a	g	-0.5862	0.099	1.11E-08	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	7237
LTA-SBP	rs492945	1p36	10723185	a	g	-0.5838	0.1005	2.10E-08	--------?	CASZ1	CASZ1	CASZ1	56109
LTA-SBP	rs13027527	2q24	164786950	a	g	-0.5768	0.0995	2.19E-08	----+----	NA	NA	GRB14	270628
LTA-SBP	rs11105364	12q21	88593407	t	g	0.9382	0.1197	3.81E-14	++++-++++	NA	ATP2B1	ATP2B1	19432
LTA-SBP	rs13021222	2q24	164756151	c	g	-0.5902	0.1008	1.60E-08	----+----	NA	NA	GRB14	301427
LTA-SBP	rs12579302	12q21	88574634	a	g	0.9342	0.1194	4.31E-14	++++-++++	NA	ATP2B1	ATP2B1	659
LTA-SBP	rs35441	12q24	114037498	t	c	-0.5471	0.0933	1.54E-08	-----+-+-	NA	NA	TBX3	431146
LTA-SBP	rs17376328	1p36	11799249	a	g	-1.1341	0.1958	2.26E-08	-----+---	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	10456
LTA-SBP	rs9292468	5p13	32854830	t	c	-0.5451	0.0911	7.76E-09	----+----	NA	C5orf23;NPR3	C5orf23	27254
LTA-SBP	rs13005481	2q24	164789612	t	c	-0.5758	0.0995	2.35E-08	----+----	NA	NA	GRB14	267966
LTA-SBP	rs4766578	12q24	110388754	a	t	-0.5599	0.0909	2.82E-09	-----+---	ATXN2	SH2B3;ATXN2	ATXN2	14353
LTA-SBP	rs17477177	7q22	106199094	t	c	-0.6322	0.1106	3.46E-08	----++--+	NA	NA	PIK3CG	94065
LTA-SBP	rs11105383	12q21	88631437	t	c	0.7644	0.1329	2.83E-08	+++++++++	NA	ATP2B1	ATP2B1	57462
LTA-SBP	rs4548524	10p12	18756873	a	g	0.544	0.0935	1.97E-08	+++++++++	CACNB2	CACNB2	CACNB2	27355
LTA-SBP	rs1275988	2p23	26767868	t	c	-0.6004	0.0917	2.61E-10	-----+--+	NA	KCNK3;CIB4	KCNK3	1254
LTA-SBP	rs2301249	15q24	72879437	t	c	0.566	0.0996	4.13E-08	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-SBP	rs6726740	2q24	164758374	t	g	0.5849	0.1008	2.15E-08	++++-++++	NA	NA	GRB14	299204
LTA-SBP	rs11687999	2q24	164774604	t	c	0.5809	0.0998	1.92E-08	++++-++++	NA	NA	GRB14	282974
LTA-SBP	rs7299436	12q21	88637201	t	g	0.7672	0.1334	2.84E-08	+++++++++	NA	NA	ATP2B1	63226
LTA-SBP	rs6100340	20q13	57118007	a	g	-0.7158	0.1261	4.31E-08	-----+---	NA	NA	SLMO2	66711

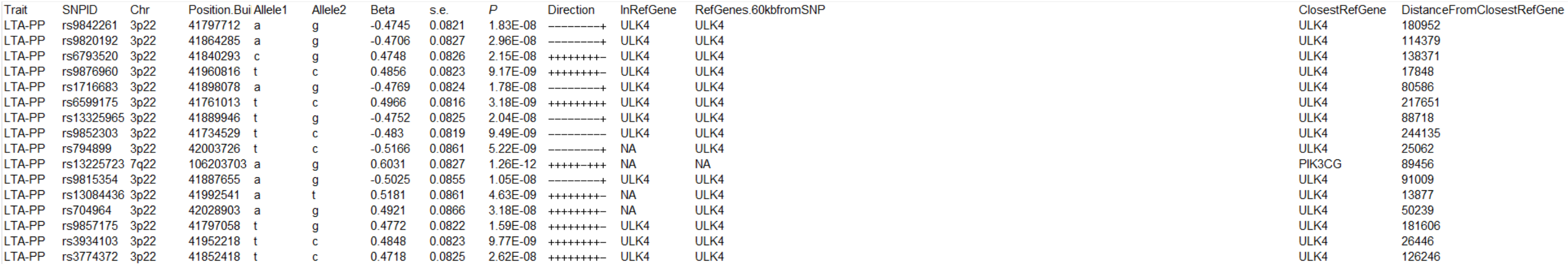
Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-SBP	rs8033381	15q24	72867738	a	g	-0.5689	0.1	3.97E-08	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-SBP	rs12995799	2q24	164798636	t	c	0.5788	0.0996	2.03E-08	++++-++++	NA	NA	GRB14	258942
LTA-SBP	rs12046278	1p36	10722164	t	c	-0.707	0.1039	5.12E-11	--------?	CASZ1	CASZ1	CASZ1	57130
LTA-SBP	rs11891401	2q24	164794993	a	t	-0.5844	0.0997	1.56E-08	----+----	NA	NA	GRB14	262585
LTA-SBP	rs7070797	10q21	63221779	a	g	-0.7415	0.1306	4.30E-08	-+---+---	NA	C10orf107	C10orf107	25684
LTA-SBP	rs4886629	15q24	72859611	c	g	-0.5728	0.1004	3.63E-08	---------	NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L	CSK	2156
LTA-SBP	rs7733331	5p13	32864603	t	c	-0.5505	0.0911	5.38E-09	----+----	NA	C5orf23;NPR3	C5orf23	37027
LTA-SBP	rs4845953	1p36	10724576	a	g	-0.5626	0.0995	4.84E-08	--------?	CASZ1	CASZ1	CASZ1	54718
LTA-SBP	rs12656497	5p13	32867696	t	c	-0.5432	0.0911	8.73E-09	----+----	NA	C5orf23;NPR3	C5orf23	40120
LTA-SBP	rs17249754	12q21	88584717	a	g	-0.9384	0.1194	3.37E-14	----+----	NA	ATP2B1	ATP2B1	10742
LTA-SBP	rs1465537	20q13	57131415	t	c	0.7232	0.127	3.86E-08	+++++-+++	NA	NA	C20orf174	68054
LTA-SBP	rs11105382	12q21	88631403	t	c	0.7637	0.1326	2.73E-08	+++++++++	NA	ATP2B1	ATP2B1	57428
LTA-SBP	rs1275985	2p23	26765249	t	c	-0.596	0.092	4.01E-10	-----+--+	NA	KCNK3;CIB4	KCNK3	3873
LTA-SBP	rs1173771	5p13	32850785	a	g	-0.5502	0.0911	5.63E-09	----+----	NA	C5orf23;NPR3	C5orf23	23209
LTA-SBP	rs35432	12q24	114039913	t	c	-0.5535	0.0945	1.58E-08	-----+-+-	NA	NA	TBX3	433561
LTA-SBP	rs10858915	12q21	88575678	a	g	0.5191	0.0903	2.92E-08	++++-++++	NA	ATP2B1	ATP2B1	1703
LTA-SBP	rs1439211	2q24	164802546	a	c	-0.5887	0.1035	4.06E-08	----+----	NA	NA	GRB14	255032
LTA-SBP	rs2050265	1p36	11802286	a	g	0.8509	0.1222	1.84E-11	+++++++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	8576
LTA-SBP	rs11014166	10p12	18748804	a	t	0.5638	0.0939	6.88E-09	+++++++++	CACNB2	CACNB2	CACNB2	19286
LTA-SBP	rs10774792	12q24	114036981	t	c	-0.5502	0.094	1.63E-08	-----+---	NA	NA	TBX3	430629
LTA-SBP	rs1173756	5p13	32825609	t	c	-0.5175	0.0896	2.52E-08	----+----	C5orf23	C5orf23;NPR3	C5orf23	908
LTA-SBP	rs1275980	2p23	26770473	t	c	-0.5947	0.0919	4.18E-10	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	1351
LTA-SBP	rs1813353	10p12	18747454	t	c	0.623	0.0968	5.31E-10	+++++-+++	CACNB2	CACNB2	CACNB2	17936
LTA-SBP	rs6676300	1p36	11847887	a	g	0.5541	0.0942	1.40E-08	+++-+-+++	NA	MTHFR;KIAA2013;NPPA;CLCN6;NPPB	NPPB	6308
LTA-SBP	rs12567136	1p36	11806318	t	c	-0.8529	0.1222	1.63E-11	---------	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA-SBP	rs2681472	12q21	88533090	a	g	0.9457	0.118	1.04E-14	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
LTA-SBP	rs17037425	1p36	11792970	a	g	-0.8574	0.1292	1.51E-10	---------	CLCN6	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	4177
LTA-SBP	rs1371181	2q24	164784974	t	c	0.5764	0.0995	2.28E-08	++++-++++	NA	NA	GRB14	272604
LTA-SBP	rs10432461	2q24	164772752	a	t	-0.5812	0.0998	1.93E-08	----+----	NA	NA	GRB14	284826
LTA-SBP	rs3184504	12q24	110368991	t	c	0.5549	0.0903	3.04E-09	+++++-+++	SH2B3	SH2B3;ATXN2	SH2B3	4818
LTA-SBP	rs11105368	12q21	88598572	c	g	-0.9371	0.1197	4.21E-14	----+----	NA	ATP2B1	ATP2B1	24597
LTA-SBP	rs13007966	2q24	164784819	t	c	-0.5762	0.0996	2.33E-08	----+----	NA	NA	GRB14	272759
LTA-SBP	rs11105378	12q21	88614872	t	c	-0.9344	0.1216	1.23E-13	----+----	NA	ATP2B1	ATP2B1	40897
LTA-SBP	rs11105328	12q21	88466521	a	g	0.8655	0.1239	1.57E-11	++++-++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	22613
LTA-SBP	rs1898841	2q24	164778453	t	c	0.5785	0.0997	2.12E-08	++++-++++	NA	NA	GRB14	279125
LTA-SBP	rs11105379	12q21	88619304	t	c	0.7704	0.1325	2.03E-08	+++++++++	NA	ATP2B1	ATP2B1	45329
LTA-SBP	rs11105358	12q21	88566273	c	g	-0.6895	0.0911	2.77E-13	----+----	ATP2B1	ATP2B1	ATP2B1	7702
LTA-SBP	rs17037390	1p36	11783430	a	g	-0.8558	0.1226	1.60E-11	---------	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	5272
LTA-SBP	rs1173766	5p13	32840285	t	c	-0.5294	0.0917	2.52E-08	----+----	NA	C5orf23;NPR3	C5orf23	12709
LTA-SBP	rs11014171	10p12	18751201	t	c	-0.5679	0.0937	4.97E-09	---------	CACNB2	CACNB2	CACNB2	21683
LTA-DBP	rs11072512	15q24	72991079	t	c	-0.3193	0.0525	5.53E-09	---------	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	4564
LTA-DBP	rs7495739	15q24	72972723	a	g	0.3158	0.0524	7.78E-09	+++++++++	MPI	COX5A;SCAMP2;C15orf17;MPI;ULK3	MPI	3261
LTA-DBP	rs7537765	1p36	11809890	a	g	0.4718	0.0714	2.36E-10	++++--+++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA-DBP	rs7085	15q24	72882536	t	c	0.3468	0.0582	1.10E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-DBP	rs198833	6p22	26222487	a	g	-0.4345	0.0741	1.91E-08	---------	NA	HIST1H1T;HIST1H2BD;HIST1H2BC;HIST1H1E;HFE;HIST1H1C;HIST1H4C;HIST1H2AC	HIST1H1T	6144
LTA-DBP	rs6495127	15q24	72981543	t	c	-0.3262	0.0571	4.40E-08	-----+---	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17;ULK3	C15orf17	2163
LTA-DBP	rs11105354	12q21	88550654	a	g	0.5235	0.0696	5.40E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-DBP	rs12246717	10q21	63129189	t	g	0.3693	0.0624	1.39E-08	+++++-++-	C10orf107	C10orf107	C10orf107	36465
LTA-DBP	rs10774625	12q24	110394602	a	g	0.3848	0.0528	2.74E-12	+++++++++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LTA-DBP	rs6092743	20q13	57133765	a	g	0.502	0.0843	1.11E-08	+++++-+++	NA	NA	C20orf174	65704
LTA-DBP	rs11634474	15q24	72903237	c	g	0.3384	0.0593	4.51E-08	+++++++++	LMAN1L	CSK;LMAN1L;CPLX3;SCAMP2;ULK3	LMAN1L	1914
LTA-DBP	rs4886636	15q24	72983229	a	g	-0.3123	0.0524	1.13E-08	---------	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17	C15orf17	3286
LTA-DBP	rs3784789	15q24	72869605	c	g	0.3166	0.0553	3.98E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	7838
LTA-DBP	rs4842666	12q21	88465680	t	c	0.5108	0.0745	4.88E-11	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-DBP	rs17367504	1p36	11785365	a	g	0.4598	0.0717	7.61E-10	++++--+++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	3337
LTA-DBP	rs11072511	15q24	72946486	a	g	0.3165	0.0525	7.35E-09	+++++++++	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	6237
LTA-DBP	rs17696736	12q24	110971201	a	g	-0.3131	0.0536	2.16E-08	---------	C12orf30	ERP29;TMEM116;C12orf30	C12orf30	22325
LTA-DBP	rs7136259	12q21	88605319	t	c	-0.3314	0.0526	1.55E-09	----+--+-	NA	ATP2B1	ATP2B1	31344
LTA-DBP	rs2681485	12q21	88549753	a	g	0.3385	0.053	9.22E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-DBP	rs1799945	6p22	26199158	c	g	-0.4226	0.074	4.33E-08	---------	HFE	HIST1H2BC;HIST1H1C;HIST1H3B;HIST1H4C;HIST1H2BB;HIST1H2AC;HIST1H1T;HIST1H2AB;HFE;HIST1H3C	HFE	3671
LTA-DBP	rs2120702	10q21	63192664	a	t	-0.3402	0.0592	3.56E-08	-----+---	C10orf107	C10orf107	C10orf107	3431
LTA-DBP	rs12258967	10p12	18767965	c	g	0.3548	0.0571	2.48E-09	+++-+-+++	CACNB2	CACNB2	CACNB2	38447
LTA-DBP	rs16916504	10q21	63122962	a	g	0.3706	0.0625	1.30E-08	+++++-++-	C10orf107	C10orf107	C10orf107	30238
LTA-DBP	rs6495126	15q24	72962079	a	g	0.3253	0.0568	4.03E-08	+++++-+++	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	7383
LTA-DBP	rs7599598	2q11	96715567	a	g	-0.314	0.0543	2.91E-08	---------	NA	FLJ10081;FER1L5;LMAN2L	FER1L5	9353
LTA-DBP	rs12230074	12q21	88614998	a	g	0.5255	0.0718	2.23E-12	+++++++++	NA	ATP2B1	ATP2B1	41023
LTA-DBP	rs11066188	12q24	111095097	a	g	0.3343	0.0539	2.76E-09	+++++++++	NA	TRAFD1	TRAFD1	19302
LTA-DBP	rs1378941	15q24	72867203	a	c	-0.3135	0.0551	4.98E-08	---------	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	5436
LTA-DBP	rs11065987	12q24	110556807	a	g	-0.3534	0.0543	4.52E-10	---------	NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-DBP	rs936226	15q24	72856335	t	c	-0.3413	0.0585	2.26E-08	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-DBP	rs2166122	10q21	63193080	t	c	-0.3932	0.0663	1.32E-08	-----+---	C10orf107	C10orf107	C10orf107	3015
LTA-DBP	rs653178	12q24	110492139	t	c	-0.3911	0.0524	7.85E-13	---------	ATXN2	ATXN2	ATXN2	29724
LTA-DBP	rs1378942	15q24	72864420	a	c	-0.3128	0.055	5.00E-08	---------	CSK	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	2653
LTA-DBP	rs11066320	12q24	111390798	a	g	0.303	0.053	4.11E-08	+++++++++	PTPN11	RPL6;PTPN11	PTPN11	41301
LTA-DBP	rs2675612	10q21	63193272	t	c	-0.3502	0.0593	1.47E-08	-----+---	C10orf107	C10orf107	C10orf107	2823
LTA-DBP	rs3765066	15q24	72927907	a	g	-0.3388	0.0563	7.81E-09	---------	SCAMP2	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	3658
LTA-DBP	rs260014	20q13	57192854	t	c	-0.4584	0.0782	1.92E-08	-----+---	NA	C20orf174	C20orf174	6615
LTA-DBP	rs11072518	15q24	73021663	t	c	0.3405	0.0552	3.29E-09	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
LTA-DBP	rs8031937	15q24	72968174	a	g	0.3264	0.057	4.01E-08	+++++-+++	NA	COX5A;MPI;CPLX3;SCAMP2;C15orf17;ULK3	MPI	1288

Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-DBP	rs1401982	12q21	88513730	a	g	0.3363	0.0529	1.06E-09	++++-++++	ATP2B1	ATP2B1	ATP2B1	7772
LTA-DBP	rs11630918	15q24	72942949	t	c	-0.3242	0.0537	7.28E-09	---------	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	9774
LTA-DBP	rs12442901	15q24	72870965	a	g	0.3399	0.0583	2.30E-08	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	9198
LTA-DBP	rs13306561	1p36	11788391	a	g	0.4789	0.0723	2.08E-10	++++--+++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	311
LTA-DBP	rs11072513	15q24	73008021	t	c	-0.3223	0.0526	4.20E-09	---------	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8350
LTA-DBP	rs2681492	12q21	88537220	t	c	0.5064	0.0676	7.02E-13	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-DBP	rs2168519	15q24	72867925	t	c	0.3402	0.0583	2.19E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
LTA-DBP	rs2393833	10q21	63115322	t	c	-0.3697	0.0624	1.36E-08	-----+--+	C10orf107	C10orf107	C10orf107	22598
LTA-DBP	rs2004776	1q42	228915325	t	c	0.3545	0.0615	3.20E-08	+++++++++	AGT	AGT;COG2;CAPN9	AGT	1239
LTA-DBP	rs4886633	15q24	72965260	a	g	-0.3276	0.057	3.49E-08	-----+---	NA	COX5A;CPLX3;SCAMP2;C15orf17;MPI;ULK3	MPI	4202
LTA-DBP	rs11856413	15q24	72986945	a	g	0.3183	0.0525	5.94E-09	+++++++++	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	430
LTA-DBP	rs1133322	15q24	72999410	a	g	0.3205	0.0526	4.96E-09	+++++++++	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	261
LTA-DBP	rs11105364	12q21	88593407	t	g	0.5264	0.0704	7.24E-13	++++-++++	NA	ATP2B1	ATP2B1	19432
LTA-DBP	rs12579302	12q21	88574634	a	g	0.5218	0.0702	1.01E-12	++++-++++	NA	ATP2B1	ATP2B1	659
LTA-DBP	rs12244842	10q21	63109192	t	g	-0.3784	0.0627	7.05E-09	-----+--+	C10orf107	C10orf107	C10orf107	16468
LTA-DBP	rs4766578	12q24	110388754	a	t	-0.3848	0.0528	2.71E-12	---------	ATXN2	SH2B3;ATXN2	ATXN2	14353
LTA-DBP	rs11105383	12q21	88631437	t	c	0.4525	0.0776	2.28E-08	+++++++-+	NA	ATP2B1	ATP2B1	57462
LTA-DBP	rs1992625	10q21	63190704	t	c	-0.3911	0.0662	1.48E-08	-----+---	C10orf107	C10orf107	C10orf107	5391
LTA-DBP	rs1133323	15q24	72999278	t	c	-0.3262	0.0526	2.66E-09	---------	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	393
LTA-DBP	rs1378940	15q24	72870547	a	c	-0.3159	0.0554	4.44E-08	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	8780
LTA-DBP	rs2301249	15q24	72879437	t	c	0.3479	0.0581	9.48E-09	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-DBP	rs1127796	15q24	72980057	t	c	0.3152	0.0525	8.37E-09	+++++++++	C15orf17	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	C15orf17	677
LTA-DBP	rs7497393	15q24	72962510	c	g	-0.3172	0.0524	6.62E-09	---------	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	6952
LTA-DBP	rs7299436	12q21	88637201	t	g	0.4541	0.0779	2.30E-08	+++++++-+	NA	NA	ATP2B1	63226
LTA-DBP	rs7162232	15q24	72902948	a	g	-0.3388	0.0593	4.35E-08	---------	LMAN1L	CPLX3;SCAMP2;CSK;ULK3;LMAN1L	LMAN1L	2203
LTA-DBP	rs198846	6p22	26215442	a	g	0.4337	0.0738	1.73E-08	+++++++++	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H1C;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H1T	177
LTA-DBP	rs8033381	15q24	72867738	a	g	-0.3403	0.0583	2.17E-08	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-DBP	rs260013	20q13	57194118	a	g	-0.4565	0.0783	2.31E-08	-----+---	NA	C20orf174	C20orf174	5351
LTA-DBP	rs3750727	10q21	63114411	a	g	0.3782	0.0626	7.09E-09	+++++-++-	C10orf107	C10orf107	C10orf107	21687
LTA-DBP	rs7070797	10q21	63221779	a	g	-0.4387	0.0761	3.30E-08	-----+--+	NA	C10orf107	C10orf107	25684
LTA-DBP	rs4886629	15q24	72859611	c	g	-0.341	0.0585	2.29E-08	---------	NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L	CSK	2156
LTA-DBP	rs17249754	12q21	88584717	a	g	-0.5256	0.0702	7.08E-13	----+----	NA	ATP2B1	ATP2B1	10742
LTA-DBP	rs11105382	12q21	88631403	t	c	0.4519	0.0774	2.21E-08	+++++++-+	NA	ATP2B1	ATP2B1	57428
LTA-DBP	rs936230	15q24	72932151	t	c	0.3335	0.0586	4.98E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	7902
LTA-DBP	rs11066301	12q24	111355755	a	g	-0.304	0.0532	4.18E-08	---------	PTPN11	RPL6;PTPN11	PTPN11	14837
LTA-DBP	rs2588992	10q21	63184677	t	c	-0.3768	0.066	4.41E-08	-----+---	C10orf107	C10orf107	C10orf107	11418
LTA-DBP	rs1130741	15q24	72976983	a	g	0.3154	0.0525	8.20E-09	+++++++++	MPI	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	MPI	635
LTA-DBP	rs2050265	1p36	11802286	a	g	0.4709	0.0715	2.68E-10	++++--+++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	8576
LTA-DBP	rs8042694	15q24	73012468	a	g	-0.3311	0.0573	2.97E-08	---+-+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	4957
LTA-DBP	rs1813353	10p12	18747454	t	c	0.342	0.0566	6.84E-09	+++-+-+++	CACNB2	CACNB2	CACNB2	17936
LTA-DBP	rs129128	6p22	26233321	t	c	-0.4462	0.0749	1.10E-08	---------	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H2BE;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H2AC	425
LTA-DBP	rs2415251	15q24	73029208	t	c	0.3255	0.0548	1.22E-08	+++++-+++	NA	COX5A;SCAMP5;MPI;RPP25;C15orf17	RPP25	5287
LTA-DBP	rs12567136	1p36	11806318	t	c	-0.4716	0.0715	2.49E-10	----++---	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA-DBP	rs2681472	12q21	88533090	a	g	0.5231	0.0691	4.01E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
LTA-DBP	rs17037425	1p36	11792970	a	g	-0.4967	0.0753	2.49E-10	----++---	CLCN6	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	4177
LTA-DBP	rs11072514	15q24	73008918	a	t	-0.3224	0.0526	4.26E-09	---------	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8507
LTA-DBP	rs3184504	12q24	110368991	t	c	0.3936	0.0524	6.08E-13	+++++++++	SH2B3	SH2B3;ATXN2	SH2B3	4818
LTA-DBP	rs11105368	12q21	88598572	c	g	-0.5267	0.0704	7.25E-13	----+----	NA	ATP2B1	ATP2B1	24597
LTA-DBP	rs198851	6p22	26212611	t	g	0.4493	0.0777	2.97E-08	+++++++++	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H1C;HIST1H4C;HIST1H2AC;HIST1H1T;HFE;HIST1H3C	HIST1H4C	68
LTA-DBP	rs11105378	12q21	88614872	t	c	-0.5253	0.0716	2.03E-12	---------	NA	ATP2B1	ATP2B1	40897
LTA-DBP	rs198823	6p22	26230912	t	g	-0.3346	0.0553	6.57E-09	----+----	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H2BC	761
LTA-DBP	rs11105328	12q21	88466521	a	g	0.4968	0.0727	5.59E-11	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	22613
LTA-DBP	rs11105379	12q21	88619304	t	c	0.4551	0.0774	1.71E-08	+++++++-+	NA	ATP2B1	ATP2B1	45329
LTA-DBP	rs11105358	12q21	88566273	c	g	-0.3434	0.0532	5.82E-10	----+----	ATP2B1	ATP2B1	ATP2B1	7702
LTA-DBP	rs17037390	1p36	11783430	a	g	-0.4687	0.0717	3.70E-10	----++---	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	5272
LTA-DBP	rs17630235	12q24	111076069	a	g	0.3354	0.0539	2.43E-09	+++++++++	NA	TRAFD1;C12orf30	TRAFD1	274
LTA-DBP	rs1378938	15q24	72883496	t	c	0.3371	0.0588	3.90E-08	+++++++++	NA	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	939
LTA-MAP	rs1275986	2p23	26765583	a	c	-0.3875	0.0616	1.80E-09	-----+--+	NA	KCNK3;CIB4	KCNK3	3539
LTA-MAP	rs10858914	12q21	88555526	t	c	0.3913	0.061	8.48E-10	++++--+++	ATP2B1	ATP2B1	ATP2B1	18449
LTA-MAP	rs6026747	20q13	57179019	a	g	0.5438	0.094	3.20E-08	+-+++++++	NA	C20orf174	C20orf174	20450
LTA-MAP	rs11072512	15q24	72991079	t	c	-0.3902	0.0605	7.19E-10	-----+---	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	4564
LTA-MAP	rs7495739	15q24	72972723	a	g	0.3859	0.0605	1.05E-09	+++++-+++	MPI	COX5A;SCAMP2;C15orf17;MPI;ULK3	MPI	3261
LTA-MAP	rs7537765	1p36	11809890	a	g	0.6026	0.0822	2.49E-12	++++-++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA-MAP	rs1275979	2p23	26777072	t	c	0.385	0.0617	2.52E-09	+++++-++-	KCNK3	KCNK3;CIB4	KCNK3	7950
LTA-MAP	rs10858911	12q21	88487272	a	g	-0.3729	0.0603	3.32E-09	----++---	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	18686
LTA-MAP	rs7085	15q24	72882536	t	c	0.4311	0.0672	8.48E-10	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-MAP	rs11905512	20q13	57187391	c	g	-0.5575	0.0944	1.66E-08	-+-------	NA	C20orf174	C20orf174	12078
LTA-MAP	rs5068	1p36	11828561	a	g	0.8103	0.1348	9.06E-09	++++--+++	NPPA	MTHFR;NPPA;CLCN6;NPPB	NPPA	199
LTA-MAP	rs6495127	15q24	72981543	t	c	-0.398	0.0658	7.53E-09	-----+---	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17;ULK3	C15orf17	2163
LTA-MAP	rs11105354	12q21	88550654	a	g	0.685	0.0801	2.98E-16	++++-++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-MAP	rs12246717	10q21	63129189	t	g	0.4361	0.072	7.13E-09	+-+++++++	C10orf107	C10orf107	C10orf107	36465
LTA-MAP	rs10774625	12q24	110394602	a	g	0.443	0.0609	3.66E-12	+++++-+++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LTA-MAP	rs882384	20q13	57132808	t	c	0.5221	0.0854	5.03E-09	+++++-+++	NA	NA	C20orf174	66661
LTA-MAP	rs6092743	20q13	57133765	a	g	0.6372	0.0971	3.60E-10	+++++++++	NA	NA	C20orf174	65704
LTA-MAP	rs11634474	15q24	72903237	c	g	0.4099	0.0685	1.05E-08	+++++++++	LMAN1L	CSK;LMAN1L;CPLX3;SCAMP2;ULK3	LMAN1L	1914
LTA-MAP	rs11105381	12q21	88630966	a	g	-0.506	0.0827	5.00E-09	---------	NA	ATP2B1	ATP2B1	56991
LTA-MAP	rs4886636	15q24	72983229	a	g	-0.387	0.0604	9.37E-10	-----+---	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17	C15orf17	3286
LTA-MAP	rs3784789	15q24	72869605	c	g	0.3899	0.0638	5.18E-09	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	7838
LTA-MAP	rs35444	12q24	114036820	a	g	0.3621	0.0626	3.20E-08	+++++-+-+	NA	NA	TBX3	430468

Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-MAP	rs4842666	12q21	88465680	t	c	0.6575	0.0857	2.22E-13	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-MAP	rs17367504	1p36	11785365	a	g	0.5888	0.0825	9.08E-12	++++-++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	3337
LTA-MAP	rs11072511	15q24	72946486	a	g	0.3859	0.0605	1.09E-09	+++++-+++	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	6237
LTA-MAP	rs17696736	12q24	110971201	a	g	-0.3667	0.0617	1.32E-08	-----+---	C12orf30	ERP29;TMEM116;C12orf30	C12orf30	22325
LTA-MAP	rs7136259	12q21	88605319	t	c	-0.4383	0.0607	4.98E-12	----+----	NA	ATP2B1	ATP2B1	31344
LTA-MAP	rs236713	20q13	57128972	a	g	-0.4742	0.0791	9.92E-09	-----+---	NA	NA	C20orf174	70497
LTA-MAP	rs2681485	12q21	88549753	a	g	0.4601	0.0611	6.24E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-MAP	rs2588918	10q21	63195030	a	t	0.4192	0.0711	1.76E-08	+-+++-+++	C10orf107	C10orf107	C10orf107	1065
LTA-MAP	rs1275923	2p23	26786300	t	c	-0.3935	0.0633	2.84E-09	-----+--+	KCNK3	KCNK3;C2orf18	KCNK3	17178
LTA-MAP	rs12487	15q24	72923747	t	c	0.3523	0.0609	3.24E-08	+++++++++	NA	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	502
LTA-MAP	rs2120702	10q21	63192664	a	t	-0.4041	0.0683	1.55E-08	-+-------	C10orf107	C10orf107	C10orf107	3431
LTA-MAP	rs12258967	10p12	18767965	c	g	0.452	0.0657	4.98E-11	+++++-+++	CACNB2	CACNB2	CACNB2	38447
LTA-MAP	rs16916504	10q21	63122962	a	g	0.4371	0.0721	6.92E-09	+-+++++++	C10orf107	C10orf107	C10orf107	30238
LTA-MAP	rs6495126	15q24	72962079	a	g	0.3953	0.0655	7.95E-09	+++++-+++	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	7383
LTA-MAP	rs6100343	20q13	57133607	a	g	0.5228	0.0854	4.92E-09	+++++-+++	NA	NA	C20orf174	65862
LTA-MAP	rs2586886	2p23	26785535	t	c	-0.3916	0.0628	2.56E-09	-----+--+	KCNK3	C2orf18;KCNK3	KCNK3	16413
LTA-MAP	rs236706	20q13	57124811	t	c	-0.4863	0.0793	4.66E-09	-----+---	NA	NA	SLMO2	73515
LTA-MAP	rs12230074	12q21	88614998	a	g	0.6822	0.0825	2.82E-15	++++-++++	NA	ATP2B1	ATP2B1	41023
LTA-MAP	rs11066188	12q24	111095097	a	g	0.3828	0.062	3.60E-09	+++++++++	NA	TRAFD1	TRAFD1	19302
LTA-MAP	rs1378941	15q24	72867203	a	c	-0.3867	0.0636	6.32E-09	---------	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	5436
LTA-MAP	rs11065987	12q24	110556807	a	g	-0.4117	0.0626	3.16E-10	---------	NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-MAP	rs936226	15q24	72856335	t	c	-0.4311	0.0676	1.08E-09	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-MAP	rs880315	1p36	10719453	t	c	-0.4597	0.067	5.49E-11	--------?	CASZ1	CASZ1	CASZ1	59841
LTA-MAP	rs2166122	10q21	63193080	t	c	-0.4812	0.0766	1.88E-09	-+---+---	C10orf107	C10orf107	C10orf107	3015
LTA-MAP	rs236714	20q13	57129635	a	t	0.4894	0.0796	4.20E-09	+++++-+++	NA	NA	C20orf174	69834
LTA-MAP	rs1869959	15q24	72934385	a	c	0.3941	0.0677	2.66E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	10136
LTA-MAP	rs16982520	20q13	57192115	a	g	-0.5643	0.0945	1.16E-08	-+-------	NA	C20orf174	C20orf174	7354
LTA-MAP	rs653178	12q24	110492139	t	c	-0.4433	0.0604	2.36E-12	-----+---	ATXN2	ATXN2	ATXN2	29724
LTA-MAP	rs6015450	20q13	57184512	a	g	-0.5552	0.0943	1.84E-08	-+-------	NA	C20orf174	C20orf174	14957
LTA-MAP	rs1378942	15q24	72864420	a	c	-0.3853	0.0635	6.63E-09	---------	CSK	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	2653
LTA-MAP	rs11066320	12q24	111390798	a	g	0.3536	0.061	3.06E-08	+++++++++	PTPN11	RPL6;PTPN11	PTPN11	41301
LTA-MAP	rs2675612	10q21	63193272	t	c	-0.4126	0.0684	8.09E-09	-+-------	C10orf107	C10orf107	C10orf107	2823
LTA-MAP	rs4842667	12q21	88490785	a	g	0.3688	0.0602	4.62E-09	++++--+++	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	15173
LTA-MAP	rs284277	1p36	10713384	a	c	-0.4569	0.0692	2.73E-10	--------?	CASZ1	CASZ1	CASZ1	65910
LTA-MAP	rs3765066	15q24	72927907	a	g	-0.4075	0.0649	1.99E-09	---------	SCAMP2	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	3658
LTA-MAP	rs1275982	2p23	26772593	t	c	-0.3813	0.0618	3.57E-09	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	3471
LTA-MAP	rs6100342	20q13	57132656	a	c	-0.5215	0.0853	5.14E-09	-----+---	NA	NA	C20orf174	66813
LTA-MAP	rs260014	20q13	57192854	t	c	-0.5518	0.0904	5.36E-09	---------	NA	C20orf174	C20orf174	6615
LTA-MAP	rs11072518	15q24	73021663	t	c	0.4315	0.0636	8.95E-11	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
LTA-MAP	rs8031937	15q24	72968174	a	g	0.397	0.0657	7.57E-09	+++++-+++	NA	COX5A;MPI;CPLX3;SCAMP2;C15orf17;ULK3	MPI	1288
LTA-MAP	rs1401982	12q21	88513730	a	g	0.4579	0.0609	6.90E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	7772
LTA-MAP	rs11630918	15q24	72942949	t	c	-0.3901	0.062	1.77E-09	-----+---	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	9774
LTA-MAP	rs998981	20q13	57133036	t	c	0.5224	0.0854	5.00E-09	+++++-+++	NA	NA	C20orf174	66433
LTA-MAP	rs2070759	12q21	88541867	t	g	0.3891	0.0608	9.54E-10	++++--+++	ATP2B1	ATP2B1	ATP2B1	32108
LTA-MAP	rs12442901	15q24	72870965	a	g	0.428	0.0673	1.23E-09	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	9198
LTA-MAP	rs13306561	1p36	11788391	a	g	0.6133	0.0832	1.83E-12	++++-++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	311
LTA-MAP	rs11072513	15q24	73008021	t	c	-0.3959	0.0606	4.27E-10	-----+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8350
LTA-MAP	rs2681492	12q21	88537220	t	c	0.6564	0.0779	8.01E-16	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-MAP	rs2168519	15q24	72867925	t	c	0.4287	0.0673	1.13E-09	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
LTA-MAP	rs1275977	2p23	26776359	a	g	-0.3812	0.0664	4.04E-08	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	7237
LTA-MAP	rs2393833	10q21	63115322	t	c	-0.4359	0.072	7.35E-09	-+-------	C10orf107	C10orf107	C10orf107	22598
LTA-MAP	rs2004776	1q42	228915325	t	c	0.4226	0.0708	1.18E-08	+++++++++	AGT	AGT;COG2;CAPN9	AGT	1239
LTA-MAP	rs4886633	15q24	72965260	a	g	-0.398	0.0656	6.81E-09	-----+---	NA	COX5A;CPLX3;SCAMP2;C15orf17;MPI;ULK3	MPI	4202
LTA-MAP	rs236715	20q13	57130490	t	c	-0.4819	0.0794	6.55E-09	-----+---	NA	NA	C20orf174	68979
LTA-MAP	rs1543927	15q24	72850626	t	c	0.4104	0.0675	6.29E-09	+++++++++	NA	CPLX3;CYP1A2;CYP1A1;CSK;LMAN1L	CSK	11141
LTA-MAP	rs492945	1p36	10723185	a	g	-0.4088	0.0674	6.62E-09	--------?	CASZ1	CASZ1	CASZ1	56109
LTA-MAP	rs11856413	15q24	72986945	a	g	0.3881	0.0605	8.56E-10	+++++-+++	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	430
LTA-MAP	rs1133322	15q24	72999410	a	g	0.393	0.0606	5.61E-10	+++++-+++	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	261
LTA-MAP	rs11105364	12q21	88593407	t	g	0.6848	0.0809	6.17E-16	++++-++++	NA	ATP2B1	ATP2B1	19432
LTA-MAP	rs6495122	15q24	72912698	a	c	0.3642	0.0611	1.23E-08	+++++++++	NA	CPLX3;SCAMP2;MPI;CSK;ULK3;LMAN1L	CPLX3	1509
LTA-MAP	rs12579302	12q21	88574634	a	g	0.6809	0.0808	7.72E-16	++++-++++	NA	ATP2B1	ATP2B1	659
LTA-MAP	rs35441	12q24	114037498	t	c	-0.3631	0.0629	3.41E-08	-----+-+-	NA	NA	TBX3	431146
LTA-MAP	rs17376328	1p36	11799249	a	g	-0.7767	0.1318	1.79E-08	----++---	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	10456
LTA-MAP	rs12244842	10q21	63109192	t	g	-0.4425	0.0723	4.97E-09	-+-------	C10orf107	C10orf107	C10orf107	16468
LTA-MAP	rs4766578	12q24	110388754	a	t	-0.4436	0.0609	3.45E-12	-----+---	ATXN2	SH2B3;ATXN2	ATXN2	14353
LTA-MAP	rs11105383	12q21	88631437	t	c	0.5824	0.0895	4.96E-10	+++++++++	NA	ATP2B1	ATP2B1	57462
LTA-MAP	rs1992625	10q21	63190704	t	c	-0.478	0.0764	2.26E-09	-+---+---	C10orf107	C10orf107	C10orf107	5391
LTA-MAP	rs4548524	10p12	18756873	a	g	0.3652	0.0631	3.10E-08	+++++++++	CACNB2	CACNB2	CACNB2	27355
LTA-MAP	rs1275988	2p23	26767868	t	c	-0.3894	0.0616	1.51E-09	-----+--+	NA	KCNK3;CIB4	KCNK3	1254
LTA-MAP	rs1133323	15q24	72999278	t	c	-0.3986	0.0606	3.22E-10	-----+---	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	393
LTA-MAP	rs1378940	15q24	72870547	a	c	-0.3902	0.0639	5.28E-09	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	8780
LTA-MAP	rs2301249	15q24	72879437	t	c	0.4315	0.0671	7.74E-10	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-MAP	rs1127796	15q24	72980057	t	c	0.3864	0.0605	1.02E-09	+++++-+++	C15orf17	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	C15orf17	677
LTA-MAP	rs4886406	15q24	72844256	t	g	-0.3941	0.0676	2.50E-08	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L	CYP1A2	8262
LTA-MAP	rs6026704	20q13	57117540	c	g	0.5037	0.0847	1.32E-08	+++++-++-	NA	NA	SLMO2	66244
LTA-MAP	rs7497393	15q24	72962510	c	g	-0.3872	0.0604	9.16E-10	-----+---	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	6952
LTA-MAP	rs7299436	12q21	88637201	t	g	0.5845	0.0898	5.02E-10	+++++++++	NA	NA	ATP2B1	63226
LTA-MAP	rs7162232	15q24	72902948	a	g	-0.4102	0.0685	1.02E-08	---------	LMAN1L	CPLX3;SCAMP2;CSK;ULK3;LMAN1L	LMAN1L	2203
LTA-MAP	rs6100340	20q13	57118007	a	g	-0.5197	0.0848	4.63E-09	-----+---	NA	NA	SLMO2	66711

Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-MAP	rs8033381	15q24	72867738	a	g	-0.4293	0.0673	1.07E-09	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-MAP	rs260013	20q13	57194118	a	g	-0.5496	0.0905	6.48E-09	---------	NA	C20orf174	C20orf174	5351
LTA-MAP	rs12046278	1p36	10722164	t	c	-0.4722	0.0693	7.26E-11	--------?	CASZ1	CASZ1	CASZ1	57130
LTA-MAP	rs3750727	10q21	63114411	a	g	0.4423	0.0723	5.01E-09	+-+++++++	C10orf107	C10orf107	C10orf107	21687
LTA-MAP	rs7362597	20q13	57112829	a	g	0.5054	0.0848	1.22E-08	+++++-++-	NA	NA	SLMO2	61533
LTA-MAP	rs7070797	10q21	63221779	a	g	-0.5456	0.0878	2.89E-09	-----+---	NA	C10orf107	C10orf107	25684
LTA-MAP	rs236705	20q13	57122065	t	c	-0.487	0.0793	4.46E-09	-----+---	NA	NA	SLMO2	70769
LTA-MAP	rs973237	10q21	63195307	a	g	0.42	0.0718	2.26E-08	+-+++++++	C10orf107	C10orf107	C10orf107	788
LTA-MAP	rs4886629	15q24	72859611	c	g	-0.4308	0.0675	1.09E-09	---------	NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L	CSK	2156
LTA-MAP	rs11854147	15q24	72839824	t	c	0.401	0.0671	1.09E-08	+++++++++	NA	CYP1A2;CYP1A1;CSK;LMAN1L	CYP1A2	3830
LTA-MAP	rs4845953	1p36	10724576	a	g	-0.3955	0.0667	1.43E-08	--------?	CASZ1	CASZ1	CASZ1	54718
LTA-MAP	rs17249754	12q21	88584717	a	g	-0.6855	0.0808	5.07E-16	----+----	NA	ATP2B1	ATP2B1	10742
LTA-MAP	rs2408046	12q21	88633468	t	c	-0.5057	0.0831	6.09E-09	---------	NA	ATP2B1	ATP2B1	59493
LTA-MAP	rs7176022	15q24	72894933	a	c	0.4115	0.0681	7.54E-09	+++++++++	LMAN1L	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	LMAN1L	2687
LTA-MAP	rs1465537	20q13	57131415	t	c	0.5218	0.0853	4.98E-09	+++++-+++	NA	NA	C20orf174	68054
LTA-MAP	rs11105382	12q21	88631403	t	c	0.5818	0.0893	4.75E-10	+++++++++	NA	ATP2B1	ATP2B1	57428
LTA-MAP	rs1275985	2p23	26765249	t	c	-0.3857	0.0618	2.39E-09	-----+--+	NA	KCNK3;CIB4	KCNK3	3873
LTA-MAP	rs4886410	15q24	72852697	c	g	-0.3871	0.064	7.21E-09	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3	CSK	9070
LTA-MAP	rs6026748	20q13	57179210	a	g	0.5518	0.0941	2.08E-08	+-+++++++	NA	C20orf174	C20orf174	20259
LTA-MAP	rs936230	15q24	72932151	t	c	0.3943	0.0677	2.53E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	7902
LTA-MAP	rs11066301	12q24	111355755	a	g	-0.3558	0.0612	2.79E-08	---------	PTPN11	RPL6;PTPN11	PTPN11	14837
LTA-MAP	rs2588992	10q21	63184677	t	c	-0.4589	0.0762	8.55E-09	-+---+---	C10orf107	C10orf107	C10orf107	11418
LTA-MAP	rs35432	12q24	114039913	t	c	-0.3676	0.0637	3.43E-08	-----+-+-	NA	NA	TBX3	433561
LTA-MAP	rs2113894	12q21	88623528	a	t	0.5072	0.0827	4.64E-09	+++++++++	NA	ATP2B1	ATP2B1	49553
LTA-MAP	rs9210	15q24	72915554	t	c	0.3887	0.0675	3.73E-08	+++++++++	ULK3	MPI;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	ULK3	43
LTA-MAP	rs1130741	15q24	72976983	a	g	0.3858	0.0605	1.07E-09	+++++-+++	MPI	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	MPI	635
LTA-MAP	rs10858915	12q21	88575678	a	g	0.3548	0.0609	2.58E-08	++++--+++	NA	ATP2B1	ATP2B1	1703
LTA-MAP	rs2050265	1p36	11802286	a	g	0.602	0.0823	2.77E-12	++++-++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	8576
LTA-MAP	rs11014166	10p12	18748804	a	t	0.3878	0.0633	4.77E-09	+++++++++	CACNB2	CACNB2	CACNB2	19286
LTA-MAP	rs12243859	10p12	18780638	t	c	-0.3739	0.0639	2.23E-08	---+-+---	CACNB2	CACNB2	CACNB2	51120
LTA-MAP	rs4590817	10q21	63137559	c	g	-0.4662	0.0816	4.72E-08	-----+--+	C10orf107	C10orf107	C10orf107	44835
LTA-MAP	rs183173	20q13	57159500	t	g	-0.5073	0.0888	4.81E-08	---------	NA	C20orf174	C20orf174	39969
LTA-MAP	rs8042694	15q24	73012468	a	g	-0.4071	0.066	3.65E-09	-----+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	4957
LTA-MAP	rs1275980	2p23	26770473	t	c	-0.3863	0.0617	2.21E-09	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	1351
LTA-MAP	rs1813353	10p12	18747454	t	c	0.439	0.0652	1.26E-10	+++++-+++	CACNB2	CACNB2	CACNB2	17936
LTA-MAP	rs6676300	1p36	11847887	a	g	0.3641	0.0634	4.03E-08	+++-+-+++	NA	MTHFR;KIAA2013;NPPA;CLCN6;NPPB	NPPB	6308
LTA-MAP	rs2415251	15q24	73029208	t	c	0.3962	0.0631	1.99E-09	+++++-+++	NA	COX5A;SCAMP5;MPI;RPP25;C15orf17	RPP25	5287
LTA-MAP	rs12567136	1p36	11806318	t	c	-0.6025	0.0823	2.64E-12	----+----	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA-MAP	rs2681472	12q21	88533090	a	g	0.6861	0.0796	1.77E-16	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
LTA-MAP	rs17037425	1p36	11792970	a	g	-0.6215	0.0868	7.76E-12	---------	CLCN6	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	4177
LTA-MAP	rs11072514	15q24	73008918	a	t	-0.396	0.0606	4.34E-10	-----+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8507
LTA-MAP	rs3184504	12q24	110368991	t	c	0.4469	0.0605	1.68E-12	+++++-+++	SH2B3	SH2B3;ATXN2	SH2B3	4818
LTA-MAP	rs11105368	12q21	88598572	c	g	-0.6845	0.081	6.61E-16	----+----	NA	ATP2B1	ATP2B1	24597
LTA-MAP	rs4845843	1p36	10724172	a	g	0.6025	0.1056	4.87E-08	++++++++?	CASZ1	CASZ1	CASZ1	55122
LTA-MAP	rs11105378	12q21	88614872	t	c	-0.6822	0.0824	2.46E-15	----+----	NA	ATP2B1	ATP2B1	40897
LTA-MAP	rs11105328	12q21	88466521	a	g	0.6393	0.0837	2.84E-13	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	22613
LTA-MAP	rs11105379	12q21	88619304	t	c	0.5869	0.0892	3.22E-10	+++++++++	NA	ATP2B1	ATP2B1	45329
LTA-MAP	rs11105358	12q21	88566273	c	g	-0.4644	0.0613	4.38E-13	----+----	ATP2B1	ATP2B1	ATP2B1	7702
LTA-MAP	rs7922049	10q21	63132371	a	g	-0.4993	0.085	2.00E-08	-+---+--+	C10orf107	C10orf107	C10orf107	39647
LTA-MAP	rs17037390	1p36	11783430	a	g	-0.6015	0.0826	3.37E-12	----+----	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	5272
LTA-MAP	rs236710	20q13	57127024	t	g	-0.4852	0.0793	5.04E-09	-----+---	NA	NA	C20orf174	72445
LTA-MAP	rs17630235	12q24	111076069	a	g	0.3848	0.062	2.94E-09	+++++++++	NA	TRAFD1;C12orf30	TRAFD1	274
LTA-MAP	rs1378938	15q24	72883496	t	c	0.4148	0.0679	5.32E-09	+++++++++	NA	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	939
LTA-MAP	rs11014171	10p12	18751201	t	c	-0.3892	0.0632	3.88E-09	---------	CACNB2	CACNB2	CACNB2	21683
LTA-PP	rs1717014	3p22	41892399	t	c	-0.4739	0.0825	2.22E-08	--------+	ULK4	ULK4	ULK4	86265
LTA-PP	rs9854833	3p22	41750581	t	c	-0.4956	0.082	3.95E-09	---------	ULK4	ULK4	ULK4	228083
LTA-PP	rs1717003	3p22	41912004	t	c	0.4803	0.0824	1.36E-08	++++++++-	ULK4	ULK4	ULK4	66660
LTA-PP	rs1717034	3p22	41930917	a	g	-0.483	0.0823	1.10E-08	--------+	ULK4	ULK4	ULK4	47747
LTA-PP	rs2469	6p21	43407301	t	c	-0.3519	0.0623	3.88E-08	---------	NA	TTBK1;ZNF318;CRIP3;SLC22A7	ZNF318	4484
LTA-PP	rs6796210	3p22	41826722	t	c	0.4691	0.082	2.58E-08	++++++++-	ULK4	ULK4	ULK4	151942
LTA-PP	rs1717007	3p22	41917203	t	c	-0.4817	0.0824	1.23E-08	--------+	ULK4	ULK4	ULK4	61461
LTA-PP	rs7634985	3p22	41994569	t	c	0.5174	0.0861	4.93E-09	++++++++-	NA	ULK4	ULK4	15905
LTA-PP	rs1052501	3p22	41900402	t	c	0.4781	0.0823	1.55E-08	++++++++-	ULK4	ULK4	ULK4	78262
LTA-PP	rs7622259	3p22	41856355	a	t	0.4706	0.0827	2.96E-08	++++++++-	ULK4	ULK4	ULK4	122309
LTA-PP	rs2272007	3p22	41971140	t	c	-0.4879	0.082	6.77E-09	--------+	ULK4	ULK4	ULK4	7524
LTA-PP	rs9874975	3p22	41739304	a	g	-0.4943	0.0819	4.26E-09	---------	ULK4	ULK4	ULK4	239360
LTA-PP	rs6783001	3p22	41837236	a	c	-0.4746	0.0825	2.13E-08	--------+	ULK4	ULK4	ULK4	141428
LTA-PP	rs2242416	6p21	43381582	a	g	0.355	0.0623	2.92E-08	+++++++++	CRIP3	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	329
LTA-PP	rs1716999	3p22	41905045	c	g	-0.479	0.0823	1.47E-08	--------+	ULK4	ULK4	ULK4	73619
LTA-PP	rs7631057	3p22	41792955	t	c	-0.4772	0.0822	1.58E-08	--------+	ULK4	ULK4	ULK4	185709
LTA-PP	rs9865780	3p22	41870806	a	g	0.4729	0.0826	2.49E-08	++++++++-	ULK4	ULK4	ULK4	107858
LTA-PP	rs1716655	3p22	41893710	a	g	-0.4739	0.0825	2.21E-08	--------+	ULK4	ULK4	ULK4	84954
LTA-PP	rs6802340	3p22	41869038	t	c	0.4709	0.0827	2.90E-08	++++++++-	ULK4	ULK4	ULK4	109626
LTA-PP	rs1717027	3p22	41962924	t	c	-0.488	0.082	6.80E-09	--------+	ULK4	ULK4	ULK4	15740
LTA-PP	rs6796078	3p22	41992824	a	t	-0.5183	0.0861	4.62E-09	--------+	NA	ULK4	ULK4	14160
LTA-PP	rs6781326	3p22	41752032	t	c	0.4963	0.0817	3.28E-09	+++++++++	ULK4	ULK4	ULK4	226632
LTA-PP	rs7632387	3p22	41828165	t	c	-0.4687	0.0821	2.67E-08	--------+	ULK4	ULK4	ULK4	150499
LTA-PP	rs1624519	3p22	41959804	a	g	0.4838	0.0823	1.05E-08	++++++++-	ULK4	ULK4	ULK4	18860
LTA-PP	rs809930	3p22	42040009	a	g	0.5026	0.0868	1.71E-08	++++++++-	NA	NA	ULK4	61345

Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-PP	rs6776724	3p22	41816274	a	g	0.4692	0.0823	2.79E-08	++++++++-	ULK4	ULK4	ULK4	162390
LTA-PP	rs6791806	3p22	41864999	t	c	-0.4709	0.0827	2.89E-08	--------+	ULK4	ULK4	ULK4	113665
LTA-PP	rs939561	3p22	42032105	a	g	0.4936	0.087	3.27E-08	++++++++-	NA	ULK4	ULK4	53441
LTA-PP	rs1717017	3p22	41890620	a	c	0.4737	0.0825	2.25E-08	++++++++-	ULK4	ULK4	ULK4	88044
LTA-PP	rs4615050	3p22	41917502	a	t	0.482	0.0824	1.20E-08	++++++++-	ULK4	ULK4	ULK4	61162
LTA-PP	rs3890604	3p22	41735629	t	c	-0.4915	0.0819	5.06E-09	---------	ULK4	ULK4	ULK4	243035
LTA-PP	rs9850310	3p22	41866102	t	c	0.4708	0.0827	2.92E-08	++++++++-	ULK4	ULK4	ULK4	112562
LTA-PP	rs12705390	7q22	106198013	a	g	0.5865	0.0759	5.40E-14	+++++-+++	NA	NA	PIK3CG	95146
LTA-PP	rs7646144	3p22	41828129	a	t	-0.4686	0.0821	2.69E-08	--------+	ULK4	ULK4	ULK4	150535
LTA-PP	rs9856088	3p22	41835486	t	g	-0.4946	0.0847	1.29E-08	--------+	ULK4	ULK4	ULK4	143178
LTA-PP	rs1016669	3p22	41869444	t	c	0.4717	0.0826	2.72E-08	++++++++-	ULK4	ULK4	ULK4	109220
LTA-PP	rs1717006	3p22	41915452	a	c	0.4791	0.082	1.29E-08	++++++++-	ULK4	ULK4	ULK4	63212
LTA-PP	rs880315	1p36	10719453	t	c	-0.421	0.0703	5.45E-09	--------?	CASZ1	CASZ1	CASZ1	59841
LTA-PP	rs1716975	3p22	41935010	t	c	-0.4837	0.0822	1.01E-08	--------+	ULK4	ULK4	ULK4	43654
LTA-PP	rs17398575	7q22	106196688	a	g	0.5732	0.075	1.02E-13	+++++-+++	NA	NA	PIK3CG	96471
LTA-PP	rs1717020	3p22	41956494	a	c	0.4829	0.082	9.73E-09	++++++++-	ULK4	ULK4	ULK4	22170
LTA-PP	rs7629767	3p22	42018513	t	g	0.4948	0.0867	2.75E-08	++++++++-	NA	ULK4	ULK4	39849
LTA-PP	rs284277	1p36	10713384	a	c	-0.4142	0.073	3.27E-08	--------?	CASZ1	CASZ1	CASZ1	65910
LTA-PP	rs17062109	3p22	41785368	t	c	-0.4773	0.082	1.46E-08	--------+	ULK4	ULK4	ULK4	193296
LTA-PP	rs1716984	3p22	41940536	a	g	0.4835	0.0823	1.06E-08	++++++++-	ULK4	ULK4	ULK4	38128
LTA-PP	rs9866759	3p22	41733422	t	c	0.483	0.0821	9.91E-09	+++++++++	ULK4	ULK4	ULK4	245242
LTA-PP	rs1716653	3p22	41950602	a	c	0.4838	0.0823	1.04E-08	++++++++-	ULK4	ULK4	ULK4	28062
LTA-PP	rs2128834	3p22	41837649	a	g	0.4694	0.0822	2.68E-08	++++++++-	ULK4	ULK4	ULK4	141015
LTA-PP	rs6599168	3p22	41725327	t	c	0.5163	0.0865	6.11E-09	+++++++++	ULK4	ULK4	ULK4	253337
LTA-PP	rs1716694	3p22	41961403	t	g	0.4864	0.0823	8.67E-09	++++++++-	ULK4	ULK4	ULK4	17261
LTA-PP	rs1613233	3p22	41920148	a	g	-0.4819	0.0824	1.22E-08	--------+	ULK4	ULK4	ULK4	58516
LTA-PP	rs9882329	3p22	41742158	t	c	0.4949	0.082	4.10E-09	+++++++++	ULK4	ULK4	ULK4	236506
LTA-PP	rs12705389	7q22	106192878	t	c	0.5759	0.0753	9.52E-14	+++++-+++	NA	NA	PIK3CG	100281
LTA-PP	rs11760498	7q22	106206208	a	g	0.4499	0.0803	4.89E-08	+++++-+++	NA	NA	PIK3CG	86951
LTA-PP	rs10212536	3p22	41802030	a	g	0.4749	0.0823	1.96E-08	++++++++-	ULK4	ULK4	ULK4	176634
LTA-PP	rs6789260	3p22	41751354	c	g	-0.4961	0.0817	3.36E-09	---------	ULK4	ULK4	ULK4	227310
LTA-PP	rs10865914	3p22	41894503	t	c	0.4741	0.0825	2.17E-08	++++++++-	ULK4	ULK4	ULK4	84161
LTA-PP	rs2949837	7p13	45960903	a	t	0.402	0.0706	2.94E-08	+++++++++	NA	IGFBP3	IGFBP3	33507
LTA-PP	rs9828398	3p22	41870897	t	c	-0.4731	0.0826	2.43E-08	--------+	ULK4	ULK4	ULK4	107767
LTA-PP	rs1615243	3p22	41940238	t	c	0.4836	0.0823	1.05E-08	++++++++-	ULK4	ULK4	ULK4	38426
LTA-PP	rs12536419	7q22	106206532	a	c	-0.4747	0.0839	3.60E-08	----++---	NA	NA	PIK3CG	86627
LTA-PP	rs7372217	3p22	41965126	a	g	0.4881	0.082	6.74E-09	++++++++-	ULK4	ULK4	ULK4	13538
LTA-PP	rs1716685	3p22	41900305	t	c	-0.4772	0.0819	1.43E-08	--------+	ULK4	ULK4	ULK4	78359
LTA-PP	rs9847006	3p22	41730363	t	c	0.4844	0.0823	1.00E-08	+++++++++	ULK4	ULK4	ULK4	248301
LTA-PP	rs13087502	3p22	41990114	t	c	0.5202	0.086	3.93E-09	++++++++-	NA	ULK4	ULK4	11450
LTA-PP	rs2125738	6p21	43435728	a	g	0.3569	0.0628	3.20E-08	+++++++++	ZNF318	CRIP3;SLC22A7;ZNF318	ZNF318	9431
LTA-PP	rs2625667	3p22	41875955	a	c	-0.4736	0.0826	2.39E-08	--------+	ULK4	ULK4	ULK4	102709
LTA-PP	rs1716983	3p22	41939132	a	g	0.4835	0.0823	1.05E-08	++++++++-	ULK4	ULK4	ULK4	39532
LTA-PP	rs1716692	3p22	41958790	a	g	0.484	0.0823	1.04E-08	++++++++-	ULK4	ULK4	ULK4	19874
LTA-PP	rs9856633	3p22	41988854	a	g	-0.4836	0.0819	9.04E-09	--------+	NA	ULK4	ULK4	10190
LTA-PP	rs1574430	6p21	43377007	a	c	0.3555	0.0625	3.04E-08	+++++++++	SLC22A7	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	3032
LTA-PP	rs939558	3p22	41951044	a	c	0.4839	0.0823	1.04E-08	++++++++-	ULK4	ULK4	ULK4	27620
LTA-PP	rs17477177	7q22	106199094	t	c	-0.589	0.0763	5.61E-14	-----+---	NA	NA	PIK3CG	94065
LTA-PP	rs10948071	6p21	43388691	t	c	-0.3846	0.0652	9.06E-09	---------	NA	CRIP3;SLC22A7;TTBK1;ZNF318	CRIP3	4183
LTA-PP	rs9823254	3p22	41869772	c	g	-0.4718	0.0826	2.69E-08	--------+	ULK4	ULK4	ULK4	108892
LTA-PP	rs4973995	3p22	41906477	t	c	-0.4796	0.0823	1.42E-08	--------+	ULK4	ULK4	ULK4	72187
LTA-PP	rs9825741	3p22	41736832	a	t	0.49	0.0817	5.25E-09	+++++++++	ULK4	ULK4	ULK4	241832
LTA-PP	rs9866092	3p22	41870971	a	c	0.4734	0.0826	2.38E-08	++++++++-	ULK4	ULK4	ULK4	107693
LTA-PP	rs6599176	3p22	41763496	t	g	0.4973	0.0818	3.23E-09	+++++++++	ULK4	ULK4	ULK4	215168
LTA-PP	rs9867627	3p22	41770845	a	c	0.4941	0.0821	4.63E-09	+++++++++	ULK4	ULK4	ULK4	207819
LTA-PP	rs9830469	3p22	41737539	a	g	0.4917	0.0819	4.96E-09	+++++++++	ULK4	ULK4	ULK4	241125
LTA-PP	rs9865127	3p22	41782452	t	c	-0.4781	0.082	1.39E-08	--------+	ULK4	ULK4	ULK4	196212
LTA-PP	rs6803560	3p22	41799484	a	g	0.4768	0.0822	1.64E-08	++++++++-	ULK4	ULK4	ULK4	179180
LTA-PP	rs2841647	6p21	43377158	a	c	-0.3538	0.0627	3.92E-08	-----?---	SLC22A7	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	3183
LTA-PP	rs1716657	3p22	41893460	t	c	0.4737	0.0825	2.24E-08	++++++++-	ULK4	ULK4	ULK4	85204
LTA-PP	rs9846634	3p22	41869053	a	g	-0.4764	0.0829	2.22E-08	--------+	ULK4	ULK4	ULK4	109611
LTA-PP	rs7650227	3p22	41769941	t	g	0.5006	0.0821	2.84E-09	+++++++++	ULK4	ULK4	ULK4	208723
LTA-PP	rs1994157	3p22	41872486	a	g	-0.4734	0.0826	2.42E-08	--------+	ULK4	ULK4	ULK4	106178
LTA-PP	rs9875107	3p22	41797317	a	t	0.4767	0.0822	1.64E-08	++++++++-	ULK4	ULK4	ULK4	181347
LTA-PP	rs11923562	3p22	41735335	t	g	-0.4917	0.0819	5.06E-09	---------	ULK4	ULK4	ULK4	243329
LTA-PP	rs7626217	3p22	41817419	a	g	0.47	0.0821	2.52E-08	++++++++-	ULK4	ULK4	ULK4	161245
LTA-PP	rs17060961	3p22	41738715	a	g	0.4946	0.0819	4.19E-09	+++++++++	ULK4	ULK4	ULK4	239949
LTA-PP	rs794902	3p22	42000943	t	c	-0.5158	0.0861	5.47E-09	--------+	NA	ULK4	ULK4	22279
LTA-PP	rs6599167	3p22	41725264	a	g	0.5164	0.0866	6.34E-09	+++++++++	ULK4	ULK4	ULK4	253400
LTA-PP	rs12635286	3p22	42026840	t	c	0.4858	0.0867	4.95E-08	++++++++-	NA	ULK4	ULK4	48176
LTA-PP	rs1716642	3p22	41940869	a	c	-0.4835	0.0823	1.06E-08	--------+	ULK4	ULK4	ULK4	37795
LTA-PP	rs7648578	3p22	41833735	t	c	-0.4694	0.0821	2.55E-08	--------+	ULK4	ULK4	ULK4	144929
LTA-PP	rs7652506	3p22	42035239	t	c	-0.49	0.0869	4.08E-08	--------+	NA	ULK4	ULK4	56575
LTA-PP	rs13088394	3p22	41926719	a	g	0.4824	0.0823	1.17E-08	++++++++-	ULK4	ULK4	ULK4	51945
LTA-PP	rs1716693	3p22	41960604	t	c	0.4857	0.0823	9.18E-09	++++++++-	ULK4	ULK4	ULK4	18060
LTA-PP	rs17063599	3p22	41836680	t	c	-0.4743	0.0825	2.16E-08	--------+	ULK4	ULK4	ULK4	141984
LTA-PP	rs2272006	3p22	41972063	t	c	0.4881	0.082	6.77E-09	++++++++-	ULK4	ULK4	ULK4	6601
LTA-PP	rs6768128	3p22	41840084	a	g	-0.4744	0.0825	2.19E-08	--------+	ULK4	ULK4	ULK4	138580
LTA-PP	rs6599179	3p22	41830288	t	c	-0.4685	0.0821	2.70E-08	--------+	ULK4	ULK4	ULK4	148376



Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-PP	rs9842261	3p22	41797712	a	g	-0.4745	0.0821	1.83E-08	--------+	ULK4	ULK4	ULK4	180952
LTA-PP	rs9820192	3p22	41864285	a	g	-0.4706	0.0827	2.96E-08	--------+	ULK4	ULK4	ULK4	114379
LTA-PP	rs6793520	3p22	41840293	c	g	0.4748	0.0826	2.15E-08	++++++++-	ULK4	ULK4	ULK4	138371
LTA-PP	rs9876960	3p22	41960816	t	c	0.4856	0.0823	9.17E-09	++++++++-	ULK4	ULK4	ULK4	17848
LTA-PP	rs1716683	3p22	41898078	a	g	-0.4769	0.0824	1.78E-08	--------+	ULK4	ULK4	ULK4	80586
LTA-PP	rs6599175	3p22	41761013	t	c	0.4966	0.0816	3.18E-09	+++++++++	ULK4	ULK4	ULK4	217651
LTA-PP	rs13325965	3p22	41889946	t	g	-0.4752	0.0825	2.04E-08	--------+	ULK4	ULK4	ULK4	88718
LTA-PP	rs9852303	3p22	41734529	t	c	-0.483	0.0819	9.49E-09	---------	ULK4	ULK4	ULK4	244135
LTA-PP	rs794899	3p22	42003726	t	c	-0.5166	0.0861	5.22E-09	--------+	NA	ULK4	ULK4	25062
LTA-PP	rs13225723	7q22	106203703	a	g	0.6031	0.0827	1.26E-12	+++++-+++	NA	NA	PIK3CG	89456
LTA-PP	rs9815354	3p22	41887655	a	g	-0.5025	0.0855	1.05E-08	--------+	ULK4	ULK4	ULK4	91009
LTA-PP	rs13084436	3p22	41992541	a	t	0.5181	0.0861	4.63E-09	++++++++-	NA	ULK4	ULK4	13877
LTA-PP	rs704964	3p22	42028903	a	g	0.4921	0.0866	3.18E-08	++++++++-	NA	ULK4	ULK4	50239
LTA-PP	rs9857175	3p22	41797058	t	g	0.4772	0.0822	1.59E-08	++++++++-	ULK4	ULK4	ULK4	181606
LTA-PP	rs3934103	3p22	41952218	t	c	0.4848	0.0823	9.77E-09	++++++++-	ULK4	ULK4	ULK4	26446
LTA-PP	rs3774372	3p22	41852418	t	c	0.4718	0.0825	2.62E-08	++++++++-	ULK4	ULK4	ULK4	126246

"Direction" corresponds to order of cohorts as listed in Supplementary Table 3.

Table S5: eQTL analysis results for the index SNP in each of the 39 loci identified in the analysis of LTA BP traits and for which eQTL data was available.

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Whole blood (CHARGE)	2.19E-72	1	11788391	3990477	MTHFR,C1orf167	cis	17.99	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	LCL (MuTHER)	1.91E-16	1	11788391	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Whole blood (PaxGene) in Japanese	1.20E-09	1	11788391	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Skin (MuTHER)	2.36E-06	1	11788391	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Subc adipose (MuTHER)	5.98E-06	1	11788391	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Whole blood (CHARGE)	2.21E-78	1	11802286	3990477	MTHFR,C1orf167	cis	18.74	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Whole blood (CHARGE)	2.64E-78	1	11806318	3990477	MTHFR,C1orf167	cis	18.73	T	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Whole blood (CHARGE)	3.23E-78	1	11809890	3990477	MTHFR,C1orf167	cis	18.72	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	LCL (MuTHER)	5.77E-19	1	11806318	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	LCL (MuTHER)	8.49E-19	1	11802286	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	LCL (MuTHER)	2.10E-18	1	11809890	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Monocytes	3.57E-14	1	11806318		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Monocytes	1.14E-13	1	11809890		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs17037429	Monocytes	2.33E-13	1	11796374		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	PaxGeneWholeBlood(Mehta)	8.44E-10	1	11809890	ILMN_1731434	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Whole blood (PaxGene) in Japanese	1.20E-09	1	11806318	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Whole blood (PaxGene) in Japanese	1.20E-09	1	11802286	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs3753584	Whole blood (PaxGene) in Japanese	1.20E-09	1	11787173	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	PaxGeneWholeBlood(Mehta)	1.44E-09	1	11806318	ILMN_1731434	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Whole blood (PaxGene) in Japanese	2.16E-09	1	11809890	A_23_P400081	MTHFR	cis	0.62			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	SchadtLiver	1.37E-07	1	11809890		CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Skin (MuTHER)	1.44E-07	1	11806318	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Skin (MuTHER)	1.50E-07	1	11802286	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Skin (MuTHER)	3.50E-07	1	11809890	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Subc adipose (MuTHER)	5.39E-07	1	11806318	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Subc adipose (MuTHER)	6.63E-07	1	11802286	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Subc adipose (MuTHER)	8.64E-07	1	11809890	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Liver(Greenawalt)	1.02E-06	1	11809890	10023816366	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Lymph	1.67E-06	1	11809890	GI_12025672-A	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Dendritic cells after Mycobacetrium tube	2.41E-06	1	11806318		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Whole blood (CHARGE)	7.04E-83	1	11783430	3990477	MTHFR,C1orf167	cis	19.29	A	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Whole blood (CHARGE)	2.88E-79	1	11785365	3990477	MTHFR,C1orf167	cis	18.85	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	LCL (MuTHER)	5.45E-18	1	11783430	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	LCL (MuTHER)	7.40E-18	1	11785365	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Whole blood (PaxGene) in Japanese	1.20E-09	1	11783430	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Whole blood (PaxGene) in Japanese	1.20E-09	1	11785365	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Subc adipose (MuTHER)	2.66E-07	1	11783430	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Skin (MuTHER)	5.16E-07	1	11783430	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Subc adipose (MuTHER)	6.16E-07	1	11785365	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Skin (MuTHER)	7.50E-07	1	11785365	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Liver (ScanDB)	9.54E-07	1	11785365		GPR116	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Lymph	1.54E-05	1	11785365	GI_12025672-A	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	omental	7.21E-05	1	11785365	10025934633	HSS00048903	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Blood(Fehrmann et al)	1.50E-27;1.9(	1	11785365	3990477;3850136	MTHFR;AL953897.6;C	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	LCL (MuTHER)	6.00E-24	1	11818262	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Whole blood (PaxGene) in Japanese	1.20E-09	1	11818262	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Skin (MuTHER)	3.72E-09	1	11818262	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Subc adipose (MuTHER)	1.56E-07	1	11818262	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Whole blood (CHARGE)	1.66E-07	1	11818262	60437	PLOD1	cis	-5.23	G	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Whole blood (CHARGE)	7.97E-95	1	11792970	3990477	MTHFR,C1orf167	cis	20.66	A	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	LCL (MuTHER)	5.98E-20	1	11792970	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Whole blood (PaxGene) in Japanese	1.20E-09	1	11792970	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Skin (MuTHER)	1.03E-08	1	11792970	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Subc adipose (MuTHER)	2.22E-08	1	11792970	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Liver(UChicago)	0.00017275	1	11792970	A_24_P302374	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	LCL (MuTHER)	2.97E-24	1	11786736	ILMN_1734830	MTHFR	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	LCL (MuTHER)	5.44E-24	1	11815237	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	LCL (MuTHER)	5.56E-24	1	11819189	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	PaxGeneWholeBlood(Mehta)	1.64E-11	1	11815237	ILMN_1731434	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Whole blood (PaxGene) in Japanese	7.49E-10	1	11819189	A_23_P400081	MTHFR	cis	0.64			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Whole blood (PaxGene) in Japanese	1.20E-09	1	11815237	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Whole blood (PaxGene) in Japanese	1.20E-09	1	11786736	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Skin (MuTHER)	2.04E-09	1	11786736	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	RNAseq(HapMapLCL)+DeepSage(blood)	3.48E-09	1	11896602	ENST0000037659	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Skin (MuTHER)	3.56E-09	1	11819189	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Skin (MuTHER)	3.63E-09	1	11815237	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Whole blood (CHARGE)	1.32E-07	1	11819189	60437	PLOD1	cis	-5.28	C	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Whole blood (CHARGE)	1.46E-07	1	11786736	60437	PLOD1	cis	-5.26	A	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Subc adipose (MuTHER)	1.65E-07	1	11815237	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Subc adipose (MuTHER)	1.75E-07	1	11819189	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Whole blood (CHARGE)	3.42E-07	1	11815237	60437	PLOD1	cis	-5.10	T	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Subc adipose (MuTHER)	4.13E-07	1	11786736	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Lung	2.34E-06	1	11786736	100146210_TGI_a	Unknown	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Monocytes (CD14+)	1.45E-05	1	11786736	TiKVCul2UleSz47	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Monocytes (CD14+)	5.10E-05	1	11815237	TiKVCul2UleSz47	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Lymph	0.00104498	1	11815237	GI_12025672-A	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Monocytes	1.43E-34;1.20	1	11819189		MTHFR;CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Blood(Fehrmann et al)	4.70E-45;2.30	1	11815237	3990477;Human_	MTHFR;AL953897.6;	cis				
rs2004776	DBP/MAP	AGT	COG2;AGT;CAPN9	2	IndexSNP		rs2004776	Cerebellum (ScanDB)	2.19E-09	1	228915325		AGT	cis				
rs2004776	DBP/MAP	AGT	COG2;AGT;CAPN9	2	LDproxy(CEU-H3)	0.754	rs1326888	Cerebellum (ScanDB)	5.13E-10	1	228929783		AGT	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Lung	2.17E-09	2	96715567	100134941_TGI_a	CNNM4	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Whole blood (CHARGE)	5.38E-08	2	96715567	1190673	LMAN2L	cis	-5.44	A	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Blood(Fehrmann et al)	1.70E-04	2	96715567	1190673	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Bcells (CD19+)	0.0008951	2	96715567	fQbX2EuV1lEh.la	ARID5A	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Lymph	0.00281896	2	96715567	GI_13540593-S	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.806	rs7582249	Whole blood (CHARGE)	2.20E-09	2	96827256	1190673	LMAN2L	cis	5.98	A	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.806	rs7582249	Skin (MuTHER)	5.64E-06	2	96827256	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs6727384	Whole blood (Battle)	4.91E-46	2	97400324		CNNM4	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Whole blood (CHARGE)	2.52E-09	2	96787353	1190673	LMAN2L	cis	5.96	C	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Whole blood (CHARGE)	3.01E-09	2	96823647	1190673	LMAN2L	cis	5.93	G	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs6727384	Whole blood (CHARGE)	3.03E-09	2	96764051	1190673	LMAN2L	cis	5.93	G	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Blood(Fehrmann et al)	5.10E-06	2	96823647	1190673	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Skin (MuTHER)	5.41E-06	2	96823647	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs6727384	Skin (MuTHER)	5.63E-06	2	96764051	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Skin (MuTHER)	5.79E-06	2	96787353	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Cerebellum (all samples)	1.79E-05	2	96823647	10025902983	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Lymph	0.00232082	2	96787353	GI_13540593-S	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Prefrontal cortex (all samples)	3.50E-02	2	96787353	10025902983	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	omental	7.82E-09;2.21	2	96823647	10023820566;100	CNNM4;LMAN2L;AN	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.771	rs994430	Whole blood (CHARGE)	2.78E-09	2	96802728	1190673	LMAN2L	cis	5.94	T	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.771	rs994430	Skin (MuTHER)	5.66E-06	2	96802728	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs6730773	Lung	1.74E-09	2	96805370	100141976_TGI_a	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs1318597	Whole blood (CHARGE)	2.40E-09	2	96826822	1190673	LMAN2L	cis	5.97	C	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs6730773	Whole blood (CHARGE)	3.04E-09	2	96805370	1190673	LMAN2L	cis	5.93	G	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs7586317	Whole blood (CHARGE)	3.21E-09	2	96811558	1190673	LMAN2L	cis	5.92	A	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs1318597	Skin (MuTHER)	5.64E-06	2	96826822	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs7586317	Skin (MuTHER)	5.66E-06	2	96811558	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs6730773	Skin (MuTHER)	5.67E-06	2	96805370	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.735	rs6576984	Whole blood (CHARGE)	1.39E-08	2	96818432	1190673	LMAN2L	cis	5.68	T	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.735	rs6576984	Skin (MuTHER)	6.41E-06	2	96818432	ILMN_1755221	LMAN2L	cis				
rs7650227	PP	ULK4	ULK4	4	IndexSNP		rs7650227	Intestine (normal ileum)	2.98E-05	3	41794937		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1615243	Whole blood (Battle)	2.92E-190	3	41965234		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	omental	4.79E-21	3	41900402	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Prefrontal cortex (all samples)	1.05E-19	3	41952218	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Parietal lobe (ScanDB)	5.85E-17	3	41952218		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Parietal lobe (ScanDB)	6.48E-17	3	41940869		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Parietal lobe (ScanDB)	6.48E-17	3	41940869		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Parietal lobe (ScanDB)	7.20E-17	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856633	Parietal lobe (ScanDB)	7.20E-17	3	41988854		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	Parietal lobe (ScanDB)	7.21E-17	3	41956494		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717024	Parietal lobe (ScanDB)	7.21E-17	3	41959892		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Parietal lobe (ScanDB)	2.54E-16	3	41802030		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Parietal lobe (ScanDB)	2.54E-16	3	42000386		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs13325965	Parietal lobe (ScanDB)	2.54E-16	3	41889946		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs17062109	Parietal lobe (ScanDB)	2.54E-16	3	41785368		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716685	Parietal lobe (ScanDB)	2.54E-16	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Parietal lobe (ScanDB)	2.54E-16	3	41905223		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717006	Parietal lobe (ScanDB)	2.54E-16	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717017	Parietal lobe (ScanDB)	2.54E-16	3	41890620		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Parietal lobe (ScanDB)	2.54E-16	3	41826722		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Parietal lobe (ScanDB)	2.54E-16	3	41799560		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	Parietal lobe (ScanDB)	2.54E-16	3	41833735		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9839399	Parietal lobe (ScanDB)	2.54E-16	3	41903048		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1016669	Parietal lobe (ScanDB)	2.55E-16	3	41869444		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128834	Parietal lobe (ScanDB)	2.55E-16	3	41837649		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	Parietal lobe (ScanDB)	2.55E-16	3	41852418		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6791806	Parietal lobe (ScanDB)	2.55E-16	3	41864999		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Parietal lobe (ScanDB)	2.55E-16	3	41859754		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Parietal lobe (ScanDB)	2.73E-16	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Parietal lobe (ScanDB)	2.80E-16	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9854833	Parietal lobe (ScanDB)	4.38E-16	3	41750581		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9854833	Cerebellum (ScanDB)	8.69E-16	3	41750581		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Parietal lobe (ScanDB)	1.21E-15	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Cerebellum (ScanDB)	1.31E-15	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Visual cortex (Huntington's)	1.39E-15	3	41900402	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Cerebellum (ScanDB)	1.39E-15	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3890604	Parietal lobe (ScanDB)	1.52E-15	3	41735629		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Parietal lobe (ScanDB)	1.52E-15	3	41736832		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Parietal lobe (ScanDB)	1.52E-15	3	41734529		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Parietal lobe (ScanDB)	1.58E-15	3	41730363		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Cerebellum (ScanDB)	2.00E-15	3	41950394		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs13325965	Cerebellum (ScanDB)	2.00E-15	3	41889946		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716685	Cerebellum (ScanDB)	2.00E-15	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Cerebellum (ScanDB)	2.00E-15	3	41905223		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717006	Cerebellum (ScanDB)	2.00E-15	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717017	Cerebellum (ScanDB)	2.00E-15	3	41890620		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128834	Cerebellum (ScanDB)	2.00E-15	3	41837649		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Cerebellum (ScanDB)	2.00E-15	3	41826722		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	Cerebellum (ScanDB)	2.00E-15	3	41833735		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9839399	Cerebellum (ScanDB)	2.00E-15	3	41903048		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1016669	Cerebellum (ScanDB)	2.01E-15	3	41869444		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	Cerebellum (ScanDB)	2.01E-15	3	41852418		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6791806	Cerebellum (ScanDB)	2.01E-15	3	41864999		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Cerebellum (ScanDB)	2.01E-15	3	41859754		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (ScanDB)	2.04E-15	3	41802030		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Cerebellum (ScanDB)	2.04E-15	3	41799560		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs17062109	Cerebellum (ScanDB)	2.05E-15	3	41785368		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Cerebellum (ScanDB)	2.20E-15	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Cerebellum (ScanDB)	2.71E-15	3	41730363		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3890604	Cerebellum (ScanDB)	2.78E-15	3	41735629		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Cerebellum (ScanDB)	2.78E-15	3	41734529		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Cerebellum (ScanDB)	2.79E-15	3	41736832		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Cerebellum (ScanDB)	2.97E-15	3	41940869		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Cerebellum (ScanDB)	3.44E-15	3	41952218		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	Cerebellum (ScanDB)	5.61E-15	3	41956494		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717024	Cerebellum (ScanDB)	5.61E-15	3	41959892		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Cerebellum (ScanDB)	5.61E-15	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856633	Cerebellum (ScanDB)	5.61E-15	3	41988854		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	Peripheral artery plaque	9.06E-14	3	41833735	100160459_TGI_	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Lung	9.75E-14	3	41799560	100149945_TGI_	ULK4	trans				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Visual cortex (all samples)	4.32E-13	3	41952218	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Liver (ScanDB)	5.57E-13	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Liver (ScanDB)	6.22E-13	3	41975390		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Liver (ScanDB)	7.34E-13	3	41734529		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Liver (ScanDB)	9.19E-13	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Liver (ScanDB)	9.88E-13	3	41952218		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	Liver (ScanDB)	1.47E-12	3	41935010		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717017	Liver (ScanDB)	3.08E-12	3	41890620		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Liver (ScanDB)	3.08E-12	3	41826722		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Peripheral artery plaque	3.91E-12	3	41736832	100149945_TGI_	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599179	Liver (ScanDB)	4.02E-12	3	41830288		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Liver(Greenawalt)	7.81E-12	3	41900402	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	Hippocampus (CA1, n=61; Kim et al.)	1.06E-11	3	41981490	232206_at	ULK4	cis	0.00			
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Liver (ScanDB)	1.24E-11	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Liver (ScanDB)	1.25E-11	3	41799560		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856633	ER+ breast tumor cells	1.31E-11	3	41988854		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	Normal dendritic cells (before Mycobacte	1.77E-11	3	41935010		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	ER+ breast tumor cells	1.95E-11	3	41852418		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716685	ER+ breast tumor cells	2.66E-11	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717006	ER+ breast tumor cells	2.66E-11	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	ER+ breast tumor cells	2.66E-11	3	41956494		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	ER+ breast tumor cells	2.66E-11	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	ER+ breast tumor cells	2.66E-11	3	41833735		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717024	ER+ breast tumor cells	2.87E-11	3	41959892		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	RNAseq(HapMapLCL)+DeepSage(blood)	4.77E-11	3	41851718	ENST0000030183	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs13325965	ER+ breast tumor cells	5.17E-11	3	41889946		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856088	Liver (ScanDB)	5.62E-11	3	41835486		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	BcellsTransformed_HapMapCEU	5.99E-11	3	41956494	2670619 in 26704	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128834	ER+ breast tumor cells	9.91E-11	3	41837649		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Liver (ScanDB)	1.02E-10	3	41802030		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs17062109	ER+ breast tumor cells	1.09E-10	3	41785368		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	ER+ breast tumor cells	1.15E-10	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Liver (ScanDB)	3.48E-10	3	41905223		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9842261	ER+ breast tumor cells	3.95E-10	3	41797712		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	ER+ breast tumor cells	7.44E-10	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599176	ER+ breast tumor cells	7.44E-10	3	41763496		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	ER+ breast tumor cells	7.44E-10	3	41736832		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Liver (ScanDB)	9.63E-10	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Liver (ScanDB)	6.65E-09	3	41859754		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Prefrontal cortex (Alzheimer's)	7.60E-09	3	41802030	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	LCL	2.70E-08	3	41971140	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	LCL	3.90E-08	3	41900402	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1994157	Liver (ScanDB)	4.07E-08	3	41872486		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	LCL	7.90E-08	3	41935010	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (Huntington's)	9.93E-07	3	41802030	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Cerebellum (normal samples)	1.1088E-05	3	41734529	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1125203	Intestine (normal ileum)	2.98E-05	3	41760895		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Intestine (normal ileum)	2.98E-05	3	41786009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Intestine (normal ileum)	2.98E-05	3	41764300		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7632387	Intestine (normal ileum)	3.61E-05	3	41853161		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Prefrontal cortex (Huntington's)	3.85E-05	3	41900402	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Intestine (normal ileum)	4.60E-05	3	41925398		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Intestine (normal ileum)	4.60E-05	3	41930219		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599179	Intestine (normal ileum)	4.60E-05	3	41855284		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Intestine (normal ileum)	4.60E-05	3	41851718		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9857175	Intestine (normal ileum)	4.60E-05	3	41822054		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1994157	Intestine (normal ileum)	5.68E-05	3	41897482		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Visual cortex (all samples)	5.95E-05	3	41734529	10023829862	AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1615243	Intestine (normal ileum)	6.89E-05	3	41965234		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716984	Intestine (normal ileum)	6.89E-05	3	41965532		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Intestine (normal ileum)	6.89E-05	3	41996136		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128835	Intestine (normal ileum)	7.22E-05	3	41862873		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	1	rs1716975	Prefrontal cortex (normal samples)	1.83E-03	3	41935010	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Lung	<2E-16	3	41730363	100125684_TGI_a	Unknown	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	omental	6.93E-17;4.74	3	41802030	10023809218;100	ULK4;AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.953	rs6599167	Visual cortex (Alzheimer's)	3.11E-08	3	41725264	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs10510731	Lung	1.40E-14	3	41828314	100160459_TGI_a	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs4299460	Lung	1.47E-14	3	41927449	100311290_TGI_a	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.861	rs17214945	ER+ breast tumor cells	2.69E-11	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.861	rs17214987	ER+ breast tumor cells	2.69E-11	3	41785485		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17218264	ER+ breast tumor cells	2.69E-11	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17283929	ER+ breast tumor cells	2.69E-11	3	41916902		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17218103	Liver (ScanDB)	5.14E-11	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17218264	Parietal lobe (ScanDB)	7.13E-11	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.861	rs17215183	Parietal lobe (ScanDB)	1.21E-10	3	41787338		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.861	rs17214945	Parietal lobe (ScanDB)	1.24E-10	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17215589	Parietal lobe (ScanDB)	1.27E-10	3	41806207		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17218103	Parietal lobe (ScanDB)	1.36E-10	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.861	rs17214945	Cerebellum (ScanDB)	3.47E-10	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17283677	ER+ breast tumor cells	3.55E-10	3	41901152		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel21	0.861	rs17215183	Cerebellum (ScanDB)	4.01E-10	3	41787338		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17215589	Cerebellum (ScanDB)	4.05E-10	3	41806207		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17218103	Cerebellum (ScanDB)	4.20E-10	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs17218264	Cerebellum (ScanDB)	4.54E-10	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel22	0.861	rs10510731	Liver (ScanDB)	4.74E-10	3	41828314		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs794894	Parietal lobe (ScanDB)	1.63E-16	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs7634985	Parietal lobe (ScanDB)	1.73E-16	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs13087502	Parietal lobe (ScanDB)	1.78E-16	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs794894	Cerebellum (ScanDB)	1.45E-13	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs7634985	Cerebellum (ScanDB)	1.56E-13	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs13087502	Cerebellum (ScanDB)	1.61E-13	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs13087502	ER+ breast tumor cells	1.55E-10	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs809930	Parietal lobe (ScanDB)	5.10E-15	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7652506	Parietal lobe (ScanDB)	6.85E-15	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs939561	Parietal lobe (ScanDB)	7.69E-15	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7629767	Parietal lobe (ScanDB)	7.83E-15	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	SubCutAdipose(Greenawalt)	1.06E-14	3	41982343	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs939561	Cerebellum (ScanDB)	5.72E-12	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7629767	Cerebellum (ScanDB)	6.08E-12	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs809930	Cerebellum (ScanDB)	6.19E-12	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7652506	Cerebellum (ScanDB)	7.19E-12	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7652506	ER+ breast tumor cells	1.07E-11	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	ER+ breast tumor cells	2.69E-11	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284313	ER+ breast tumor cells	2.69E-11	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284472	ER+ breast tumor cells	2.69E-11	3	41971308		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284313	Parietal lobe (ScanDB)	7.62E-11	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Parietal lobe (ScanDB)	7.64E-11	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284472	Parietal lobe (ScanDB)	7.64E-11	3	41971308		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs809930	ER+ breast tumor cells	9.77E-11	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Liver (ScanDB)	1.11E-10	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284313	Cerebellum (ScanDB)	4.41E-10	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Cerebellum (ScanDB)	4.42E-10	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284472	Cerebellum (ScanDB)	4.42E-10	3	41971308		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Stomach	8.32E-10	3	41982343	100311290	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Cerebellum (Alzheimer's)	5.26E-02	3	41982343	10023829862	AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.762	rs794899	LCL	1.30E-07	3	42003726	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Parietal lobe (ScanDB)	7.75E-15	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Cerebellum (ScanDB)	6.72E-12	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Liver (ScanDB)	1.85E-08	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Liver(Greenawalt)	1.76E-07	3	42026840	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Cerebellum (Alzheimer's)	2.92E-05	3	42026840	10025919071	CTNNB1	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2:	0.967	rs12656497	Lung	1.67E-07	5	32867696	100142475_TGI_a	NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2:	0.84	rs1173766	Lung	7.02E-08	5	32840285	100303568_TGI_a	NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-H3)	0.784	rs1173756	Lung	1.91E-08	5	32825609	100145622_TGI_a	NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-1kg)	0.781	rs1173743	Primary PHA-stimulated T cells (GenCord	5.68E-07	5	32775047		ENSG00000056097.1(	cis	0.36			
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Cerebellum	5.54E-21	6	26230912	ILMN_2075334	HIST1H4C	cis				
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Whole blood (CHARGE)	1.30E-15	6	26230912	2970019	HIST1H4H	cis	-7.99	G	6	26393396
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Temporal cortex	2.59E-13	6	26230912	ILMN_2075334	HIST1H4C	cis				
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Liver(UChicago)	0.02226068	6	26230912	A_23_P395374	HIST1H4D	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	IndexSNP		rs10948071	Whole blood (CHARGE)	6.44E-09	6	43388691	7050040	ZNF318	cis	-5.81	C	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	IndexSNP		rs10948071	LCL (MuTHER)	1.82E-06	6	43388691	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	IndexSNP		rs10948071	Skin (MuTHER)	2.56E-05	6	43388691	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Whole blood (Battle)	4.88E-53	6	43273604		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	Whole blood (CHARGE)	2.71E-16	6	43377007	50193	ZNF318	cis	-8.19	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Whole blood (CHARGE)	2.83E-16	6	43381582	50193	ZNF318	cis	-8.18	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Whole blood (CHARGE)	4.13E-16	6	43407301	50193	ZNF318	cis	-8.13	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	Intestine (normal ileum)	5.70E-14	6	43269029		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2841648	Intestine (normal ileum)	5.70E-14	6	43269179		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Intestine (normal ileum)	1.37E-13	6	43273604		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Blood(Fehrmann et al)	5.90E-06	6	43381582	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Blood(Fehrmann et al)	5.90E-06	6	43407301	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Skin (MuTHER)	1.11E-05	6	43407301	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2841648	Skin (MuTHER)	1.46E-05	6	43377157	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	Skin (MuTHER)	1.46E-05	6	43377007	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Skin (MuTHER)	1.97E-05	6	43381582	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2841648	LCL (MuTHER)	2.12E-05	6	43377157	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	LCL (MuTHER)	2.13E-05	6	43377007	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	LCL (MuTHER)	2.27E-05	6	43381582	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	LCL (MuTHER)	2.74E-05	6	43407301	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Lymph	0.00015064	6	43407301	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Liver(UChicago)	0.00071416	6	43381582	A_23_P156562	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Liver(Greenawalt)	1.75E-06;2.2!	6	43407301	10025906643;100	SLC22A7;SLC22A7	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	Whole blood (CHARGE)	1.78E-18	6	43435728	50193	ZNF318	cis	-8.77	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125737	Whole blood (CHARGE)	1.53E-16	6	43435514	50193	ZNF318	cis	-8.25	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs4714677	Whole blood (CHARGE)	1.53E-16	6	43435017	50193	ZNF318	cis	-8.25	G	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9369407	Whole blood (CHARGE)	1.53E-16	6	43435353	50193	ZNF318	cis	-8.25	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	Whole blood (CHARGE)	1.53E-16	6	43428388	50193	ZNF318	cis	-8.25	T	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2841642	Whole blood (CHARGE)	1.66E-16	6	43410263	50193	ZNF318	cis	-8.24	G	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	Intestine (normal ileum)	5.70E-14	6	43276390		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	Monocytes	4.97E-12	6	43435728		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	Blood(Fehrmann et al)	2.50E-06	6	43428388	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	Skin (MuTHER)	1.29E-05	6	43384368	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125737	LCL (MuTHER)	1.59E-05	6	43435514	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9369407	LCL (MuTHER)	1.59E-05	6	43435353	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs4714677	LCL (MuTHER)	1.59E-05	6	43435017	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2841642	LCL (MuTHER)	1.63E-05	6	43410263	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	LCL (MuTHER)	1.63E-05	6	43428388	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	LCL (MuTHER)	1.97E-05	6	43435728	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	LCL (MuTHER)	2.39E-05	6	43384368	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9369407	Skin (MuTHER)	2.98E-05	6	43435353	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125737	Skin (MuTHER)	2.98E-05	6	43435514	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs4714677	Skin (MuTHER)	2.98E-05	6	43435017	ILMN_1694711	MAD2L1BP	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2841642	Skin (MuTHER)	3.15E-05	6	43410263	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	Skin (MuTHER)	3.15E-05	6	43428388	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	Skin (MuTHER)	3.27E-05	6	43435728	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	Lymph	0.00025613	6	43384368	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931	rs9369408	Whole blood (CHARGE)	1.72E-16	6	43440164	50193	ZNF318	cis	-8.24	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931	rs9369408	Skin (MuTHER)	6.63E-06	6	43440164	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931	rs9369408	LCL (MuTHER)	1.72E-05	6	43440164	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892	rs2396002	LCL (MuTHER)	5.60E-07	6	43367990	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892	rs2396002	Whole blood (CHARGE)	5.68E-07	6	43367990	7050040	ZNF318	cis	-5.00	C	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892	rs2396002	Skin (MuTHER)	8.40E-06	6	43367990	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828	rs2841647	Whole blood (CHARGE)	3.05E-16	6	43377157	50193	ZNF318	cis	-8.17	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828	rs2841647	Skin (MuTHER)	1.15E-05	6	43377158	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828	rs2841647	LCL (MuTHER)	2.68E-05	6	43377158	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Liver(Greenawalt)	1.26E-28	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	Monocytes	1.18E-26	6	43368638		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Visual cortex (all samples)	2.69E-25	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	omental	4.72E-23	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	SubCutAdipose(Greenawalt)	6.30E-19	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	Whole blood (CHARGE)	5.81E-18	6	43368638	7050040	ZNF318	cis	-8.64	C	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs16896398	Whole blood (CHARGE)	8.93E-18	6	43370682	7050040	ZNF318	cis	-8.59	T	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Whole blood (CHARGE)	1.55E-17	6	43387699	7050040	ZNF318	cis	-8.52	A	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Prefrontal cortex (normal samples)	8.53E-17	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Whole blood (PAX) in breast cancer survi	6.97E-11	6	43387699	6200307	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Intestine (normal ileum)	5.10E-10	6	43279721		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Cerebellum (Huntington's)	8.76E-10	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Liver(Schroder)	1.82E-09	6	43387699		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Lymph	3.44E-08	6	43387699	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	LCL (MuTHER)	1.72E-05	6	43368638	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Tcells	1.83E-05	6	43387699		PTK7	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	Skin (MuTHER)	2.15E-05	6	43368638	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	LCL (MuTHER)	2.20E-05	6	43387699	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Skin (MuTHER)	2.97E-05	6	43387699	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Blood(Fehrmann et al)	5.10E-20;1.0	6	43387699	50193;7210484	ZNF318;RP3-330M21	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	Whole blood (CHARGE)	1.75E-17	6	43407036	7050040	ZNF318	cis	-8.51	G	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	Intestine (normal ileum)	4.60E-10	6	43299058		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	LCL (MuTHER)	1.75E-05	6	43407036	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	Skin (MuTHER)	2.70E-05	6	43407036	ILMN_1694711	MAD2L1BP	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1	rs2393833	Liver (ScanDB)	8.10E-07	10	63115322		SGTA	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1	rs12246717	Liver (ScanDB)	9.54E-07	10	63129189		SERPIND1	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1	rs2393833	Blood	0.0000286	10	63115322	HSG00268758	LOC219790	cis				
rs7070797	SBP	NA	C10orf107	9	LDproxy(CEU-Rel2	0.786	rs10509158	Adipose	0.0000037	10	63177675	HSG00269025	NM_173554	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.778	rs2588918	EndometrialTumor	0.00379818	10	63195030		C10orf107	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.734	rs973237	Liver (ScanDB)	5.92E-07	10	63195307		FUCA1	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.734	rs973237	Prefrontal cortex (Alzheimer's)	9.15E-05	10	63195307	10025902662	C10orf107	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP		rs2681472	Whole blood (CHARGE)	1.83E-15	12	88533090	7320717	WDR51B	cis	7.95	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP		rs2681472	Liver (ScanDB)	3.74E-07	12	88533090		LOC100131662	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP		rs2681472	Blood(Fehrmann et al)	2.20E-08;2.2	12	88533090	6650035;7320717	;WDR51B;ATP2B1	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs11105368	Whole blood (CHARGE)	3.56E-15	12	88598572	7320717	WDR51B	cis	7.87	C	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs11105364	Whole blood (CHARGE)	3.80E-15	12	88593407	7320717	WDR51B	cis	7.86	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs11105354	Whole blood (CHARGE)	3.82E-15	12	88550654	7320717	WDR51B	cis	7.86	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs17249754	Whole blood (CHARGE)	4.81E-15	12	88584717	7320717	WDR51B	cis	7.83	A	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs12579302	Whole blood (CHARGE)	5.09E-15	12	88574634	7320717	WDR51B	cis	7.82	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	1	rs12230074	Whole blood (CHARGE)	5.11E-15	12	88614998	7320717	WDR51B	cis	7.82	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	1	rs11105378	Whole blood (CHARGE)	7.12E-15	12	88614872	7320717	WDR51B	cis	7.78	T	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92	rs2681492	Whole blood (CHARGE)	7.76E-13	12	88537220	7320717	WDR51B	cis	7.17	C	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92	rs2681492	Liver (ScanDB)	3.15E-07	12	88537220		LOC100131662	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92	rs2681492	Blood(Fehrmann et al)	2.10E-08;5.9	12	88537220	6650035;7320717	;WDR51B;ATP2B1	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	0.915	rs4842666	Whole blood (CHARGE)	3.74E-07	12	88465680	7160609	WDR51B	cis	-5.08	C	12	88337954
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	0.915	rs4842666	Monocytes (CD14+)	4.35E-05	12	88465680	9N1yRYl6R8pJ.S	GALNT4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-H3)	0.805	rs11105328	Monocytes (CD14+)	5.41E-05	12	88466521	9N1yRYl6R8pJ.Sv	GALNT4	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Liver(Greenawalt)	4.63E-26	12	110368991	10023848139	AL049919	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs4766578	Whole blood (CHARGE)	5.62E-20	12	110388754	6560301	SH2B3	cis	9.15	T	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Whole blood (CHARGE)	5.02E-19	12	110368991	6560301	SH2B3	cis	8.91	T	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Visual cortex (Huntington's)	1.75E-12	12	110368991	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Prefrontal cortex (normal samples)	7.00E-11	12	110368991	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Whole blood (CHARGE)	2.00E-07	12	110368991	7570673	UPP1	trans	5.20	T	7	48114477
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Blood(Fehrmann et al)	3.50E-07	12	110368991	6560301	SH2B3;ATXN2	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Blood	0.0002037	12	110368991	HSG00276844	FLJ21127	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs10774625	Whole blood (CHARGE)	8.15E-20	12	110394602	6560301	SH2B3	cis	9.11	A	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Whole blood (CHARGE)	1.68E-19	12	110492139	6560301	SH2B3	cis	9.03	C	12	110373489
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs10774625	Whole blood (CHARGE)	3.56E-08	12	110394602	2070170	UBE2L6	trans	5.51	A	11	57075756
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Cerebellum (all samples)	9.56E-08	12	110492139	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Whole blood (CHARGE)	4.37E-07	12	110492139	7570673	UPP1	trans	5.05	C	7	48114477
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Blood(Fehrmann et al)	2.20E-07;9.8	12	110492139	6560301;840253	SH2B3;ATXN2;ALDH2	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Liver(Greenawalt)	4.63E-26	12	110368991	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs4766578	Whole blood (CHARGE)	5.62E-20	12	110388754	6560301	SH2B3	cis	9.15	T	12	110373489
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Whole blood (CHARGE)	5.02E-19	12	110368991	6560301	SH2B3	cis	8.91	T	12	110373489
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Visual cortex (Huntington's)	1.75E-12	12	110368991	10023848139	AL049919	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Prefrontal cortex (normal samples)	7.00E-11	12	110368991	10023848139	AL049919	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Whole blood (CHARGE)	2.00E-07	12	110368991	7570673	UPP1	trans	5.20	T	7	48114477
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Blood(Fehrmann et al)	3.50E-07	12	110368991	6560301	SH2B3;ATXN2	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Blood	0.0002037	12	110368991	HSG00276844	FLJ21127	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Whole blood (CHARGE)	1.57E-34	15	73021663	4480132	ULK3	cis	12.26	T	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	omental	1.11E-13	15	73021663	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Subc adipose (MuTHER)	8.68E-09	15	73021663	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Lymph	8.12E-08	15	73021663	GI_4505234-S	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	LCL (MuTHER)	5.27E-07	15	73021663	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Skin (MuTHER)	7.69E-07	15	73021663	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Bcells (CD19+)	3.32E-06	15	73021663	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Prefrontal cortex (Alzheimer's)	3.32E-04	15	73021663	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Monocytes (CD14+)	0.000374	15	73021663	r_tdN3VF1vV3q	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Blood(Fehrmann et al)	1.90E-27;7.9	15	73021663	3170239;4480132	CSK;ULK3;COX5A;SC	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Whole blood (CHARGE)	5.55E-45	15	72927907	4480132	ULK3	cis	14.07	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	LCL in asthmatics (Liang 1kg)	1.06E-23	15	72927907	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Subc adipose (MuTHER)	1.16E-09	15	72927907	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Skin (MuTHER)	1.15E-08	15	72927907	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Lung	1.32E-07	15	72927907	100151075_TGI_	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Bcells (CD19+)	4.65E-07	15	72927907	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	LCL (MuTHER)	4.26E-06	15	72927907	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Whole blood (CHARGE)	2.10E-47	15	73012468	4480132	ULK3	cis	14.46	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Subc adipose (MuTHER)	3.46E-12	15	73012468	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	LCL (MuTHER)	4.95E-08	15	73012468	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Skin (MuTHER)	6.16E-07	15	73012468	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Lymph	1.02E-05	15	73012468	GI_4505234-S	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Cerebellum (all samples)	9.88E-05	15	73012468	10025904895	C15orf17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Monocytes	4.69E-54	15	72962079		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Whole blood (CHARGE)	4.20E-48	15	72968174	4480132	ULK3	cis	14.57	A	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Whole blood (CHARGE)	4.69E-48	15	72962079	4480132	ULK3	cis	14.57	A	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Whole blood (CHARGE)	5.76E-48	15	72981543	4480132	ULK3	cis	14.55	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	LCL in asthmatics (Liang 1kg)	4.58E-23	15	72968174	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	LCL in asthmatics (Liang 1kg)	5.33E-23	15	72962079	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs7497201	LCL in asthmatics (Liang 1kg)	2.74E-22	15	72977743	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Subc adipose (MuTHER)	2.11E-12	15	72968174	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Subc adipose (MuTHER)	2.18E-12	15	72962079	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Subc adipose (MuTHER)	2.66E-12	15	72981543	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Whole blood (Battle)	3.91E-11	15	75194490		COX5A	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Cerebellum (all samples)	3.89E-10	15	72962079	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Visual cortex (normal samples)	2.40E-08	15	72962079	10025927424	ULK3	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	LCL (MuTHER)	1.36E-07	15	72981543	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	LCL (MuTHER)	2.10E-07	15	72968174	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	LCL (MuTHER)	3.69E-07	15	72962079	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Lymph	7.22E-07	15	72962079	GI_4505234-S	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Skin (MuTHER)	1.01E-06	15	72981543	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Skin (MuTHER)	1.52E-06	15	72968174	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Skin (MuTHER)	3.23E-06	15	72962079	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs7497201	Bcells (CD19+)	3.92E-06	15	72977743	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Bcells (CD19+)	4.00E-06	15	72981543	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Blood	0.00000646	15	72962079	HSG00291325	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Bcells (CD19+)	6.61E-06	15	72968174	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	SchadtLiver	8.60E-06	15	72962079		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Bcells (CD19+)	8.77E-06	15	72962079	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Monocytes (CD14+)	7.18E-05	15	72962079	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Monocytes (CD14+)	7.50E-05	15	72981543	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Monocytes (CD14+)	0.000101	15	72968174	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs7497201	Monocytes (CD14+)	0.000152	15	72977743	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Adipose	0.0001963	15	72962079	HSG00291325	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Induced sputum (COPD cases)	0.00037621	15	72962079	224805_s_at	C15orf17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Blood(Fehrmann et al)	2.00E-28;3.0	15	72962079	3170239;4480132	CSK;ULK3;C15orf17;C	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.751	rs11636952	LCL in asthmatics (Liang 1kg)	2.98E-23	15	72901375	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.751	rs11636952	Bcells (CD19+)	1.06E-08	15	72901375	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Monocytes	8.25E-26	15	72999278		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Whole blood (CHARGE)	5.97E-21	15	72999278	4480132	ULK3	cis	-9.39	T	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	LCL (MuTHER)	3.18E-08	15	72999278	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Skin (MuTHER)	1.30E-05	15	72999278	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Subc adipose (MuTHER)	2.40E-05	15	72999278	ILMN_2364535	SNUPN	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Bcells (CD19+)	3.86E-05	15	72999278	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.735	rs4886633	Whole blood (CHARGE)	3.99E-48	15	72965260	4480132	ULK3	cis	14.58	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.735	rs4886633	LCL in asthmatics (Liang 1kg)	5.73E-23	15	72965260	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Monocytes	3.21E-35	15	72864420		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Whole blood (CHARGE)	6.15E-35	15	72870547	4480132	ULK3	cis	12.33	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Whole blood (CHARGE)	3.65E-34	15	72869605	4480132	ULK3	cis	12.19	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	Whole blood (CHARGE)	4.77E-34	15	72867203	4480132	ULK3	cis	12.17	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	Whole blood (CHARGE)	6.23E-34	15	72852697	4480132	ULK3	cis	12.14	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Whole blood (CHARGE)	5.71E-33	15	72864420	4480132	ULK3	cis	11.96	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Whole blood (Battle)	1.79E-27	15	75083494		CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Bcells (CD19+)	1.33E-08	15	72870547	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Skin (MuTHER)	1.37E-08	15	72870547	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Skin (MuTHER)	1.75E-08	15	72869605	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	Skin (MuTHER)	2.59E-08	15	72867203	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Skin (MuTHER)	3.12E-08	15	72864420	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	Skin (MuTHER)	3.16E-08	15	72852697	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Subc adipose (MuTHER)	4.43E-08	15	72869605	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	Subc adipose (MuTHER)	4.62E-08	15	72867203	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Subc adipose (MuTHER)	4.72E-08	15	72870547	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Subc adipose (MuTHER)	6.30E-08	15	72864420	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	Subc adipose (MuTHER)	7.48E-08	15	72852697	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Whole blood (DeepSAGESeq)	1.48E-06	15	75082552	15_75095325	None:15_75095325	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	LCL (MuTHER)	3.79E-06	15	72852697	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	LCL (MuTHER)	4.06E-06	15	72870547	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	LCL (MuTHER)	4.16E-06	15	72867203	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	LCL (MuTHER)	4.43E-06	15	72869605	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	LCL (MuTHER)	4.49E-06	15	72864420	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Lung	3.02E-05	15	72864420	100132373_TGI_a	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Blood(Fehrmann et al)	2.00E-45;3.2	15	72864420	3170239;4480132	CSK;ULK3;COX5A	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.719	rs12591513	LCL in asthmatics (Liang 1kg)	1.92E-22	15	72889767	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	Whole blood (CHARGE)	6.50E-29	15	72844800	4480132	ULK3	cis	11.16	A	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	Skin (MuTHER)	7.34E-08	15	72844800	ILMN_1679495	ULK3	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	Subc adipose (MuTHER)	8.91E-08	15	72844800	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	LCL (MuTHER)	6.38E-06	15	72844800	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Monocytes	8.25E-26	15	72999278		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Whole blood (CHARGE)	5.97E-21	15	72999278	4480132	ULK3	cis	-9.39	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	LCL (MuTHER)	3.18E-08	15	72999278	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Skin (MuTHER)	1.30E-05	15	72999278	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Subc adipose (MuTHER)	2.40E-05	15	72999278	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Bcells (CD19+)	3.86E-05	15	72999278	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	Whole blood (Battle)	7.31E-79	15	75183935		SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Monocytes	8.85E-27	15	72999410		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11857695	LCL in asthmatics (Liang 1kg)	3.41E-21	15	72952804	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs12911254	LCL in asthmatics (Liang 1kg)	3.41E-21	15	72953388	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	LCL in asthmatics (Liang 1kg)	5.92E-21	15	72970988	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11633472	LCL in asthmatics (Liang 1kg)	5.99E-21	15	72971137	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Whole blood (CHARGE)	6.01E-21	15	72999410	4480132	ULK3	cis	-9.39	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	Whole blood (CHARGE)	6.51E-21	15	73008021	4480132	ULK3	cis	-9.38	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Whole blood (CHARGE)	7.20E-21	15	73008918	4480132	ULK3	cis	-9.37	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	1	rs12909335	LCL in asthmatics (Liang 1kg)	2.70E-20	15	73001842	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	LCL in asthmatics (Liang 1kg)	4.20E-20	15	73008021	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs12912839	LCL in asthmatics (Liang 1kg)	1.09E-19	15	73008298	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	LCL in asthmatics (Liang 1kg)	1.10E-19	15	73008918	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs62029167	LCL in asthmatics (Liang 1kg)	2.14E-19	15	73015403	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs12901190	LCL in asthmatics (Liang 1kg)	4.25E-19	15	73018505	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Hippocampus (CA1, n=61; Kim et al.)	5.88E-11	15	75212357	229426_at	COX5A	cis	0.00			
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	LCL (MuTHER)	3.12E-09	15	72999410	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	LCL (MuTHER)	2.97E-08	15	73008021	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	LCL (MuTHER)	3.03E-08	15	73008918	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Skin (MuTHER)	1.37E-05	15	73008918	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	Skin (MuTHER)	1.39E-05	15	73008021	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	Subc adipose (MuTHER)	1.98E-05	15	73008021	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Subc adipose (MuTHER)	2.04E-05	15	73008918	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Subc adipose (MuTHER)	2.19E-05	15	72999410	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Skin (MuTHER)	3.02E-05	15	72999410	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Bcells (CD19+)	3.21E-05	15	72999410	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11633472	Bcells (CD19+)	3.86E-05	15	72971137	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	Bcells (CD19+)	3.86E-05	15	72970988	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Monocytes (CD14+)	0.0001945	15	72999410	r_tdN3VF1vV3q\	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	LCL in asthmatics (Liang 1kg)	1.02E-20	15	72986945	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Whole blood (CHARGE)	3.32E-20	15	72986945	4480132	ULK3	cis	-9.21	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Liver(Greenawalt)	1.34E-18	15	72986945	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	LCL (MuTHER)	3.91E-08	15	72986945	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Lymph	4.27E-06	15	72986945	GI_4505234-S	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Skin (MuTHER)	1.33E-05	15	72986945	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Prefrontal cortex (all samples)	1.3997E-05	15	72986945	10026392220	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Subc adipose (MuTHER)	3.12E-05	15	72986945	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Bcells (CD19+)	3.86E-05	15	72986945	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Induced sputum (COPD cases)	0.00015722	15	72986945	224805_s_at	C15orf17	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Blood(Fehrmann et al)	2.20E-21;2.2(	15	72986945	3170239;50341;4	CSK;SCAMP2;ULK3;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Whole blood (Battle)	4.09E-124	15	75189930		MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	Monocytes	3.25E-29	15	72972723		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	LCL in asthmatics (Liang 1kg)	5.96E-29	15	72972723	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	LCL in asthmatics (Liang 1kg)	1.45E-28	15	72976983	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	LCL in asthmatics (Liang 1kg)	3.40E-28	15	72991079	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	LCL in asthmatics (Liang 1kg)	3.40E-28	15	72983229	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Monocytes	6.08E-27	15	72980057		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Whole blood (CHARGE)	1.49E-22	15	72983229	4480132	ULK3	cis	-9.77	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Whole blood (CHARGE)	5.14E-22	15	72976983	4480132	ULK3	cis	-9.65	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	Whole blood (CHARGE)	5.40E-22	15	72972723	4480132	ULK3	cis	-9.64	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	Whole blood (CHARGE)	5.71E-22	15	72962510	4480132	ULK3	cis	-9.63	C	15	72915933

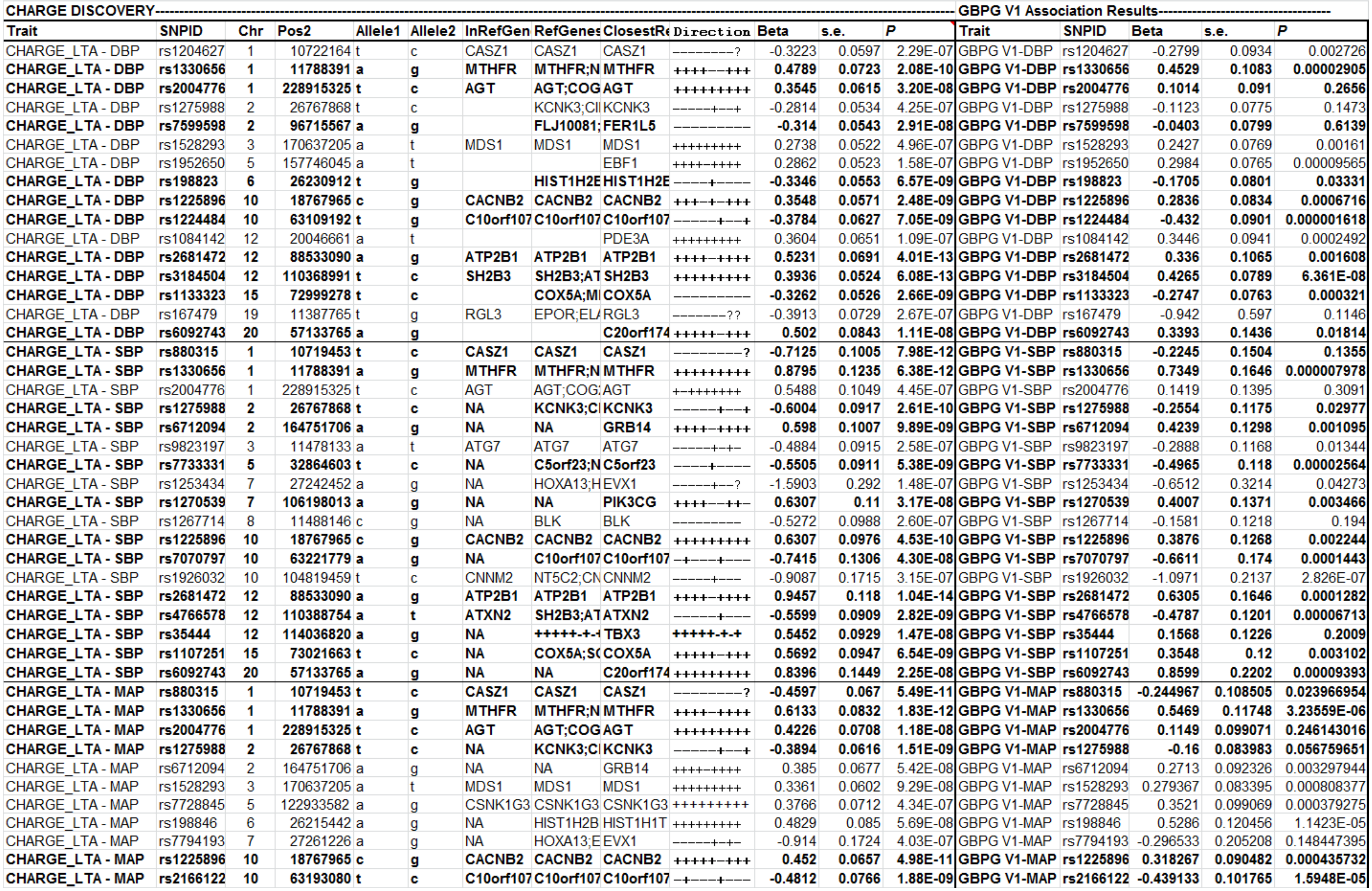
IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Whole blood (CHARGE)	1.00E-21	15	72980057	4480132	ULK3	cis	-9.58	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	Whole blood (CHARGE)	1.61E-21	15	72946486	4480132	ULK3	cis	-9.53	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	LCL in asthmatics (Liang 1kg)	3.92E-21	15	72999278	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Whole blood (CHARGE)	7.79E-21	15	72991079	4480132	ULK3	cis	-9.36	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	LCL in asthmatics (Liang 1kg)	5.64E-20	15	72946486	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	SubCutAdipose(Greenawalt)	7.68E-11	15	72983229	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	LCL (MuTHER)	3.00E-09	15	72983229	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	LCL (MuTHER)	3.10E-09	15	72991079	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	LCL (MuTHER)	4.61E-09	15	72980057	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	LCL (MuTHER)	4.89E-09	15	72976983	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	LCL (MuTHER)	5.54E-09	15	72972723	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	LCL (MuTHER)	6.47E-09	15	72946486	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	LCL (MuTHER)	8.74E-08	15	72962510	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	RNAseq(HapMapLCL)+DeepSage(blood)	2.76E-07	15	75185670	ENST0000037969	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	Subc adipose (MuTHER)	1.49E-05	15	72962510	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	Subc adipose (MuTHER)	1.53E-05	15	72946486	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Subc adipose (MuTHER)	1.94E-05	15	72983229	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	Subc adipose (MuTHER)	2.20E-05	15	72972723	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Subc adipose (MuTHER)	2.25E-05	15	72976983	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	Skin (MuTHER)	2.44E-05	15	72962510	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Subc adipose (MuTHER)	2.49E-05	15	72980057	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Induced sputum (COPD cases)	2.56E-05	15	72983229	224805_s_at	C15orf17	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Subc adipose (MuTHER)	2.61E-05	15	72991079	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Skin (MuTHER)	3.01E-05	15	72991079	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Bcells (CD19+)	3.21E-05	15	72991079	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Bcells (CD19+)	3.21E-05	15	72980057	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Bcells (CD19+)	3.35E-05	15	72983229	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Bcells (CD19+)	4.67E-05	15	72976983	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Monocytes (CD14+)	0.000135	15	72983229	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	Bcells (CD19+)	0.0001942	15	72946486	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Monocytes (CD14+)	0.0001945	15	72991079	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Monocytes (CD14+)	0.0001945	15	72980057	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Visual cortex (all samples)	2.80E-04	15	72983229	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Monocytes (CD14+)	0.0003045	15	72976983	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Liver(UChicago)	0.000119825;	15	72983229	A_23_P60579;A_	MPI;SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Blood(Fehrmann et al)	1.60E-19;1.1	15	72983229	3170239;50341;4	CSK;SCAMP2;ULK3;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs12902515	LCL in asthmatics (Liang 1kg)	4.40E-20	15	72948051	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Whole blood (CHARGE)	1.49E-19	15	73029208	4480132	ULK3	cis	-9.05	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs4886641	LCL in asthmatics (Liang 1kg)	2.23E-19	15	73015708	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs11639413	LCL in asthmatics (Liang 1kg)	2.55E-19	15	73030347	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	LCL in asthmatics (Liang 1kg)	2.58E-19	15	73029208	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	omental	3.08E-19	15	73029208	10025911367	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415249	LCL in asthmatics (Liang 1kg)	4.75E-19	15	73029093	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	LCL (MuTHER)	4.19E-08	15	73029208	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Subc adipose (MuTHER)	2.09E-05	15	73029208	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Skin (MuTHER)	2.46E-05	15	73029208	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Bcells (CD19+)	3.17E-05	15	73029208	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11854704	LCL in asthmatics (Liang 1kg)	4.96E-28	15	73008068	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Whole blood (CHARGE)	1.26E-22	15	72942949	4480132	ULK3	cis	-9.79	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	LCL in asthmatics (Liang 1kg)	1.94E-20	15	72942949	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	LCL (MuTHER)	6.46E-08	15	72942949	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Lung	2.86E-06	15	72942949	100161886_TGI_	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Skin (MuTHER)	4.23E-06	15	72942949	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Subc adipose (MuTHER)	3.77E-05	15	72942949	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Bcells (CD19+)	5.10E-05	15	72942949	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs12913293	LCL in asthmatics (Liang 1kg)	5.44E-29	15	72971511	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs8025447	LCL in asthmatics (Liang 1kg)	1.59E-28	15	72979275	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs12907898	LCL in asthmatics (Liang 1kg)	3.26E-28	15	72994925	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs12904897	LCL in asthmatics (Liang 1kg)	3.85E-28	15	73004739	202472_at	MPI	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs59945415	LCL in asthmatics (Liang 1kg)	8.04E-28	15	73015480	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Monocytes	5.36E-26	15	72923747		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Whole blood (CHARGE)	3.69E-24	15	72923747	4480132	ULK3	cis	-10.14	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	LCL in asthmatics (Liang 1kg)	9.19E-21	15	72923747	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	LCL (MuTHER)	2.37E-07	15	72923747	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Skin (MuTHER)	3.95E-06	15	72923747	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Subc adipose (MuTHER)	4.58E-05	15	72923747	ILMN_1695271	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.9	rs4480762	LCL in asthmatics (Liang 1kg)	9.19E-21	15	72926479	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Whole blood (CHARGE)	3.44E-23	15	72912698	4480132	ULK3	cis	-9.92	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	LCL in asthmatics (Liang 1kg)	4.34E-20	15	72912698	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Cerebellum (Alzheimer's)	7.49E-10	15	72912698	10025927424	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Bcells (CD19+)	3.92E-07	15	72912698	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Lymph	4.47E-07	15	72912698	GI_39930360-S	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	LCL (MuTHER)	6.72E-07	15	72912698	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Skin (MuTHER)	5.50E-06	15	72912698	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Subc adipose (MuTHER)	3.13E-05	15	72912698	ILMN_1695271	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Monocytes (CD14+)	9.64E-05	15	72912698	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Blood	0.0002728	15	72912698	HSG00290189	ARID3B	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Lung	<2E-16	15	72912698	100312245_TGI_	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Blood(Fehrmann et al)	1.00E-25;1.5	15	72912698	3170239;4480132	CSK;ULK3;SCAMP2;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.832	rs34063670	LCL in asthmatics (Liang 1kg)	1.28E-18	15	73034209	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.832	rs11636892	LCL in asthmatics (Liang 1kg)	2.81E-18	15	73053102	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.808	rs12917376	LCL in asthmatics (Liang 1kg)	1.61E-22	15	72903220	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.801	rs56338926	LCL in asthmatics (Liang 1kg)	1.23E-18	15	73046388	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.801	rs35556055	LCL in asthmatics (Liang 1kg)	2.88E-18	15	73040467	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.801	rs35556055	Bcells (CD19+)	0.0001316	15	73040467	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	Whole blood (CHARGE)	3.19E-20	15	72916647	4480132	ULK3	cis	-9.21	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	LCL in asthmatics (Liang 1kg)	3.77E-20	15	72916647	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	LCL (MuTHER)	3.57E-07	15	72916647	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	Skin (MuTHER)	8.85E-06	15	72916647	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.798	rs11630087	LCL in asthmatics (Liang 1kg)	1.82E-18	15	73048726	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.798	rs62029217	LCL in asthmatics (Liang 1kg)	3.24E-18	15	73048952	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.771	rs12912343	LCL in asthmatics (Liang 1kg)	1.30E-18	15	73038094	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.767	rs4886413	LCL in asthmatics (Liang 1kg)	3.29E-18	15	73049363	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Whole blood (CHARGE)	1.57E-34	15	73021663	4480132	ULK3	cis	12.26	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	omental	1.11E-13	15	73021663	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Subc adipose (MuTHER)	8.68E-09	15	73021663	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Lymph	8.12E-08	15	73021663	GI_4505234-S	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	LCL (MuTHER)	5.27E-07	15	73021663	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Skin (MuTHER)	7.69E-07	15	73021663	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Bcells (CD19+)	3.32E-06	15	73021663	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Prefrontal cortex (Alzheimer's)	3.32E-04	15	73021663	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Monocytes (CD14+)	0.000374	15	73021663	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Blood(Fehrmann et al)	1.90E-27;7.9	15	73021663	3170239;4480132	CSK;ULK3;COX5A;SC	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Whole blood (CHARGE)	2.42E-29	15	72917626	4480132	ULK3	cis	11.25	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	LCL (MuTHER)	1.67E-07	15	72917626	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Subc adipose (MuTHER)	1.58E-06	15	72917626	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Bcells (CD19+)	5.64E-06	15	72917626	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Skin (MuTHER)	1.83E-05	15	72917626	ILMN_1679495	ULK3	cis				
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs6026704	Whole blood (CHARGE)	1.59E-08	20	57117540	4220259	CTSZ	cis	5.65	C	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs7362597	Whole blood (CHARGE)	1.60E-08	20	57112829	4220259	CTSZ	cis	5.65	A	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs6100342	Whole blood (CHARGE)	2.28E-08	20	57132656	4220259	CTSZ	cis	5.59	C	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs882384	Whole blood (CHARGE)	2.28E-08	20	57132808	4220259	CTSZ	cis	5.59	T	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs998981	Whole blood (CHARGE)	2.44E-08	20	57133036	4220259	CTSZ	cis	5.58	T	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs6100343	Whole blood (CHARGE)	2.70E-08	20	57133607	4220259	CTSZ	cis	5.56	A	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	0.915	rs1465537	Whole blood (CHARGE)	2.37E-08	20	57131415	4220259	CTSZ	cis	5.58	T	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	0.85	rs6100340	Whole blood (CHARGE)	2.53E-08	20	57118007	4220259	CTSZ	cis	5.57	G	20	57003893

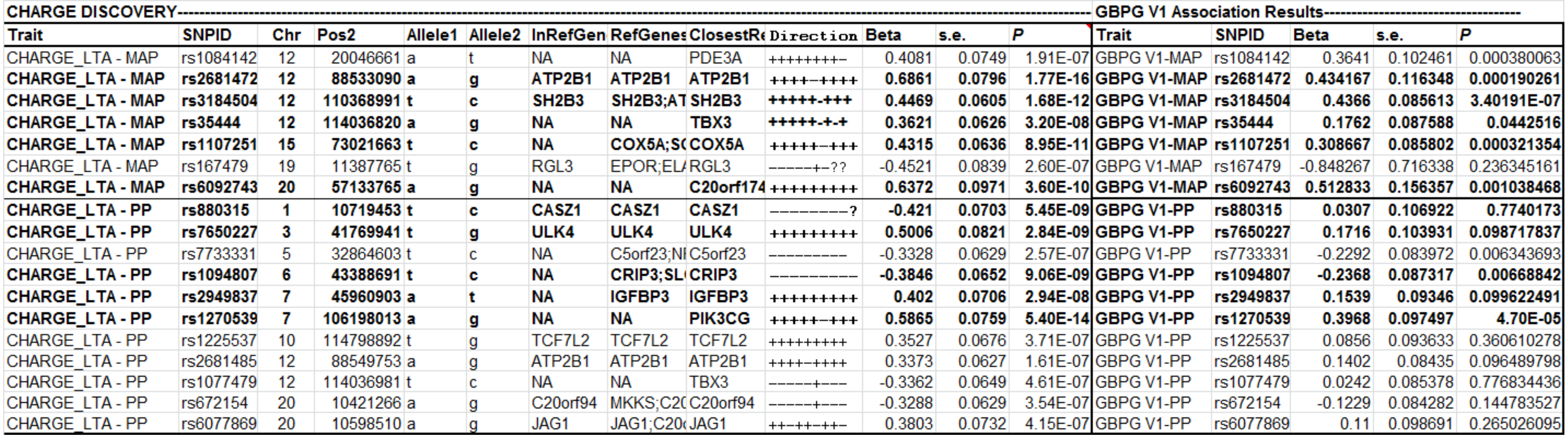
Table S6: PUUMA cohort characteristics.

N	Age, years (sd)	BMI, kg/m2 (sd)	SBP, mmHg (sd)	DBP, mmHg (sd)	Anti-hypertensive therapy (%)	SBP, mmHg, adjusted for antihypertensive therapy (sd)	DBP, mmHg, adjusted for antihypertensive therapy (sd)
5,605	57.35 (9.02)	26.07 (3.38)	133.92 (16.61)	74.92 (9.95)	33.52%	138.95 (19.88)	78.27 (11.42)

Table S7: LTA discovery analysis summary for loci with SNP association(s) *P* value < 5x10-7, and association results in GBPG Visit 1 BP analyses.A1



CHARGE DISCOVERY------------------------													GBPG V1 Association Results------------				
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGenes	ClosestR	Direction	Beta	s.e.	*P*	Trait	SNPID	Beta	s.e.	*P*
CHARGE_LTA - DBP	rs1204627	1	10722164	t	c	CASZ1	CASZ1	CASZ1	--------?	-0.3223	0.0597	2.29E-07	GBPG V1-DBP	rs1204627	-0.2799	0.0934	0.002726
CHARGE_LTA - DBP	**rs1330656**	**1**	**11788391**	**a**	**g**	**MTHFR**	**MTHFR;N**	**MTHFR**	**++++--+++**	**0.4789**	**0.0723**	**2.08E-10**	**GBPG V1-DBP**	**rs1330656**	**0.4529**	**0.1083**	**0.00002905**
CHARGE_LTA - DBP	**rs2004776**	**1**	**228915325**	**t**	**c**	**AGT**	**AGT;COG**	**AGT**	**+++++++++**	**0.3545**	**0.0615**	**3.20E-08**	**GBPG V1-DBP**	**rs2004776**	**0.1014**	**0.091**	**0.2656**
CHARGE_LTA - DBP	rs1275988	2	26767868	t	c		KCNK3;CI	KCNK3	-----+--+	-0.2814	0.0534	4.25E-07	GBPG V1-DBP	rs1275988	-0.1123	0.0775	0.1473
CHARGE_LTA - DBP	**rs7599598**	**2**	**96715567**	**a**	**g**		**FLJ10081;**	**FER1L5**	**---------**	**-0.314**	**0.0543**	**2.91E-08**	**GBPG V1-DBP**	**rs7599598**	**-0.0403**	**0.0799**	**0.6139**
CHARGE_LTA - DBP	rs1528293	3	170637205	a	t	MDS1	MDS1	MDS1	+++++++++	0.2738	0.0522	4.96E-07	GBPG V1-DBP	rs1528293	0.2427	0.0769	0.00161
CHARGE_LTA - DBP	rs1952650	5	157746045	a	t			EBF1	++++-++++	0.2862	0.0523	1.58E-07	GBPG V1-DBP	rs1952650	0.2984	0.0765	0.00009565
CHARGE_LTA - DBP	**rs198823**	**6**	**26230912**	**t**	**g**		**HIST1H2E**	**HIST1H2E**	**----+----**	**-0.3346**	**0.0553**	**6.57E-09**	**GBPG V1-DBP**	**rs198823**	**-0.1705**	**0.0801**	**0.03331**
CHARGE_LTA - DBP	**rs1225896**	**10**	**18767965**	**c**	**g**	**CACNB2**	**CACNB2**	**CACNB2**	**+++-+-+++**	**0.3548**	**0.0571**	**2.48E-09**	**GBPG V1-DBP**	**rs1225896**	**0.2836**	**0.0834**	**0.0006716**
CHARGE_LTA - DBP	**rs1224484**	**10**	**63109192**	**t**	**g**	**C10orf107**	**C10orf107**	**C10orf107**	**-----+--+**	**-0.3784**	**0.0627**	**7.05E-09**	**GBPG V1-DBP**	**rs1224484**	**-0.432**	**0.0901**	**0.000001618**
CHARGE_LTA - DBP	rs1084142	12	20046661	a	t			PDE3A	+++++++++	0.3604	0.0651	1.09E-07	GBPG V1-DBP	rs1084142	0.3446	0.0941	0.0002492
CHARGE_LTA - DBP	**rs2681472**	**12**	**88533090**	**a**	**g**	**ATP2B1**	**ATP2B1**	**ATP2B1**	**++++-++++**	**0.5231**	**0.0691**	**4.01E-13**	**GBPG V1-DBP**	**rs2681472**	**0.336**	**0.1065**	**0.001608**
CHARGE_LTA - DBP	**rs3184504**	**12**	**110368991**	**t**	**c**	**SH2B3**	**SH2B3;AT**	**SH2B3**	**+++++++++**	**0.3936**	**0.0524**	**6.08E-13**	**GBPG V1-DBP**	**rs3184504**	**0.4265**	**0.0789**	**6.361E-08**
CHARGE_LTA - DBP	**rs1133323**	**15**	**72999278**	**t**	**c**		**COX5A;MI**	**COX5A**	**---------**	**-0.3262**	**0.0526**	**2.66E-09**	**GBPG V1-DBP**	**rs1133323**	**-0.2747**	**0.0763**	**0.000321**
CHARGE_LTA - DBP	rs167479	19	11387765	t	g	RGL3	EPOR;EL	RGL3	-------??	-0.3913	0.0729	2.67E-07	GBPG V1-DBP	rs167479	-0.942	0.597	0.1146
CHARGE_LTA - DBP	**rs6092743**	**20**	**57133765**	**a**	**g**			**C20orf174**	**+++++-+++**	**0.502**	**0.0843**	**1.11E-08**	**GBPG V1-DBP**	**rs6092743**	**0.3393**	**0.1436**	**0.01814**
CHARGE_LTA - SBP	**rs880315**	**1**	**10719453**	**t**	**c**	**CASZ1**	**CASZ1**	**CASZ1**	**--------?**	**-0.7125**	**0.1005**	**7.98E-12**	**GBPG V1-SBP**	**rs880315**	**-0.2245**	**0.1504**	**0.1355**
CHARGE_LTA - SBP	**rs1330656**	**1**	**11788391**	**a**	**g**	**MTHFR**	**MTHFR;N**	**MTHFR**	**+++++++++**	**0.8795**	**0.1235**	**6.38E-12**	**GBPG V1-SBP**	**rs1330656**	**0.7349**	**0.1646**	**0.000007978**
CHARGE_LTA - SBP	rs2004776	1	228915325	t	c	AGT	AGT;COG	AGT	+-+++++++	0.5488	0.1049	4.45E-07	GBPG V1-SBP	rs2004776	0.1419	0.1395	0.3091
CHARGE_LTA - SBP	**rs1275988**	**2**	**26767868**	**t**	**c**	**NA**	**KCNK3;CI**	**KCNK3**	**-----+--+**	**-0.6004**	**0.0917**	**2.61E-10**	**GBPG V1-SBP**	**rs1275988**	**-0.2554**	**0.1175**	**0.02977**
CHARGE_LTA - SBP	**rs6712094**	**2**	**164751706**	**a**	**g**	**NA**	**NA**	**GRB14**	**++++-++++**	**0.598**	**0.1007**	**9.89E-09**	**GBPG V1-SBP**	**rs6712094**	**0.4239**	**0.1298**	**0.001095**
CHARGE_LTA - SBP	rs9823197	3	11478133	a	t	ATG7	ATG7	ATG7	-----+-+-	-0.4884	0.0915	2.58E-07	GBPG V1-SBP	rs9823197	-0.2888	0.1168	0.01344
CHARGE_LTA - SBP	**rs7733331**	**5**	**32864603**	**t**	**c**	**NA**	**C5orf23;N**	**C5orf23**	**----+----**	**-0.5505**	**0.0911**	**5.38E-09**	**GBPG V1-SBP**	**rs7733331**	**-0.4965**	**0.118**	**0.00002564**
CHARGE_LTA - SBP	rs1253434	7	27242452	a	g	NA	HOXA13;H	EVX1	-----+--?	-1.5903	0.292	1.48E-07	GBPG V1-SBP	rs1253434	-0.6512	0.3214	0.04273
CHARGE_LTA - SBP	**rs1270539**	**7**	**106198013**	**a**	**g**	**NA**	**NA**	**PIK3CG**	**++++--++-**	**0.6307**	**0.11**	**3.17E-08**	**GBPG V1-SBP**	**rs1270539**	**0.4007**	**0.1371**	**0.003466**
CHARGE_LTA - SBP	rs1267714	8	11488146	c	g	NA	BLK	BLK	---------	-0.5272	0.0988	2.60E-07	GBPG V1-SBP	rs1267714	-0.1581	0.1218	0.194
CHARGE_LTA - SBP	**rs1225896**	**10**	**18767965**	**c**	**g**	**CACNB2**	**CACNB2**	**CACNB2**	**+++++++++**	**0.6307**	**0.0976**	**4.53E-10**	**GBPG V1-SBP**	**rs1225896**	**0.3876**	**0.1268**	**0.002244**
CHARGE_LTA - SBP	**rs7070797**	**10**	**63221779**	**a**	**g**	**NA**	**C10orf107**	**C10orf107**	**-+---+---**	**-0.7415**	**0.1306**	**4.30E-08**	**GBPG V1-SBP**	**rs7070797**	**-0.6611**	**0.174**	**0.0001443**
CHARGE_LTA - SBP	rs1926032	10	104819459	t	c	CNNM2	NT5C2;CN	CNNM2	-----+---	-0.9087	0.1715	3.15E-07	GBPG V1-SBP	rs1926032	-1.0971	0.2137	2.826E-07
CHARGE_LTA - SBP	**rs2681472**	**12**	**88533090**	**a**	**g**	**ATP2B1**	**ATP2B1**	**ATP2B1**	**++++-++++**	**0.9457**	**0.118**	**1.04E-14**	**GBPG V1-SBP**	**rs2681472**	**0.6305**	**0.1646**	**0.0001282**
CHARGE_LTA - SBP	**rs4766578**	**12**	**110388754**	**a**	**t**	**ATXN2**	**SH2B3;AT**	**ATXN2**	**-----+---**	**-0.5599**	**0.0909**	**2.82E-09**	**GBPG V1-SBP**	**rs4766578**	**-0.4787**	**0.1201**	**0.00006713**
CHARGE_LTA - SBP	**rs35444**	**12**	**114036820**	**a**	**g**	**NA**	**+++++-+-**	**TBX3**	**+++++-+-+**	**0.5452**	**0.0929**	**1.47E-08**	**GBPG V1-SBP**	**rs35444**	**0.1568**	**0.1226**	**0.2009**
CHARGE_LTA - SBP	**rs1107251**	**15**	**73021663**	**t**	**c**	**NA**	**COX5A;S**	**COX5A**	**+++++-+++**	**0.5692**	**0.0947**	**6.54E-09**	**GBPG V1-SBP**	**rs1107251**	**0.3548**	**0.12**	**0.003102**
CHARGE_LTA - SBP	**rs6092743**	**20**	**57133765**	**a**	**g**	**NA**	**NA**	**C20orf174**	**+++++++++**	**0.8396**	**0.1449**	**2.25E-08**	**GBPG V1-SBP**	**rs6092743**	**0.8599**	**0.2202**	**0.00009393**
CHARGE_LTA - MAP	**rs880315**	**1**	**10719453**	**t**	**c**	**CASZ1**	**CASZ1**	**CASZ1**	**--------?**	**-0.4597**	**0.067**	**5.49E-11**	**GBPG V1-MAP**	**rs880315**	**-0.244967**	**0.108505**	**0.023966954**
CHARGE_LTA - MAP	**rs1330656**	**1**	**11788391**	**a**	**g**	**MTHFR**	**MTHFR;N**	**MTHFR**	**++++-++++**	**0.6133**	**0.0832**	**1.83E-12**	**GBPG V1-MAP**	**rs1330656**	**0.5469**	**0.11748**	**3.23559E-06**
CHARGE_LTA - MAP	**rs2004776**	**1**	**228915325**	**t**	**c**	**AGT**	**AGT;COG**	**AGT**	**+++++++++**	**0.4226**	**0.0708**	**1.18E-08**	**GBPG V1-MAP**	**rs2004776**	**0.1149**	**0.099071**	**0.246143016**
CHARGE_LTA - MAP	**rs1275988**	**2**	**26767868**	**t**	**c**	**NA**	**KCNK3;CI**	**KCNK3**	**-----+--+**	**-0.3894**	**0.0616**	**1.51E-09**	**GBPG V1-MAP**	**rs1275988**	**-0.16**	**0.083983**	**0.056759651**
CHARGE_LTA - MAP	rs6712094	2	164751706	a	g	NA	NA	GRB14	++++-++++	0.385	0.0677	5.42E-08	GBPG V1-MAP	rs6712094	0.2713	0.092326	0.003297944
CHARGE_LTA - MAP	rs1528293	3	170637205	a	t	MDS1	MDS1	MDS1	+++++++++	0.3361	0.0602	9.29E-08	GBPG V1-MAP	rs1528293	0.279367	0.083395	0.000808377
CHARGE_LTA - MAP	rs7728845	5	122933582	a	g	CSNK1G3	CSNK1G3	CSNK1G3	+++++++++	0.3766	0.0712	4.34E-07	GBPG V1-MAP	rs7728845	0.3521	0.099069	0.000379275
CHARGE_LTA - MAP	rs198846	6	26215442	a	g	NA	HIST1H2B	HIST1H1T	+++++++++	0.4829	0.085	5.69E-08	GBPG V1-MAP	rs198846	0.5286	0.120456	1.1423E-05
CHARGE_LTA - MAP	rs7794193	7	27261226	a	g	NA	HOXA13;E	EVX1	-----+-+-	-0.914	0.1724	4.03E-07	GBPG V1-MAP	rs7794193	-0.296533	0.205208	0.148447395
CHARGE_LTA - MAP	**rs1225896**	**10**	**18767965**	**c**	**g**	**CACNB2**	**CACNB2**	**CACNB2**	**+++++-+++**	**0.452**	**0.0657**	**4.98E-11**	**GBPG V1-MAP**	**rs1225896**	**0.318267**	**0.090482**	**0.000435732**
CHARGE_LTA - MAP	**rs2166122**	**10**	**63193080**	**t**	**c**	**C10orf107**	**C10orf107**	**C10orf107**	**-+---+---**	**-0.4812**	**0.0766**	**1.88E-09**	**GBPG V1-MAP**	**rs2166122**	**-0.439133**	**0.101765**	**1.5948E-05**



CHARGE DISCOVERY													GBPG V1 Association Results				
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGenes	ClosestR	Direction	Beta	s.e.	*P*	Trait	SNPID	Beta	s.e.	*P*
CHARGE_LTA - MAP	rs1084142	12	20046661	a	t	NA	NA	PDE3A	++++++++–	0.4081	0.0749	1.91E-07	GBPG V1-MAP	rs1084142	0.3641	0.102461	0.000380063
CHARGE_LTA - MAP	**rs2681472**	**12**	**88533090**	**a**	**g**	**ATP2B1**	**ATP2B1**	**ATP2B1**	**++++–++++**	**0.6861**	**0.0796**	**1.77E-16**	**GBPG V1-MAP**	**rs2681472**	**0.434167**	**0.116348**	**0.000190261**
CHARGE_LTA - MAP	**rs3184504**	**12**	**110368991**	**t**	**c**	**SH2B3**	**SH2B3;AT**	**SH2B3**	**+++++-+++**	**0.4469**	**0.0605**	**1.68E-12**	**GBPG V1-MAP**	**rs3184504**	**0.4366**	**0.085613**	**3.40191E-07**
CHARGE_LTA - MAP	**rs35444**	**12**	**114036820**	**a**	**g**	**NA**	**NA**	**TBX3**	**+++++-+-+**	**0.3621**	**0.0626**	**3.20E-08**	**GBPG V1-MAP**	**rs35444**	**0.1762**	**0.087588**	**0.0442516**
CHARGE_LTA - MAP	**rs1107251**	**15**	**73021663**	**t**	**c**	**NA**	**COX5A;S**	**COX5A**	**+++++–+++**	**0.4315**	**0.0636**	**8.95E-11**	**GBPG V1-MAP**	**rs1107251**	**0.308667**	**0.085802**	**0.000321354**
CHARGE_LTA - MAP	rs167479	19	11387765	t	g	RGL3	EPOR;EL	RGL3	–––––+–??	-0.4521	0.0839	2.60E-07	GBPG V1-MAP	rs167479	-0.848267	0.716338	0.236345161
CHARGE_LTA - MAP	**rs6092743**	**20**	**57133765**	**a**	**g**	**NA**	**NA**	**C20orf174**	**+++++++++**	**0.6372**	**0.0971**	**3.60E-10**	**GBPG V1-MAP**	**rs6092743**	**0.512833**	**0.156357**	**0.001038468**
CHARGE_LTA - PP	**rs880315**	**1**	**10719453**	**t**	**c**	**CASZ1**	**CASZ1**	**CASZ1**	**––––––––?**	**-0.421**	**0.0703**	**5.45E-09**	**GBPG V1-PP**	**rs880315**	**0.0307**	**0.106922**	**0.7740173**
CHARGE_LTA - PP	**rs7650227**	**3**	**41769941**	**t**	**g**	**ULK4**	**ULK4**	**ULK4**	**+++++++++**	**0.5006**	**0.0821**	**2.84E-09**	**GBPG V1-PP**	**rs7650227**	**0.1716**	**0.103931**	**0.098717837**
CHARGE_LTA - PP	rs7733331	5	32864603	t	c	NA	C5orf23;N	C5orf23	–––––––––	-0.3328	0.0629	2.57E-07	GBPG V1-PP	rs7733331	-0.2292	0.083972	0.006343693
CHARGE_LTA - PP	**rs1094807**	**6**	**43388691**	**t**	**c**	**NA**	**CRIP3;SL**	**CRIP3**	**–––––––––**	**-0.3846**	**0.0652**	**9.06E-09**	**GBPG V1-PP**	**rs1094807**	**-0.2368**	**0.087317**	**0.00668842**
CHARGE_LTA - PP	**rs2949837**	**7**	**45960903**	**a**	**t**	**NA**	**IGFBP3**	**IGFBP3**	**+++++++++**	**0.402**	**0.0706**	**2.94E-08**	**GBPG V1-PP**	**rs2949837**	**0.1539**	**0.09346**	**0.099622491**
CHARGE_LTA - PP	**rs1270539**	**7**	**106198013**	**a**	**g**	**NA**	**NA**	**PIK3CG**	**+++++–+++**	**0.5865**	**0.0759**	**5.40E-14**	**GBPG V1-PP**	**rs1270539**	**0.3968**	**0.097497**	**4.70E-05**
CHARGE_LTA - PP	rs1225537	10	114798892	t	g	TCF7L2	TCF7L2	TCF7L2	+++++++++	0.3527	0.0676	3.71E-07	GBPG V1-PP	rs1225537	0.0856	0.093633	0.360610278
CHARGE_LTA - PP	rs2681485	12	88549753	a	g	ATP2B1	ATP2B1	ATP2B1	++++–++++	0.3373	0.0627	1.61E-07	GBPG V1-PP	rs2681485	0.1402	0.08435	0.096489798
CHARGE_LTA - PP	rs1077479	12	114036981	t	c	NA	NA	TBX3	–––––+–––	-0.3362	0.0649	4.61E-07	GBPG V1-PP	rs1077479	0.0242	0.085378	0.776834436
CHARGE_LTA - PP	rs672154	20	10421266	a	g	C20orf94	MKKS;C2	C20orf94	–––––+–––	-0.3288	0.0629	3.54E-07	GBPG V1-PP	rs672154	-0.1229	0.084282	0.144783527
CHARGE_LTA - PP	rs6077869	20	10598510	a	g	JAG1	JAG1;C20	JAG1	++–++–++–	0.3803	0.0732	4.15E-07	GBPG V1-PP	rs6077869	0.11	0.098691	0.265026095

Rows in **bold** show LTA analysis *P* values < $5x10^{-8}$.

Table S8: Summary of number of SNPs and loci identified by LTA

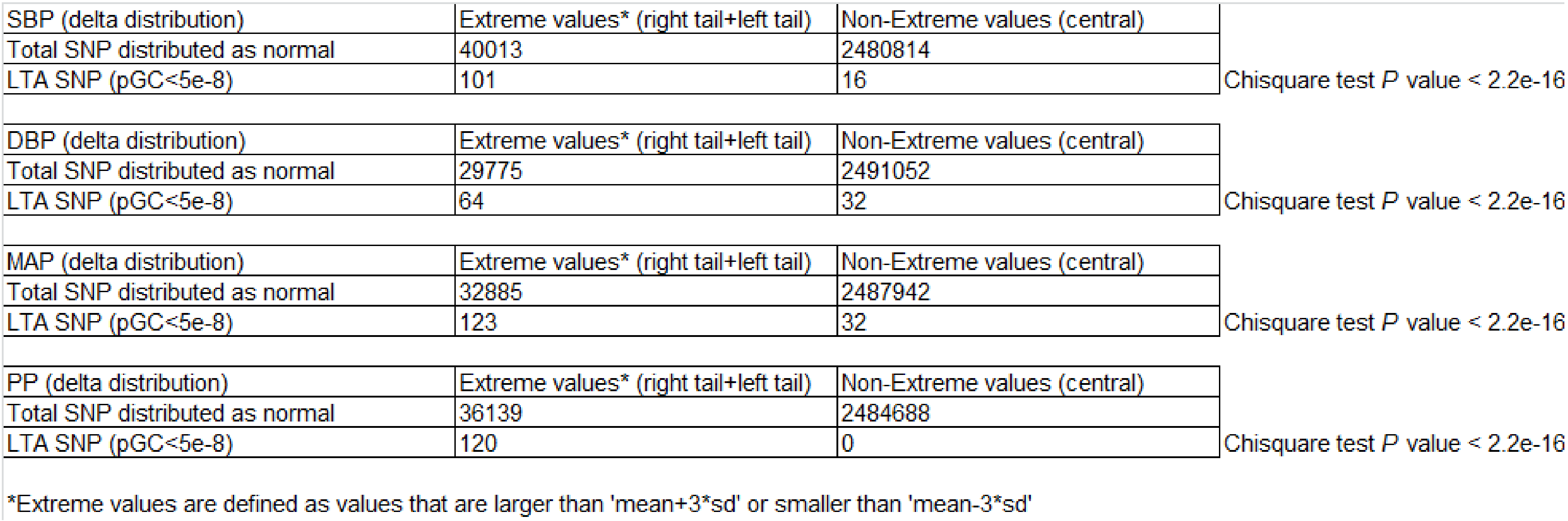
Number of significant SNPs

	P value < $5x10^{-8}$	
	#LTA SNPs	#V1 SNPs
SBP	117	122
DBP	96	126
MAP	155	153
PP	120	1
Total	488	402

Number of significant Loci

	P value < $5x10^{-8}$	
	#LTA loci	#V1 loci
SBP	13	8
DBP	10	9
MAP	11	9
PP	5	1
Total	39	27

Table S9: Distribution of LTA *P* values as compared to the corresponding V1 BP trait analysis *P* values



SBP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	40013	2480814	
LTA SNP (pGC<5e-8)	101	16	Chisquare test *P* value < 2.2e-16

DBP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	29775	2491052	
LTA SNP (pGC<5e-8)	64	32	Chisquare test *P* value < 2.2e-16

MAP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	32885	2487942	
LTA SNP (pGC<5e-8)	123	32	Chisquare test *P* value < 2.2e-16

PP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	36139	2484688	
LTA SNP (pGC<5e-8)	120	0	Chisquare test *P* value < 2.2e-16

*Extreme values are defined as values that are larger than 'mean+3*sd' or smaller than 'mean-3*sd'

Table S10: Power simulations for the application of LTA to SBP.

a: Correlation between the 4 visits for SBP residual adjusted for BMI, age, and age*age and gender in ARIC.

	SBP V1	**SBP V2**	**SBP V3**	**SBP V4**
SBP V1	1.00	0.73	0.65	0.60
SBP V2	0.73	1.00	0.72	0.64
SBP V3	0.65	0.72	1.00	0.70
SBP V4	0.60	0.64	0.70	1.00

b1: Power Estimates. Sample size N = 1000 and testing at alpha=0.05. The true effect size is 0.1. Monte Carlo size 10,000.

q	**0.05**	**0.10**	**0.20**	**0.30**	**0.40**
Visit 1	0.16	0.27	0.43	0.52	0.59
LTA	0.19	0.33	0.52	0.63	0.70
GEE (4 visits)	0.20	0.34	0.52	0.64	0.70

b2: Power Estimates, Null Hypothesis. Sample size N = 1000 and testing at alpha=0.05. The true effect size is 0. Monte Carlo size 10,000.

q	**0.05**	**0.10**	**0.20**	**0.30**	**0.40**
Visit 1	0.050	0.048	0.048	0.050	0.047
LTA	0.053	0.051	0.052	0.048	0.048
GEE (4 visits)	0.059	0.052	0.051	0.051	0.050

c: Sample size N = 10000 and testing at alpha = 5x10-8. The true effect size is 0.05. Monte Carlo size 5,000.

	0.05	**0.1**	**0.2**	**0.3**	**0.4**
Visit 1	0	0.001	0.005	0.011	0.023
LTA	0	0.002	0.015	0.039	0.070
GEE (4 visits)	0	0.002	0.015	0.039	0.071

Table S11: Enrichment analysis results

Stronger results in LTA versus V1 analysis	**Summary of lead SNPs and LTA and V1 results**										**Tested Region**			Pvalue of Kolmogorov–Smirnov statistics with 10000 permutation		Pvalue of 10000 times Bootstrapping compared to the statistics from the	
	trait	**SNPID**	**Allele1**	**Chr**	**Position**	**InRefGene**	**RefGenes.60kbfron**	**ClosestRefGene**	**LTA P value**	**V1 P value**	**Position Start**	**Position End**	**# SNPs**	**D-.*P*value**	**D+.*P*value**	**D-.*P*value**	**D+.*P*value**
LTA	SBP	rs13306561	a	1p36	11788391	MTHFR	MTHFR;NPPA;CLCN	MTHFR	6.38E-12	1.11E-07	11775103	11847887	102	0.4522	**1.00E-04**	0.3983	**<0.0001**
LTA	SBP	rs1275988	t	2p23	26767868	NA	KCNK3;CIB4	KCNK3	2.61E-10	1.38E-05	26765249	26786300	10	1	**<0.0001**	1	**<0.0001**
LTA	SBP	rs6712094	a	2q24	164751706	NA	NA	GRB14	9.89E-09	5.22E-07	164722539	164839114	175	0.6859	**2.00E-04**	0.7081	**<0.0001**
LTA	SBP	rs7733331	t	5p13	32864603	NA	C5orf23;NPR3	C5orf23	5.38E-09	0.000141351	32810804	32867696	43	1	**0.0016**	1	**4.00E-04**
LTA	SBP	rs12705390	a	7q22	106198013	NA	NA	PIK3CG	3.17E-08	2.63E-05	106192878	106199094	20	0.956	**4.00E-04**	0.9823	**1.00E-04**
LTA	SBP	rs7070797	a	10q21	63221779	NA	C10orf107	C10orf107	4.30E-08	1.17E-06	63190704	63221779	48	0.7187	**0.0024**	0.7434	**1.00E-04**
LTA	DBP	rs13306561	a	1p36	11788391	MTHFR	MTHFR;NPPA;CLCN	MTHFR	2.08E-10	1.28E-07	11783430	11828561	83	0.7217	**<0.0001**	0.7821	**<0.0001**
LTA	DBP	rs1952650	a	5q33	157746045	NA	NA	EBF1	1.58E-07	2.16E-05	157746045	157746045	82	0.3685	**<0.0001**	0.3102	**<0.0001**
LTA	DBP	rs198823	t	6p22	26230912	NA	HIST1H2BD;HIST1H2	HIST1H2BC	6.57E-09	4.52E-06	26150218	26233321	155	0.8544	**<0.0001**	0.8949	**<0.0001**
LTA	DBP	rs3184504	t	12q24	110368991	SH2B3	SH2B3;ATXN2	SH2B3	6.08E-13	1.26E-08	110368991	111390798	277	0.9517	**<0.0001**	0.9721	**<0.0001**
LTA	MAP	rs880315	t	1p36	10719453	CASZ1	CASZ1	CASZ1	5.49E-11	1.47E-07	10713384	10724576	9	0.856	**0.0081**	0.9464	**0.0042**
LTA	MAP	rs13306561	a	1p36	11788391	MTHFR	MTHFR;NPPA;CLCN	MTHFR	1.83E-12	1.48E-08	11775103	11847887	104	0.7774	**1.00E-04**	0.8154	**<0.0001**
LTA	MAP	rs1275988	t	2p23	26767868	NA	KCNK3;CIB4	KCNK3	1.51E-09	7.06E-06	26765249	26786300	10	1	**3.00E-04**	1	**<0.0001**
LTA	MAP	rs2681472	a	12q21	88533090	ATP2B1	ATP2B1	ATP2B1	1.77E-16	1.70E-12	88465680	88637201	132	0.3985	**<0.0001**	0.3285	**<0.0001**
LTA	PP	rs10948071	t	6p21	43388691	NA	CRIP3;SLC22A7;TTE	CRIP3	9.06E-09	0.000111242	43367990	43440164	49	0.9211	**<0.0001**	0.9491	**<0.0001**
LTA	PP	rs2949837	a	7p13	45960903	NA	IGFBP3	IGFBP3	2.94E-08	6.88E-06	45929639	45960903	49	1	**<0.0001**	1	**<0.0001**
LTA	PP	rs12705390	a	7q22	106198013	NA	NA	PIK3CG	5.40E-14	1.20E-06	106192878	106206532	24	0.612	**5.00E-04**	0.7028	**<0.0001**
V1	SBP	rs2004776	t	1q42	228915325	AGT	AGT;COG2;CAPN9	AGT	4.45E-07	4.63E-08	228903667	228916422	76	**0.0061**	0.9914	**4.00E-04**	1
V1	SBP	rs4766578	a	12q24	110388754	ATXN2	SH2B3;ATXN2	ATXN2	2.82E-09	1.18E-09	110368991	110556807	201	**<0.0001**	0.7427	**<0.0001**	0.7695
V1	SBP	rs11072518	t	15q24	73021663	NA	COX5A;SCAMP5;RP	COX5A	6.54E-09	2.93E-11	72820453	73029208	90	**<0.0001**	0.7609	**<0.0001**	0.8024
V1	SBP	rs6092743	a	20q13	57133765	NA	NA	C20orf174	2.25E-08	2.18E-09	57112829	57194118	67	**1.00E-04**	0.9868	**<0.0001**	0.9975
V1	DBP	rs2004776	t	1q42	228915325	AGT	AGT;COG2;CAPN9	AGT	3.20E-08	1.53E-08	228915325	228915982	50	**0.0057**	0.9252	**0.001**	0.9622
V1	DBP	rs12258967	c	10p12	18767965	CACNB2	CACNB2	CACNB2	2.48E-09	3.71E-09	18747454	18780638	51	**0.0195**	0.7355	**0.0048**	0.7591
V1	DBP	rs1133323	t	15q24	72999278	NA	COX5A;MPI;SCAMP2	COX5A	2.66E-09	4.89E-10	72806502	73029208	109	**<0.0001**	0.3275	**<0.0001**	0.2717
V1	DBP	rs6092743	a	20q13	57133765	NA	NA	C20orf174	1.11E-08	3.37E-11	57108080	57194118	71	**<0.0001**	0.7041	**<0.0001**	0.7368
V1	MAP	rs2004776	t	1q42	228915325	AGT	AGT;COG2;CAPN9	AGT	1.18E-08	2.45E-09	228882807	228929783	105	**0.0336**	0.9726	**0.0078**	0.9898
V1	MAP	rs12258967	c	10p12	18767965	CACNB2	CACNB2	CACNB2	4.98E-11	5.57E-10	18726458	18780638	91	0.0843	0.4946	**0.0355**	0.4722
V1	MAP	rs11072518	t	15q24	73021663	NA	COX5A;SCAMP5;RP	COX5A	8.95E-11	1.86E-12	72806502	73029208	95	**<0.0001**	0.5105	**<0.0001**	0.4795
Mixed effect	DBP	rs12244842	t	10q21	63109192	C10orf107	C10orf107	C10orf107	7.05E-09	6.15E-08	63109192	63221779	158	**0.0348**	**<0.0001**	**0.0101**	**<0.0001**
Mixed effect	MAP	rs2166122	t	10q21	63193080	C10orf107	C10orf107	C10orf107	1.88E-09	4.76E-08	63109192	63221779	142	0.0565	**<0.0001**	**0.0184**	**<0.0001**
Mixed effect	MAP	rs3184504	t	12q24	110368991	SH2B3	SH2B3;ATXN2	SH2B3	1.68E-12	3.71E-10	110368991	111390798	316	**<0.0001**	0.06	**<0.0001**	**0.0192**
Mixed effect	MAP	rs6092743	a	20q13	57133765	NA	NA	C20orf174	3.60E-10	1.12E-11	57108080	57194118	73	**<0.0001**	0.0924	**<0.0001**	**0.0439**
Mixed effect	PP	rs7650227	t	3p22	41769941	ULK4	ULK4	ULK4	2.84E-09	4.38E-06	41725264	42040009	201	**0.0042**	**<0.0001**	**8.00E-04**	**<0.0001**
No difference	SBP	rs880315	t	1p36	10719453	CASZ1	CASZ1	CASZ1	7.98E-12	7.20E-09	10713384	10724576	9	0.8669	0.2722	0.9464	0.3158
No difference	SBP	rs12258967	c	10p12	18767965	CACNB2	CACNB2	CACNB2	4.53E-10	1.53E-08	18726458	18780638	91	0.9551	0.2148	0.9822	0.1264
No difference	SBP	rs2681472	a	12q21	88533090	ATP2B1	ATP2B1	ATP2B1	1.04E-14	1.69E-11	88465680	88637201	132	0.1781	0.2263	0.1116	0.1561
No difference	SBP	rs35444	a	12q24	114036820	NA	NA	TBX3	1.47E-08	2.63E-06	114036820	114039913	14	0.7564	0.3222	0.7963	0.2573
No difference	DBP	rs7599598	a	2q11	96715567	NA	FLJ10081;FER1L5;LI	FER1L5	2.91E-08	6.54E-08	96715567	rs7599598	1	1	0.4993	1	0.5046
No difference	DBP	rs1801253	c	10q25	115795046	ADRB1	ADRB1	ADRB1	7.22E-06	2.58E-08	115782052	115795046	9	0.1765	0.8999	0.112	0.9477
No difference	DBP	rs2681472	a	12q21	88533090	ATP2B1	ATP2B1	ATP2B1	4.01E-13	8.68E-11	88465680	88637201	132	0.1105	0.3348	0.0576	0.2681
No difference	MAP	rs1801253	c	10q25	115795046	ADRB1	ADRB1	ADRB1	7.32E-07	7.10E-09	115779365	115795046	9	0.1665	0.8955	0.1032	0.9494
No difference	MAP	rs35444	a	12q24	114036820	NA	NA	TBX3	3.20E-08	8.38E-07	114036820	114039913	14	0.7605	0.3228	0.7945	0.2617
No difference	PP	rs880315	t	1p36	10719453	CASZ1	CASZ1	CASZ1	5.45E-09	3.31E-06	10713384	10722164	6	0.8323	0.1492	0.8929	0.1943
No difference	PP	rs12631867	a	3p24	30437485	NA	NA	TGFBR2	0.023903474	9.25E-10	30437485	rs12631867	1	0.5002	1	0.5043	1

SUPPLEMENTAL COHORT DESCRIPTIONS

Cohort Descriptions

Discovery cohorts

The CHARGE Consortium[1] includes cohort studies that completed genome-wide genotyping and had extensive data on multiple phenotypes including blood pressure. Each study adopted collaboration guidelines and established a consensus on phenotype harmonization, covariate selection and an analytical plan for within-study genome-wide association and prospective meta-analysis of results across studies. Each study received institutional review board approval of its consent procedures, examination and surveillance components, data security measures, and DNA collection and its use for genetic research. All participants provided written informed consent.

In the current analysis, most of the participating cohorts were general population samples (AGES, ARIC, CHS, FHS, RS, MESA, CARDIA). Demographic information, blood pressure, height, and weight were directly measured in all participants, except for the Women's Genome Health Study as described. All studies with GWAS data used hidden Markov model approaches[2-4] and HapMap reference panels[5] to impute genotypes at unmeasured SNPs and excluded SNPs, so that a common set of ~2.5M HapMap SNPs were available across the discovery samples[4,6]. All studies with GWAS data used hidden Markov model approaches1-3 and HapMap reference panels4 to impute genotypes at unmeasured SNPs and excluded SNPs, so that a common set of ~2.5M HapMap SNPs were available across the discovery samples[4,6].

AGES Reykjavik

The Age Gene/Environment Susceptibility-Reykjavik (AGES- Reykjavik) Study cohort originally comprised a random sample of 30,795 men and women born in 1907-1935 and living in Reykjavik in 1967. A total of 19,381 people attended, resulting in 71% recruitment rate. The study sample was divided into six groups by birth year and birth date within month. One group was designated for longitudinal follow up and was examined in all stages. One group was designated a control group and was not included in examinations until 1991. Other groups were invited to participate in specific stages of the study. Between 2002 and 2006, the AGES-Reykjavik study re-examined 5764 survivors of the original cohort who had participated before in the Reykjavik Study.[7] The midlife data blood pressure measurement was taken from stage 3 of the Reykjavik Study (1974-1979), if available. Half of the cohort attended during this period. Otherwise an observation was selected closest in time to the stage 3 visit. Participants came in a fasting state to the clinic. The supine blood pressure was measured twice by a nurse using a mercury sphygmomanometer after a 5-min rest. Blood pressure was measured according to World Health Organization recommendations. Individuals with previous MI were excluded from the analyses (n=12). Successful genotyping was available for 3219 AGES participants who were eligible for this study. The AGES Reykjavik Study GWAS was approved by the National Bioethics Committee and the Data Protection Authority.

ARIC

The Atherosclerosis Risk In Communities Study (ARIC) study is a population-based prospective cohort study of cardiovascular disease sponsored by National Heart, Lung, and Blood Institute (NHLBI). ARIC included 15,792 individuals aged 45-64 years at baseline (1987-89), chosen by probability sampling from four US communities[8] Cohort members completed four clinic examinations, conducted three years apart between 1987 and 1998. The data used in this study are from all four visits. A detailed study protocol is available on the ARIC study website (http://www.cscc.unc.edu/aric). Clinic examinations included assessment of cardiovascular disease risk factors, a detailed medical and psychosocial history, and measurement of various clinical and laboratory variables. The physical examination included measurements of weight and height from which the body mass index (BMI) was calculated. Blood pressure was measured using a standardized Hawskley random-zero mercury column sphygmomanometer with participants in sitting position after a resting period of 5 minutes. The size of the cuff was chosen according to the arm circumference. For the first three visits, three sequential recordings for systolic and diastolic blood pressure were obtained and the mean of the last two measurements used in this analysis. At the fourth visit, two blood pressure measurements were taken and averaged. Blood pressure lowering medication use was recorded from the medication history. Outliers (>4SD from the mean) with respect to the systolic or diastolic blood pressure distribution were excluded from the analysis. For this investigation we limited the sample to individuals of European descent by self-report and in whom GWAS was carried out.

CARDIA

The Coronary Artery Risk Development in Young Adults (CARDIA) is a prospective multicenter study with 5115 adults Caucasian and African American participants of the age group 18-30 years, recruited from four centers at the baseline examination in 1985-1986. The recruitment was done from the total community in Birmingham, AL, from selected census tracts in Chicago, IL and Minneapolis, MN; and from the Kaiser Permanente health plan membership in Oakland, CA. The details of the study design for the CARDIA study have been previously published.[17] Eight examinations have been completed since initiation of the study, respectively in the years 0, 2, 5, 7, 10, 15, 20 and 25. Written informed consent was obtained from participants at each examination and all study protocols were approved by the institutional review boards of the participating institutions. At each examination, systolic and diastolic blood pressure was measured in triplicate on the right arm using a random-zero sphygmomanometer with the participant seated and following a 5-min. rest. The average of the second and third measurements was taken as the blood pressure value. Blood pressure medication use was obtained by questionnaire. Blood pressure data measured at year 7 through year 20 were used in this study. In addition, the sample was restricted to individuals of European descent by self-report and principal component analysis using genome-wide genotypes.

CHS

The CHS is a population-based cohort study of risk factors for cardiovascular disease in adults 65 years of age or older conducted across four field centers. The original predominantly white cohort of 5201 persons was recruited in 1989-1990 from random samples of the Medicare eligibility lists and an additional 687 African-Americans were enrolled in 1992-93 for a total sample of 5888. Details of the study design are summarized elsewhere[9]. A total of 1908 persons were excluded from the study sample due to 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). Participants with missing BMI (n=10) or BP measurements (n=8) were excluded. CHS participants completed standardized clinical examinations and questionnaires at study baseline and at nine annual follow-up visits. Research staff who received central training in blood pressure measurement assessed repeat right-arm seated systolic and diastolic blood pressure levels at baseline with a

Hawksley random-zero sphygmomanometer. Means of the repeated blood pressure measurements from the baseline examination were used for GWAS analyses. Because the other cohorts were predominantly white, African American participants were excluded from this analysis. 3,159 CHS subjects contributed to this analysis.

FHS

The Framingham Heart Study (FHS) began in 1948 with the recruitment of an original cohort of 5,209 men and women who were 28 to 62 years of age (mean age 44 years; 55 percent women) at entry. In 1971 enrollment of a second generation of study participants took place; this cohort consisted of 5,124 children and spouses of children of the original cohort. The mean age of the offspring cohort was 37 years; 52 percent were women. A third generation cohort The FHS began in 1948 with the recruitment of an original cohort of 5,209 men and women who were 28 to 62 years of age (mean age 44 years; 55 percent women) at entry. In 1971 enrollment of a second generation of study participants took place; this cohort consisted of 5,124 children and spouses of children of the original cohort. The mean age of the offspring cohort was 37 years; 52 percent were women.[10-12] At each clinic visit, a medical history was obtained with a focus on cardiovascular content, and participants underwent a physical examination including measurement of height and weight from which BMI was calculated. Systolic and diastolic blood pressures were measured twice by a physician on the left arm of the resting and seated participant using a mercury column sphygmomanometer. Pressures were recorded to the nearest even number. The means of two separate systolic and diastolic blood pressure readings at the first clinic examination of each cohort were used for GWAS analyses. For a subset of offspring cohort participants only one measurement was obtained. Individuals under 20 years of age, those who had a myocardial infarction, or congestive heart failure were excluded from the analyses because those conditions may affect blood pressure levels.

MESA

The Multi-Ethnic Study of Atherosclerosis investigation is a population-based study of 6,814 men and women age 45 to 85 years, without clinical cardiovascular disease, recruited from six United States communities (Baltimore, MD; Chicago, IL; Forsyth County, NC; Los Angeles County, CA; northern Manhattan, NY; and St. Paul, MN). The main objective of MESA is to determine the characteristics of subclinical cardiovascular disease and its progression. Sampling and recruitment procedures have been previously described in detail.[15] Adults with symptoms or history of medical or surgical treatment for cardiovascular disease were excluded. During the recruitment process, potential participants were asked about their race/ethnicity. Self-reported ethnicity was used to classify participants into groups.[16] After a 5-minute rest BP was measured three times at 1 minute intervals using a Dinamap PRO 100 automated oscillometric device (Critikon, Tampa, FL) with the subject in seated, and the average of the second and third BP measurements was recorded for each visit. Data from white participants, collected at MESA exams 1 through 4, was used in this analysis.

Rotterdam Study - RS1, RS2

The RS is a prospective population-based cohort study comprising 7,983 subjects aged 55 years or older. Participants completed an interview at home and at the research center, where participants were subsequently examined. Baseline data were collected between 1990 and 1993. In 1999, inhabitants who turned 55 years of age or moved into the study district since the start of the study were invited to participate in an extension of the RS (RES) of whom 3011 participated (67% response rate). The rationale and design of the RS have been described in detail elsewhere.[13] At the research center, we obtained two seated blood pressure measurements in the right brachial artery with a random zero sphygmomanometer. The mean of two consecutive measurements was used in association analyses. We excluded participants who were older than 85 years of age and those who had a history myocardial infarction or congestive heart failure, because of the impact of these conditions on blood pressure levels.

WGHS

The Women's Genome Health Study (WGHS)[14] is a prospective cohort of female North American health care professionals representing participants in the Women's Health Study (WHS) trial who provided a blood sample at baseline and consent for blood-based analyses. Participants in the WHS were 45 years or older at enrolment and free of cardiovascular disease, cancer or other major chronic illness. For the primary WHS endpoints of cardiovascular disease, full medical records were obtained for reported endpoints and reviewed by an endpoints committee of physicians unaware of assignment. The current data are derived from 23,294 WGHS participants for whom whole genome genotype information was available at the time of analysis and for whom self-reported European ancestry could be confirmed by multidimensional scaling analysis of 1,443 ancestry informative markers in PLINK v. 1.06. Baseline BP in the WGHS was ascertained by a self-reported questionnaire, an approach which has been validated in the WGHS demographic, namely female health care professionals. Questionnaires recorded systolic blood pressure in 9 categories (<110, 110-119, 120-129, 130- 139, 140-149, 150-159, 160-169, 170-179, ≥180 mmHg), and diastolic blood pressure in 7 categories (<65, 65-74, 75-84, 85-89, 90-94, 95-104, ≥105 mmHg). The midpoint of each category was used for analysis. Hypertension was defined as a history of physician-diagnosed HTN and ongoing HTN treatment, or SBP ≥ 140 or DBP ≥ 90 mmHg. To account for treatment effects, 10 and 5 mmHg were added to the measured systolic and diastolic blood pressures respectively, if a participant was taking antihypertensive medication.

Replication Cohorts

The replication cohorts in this analysis were used to test the reproducibility of novel discovered loci which were identified by the use of the LTA method. The replication cohorts all provided single-visit BP traits. All participants provided written informed consent and studies were approved by their local Institutional Review Boards or Research Ethics Committees.

Global BP Gen (GBPG)

Single-visit BP traits were previously analyzed in 17 cohorts, and the results of the meta-analysis have been previously reported.[18] Adjustment was performed for the use of anti-hypertensive medications using similar methods as we used in the discovery analysis. The same covariates were included in the individual cohort analyses, including age, age-squared, body mass index, and gender, as in the LTA discovery analyses.

Peking University – University of Michigan Study of Atherosclerosis (PUUMA) Beijing Shijensheng Cohort

The Peking University – University of Michigan Study of Atherosclerosis (PUUMA) is based upon the enrollment of individuals at two hospitals in the Peking University Health Science system: PKU First Hospital and PKU Third Hospital. There were several sources of samples, including the cardiac catheterization laboratories of the hospitals and a community-based enrollment in Beijing Shijengsheng district. The single-visit BP analyses reported in this study were based upon the community based enrollment of 5,065 unrelated individuals (confirmed by exome wide genotypes) which represents a population sample of Han Chinese from Beijing. Blood pressure was recorded using the Omron 7100 machine three times at 2-minute interval in a seated position. The average of three readings was used for the analysis. Genotyping was performed using the Illumina Exome Plus chip with additional custom content based upon sequencing of additional individuals of Asian ancestry and candidate SNPs identified in prior BP association studies. QC was performed as described elsewhere (manuscript in preparation). Association analyses were implemented in PLINK, and genomic control was applied to the final association statistics.

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LTA Discovery Cohorts:

AGES: Age, Gene/Environment Susceptibility (AGES) Reykjavik Study is funded by NIH contract N01-AG-12100, the NIA Intramural Research Program, Hjartavernd (the Icelandic Heart Association) and the Althingi (the Icelandic Parliament). The study is approved by the Icelandic National Bioethics Committee, VSN: 00-063.

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__Reproducibility studies with single-visit BP traits:__

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Supplemental References

1. Psaty, B.M. *et al.* Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: Design of prospective meta-analyses of genome-wide association studies from 5 cohorts. *Circ Cardiovasc Genet* **2**, 73-80 (2009).
2. Servin, B. & Stephens, M. Imputation-based analysis of association studies: candidate regions and quantitative traits. *PLoS Genet* **3**, e114 (2007).
3. Marchini, J. & Howie, B. Genotype imputation for genome-wide association studies. *Nat Rev Genet* **11**, 499-511.
4. Li, Y., Willer, C., Sanna, S. & Abecasis, G. Genotype imputation. *Annu Rev Genomics Hum Genet* **10**, 387-406 (2009).
5. International HapMap, C. The International HapMap Project. *Nature* **426**, 789-96 (2003).
6. Guan, Y. & Stephens, M. Practical issues in imputation-based association mapping. *PLoS Genet* **4**, e1000279 (2008).
7. Harris, T.B. *et al.* Age, Gene/Environment Susceptibility-Reykjavik Study: multidisciplinary applied phenomics. *Am J Epidemiol* **165**, 1076-87 (2007).
8. The Atherosclerosis Risk in Communities (ARIC) Study: design and objectives. The ARIC investigators. *Am J Epidemiol* **129**, 687-702 (1989).
9. Fried, L.P. *et al.* The Cardiovascular Health Study: design and rationale. *Ann Epidemiol* **1**, 263-76 (1991).
10. Dawber, T.R., Meadors, G.F. & Moore, F.E., Jr. Epidemiological approaches to heart disease: the Framingham Study. *Am J Public Health Nations Health* **41**, 279-81 (1951).
11. Feinleib, M., Kannel, W.B., Garrison, R.J., McNamara, P.M. & Castelli, W.P. The Framingham Offspring Study. Design and preliminary data. *Prev Med* **4**, 518-25 (1975).
12. Splansky, G.L. *et al.* The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. *Am J Epidemiol* **165**, 1328-35 (2007).
13. Hofman, A. *et al.* The Rotterdam Study: objectives and design update. *Eur J Epidemiol* **22**, 819-29 (2007).
14. Ridker, P.M. *et al.* Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy american women. *Clin Chem* **54**, 249-55 (2008).
15. Kramer, H. *et al.* Racial/ethnic differences in hypertension and hypertension treatment and control in the multi-ethnic study of atherosclerosis (MESA). *Am J Hypertens* **17**, 963-70 (2004).
16. Bild, D.E. *et al.* Multi-ethnic study of atherosclerosis: objectives and design. *Am J Epidemiol* **156**, 871-81 (2002).
17. Friedman, G.D. *et al.* CARDIA: study design, recruitment, and some characteristics of the examined subjects. *J Clin Epidemiol* **41**, 1105-16 (1988).
18. Newton-Cheh, C. *et al.* Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet* (2009).
19. Johnson, A.D. *et al.* SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. *Bioinformatics.* **24**, 2938-2939 (2008).
20. Goring, H.H. *et al.* Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. *Nat.Genet.* **39**, 1208-1216 (2007).
21. Idaghdour, Y. *et al.* Geographical genomics of human leukocyte gene expression variation in southern Morocco. *Nat Genet* **42**, 62-67.

22. Heap, G.A. *et al.* Complex nature of SNP genotype effects on gene expression in primary human leucocytes. *BMC Med Genomics* **2**, 1 (2009).
23. The Genotype-Tissue Expression (GTEx) project. *Nat.Genet.* **45**, 580-585 (2013).
24. Battle, A. *et al.* Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. *Genome Res.* **24**, 14-24 (2014).
25. Benton, M.C. *et al.* Mapping eQTLs in the Norfolk Island genetic isolate identifies candidate genes for CVD risk traits. *Am.J.Hum.Genet.* **93**, 1087-1099 (2013).
26. Emilsson, V. *et al.* Genetics of gene expression and its effect on disease. *Nature* **452**, 423-428 (2008).
27. Fehrmann, R.S. *et al.* Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. *PLoS Genet* **7**, e1002197.
28. Landmark-Hoyvik, H. *et al.* Genome-wide association study in breast cancer survivors reveals SNPs associated with gene expression of genes belonging to MHC class I and II. *Genomics* **102**, 278-287 (2013).
29. Mehta, D. *et al.* Impact of common regulatory single-nucleotide variants on gene expression profiles in whole blood. *Eur.J.Hum.Genet.* **21**, 48-54 (2013).
30. Sasayama, D. *et al.* Identification of single nucleotide polymorphisms regulating peripheral blood mRNA expression with genome-wide significance: an eQTL study in the Japanese population. *PLoS.One.* **8**, e54967 (2013).
31. van Eijk, K.R. *et al.* Genetic analysis of DNA methylation and gene expression levels in whole blood of healthy human subjects. *BMC.Genomics* **13**, 636 (2012).
32. Westra, H.J. *et al.* Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nat.Genet.* **45**, 1238-1243 (2013).
33. Zhernakova, D.V. *et al.* DeepSAGE Reveals Genetic Variants Associated with Alternative Polyadenylation and Expression of Coding and Non-coding Transcripts. *PLoS.Genet.* **9**, e1003594 (2013).
34. Dixon, A.L. *et al.* A genome-wide association study of global gene expression. *Nat Genet* **39**, 1202-1207 (2007).
35. Liang, L. *et al.* A cross-platform analysis of 14,177 expression quantitative trait loci derived from lymphoblastoid cell lines. *Genome Res.* (2013).
36. Stranger, B.E. *et al.* Patterns of cis regulatory variation in diverse human populations. *PLoS Genet.* **8**, e1002639 (2012).
37. Kwan, T. *et al.* Genome-wide analysis of transcript isoform variation in humans. *Nat.Genet.* **40**, 225-231 (2008).
38. Cusanovich, D.A. *et al.* The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. *Hum.Mol.Genet.* **21**, 2111-2123 (2012).
39. Dimas, A.S. *et al.* Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science* **325**, 1246-1250 (2009).
40. Grundberg, E. *et al.* Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nat.Genet.* **44**, 1084-1089 (2012).
41. Gutierrez-Arcelus, M. *et al.* Passive and active DNA methylation and the interplay with genetic variation in gene regulation. *Elife.* **2**, e00523 (2013).
42. Mangravite, L.M. *et al.* A statin-dependent QTL for GATM expression is associated with statin-induced myopathy. *Nature* **502**, 377-380 (2013).
43. Fairfax, B.P. *et al.* Genetics of gene expression in primary immune cells identifies cell type-specific master regulators and roles of HLA alleles. *Nat.Genet.* **44**, 502-510 (2012).

44. Murphy, A. *et al.* Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. *Hum Mol Genet* **19**, 4745-4757.

45. Heinzen, E.L. *et al.* Tissue-specific genetic control of splicing: implications for the study of complex traits. *PLoS Biol* **6**, e1 (2008).

46. Zeller, T. *et al.* Genetics and beyond--the transcriptome of human monocytes and disease susceptibility. *PLoS One* **5**, e10693.

47. Barreiro, L.B. *et al.* Deciphering the genetic architecture of variation in the immune response to Mycobacterium tuberculosis infection. *Proc.Natl.Acad.Sci.U.S.A* **109**, 1204-1209 (2012).

48. Huang, R.S. *et al.* Population differences in microRNA expression and biological implications. *RNA.Biol.* **8**, 692-701 (2011).

49. Degner, J.F. *et al.* DNase I sensitivity QTLs are a major determinant of human expression variation. *Nature* **482**, 390-394 (2012).

50. Greenawalt, D.M. *et al.* A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. *Genome Res* **21**, 1008-1016.

51. Kompass, K.S. & Witte, J.S. Co-regulatory expression quantitative trait loci mapping: method and application to endometrial cancer. *BMC.Med.Genomics* **4**, 6 (2011).

52. Li, Q. *et al.* Integrative eQTL-based analyses reveal the biology of breast cancer risk loci. *Cell* **152**, 633-641 (2013).

53. Webster, J.A. *et al.* Genetic control of human brain transcript expression in Alzheimer disease. *Am J Hum Genet* **84**, 445-458 (2009).

54. Zou, F. *et al.* Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. *PLoS Genet* **8**, e1002707.

55. Colantuoni, C. *et al.* Temporal dynamics and genetic control of transcription in the human prefrontal cortex. *Nature* **478**, 519-523.

56. Kim, S., Cho, H., Lee, D. & Webster, M.J. Association between SNPs and gene expression in multiple regions of the human brain. *Transl.Psychiatry* **2**, e113 (2012).

57. Liu, C. *et al.* Whole-genome association mapping of gene expression in the human prefrontal cortex. *Mol Psychiatry* **15**, 779-784.

58. Gamazon, E.R. *et al.* Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. *Mol.Psychiatry* **18**, 340-346 (2013).

59. Gibbs, J.R. *et al.* Abundant quantitative trait loci exist for DNA methylation and gene expression in human brain. *PLoS Genet* **6**, e1000952.

60. Zhang, B. *et al.* Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. *Cell* **153**, 707-720 (2013).

61. Innocenti, F. *et al.* Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. *PLoS Genet* **7**, e1002078.

62. Schadt, E.E. *et al.* Mapping the genetic architecture of gene expression in human liver. *PLoS Biol* **6**, e107 (2008).

63. Schroder, A. *et al.* Genomics of ADME gene expression: mapping expression quantitative trait loci relevant for absorption, distribution, metabolism and excretion of drugs in human liver. *Pharmacogenomics.J.* **13**, 12-20 (2013).

64. Grundberg, E. *et al.* Population genomics in a disease targeted primary cell model. *Genome Res.* **19**, 1942-1952 (2009).

65. Kabakchiev, B. & Silverberg, M.S. Expression quantitative trait loci analysis identifies associations between genotype and gene expression in human intestine. *Gastroenterology* **144**, 1488-96, 1496 (2013).

66. Keildson, S. *et al.* Skeletal Muscle Expression of Phosphofructokinase is Influenced by Genetic Variation and Associated with Insulin Sensitivity. *Diabetes* (2013).
67. Quigley, D.A. *et al.* The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogen-receptor positive tumors. *Mol.Oncol.* (2013).
68. Gao, C. *et al.* HEFT: eQTL analysis of many thousands of expressed genes while simultaneously controlling for hidden factors. *Bioinformatics.* (2013).
69. Hao, K. *et al.* Lung eQTLs to help reveal the molecular underpinnings of asthma. *PLoS.Genet.* **8**, e1003029 (2012).
70. Ding, J. *et al.* Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. *Am.J.Hum.Genet.* **87**, 779-789 (2010).
71. Qiu, W. *et al.* Genetics of sputum gene expression in chronic obstructive pulmonary disease. *PLoS.One.* **6**, e24395 (2011).
72. Lin, H. *et al.* Gene expression and genetic variation in human atria. *Heart Rhythm.* (2013).
73. Rantalainen, M. *et al.* MicroRNA expression in abdominal and gluteal adipose tissue is associated with mRNA expression levels and partly genetically driven. *PLoS One* **6**, e27338 (2011).

FIGURE S1: Study design summary.

The study design of the long-term averaged (LTA) analysis is summarized to accomplish the goals of firstly, identifying novel BP associations, which were replicated in an independent sample, and secondly characterizing the impact of LTA on genetic associations as compared to single-visit (V1) BP associations.

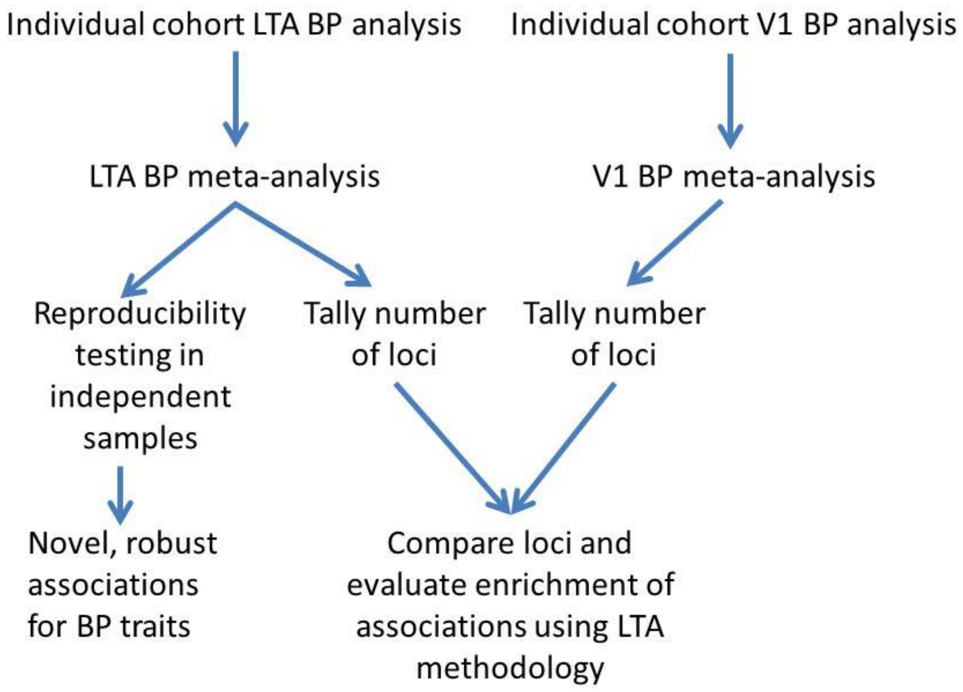


FIGURE S2. QQ plots for LTA BP traits and single visit (V1) SBP and DBP.

Quantile-quantile (QQ) plots are shown for (a) LTA and V1 SBP traits, (b) LTA and V1 DBP traits, (c) LTA-MAP and (d) LTA-PP. The null hypothesis is shown as the orange line. The 95% confidence interval around the null is shown in gray.

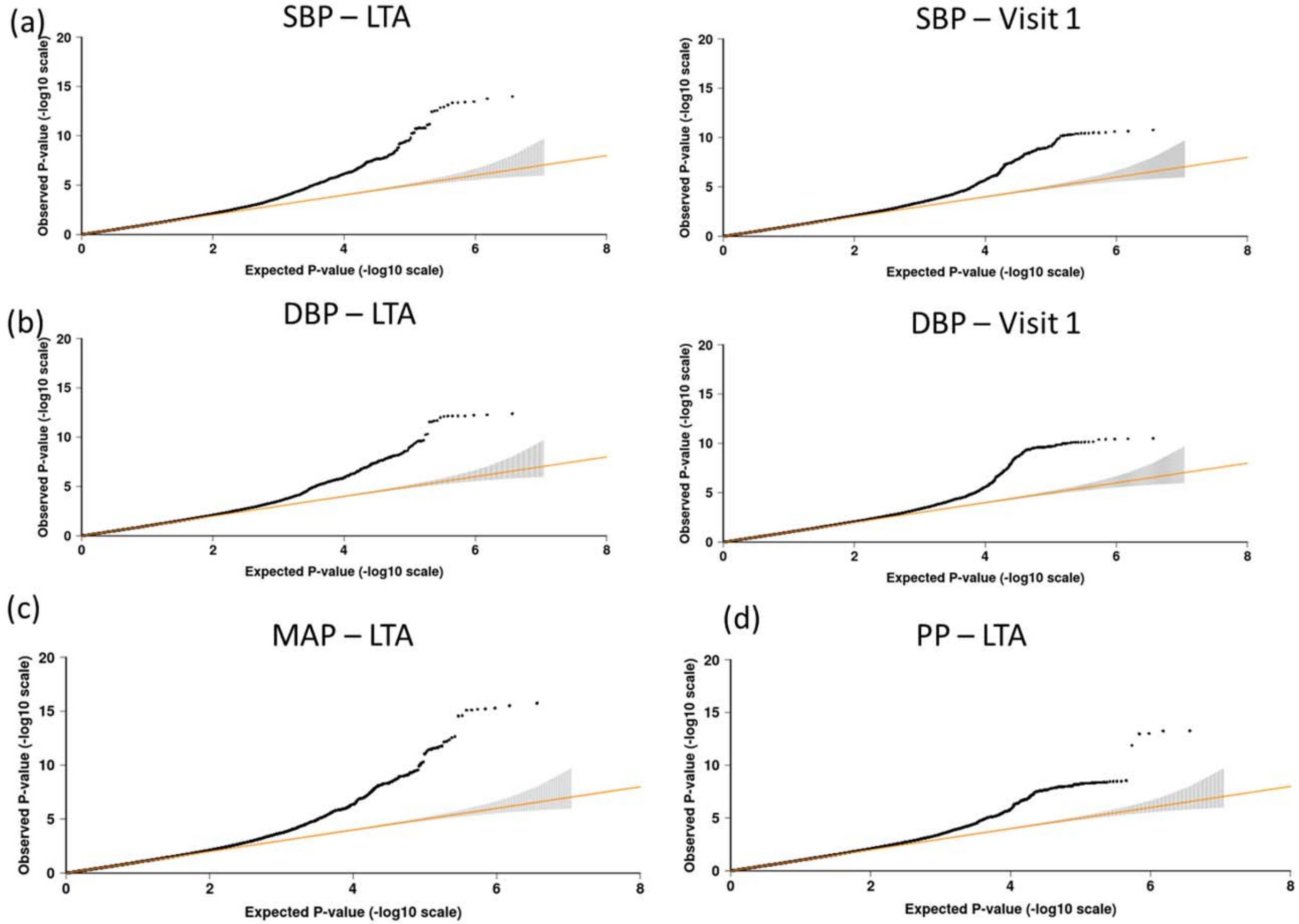
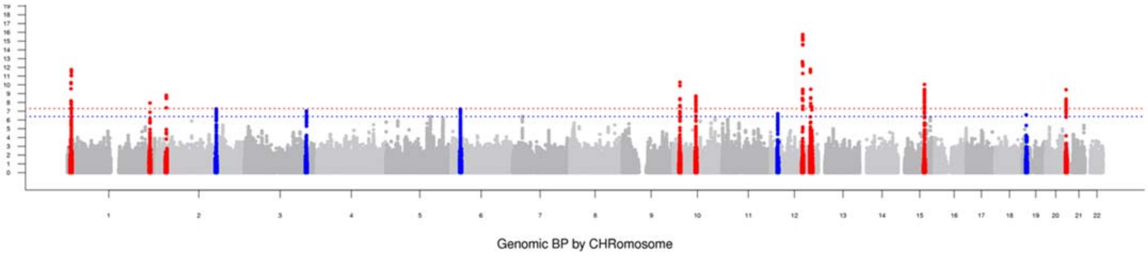


FIGURE S3. Genome-wide association studies: –log*P* values for (a) LTA-MAP and (b) LTA-PP.

Genome wide association studies' –log*P* plots are shown for LTA-MAP and LTA-PP traits. Regions with SNP associations reaching *P* value < 5 x 10^{-8} are shown in red, and regions reaching *P* value < 5x10^{-7} are shown in blue.

(a) LTA-MAP



(b) LTA-PP

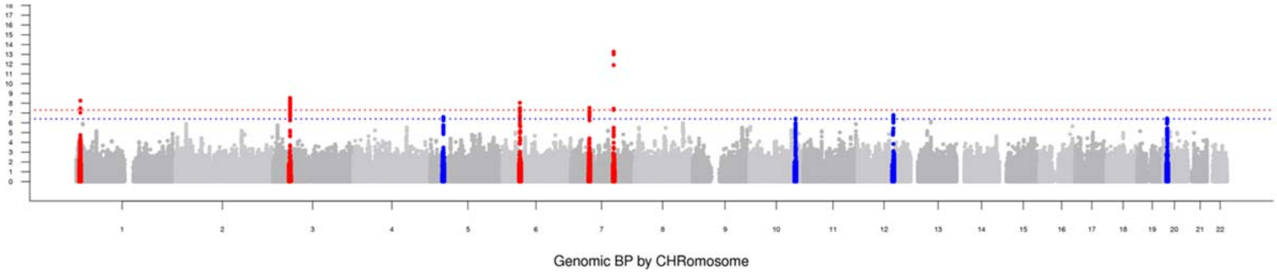


FIGURE S4. QQ plots for SBP and DBP traits showing associations statistics for both LTA and V1 traits.

Genome-wide association statistics for SBP and DBP analyses using LTA versus V1 only in quantile-quantile plots of LTA-SBP and LTA-DBP, with corresponding V1-SBP and V1-DBP results. The distribution of *P* values is shown with SNPs plotted in blue corresponding to V1 results, and SNPs plotted in green corresponding to LTA analysis results.

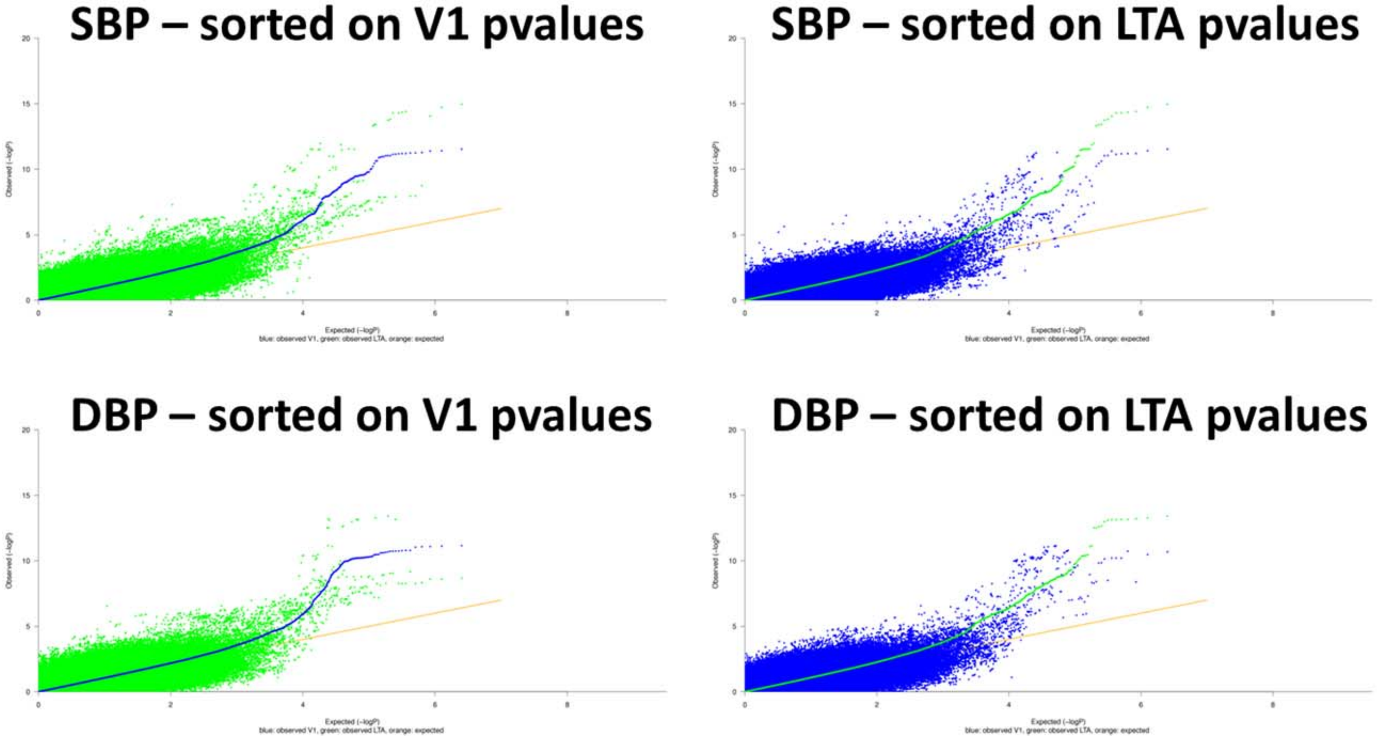


FIGURE S5. Genome-wide association statistics for SBP and DBP analyses using LTA versus V1.

Genome-wide association statistics for SBP and DBP analyses using LTA versus V1, with LTA values plotted on the X-axis and V1 on the Y-axis, for the effect size (beta, regression) estimate, standard error, chi-squared values and the normalized regression estimate (beta recalculated as the raw beta divided by the standard deviation of the phenotype).

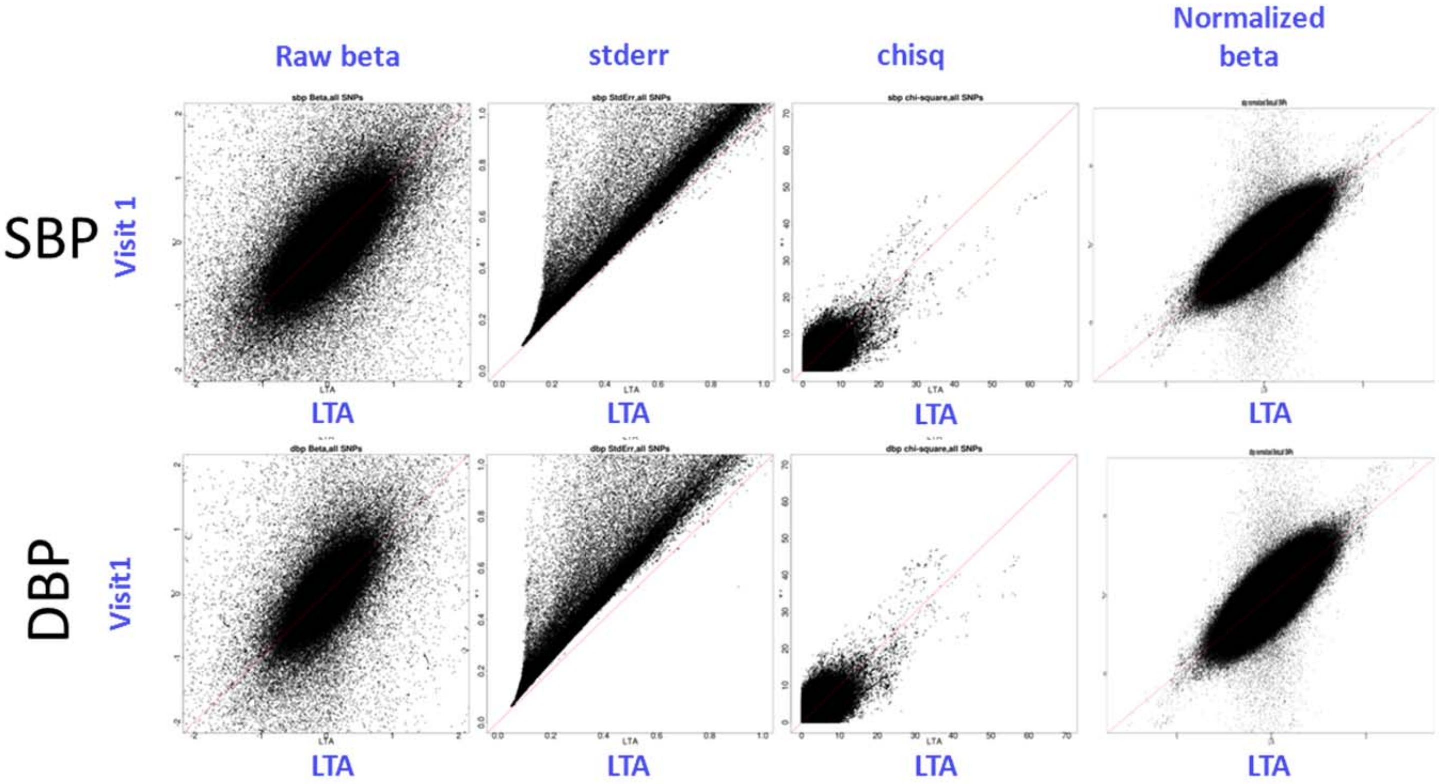
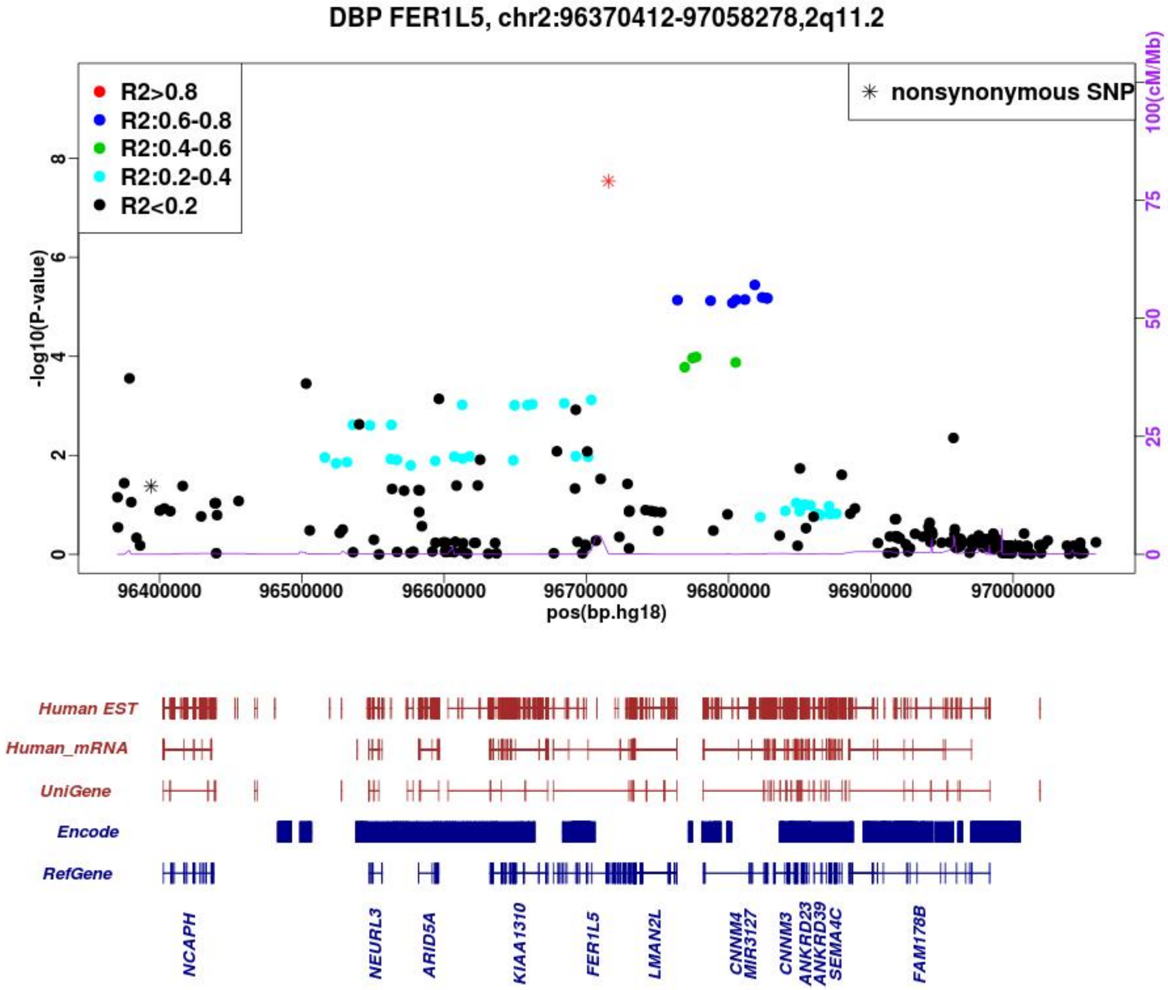
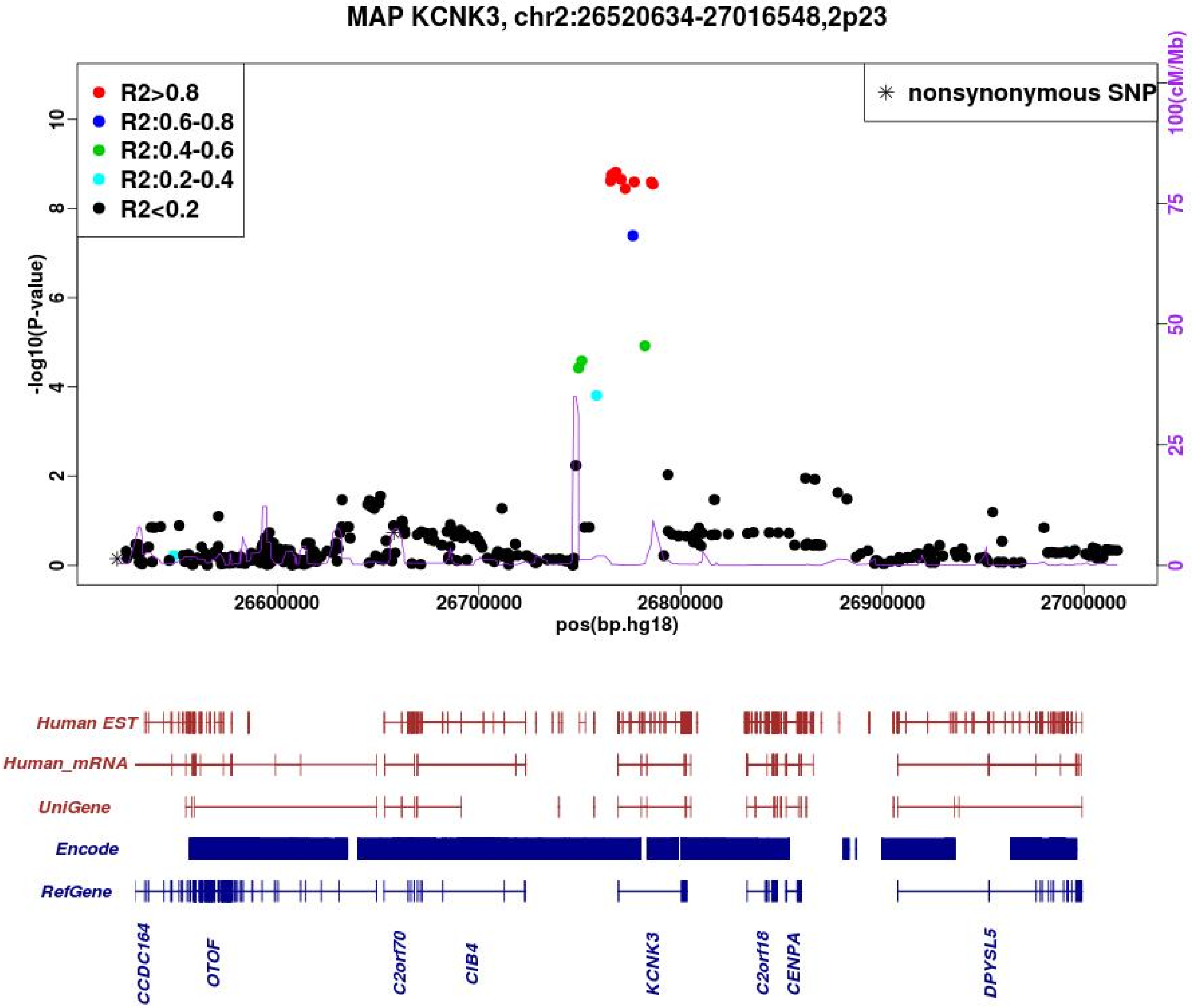


FIGURE S6. -log*P* value plots for regions identified in the LTA analysis incorporating LD estimates and annotation of nonsynonymous SNPs for each of the new 5 SNP-trait associations we identified in the LTA analysis (a-e).

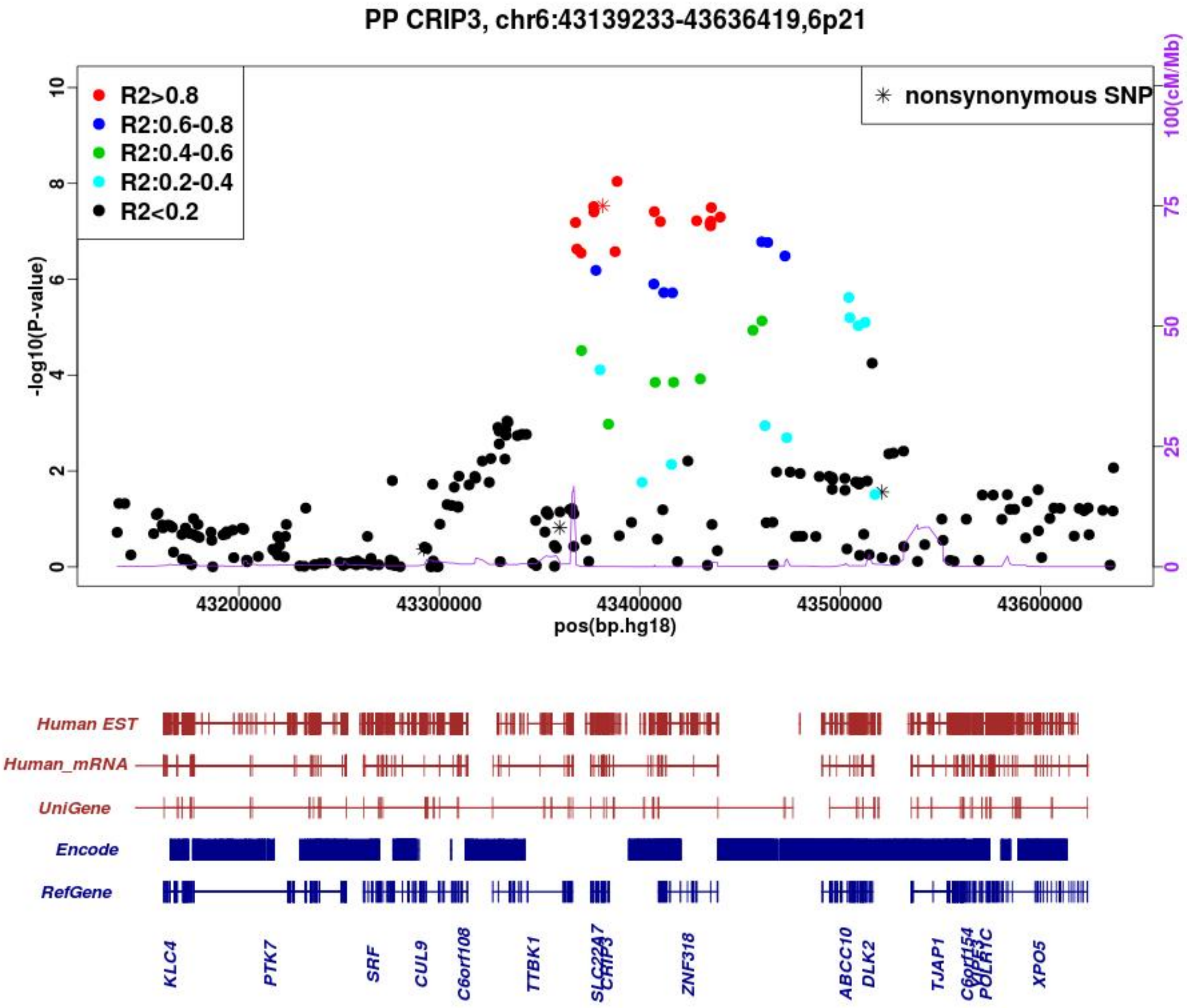
(a)



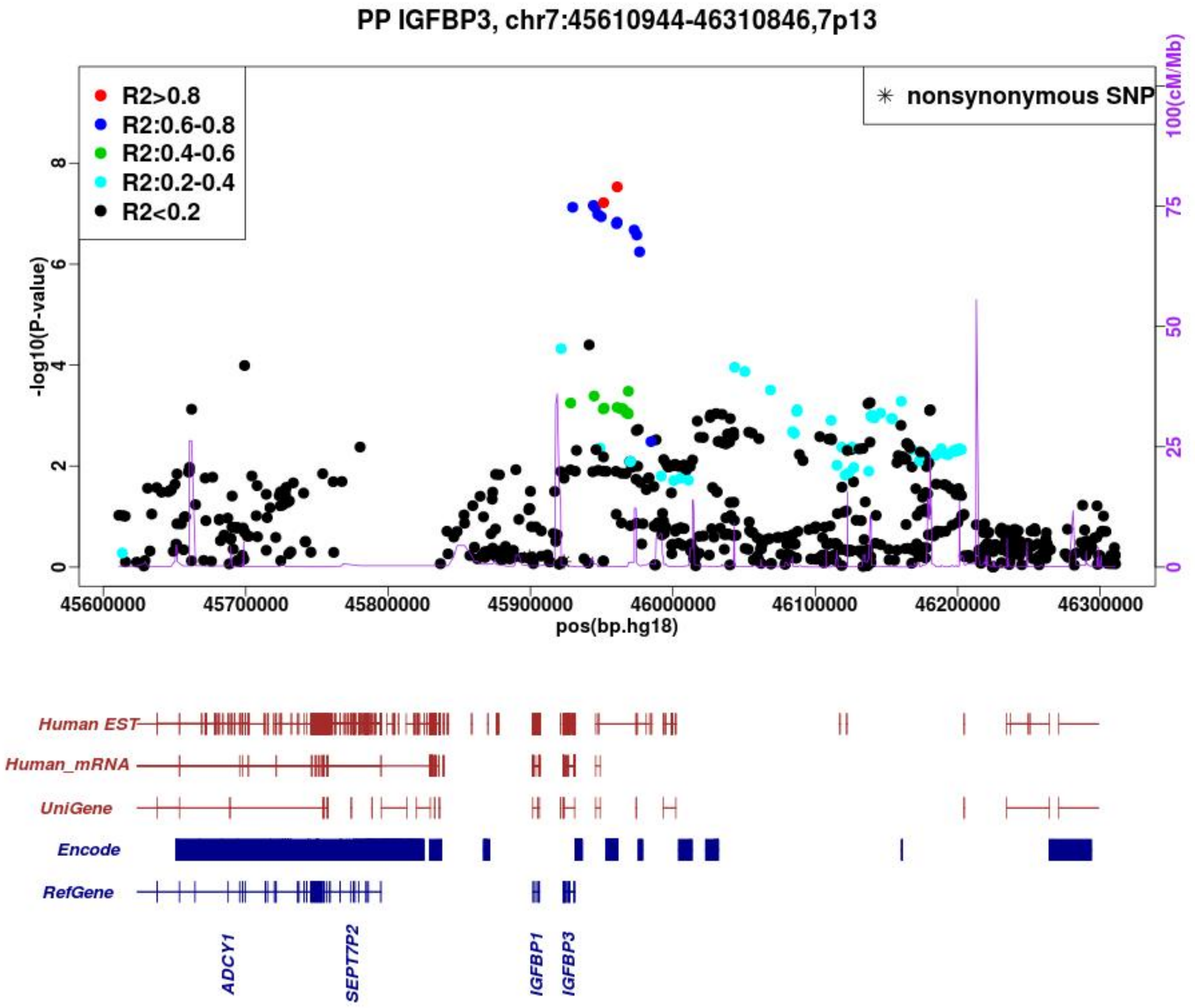
(b)


MAP KCNK3, chr2:26520634-27016548,2p23
● R2>0.8
● R2:0.6-0.8
● R2:0.4-0.6
● R2:0.2-0.4
● R2<0.2
✳ nonsynonymous SNP
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
26600000
26700000
26800000
26900000
27000000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
CCDC164
OTOF
C2orf70
CIB4
KCNK3
C2orf18
CENPA
DPYSL5

(c)


PP CRIP3, chr6:43139233-43636419,6p21
● R2>0.8
● R2:0.6-0.8
● R2:0.4-0.6
● R2:0.2-0.4
● R2<0.2
✳ nonsynonymous SNP
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
43200000
43300000
43400000
43500000
43600000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
KLC4
PTK7
SRF
CUL9
C6orf108
TTBK1
SLC22A7
CRIP3
ZNF318
ABCC10
DLK2
TJAP1
C6orf154
YIPF3
POLR1C
XPO5

(d)


PP IGFBP3, chr7:45610944-46310846,7p13
R2>0.8
R2:0.6-0.8
R2:0.4-0.6
R2:0.2-0.4
R2<0.2
✳ nonsynonymous SNP
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
45600000
45700000
45800000
45900000
46000000
46100000
46200000
46300000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
ADCY1
SEPT7P2
IGFBP1
IGFBP3

(e)

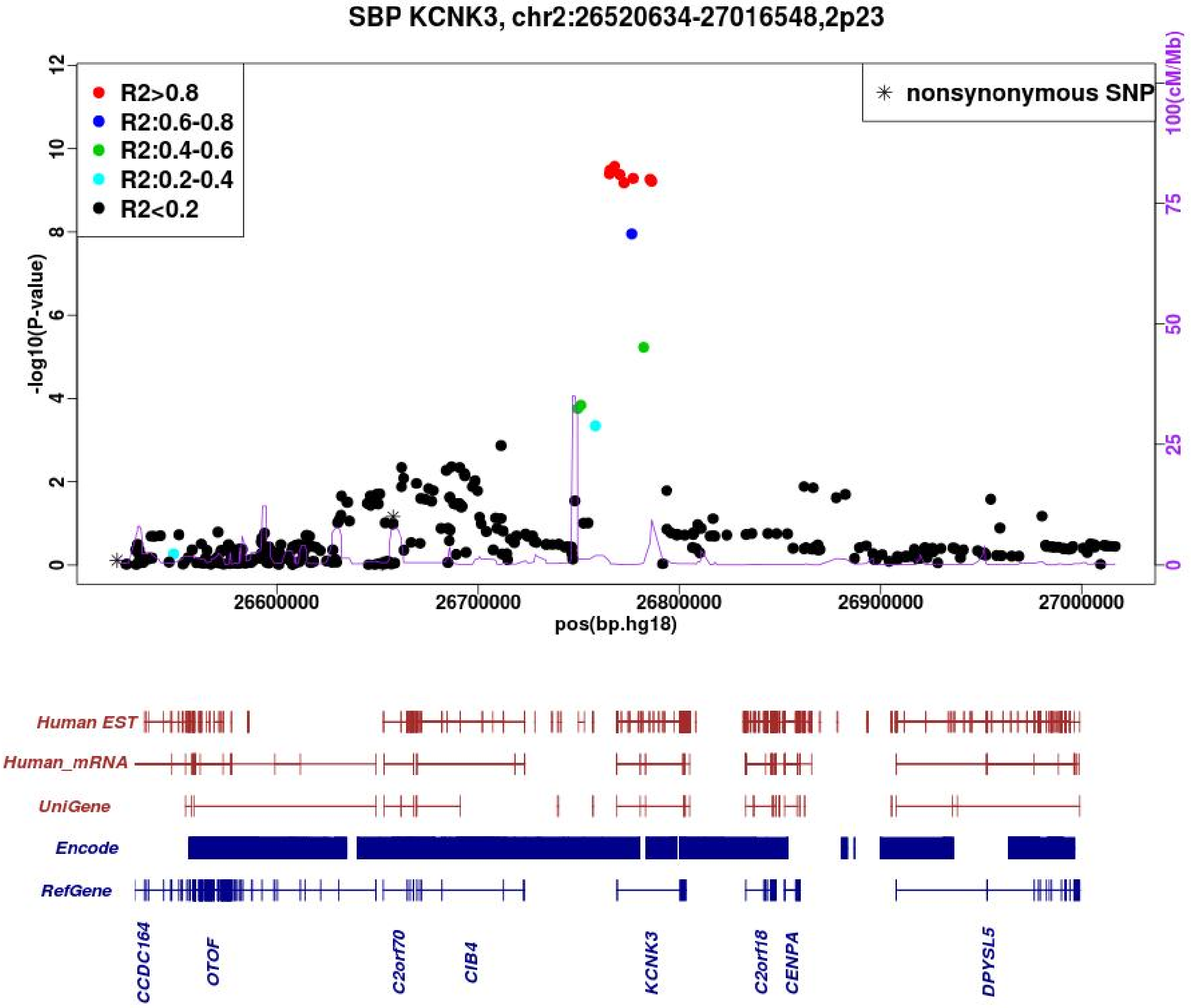
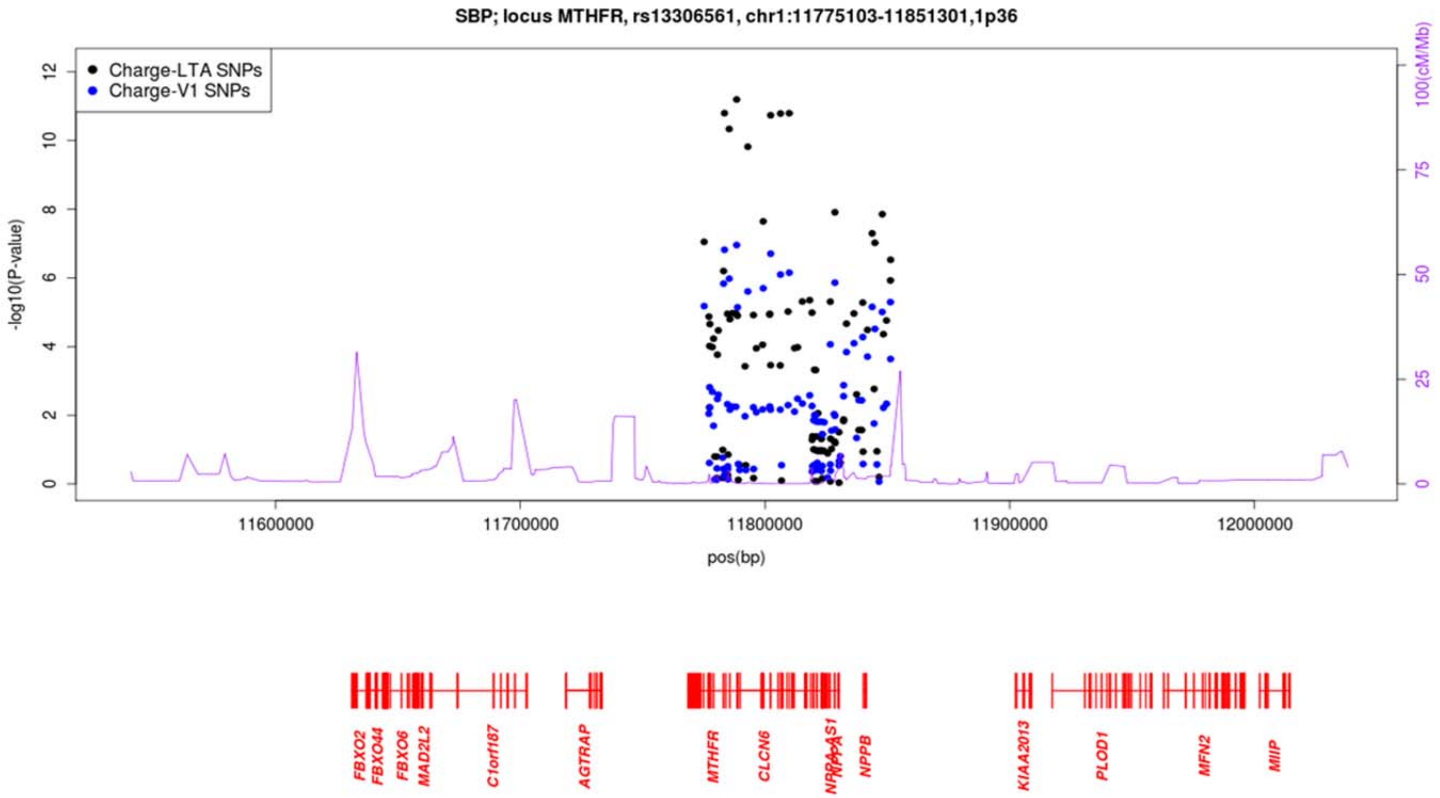

SBP KCNK3, chr2:26520634-27016548,2p23
R2>0.8
R2:0.6-0.8
R2:0.4-0.6
R2:0.2-0.4
R2<0.2
✳ nonsynonymous SNP
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
26600000
26700000
26800000
26900000
27000000
pos(bp.hg18)
Human EST
Human_mRNA
UniGene
Encode
RefGene
CCDC164
OTOF
C2orf70
CIB4
KCNK3
C2orf18
CENPA
DPYSL5

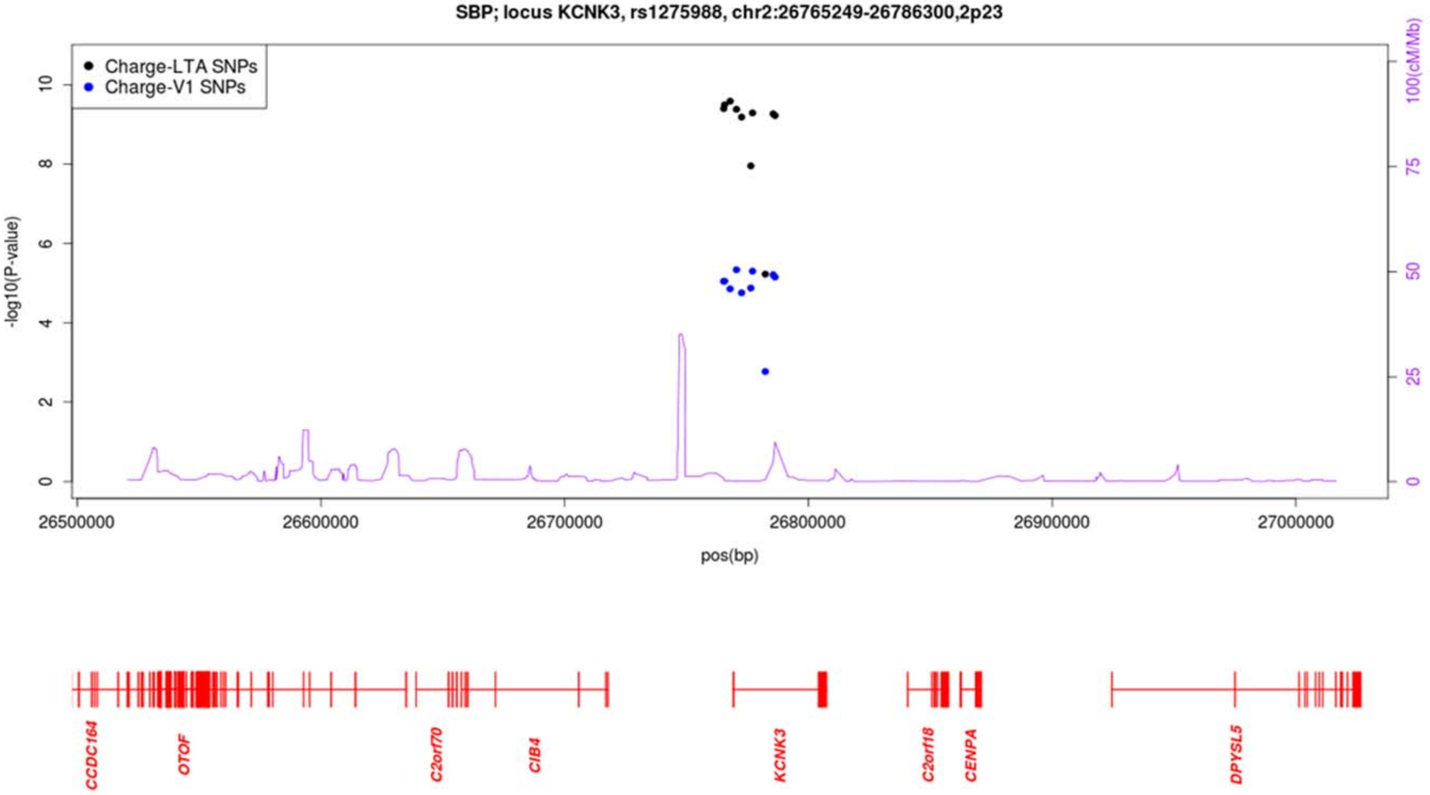
FIGURE S7. -log*P* value plots for regions identified in the LTA analysis.

–log*P* values of association tests are shown for all regions identified in the LTA analyses for (a) regions with enrichment in the LTA analysis compared to the corresponding V1 analyses (rank test *P* value < 0.001), (b) regions with enrichment in the V1 analysis compared to the corresponding LTA analyses (rank test *P* value < 0.001), (c) one region with enrichment of some SNP by LTA and other SNPs by V1 (*P* Value < 0.001) and (d) regions without enrichment by either LTA or V1 within the locus. The results of the LTA-SBP analysis are plotted in black and the results of the corresponding V1-SBP analysis of the same individuals are plotted in blue.

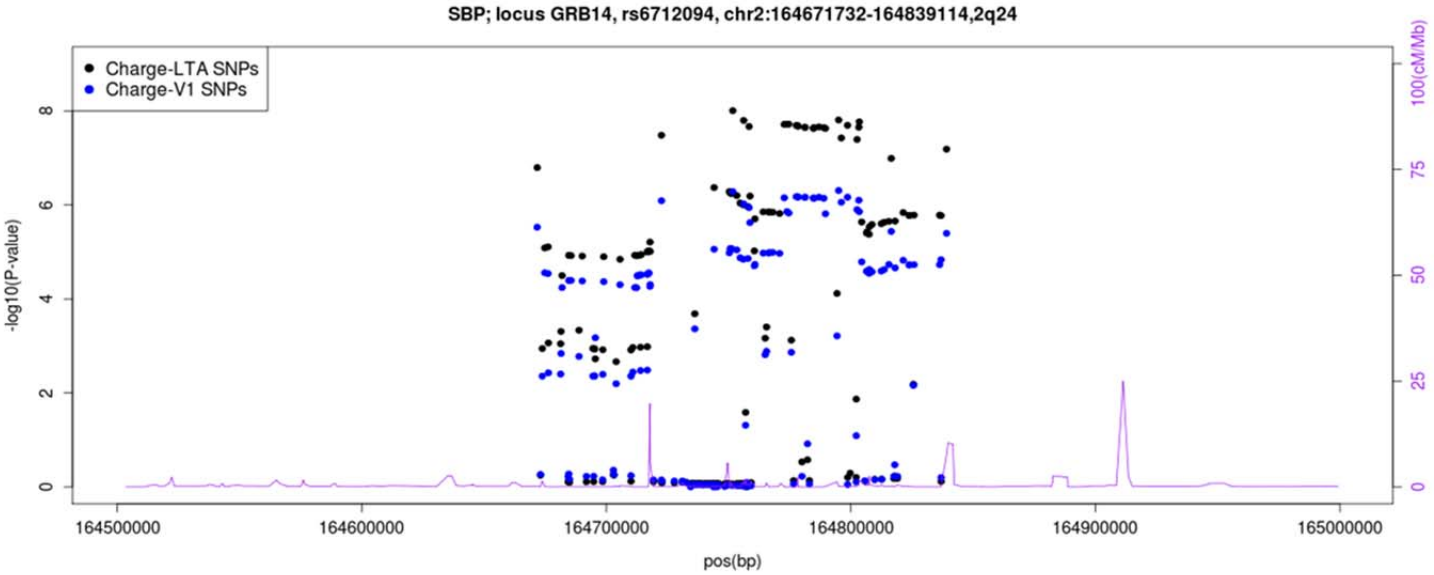
(a1)


SBP; locus MTHFR, rs13306561, chr1:11775103-11851301,1p36
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
11600000
11700000
11800000
11900000
12000000
pos(bp)
FBXO2
FBXO44
FBXO6
MAD2L2
C1orf187
AGTRAP
MTHFR
CLCN6
NPPA-AS1
NPPA
NPPB
KIAA2013
PLOD1
MFN2
MIIP

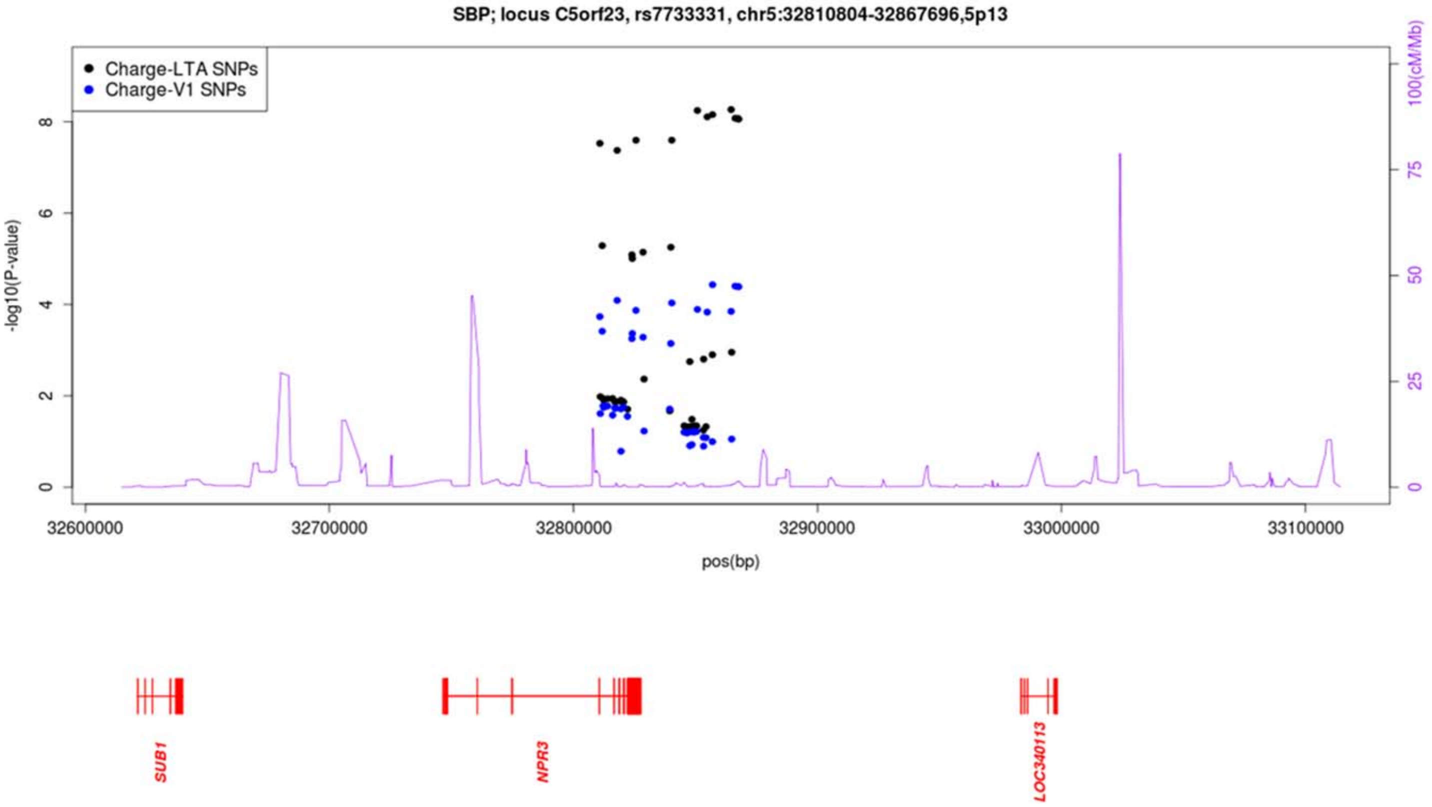
(a2)


SBP; locus KCNK3, rs1275988, chr2:26765249-26786300,2p23
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
26500000
26600000
26700000
26800000
26900000
27000000
pos(bp)
CCDC164
OTOF
C2orf70
CIB4
KCNK3
C2orf18
CENPA
DPYSL5

(a3)

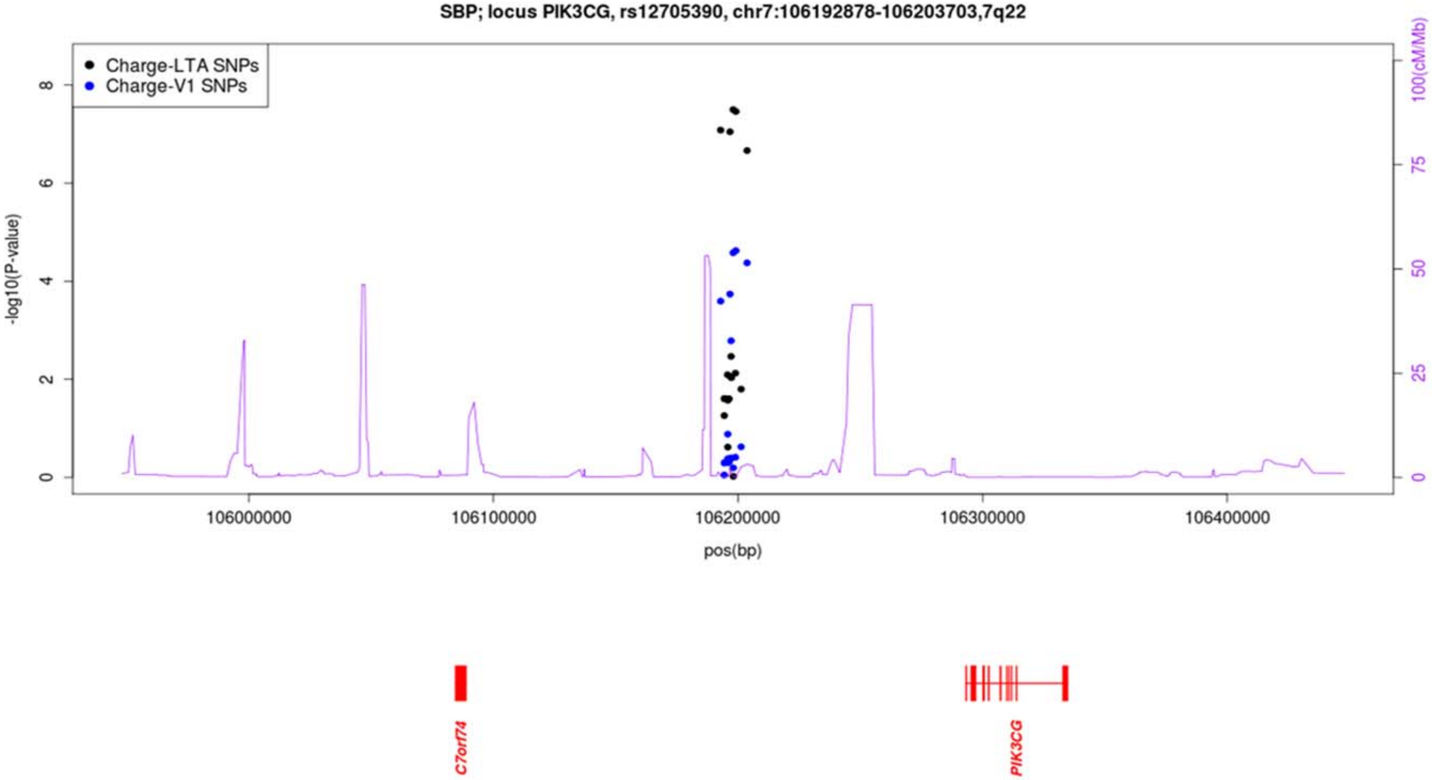

SBP; locus GRB14, rs6712094, chr2:164671732-164839114,2q24
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
164500000
164600000
164700000
164800000
164900000
165000000
pos(bp)

(a4)

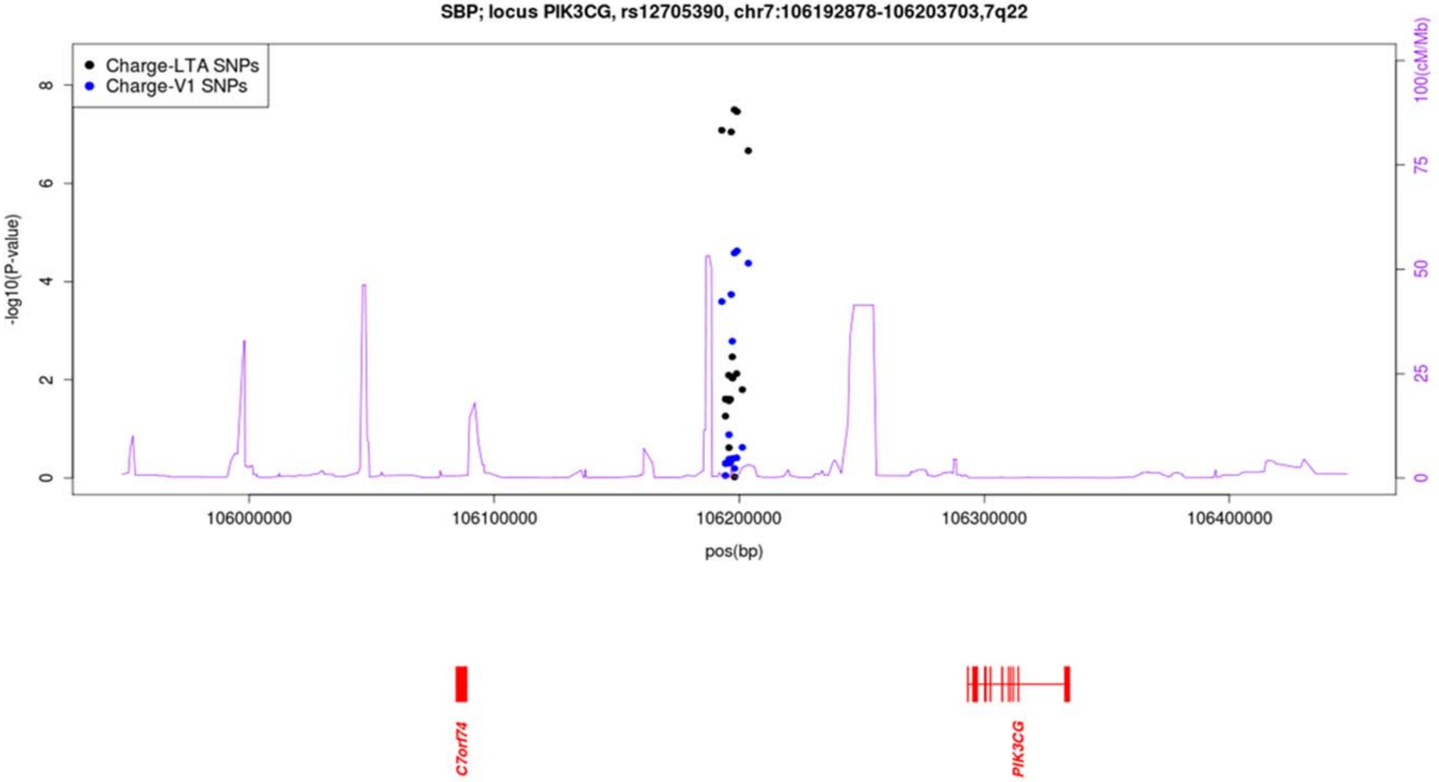


SBP; locus C5orf23, rs7733331, chr5:32810804-32867696,5p13

(a5)

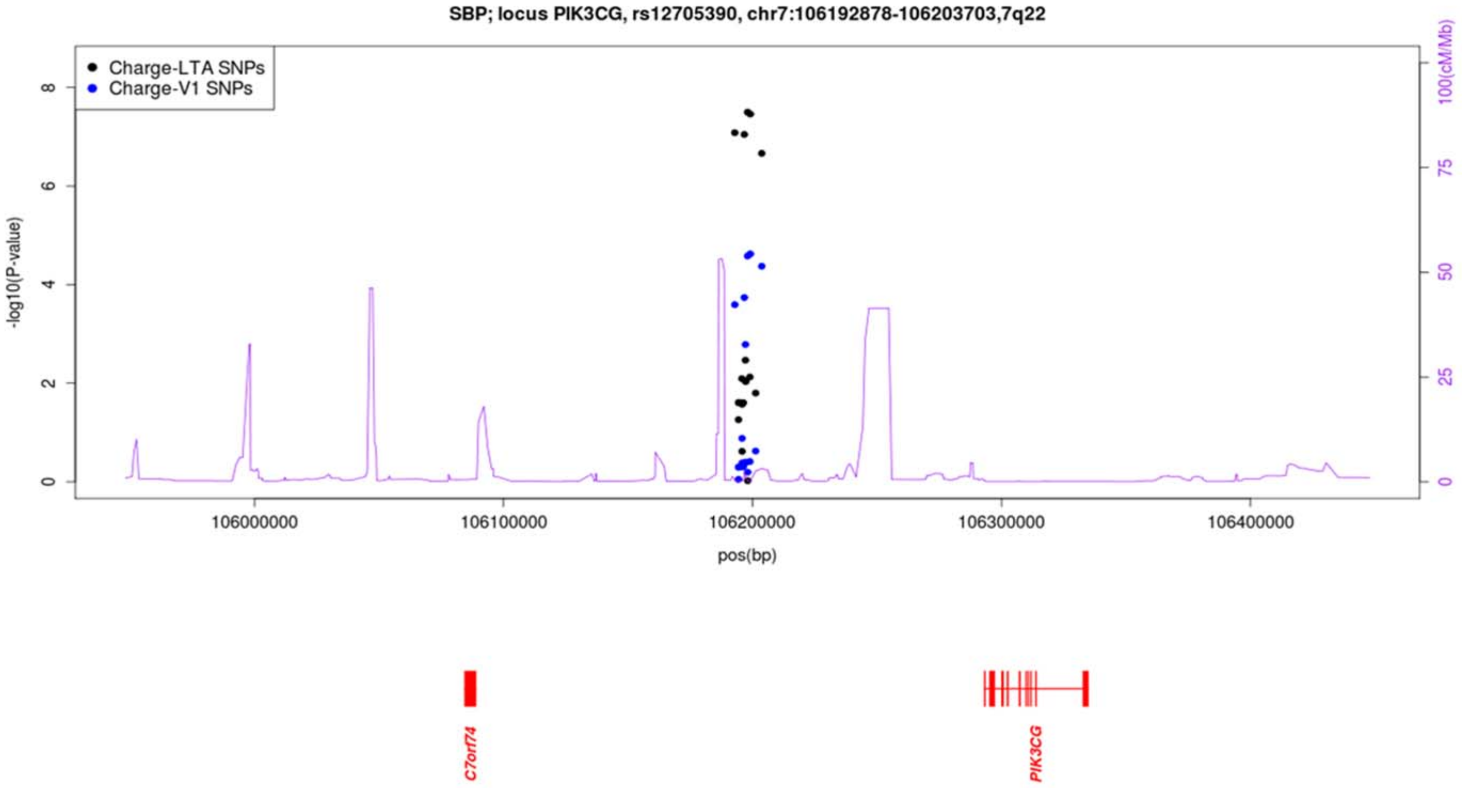

SBP; locus PIK3CG, rs12705390, chr7:106192878-106203703,7q22
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
106000000
106100000
106200000
106300000
106400000
pos(bp)
C7orf74
PIK3CG

(a6)

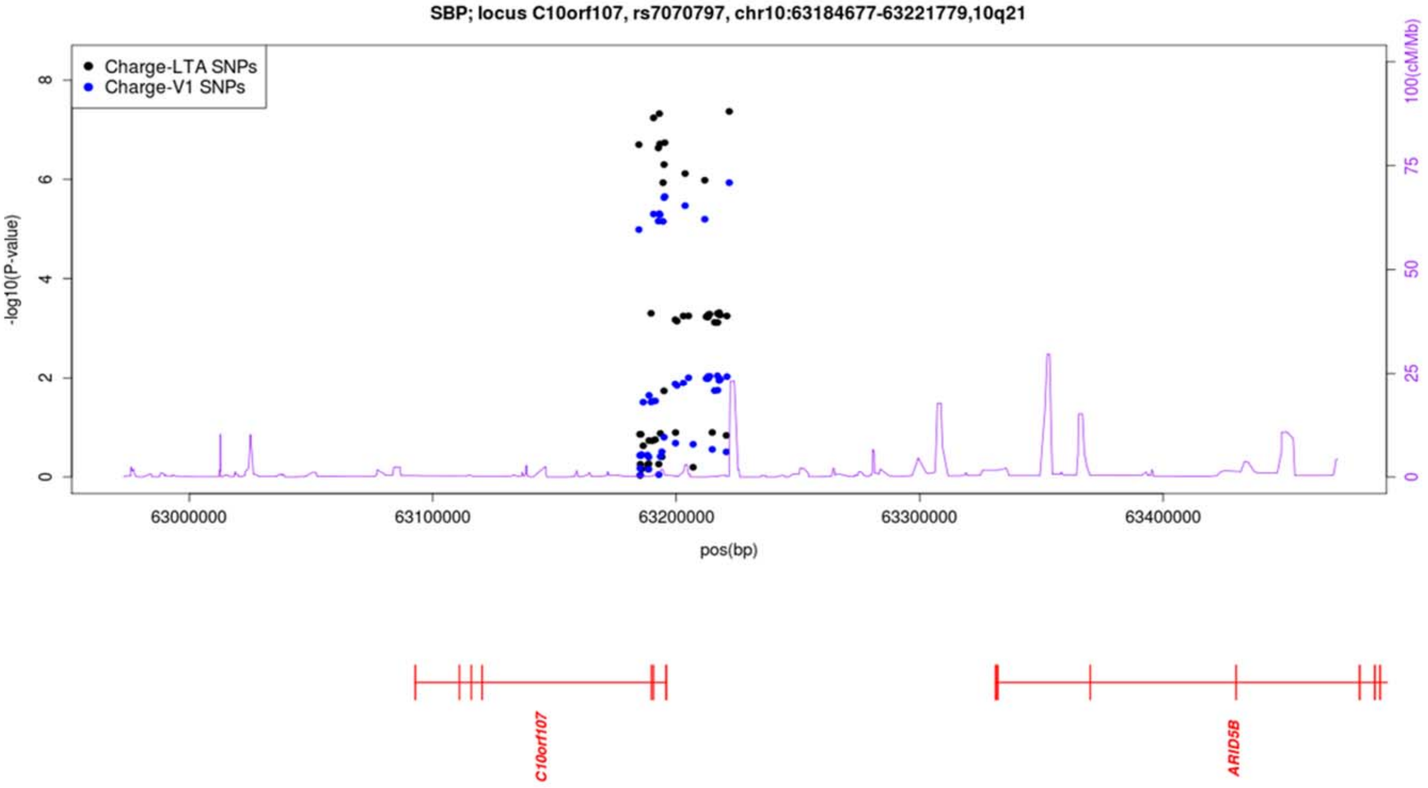


SBP; locus PIK3CG, rs12705390, chr7:106192878-106203703,7q22
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
106000000
106100000
106200000
106300000
106400000
pos(bp)
C7orf74
PIK3CG

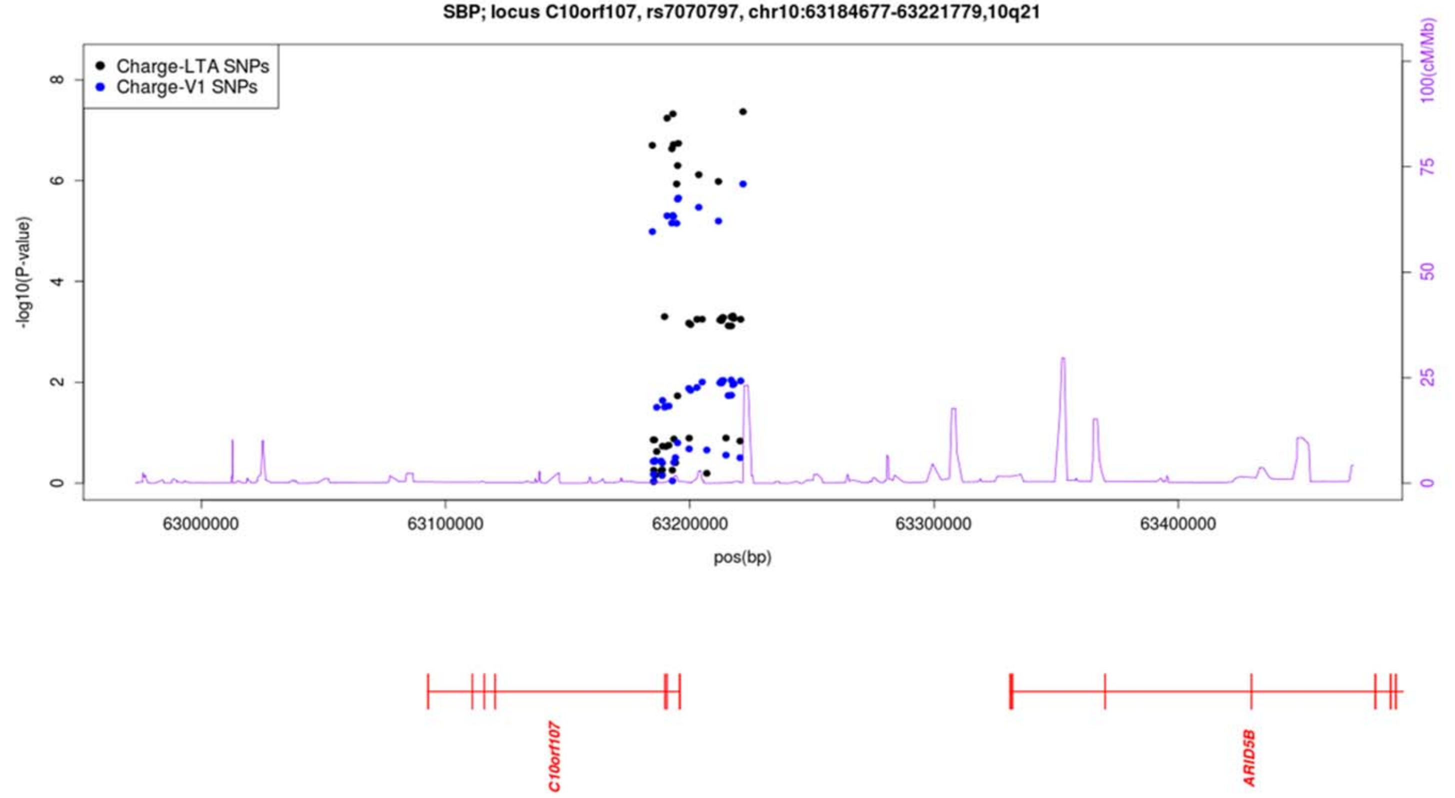
(a7)


SBP; locus PIK3CG, rs12705390, chr7:106192878-106203703,7q22
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
106000000
106100000
106200000
106300000
106400000
pos(bp)
C7orf74
PIK3CG

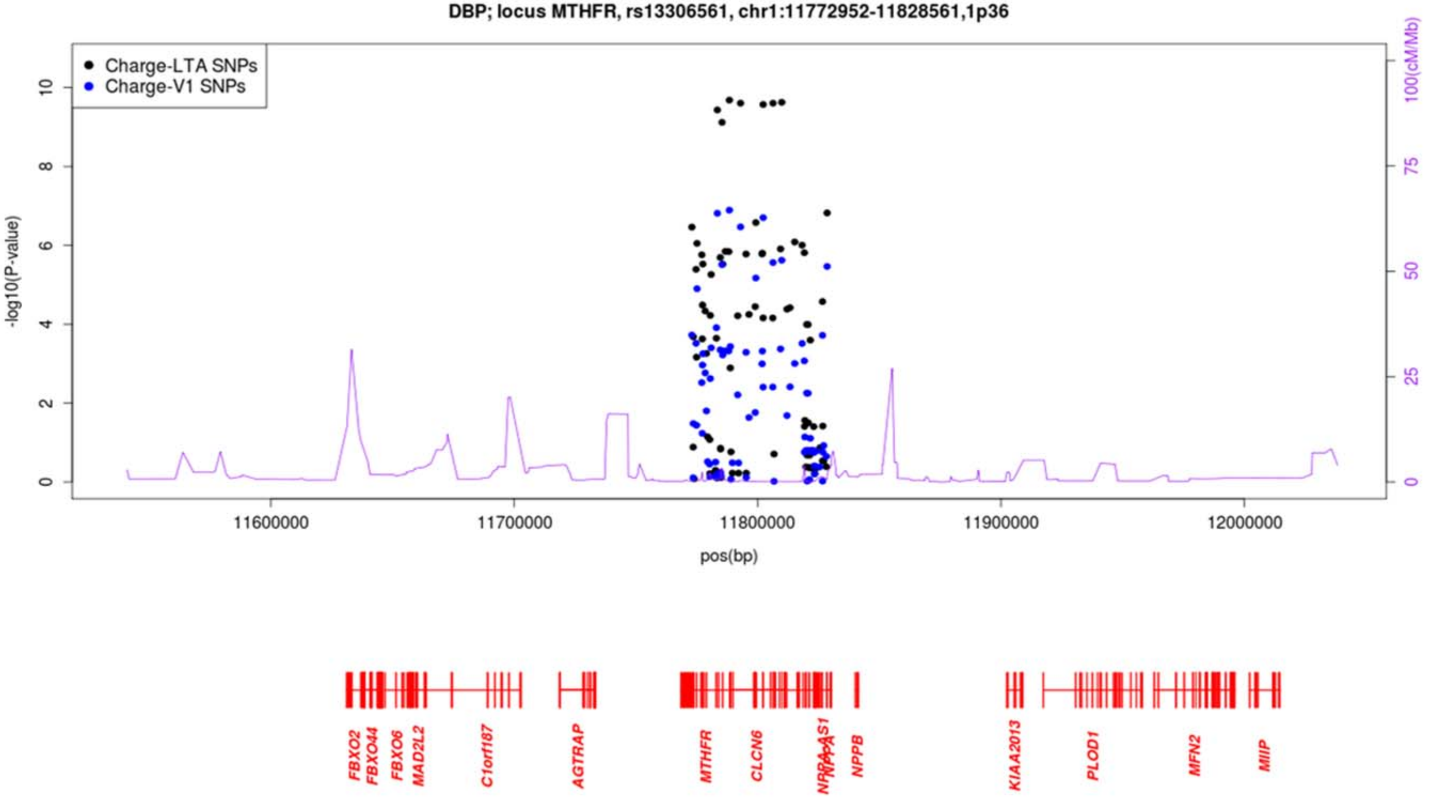
(a8)


SBP; locus C10orf107, rs7070797, chr10:63184677-63221779,10q21
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
63000000
63100000
63200000
63300000
63400000
pos(bp)
C10orf107
ARID5B

(a9)

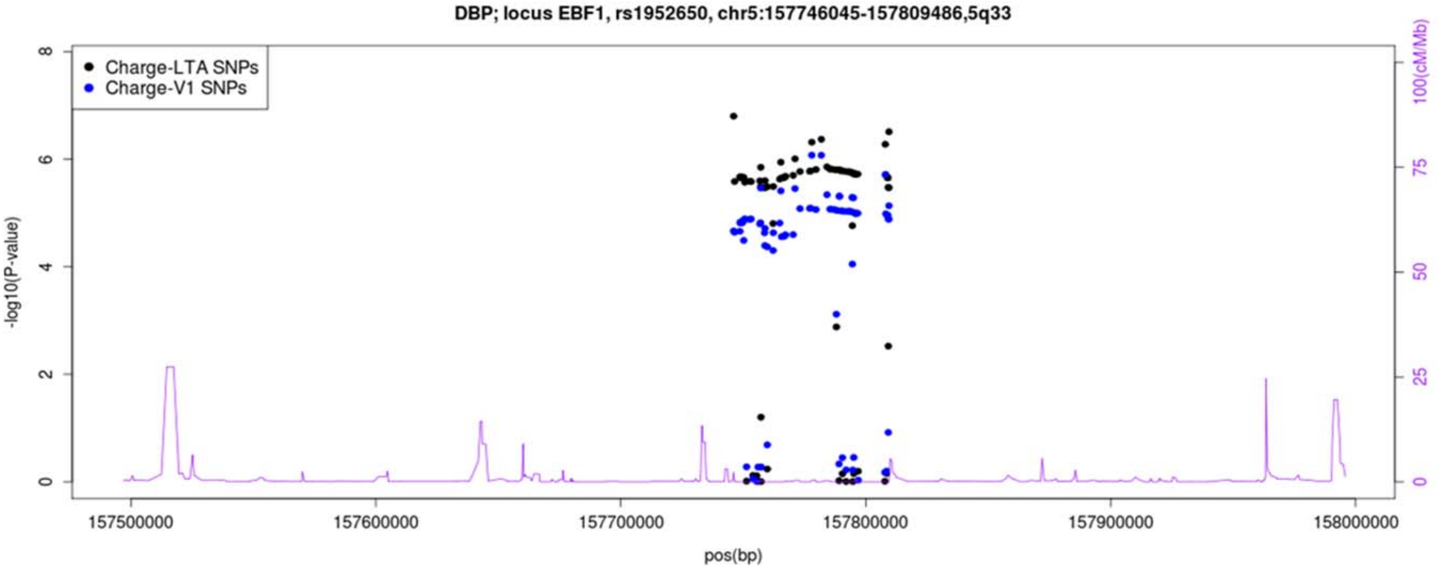

SBP; locus C10orf107, rs7070797, chr10:63184677-63221779,10q21
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
63000000
63100000
63200000
63300000
63400000
pos(bp)
C10orf107
ARID5B

(a10)

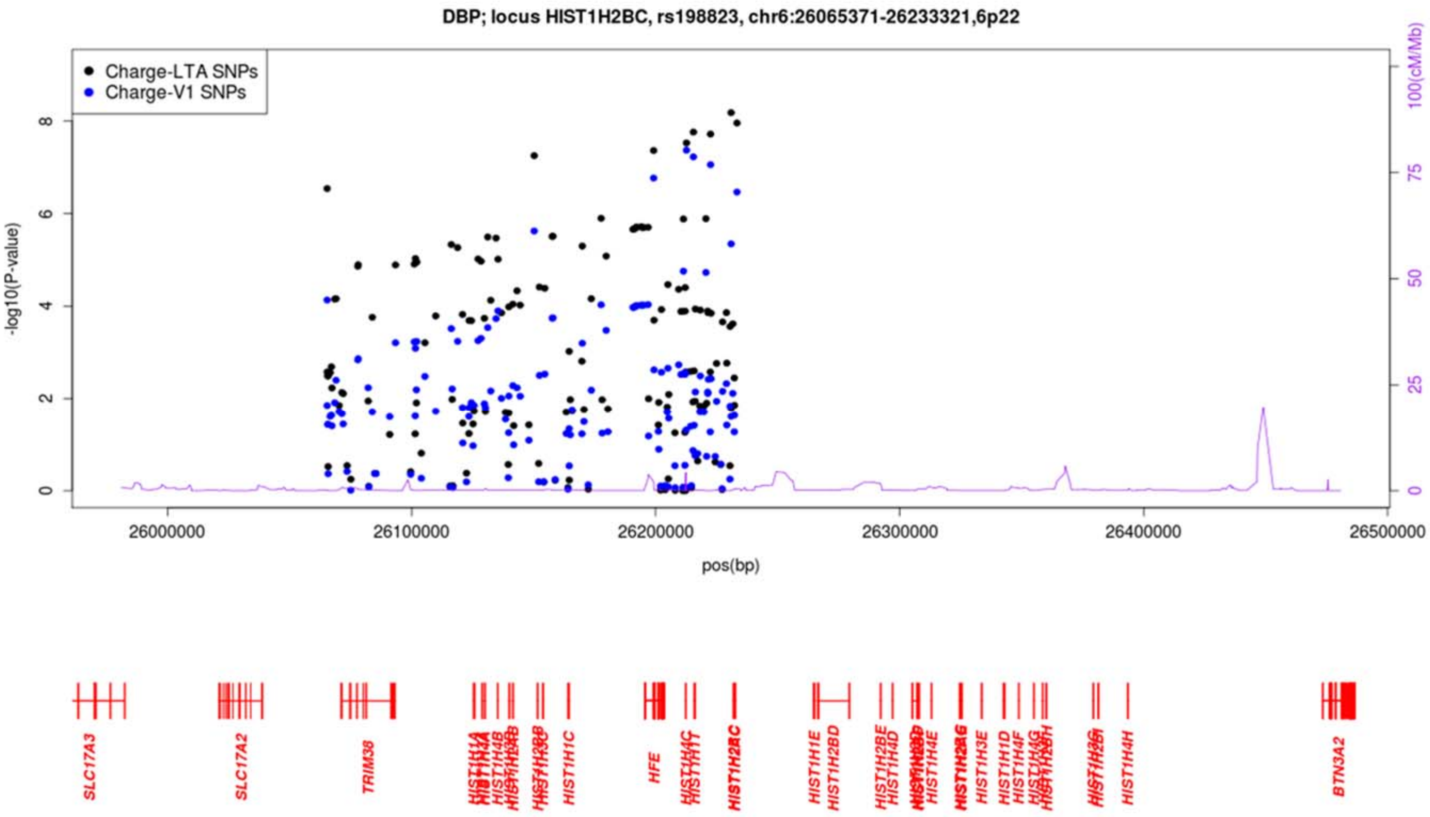


DBP; locus MTHFR, rs13306561, chr1:11772952-11828561,1p36

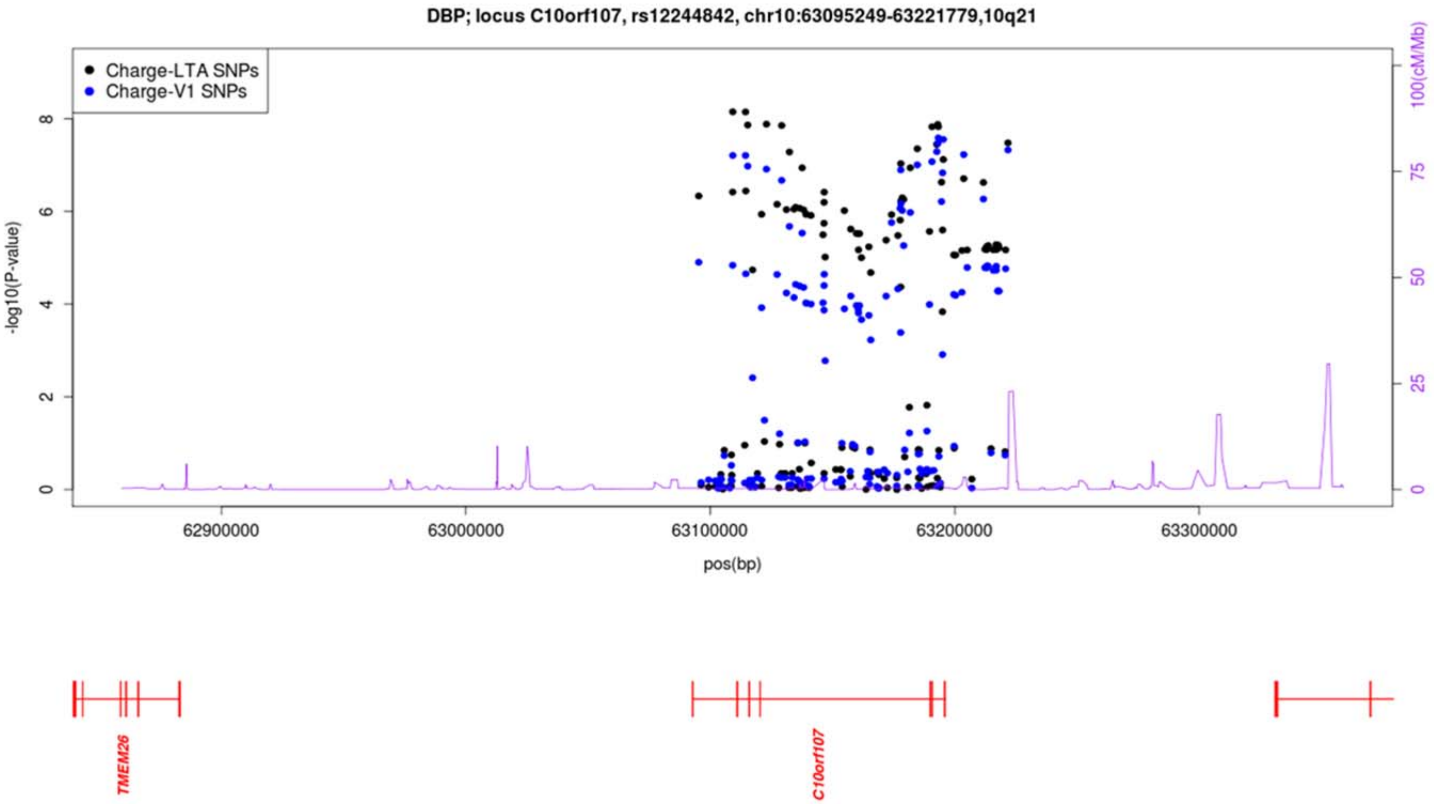
(a11)


DBP; locus EBF1, rs1952650, chr5:157746045-157809486,5q33
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
157500000
157600000
157700000
157800000
157900000
158000000
pos(bp)

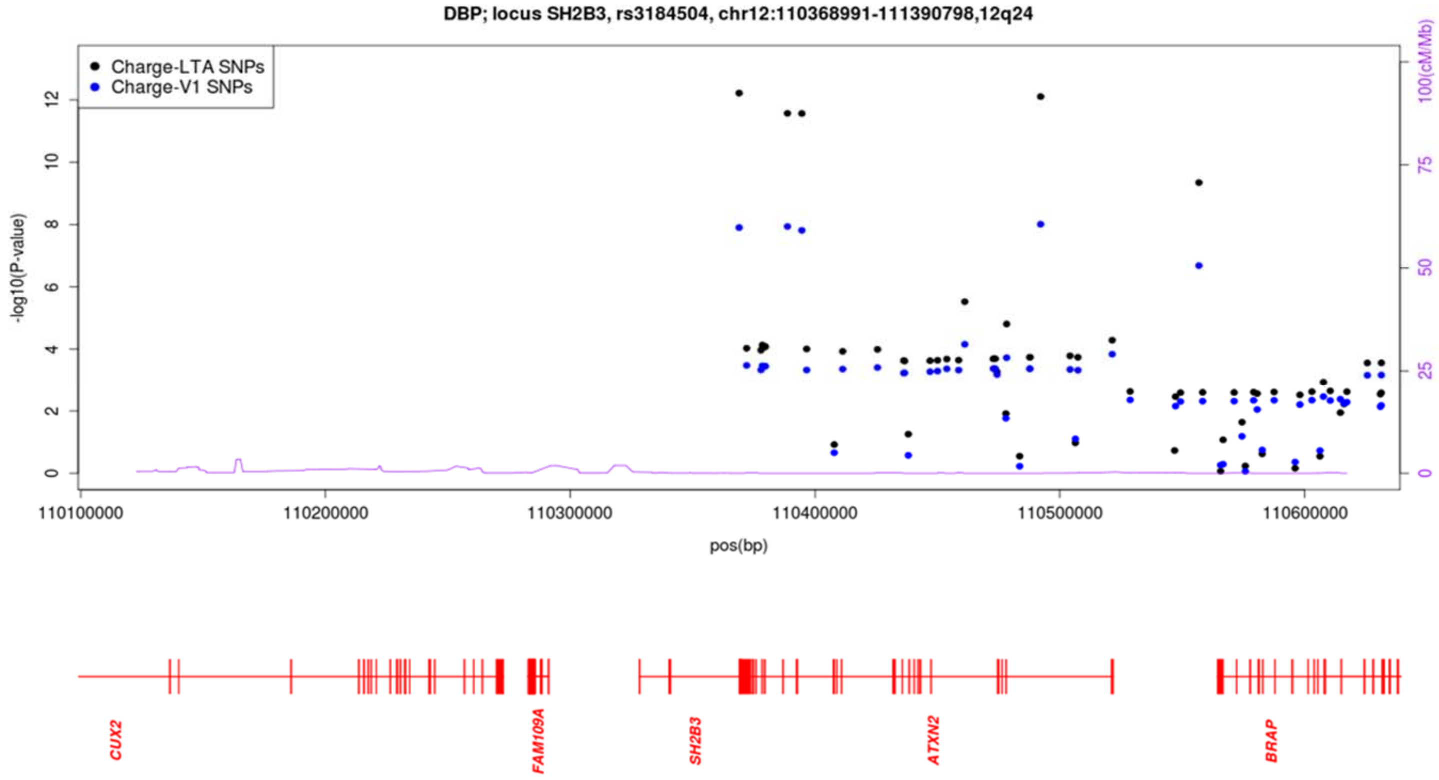
(a12)


DBP; locus HIST1H2BC, rs198823, chr6:26065371-26233321,6p22
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
26000000
26100000
26200000
26300000
26400000
26500000
pos(bp)
SLC17A3
SLC17A2
TRIM38
HIST1H1A
HIST1H4B
HIST1H1C
HFE
HIST1H4C
HIST1H1T
HIST1H2AC
HIST1H1E
HIST1H2BD
HIST1H2BE
HIST1H4D
HIST1H4E
HIST1H2AG
HIST1H3E
HIST1H1D
HIST1H4F
HIST1H4G
HIST1H4H
BTN3A2

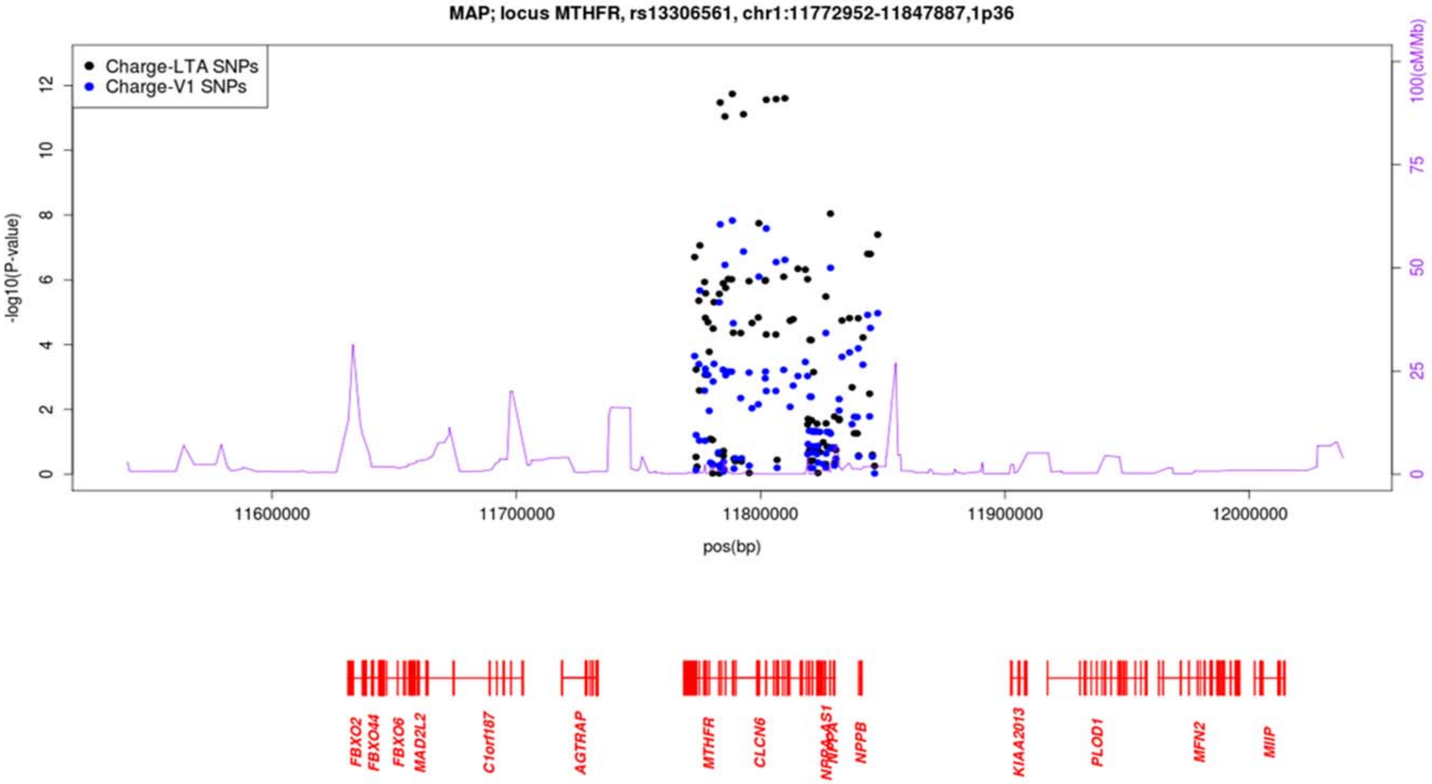
(a13)


DBP; locus C10orf107, rs12244842, chr10:63095249-63221779,10q21
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
62900000
63000000
63100000
63200000
63300000
pos(bp)
TMEM26
C10orf107

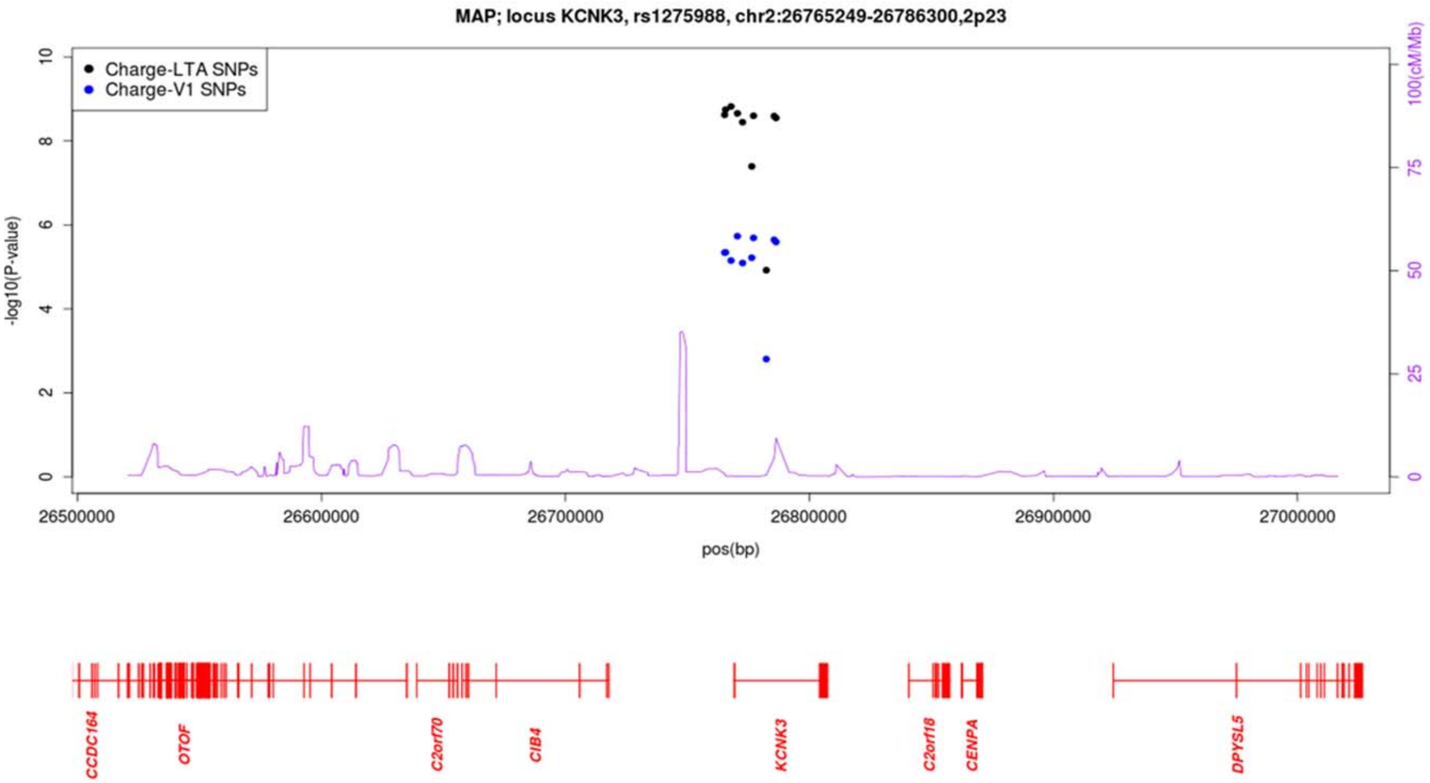
(a14)


DBP; locus SH2B3, rs3184504, chr12:110368991-111390798,12q24
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
110100000
110200000
110300000
110400000
110500000
110600000
pos(bp)
CUX2
FAM109A
SH2B3
ATXN2
BRAP

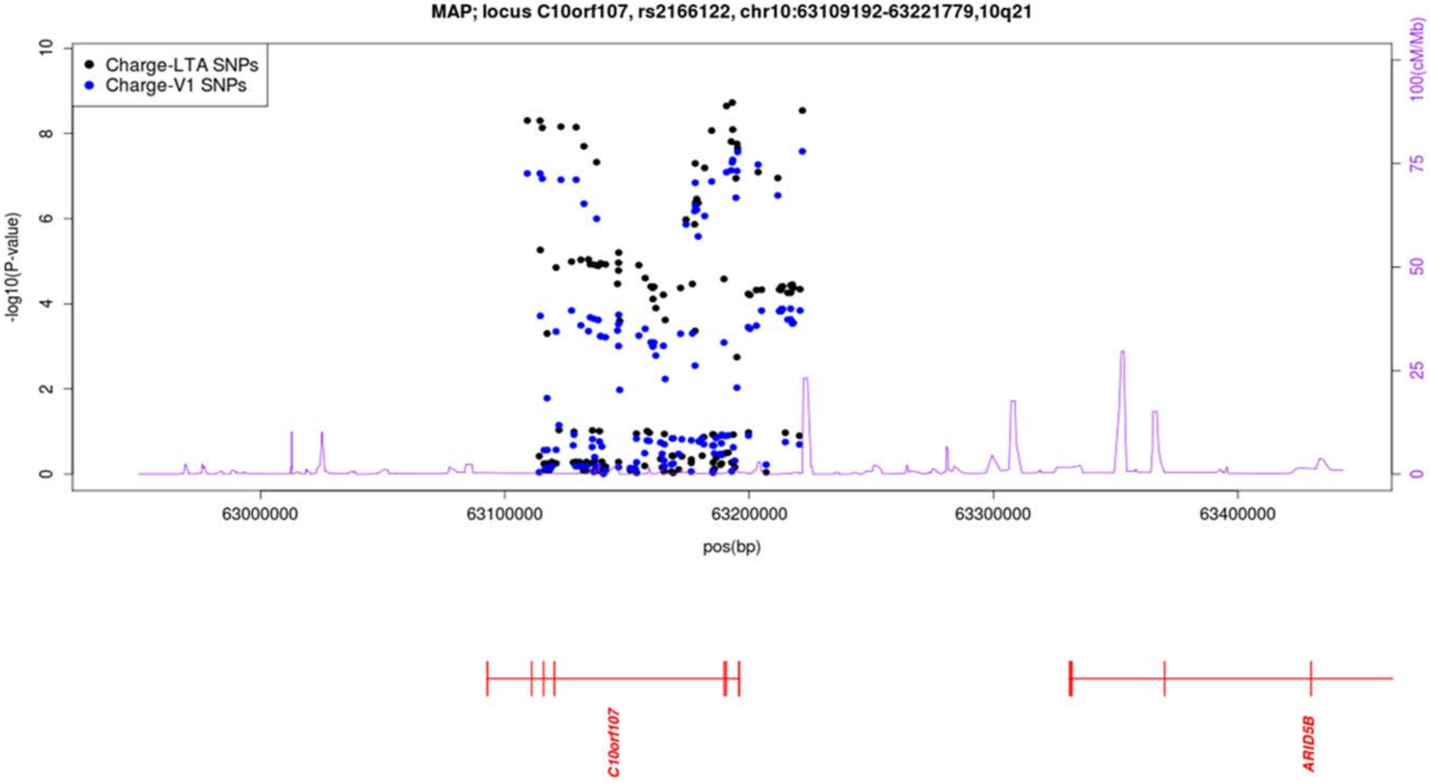
(a15)


MAP; locus MTHFR, rs13306561, chr1:11772952-11847887,1p36
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
11600000
11700000
11800000
11900000
12000000
pos(bp)
FBXO2
FBXO44
FBXO6
MAD2L2
C1orf187
AGTRAP
MTHFR
CLCN6
NPPA-AS1
NPPA
NPPB
KIAA2013
PLOD1
MFN2
MIIP

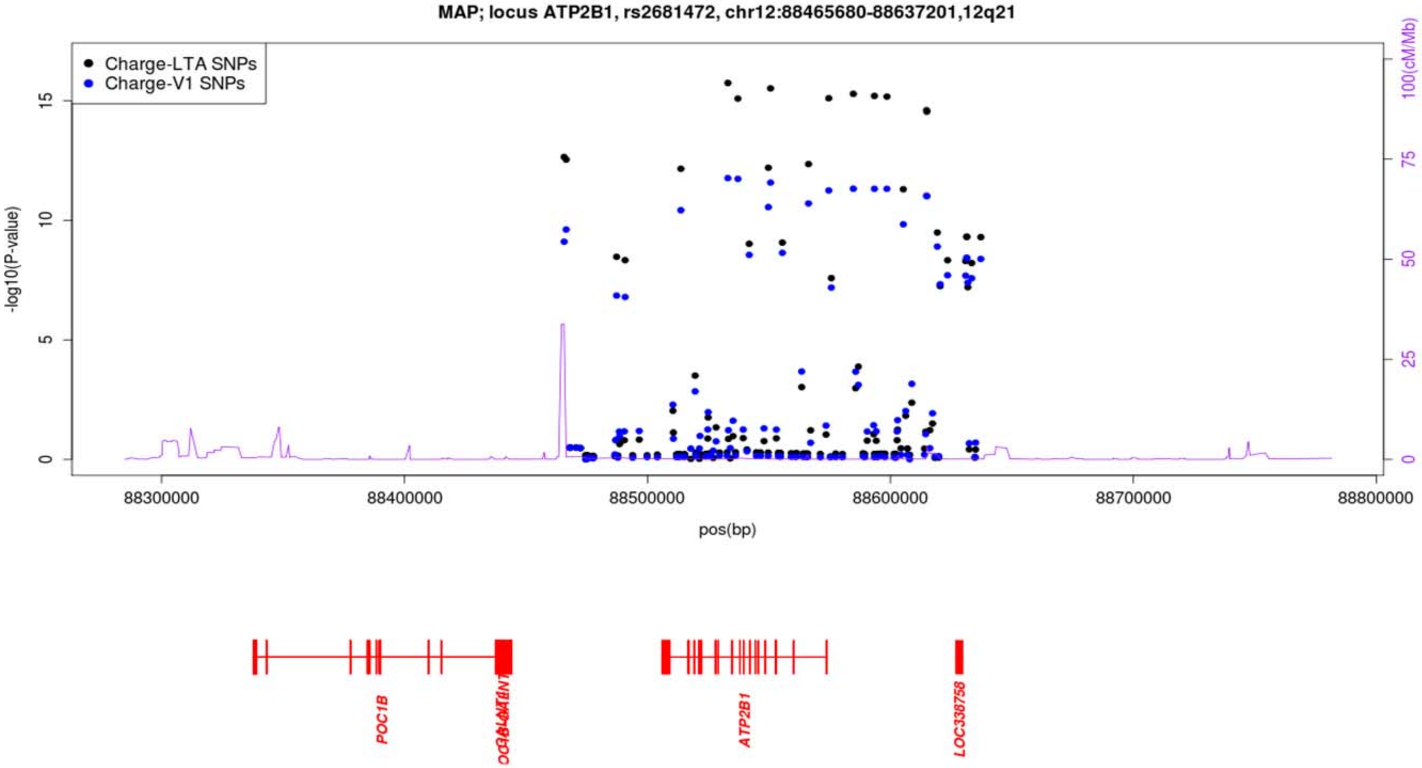
(a16)


MAP; locus KCNK3, rs1275988, chr2:26765249-26786300,2p23
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
26500000
26600000
26700000
26800000
26900000
27000000
pos(bp)
CCDC164
OTOF
C2orf70
CIB4
KCNK3
C2orf18
CENPA
DPYSL5

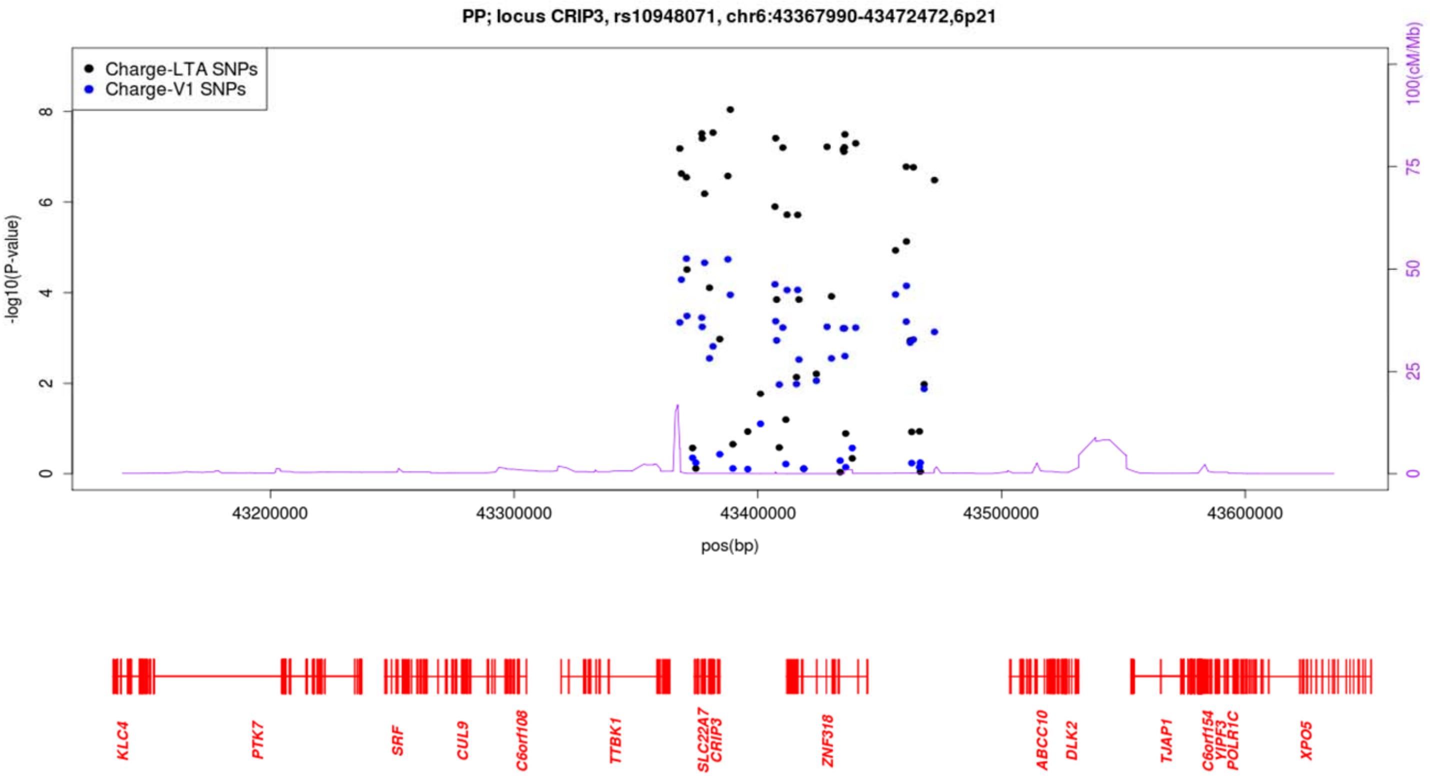
(a17)


MAP; locus C10orf107, rs2166122, chr10:63109192-63221779,10q21
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
63000000
63100000
63200000
63300000
63400000
pos(bp)
C10orf107
ARID5B

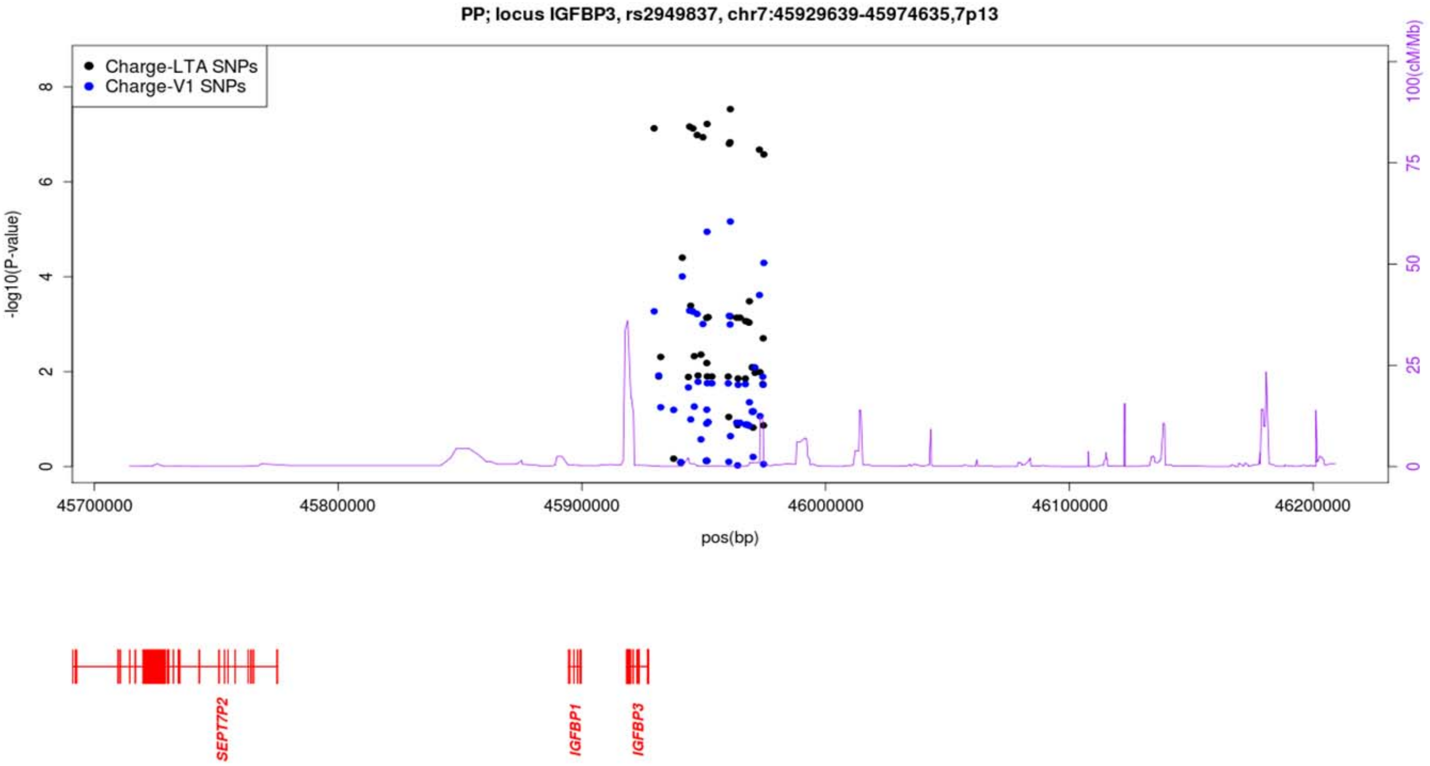
(a18)


MAP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
5
10
15
100(cM/Mb)
0
25
50
75
100
88300000
88400000
88500000
88600000
88700000
88800000
pos(bp)
POC1B
ATP2B1
LOC338758

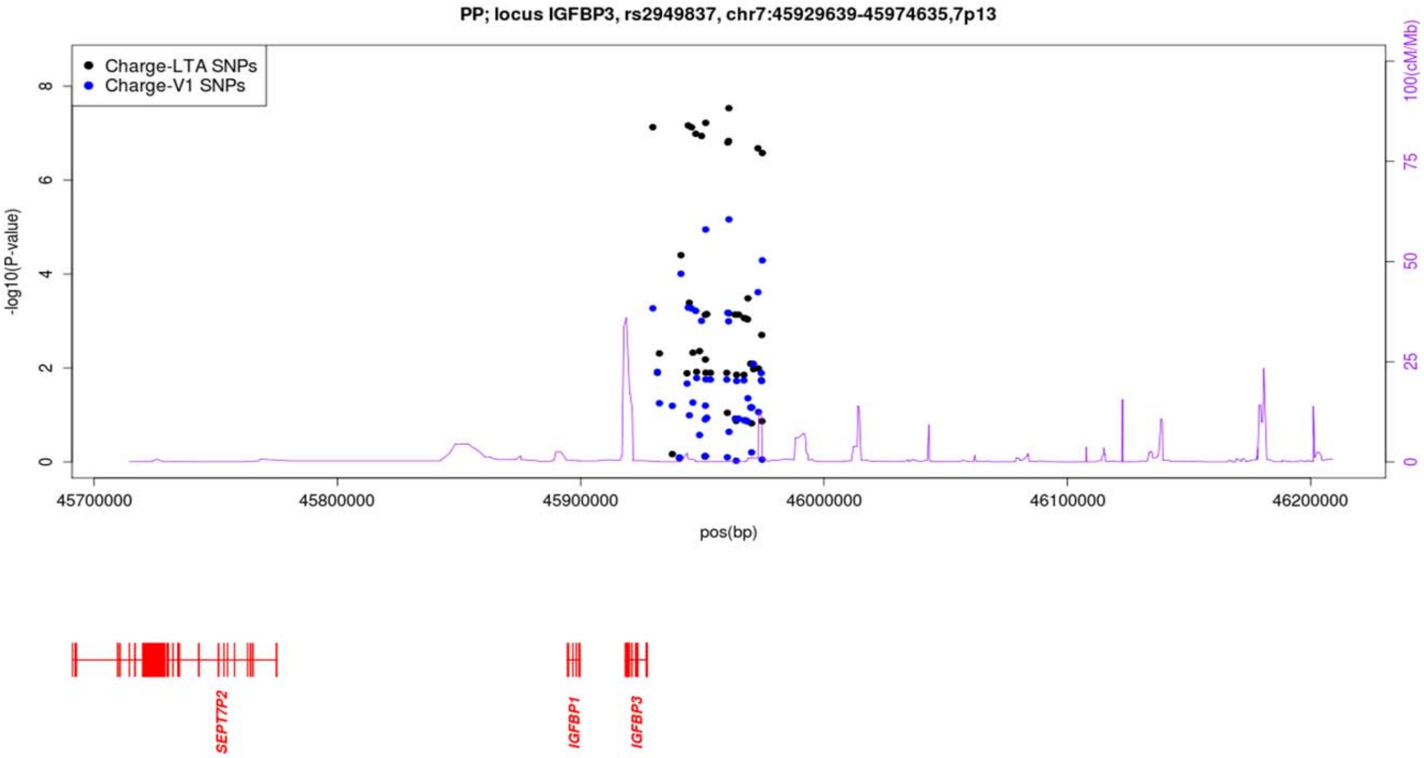
(a19)


PP; locus CRIP3, rs10948071, chr6:43367990-43472472,6p21
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
43200000
43300000
43400000
43500000
43600000
pos(bp)
KLC4
PTK7
SRF
CUL9
C6orf108
TTBK1
SLC22A7
CRIP3
ZNF318
ABCC10
DLK2
TJAP1
C6orf154
YIPF3
POLR1C
XPO5

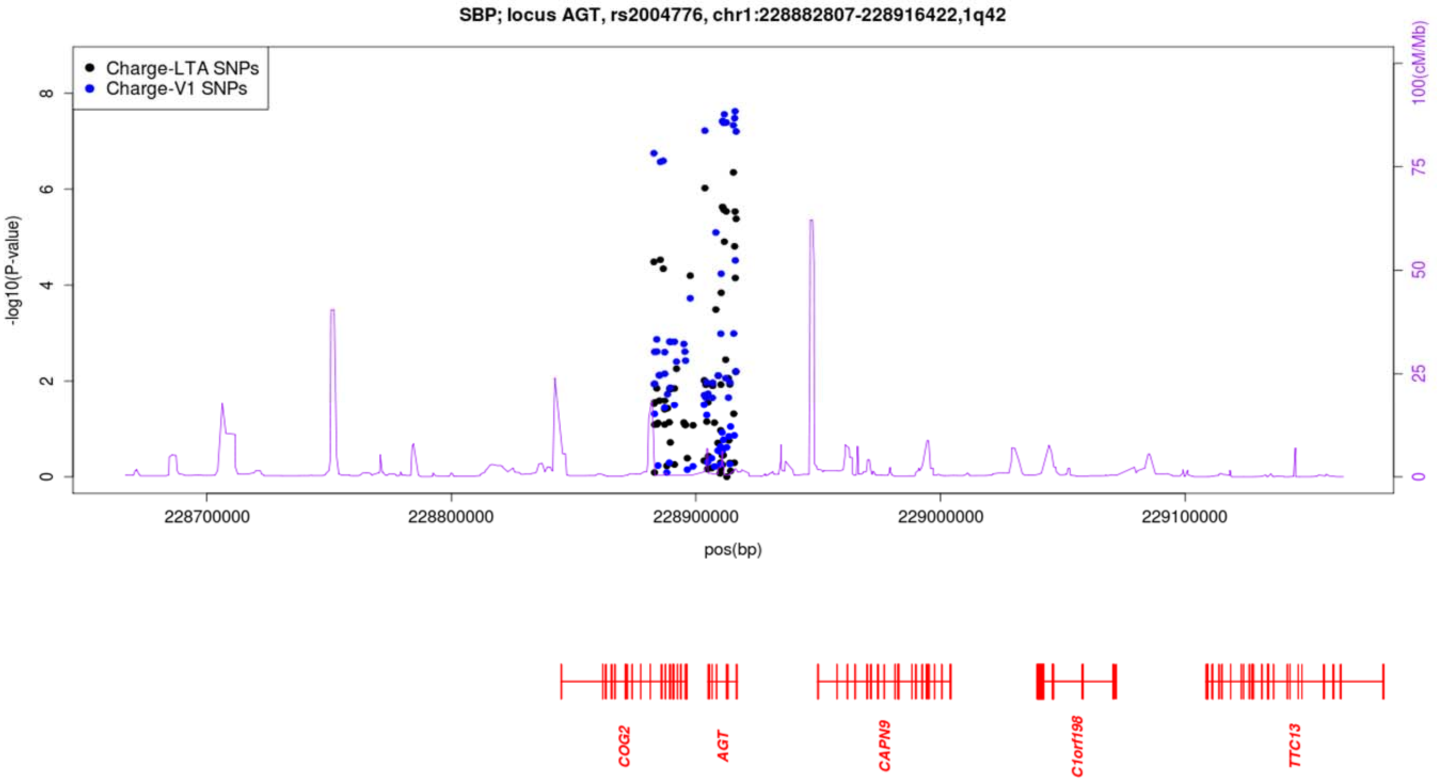
(a20)


PP; locus IGFBP3, rs2949837, chr7:45929639-45974635,7p13
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
45700000
45800000
45900000
46000000
46100000
46200000
pos(bp)
SEPT7P2
IGFBP1
IGFBP3

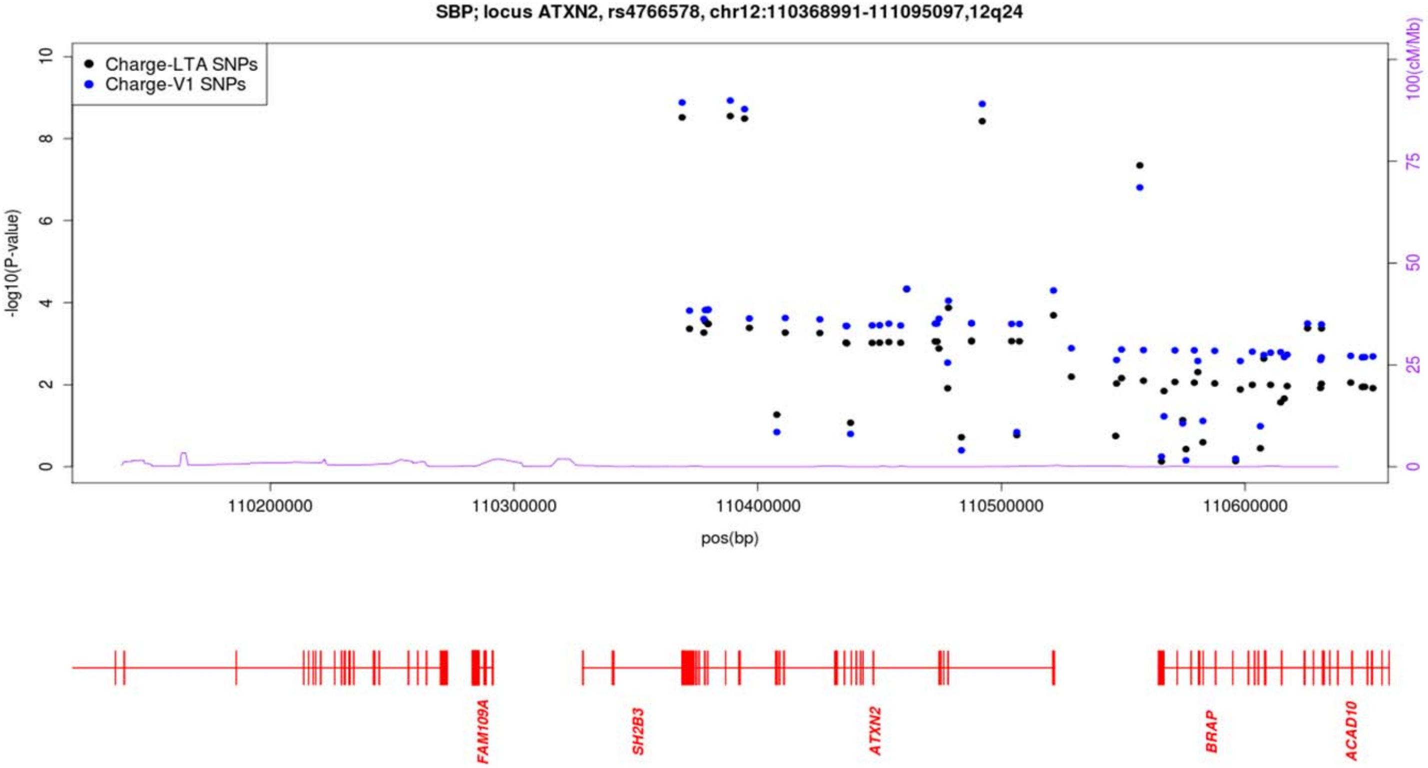
(a21)


PP; locus IGFBP3, rs2949837, chr7:45929639-45974635,7p13
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
45700000
45800000
45900000
46000000
46100000
46200000
pos(bp)
SEPT7P2
IGFBP1
IGFBP3

(b1)

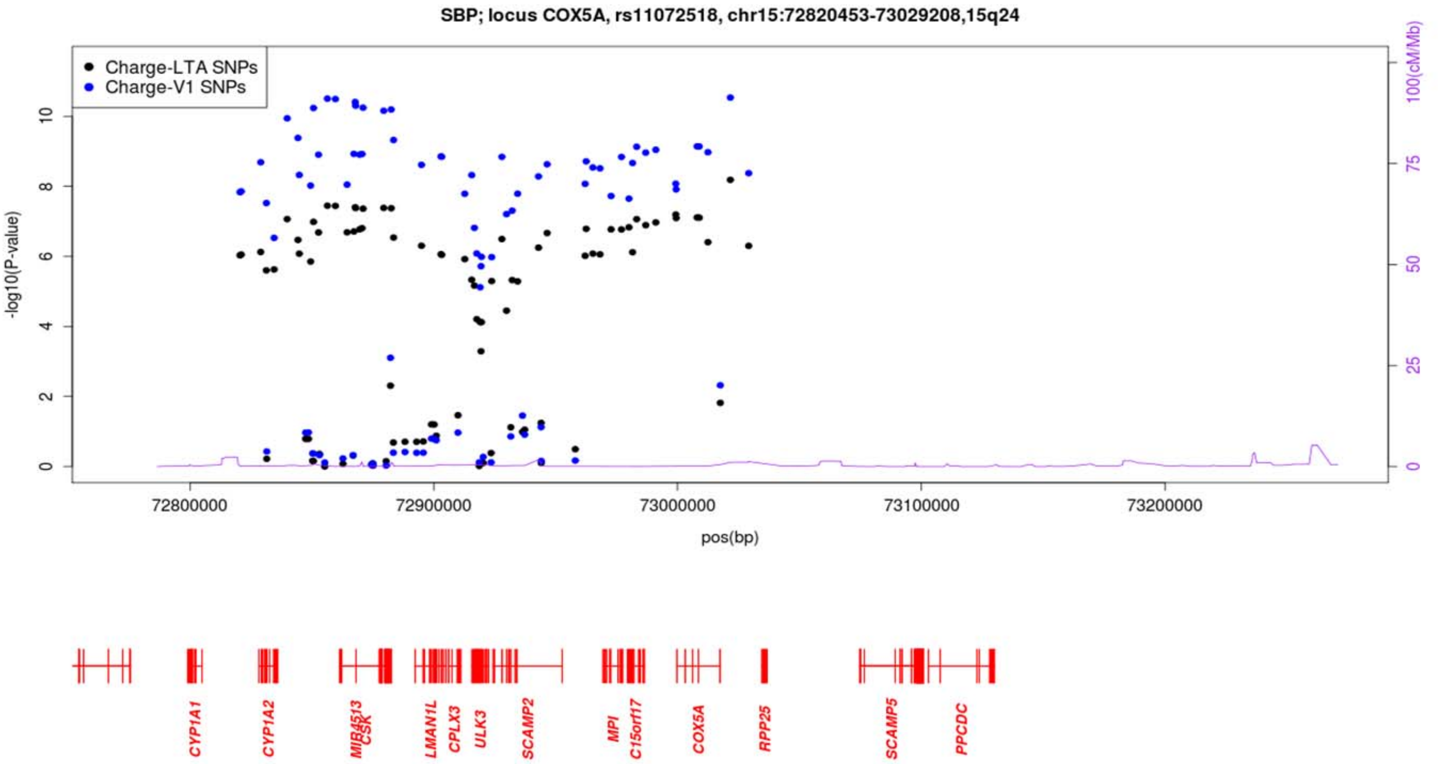

SBP; locus AGT, rs2004776, chr1:228882807-228916422,1q42
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
100(cM/Mb)
0
25
50
75
228700000
228800000
228900000
229000000
229100000
pos(bp)
COG2
AGT
CAPN9
C1orf198
TTC13

(b2)

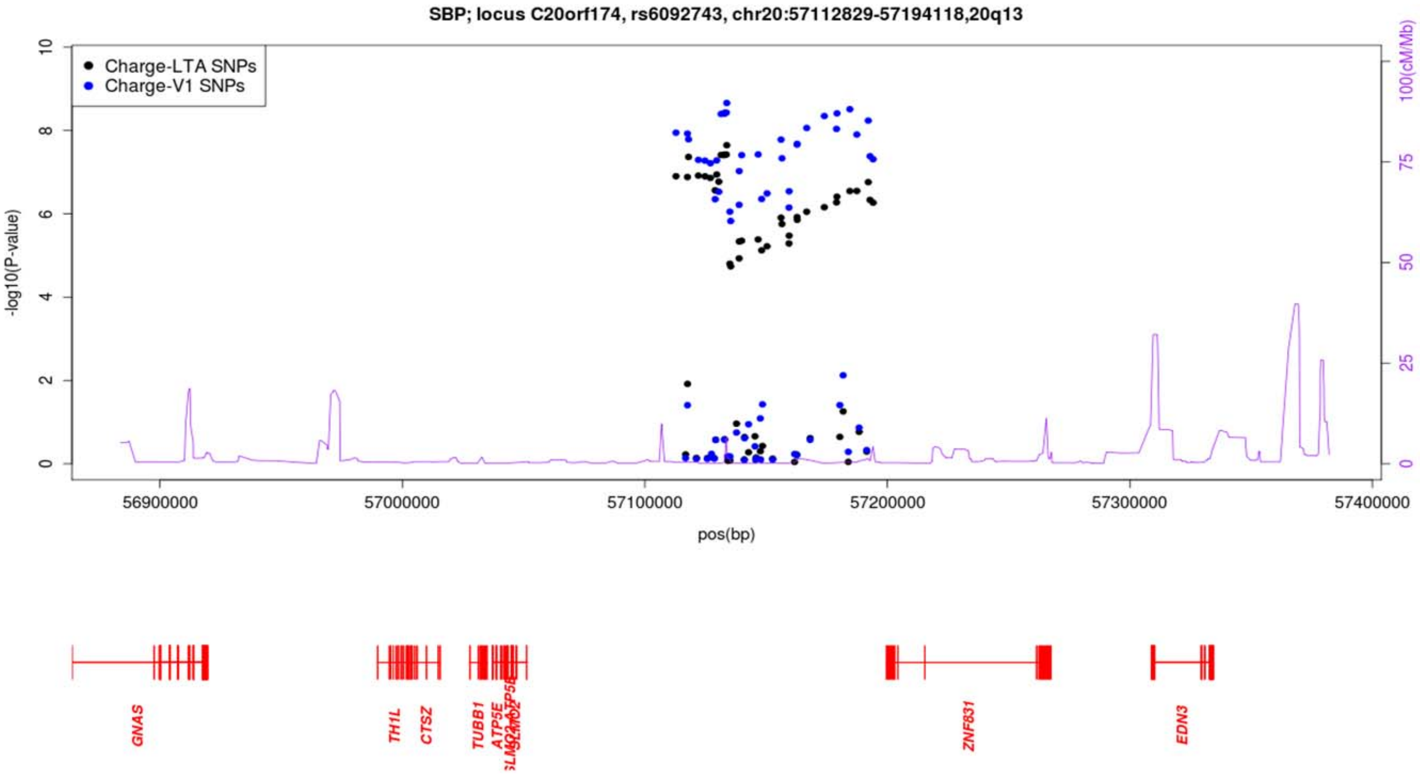


SBP; locus ATXN2, rs4766578, chr12:110368991-111095097,12q24
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
110200000
110300000
110400000
110500000
110600000
pos(bp)
FAM109A
SH2B3
ATXN2
BRAP
ACAD10

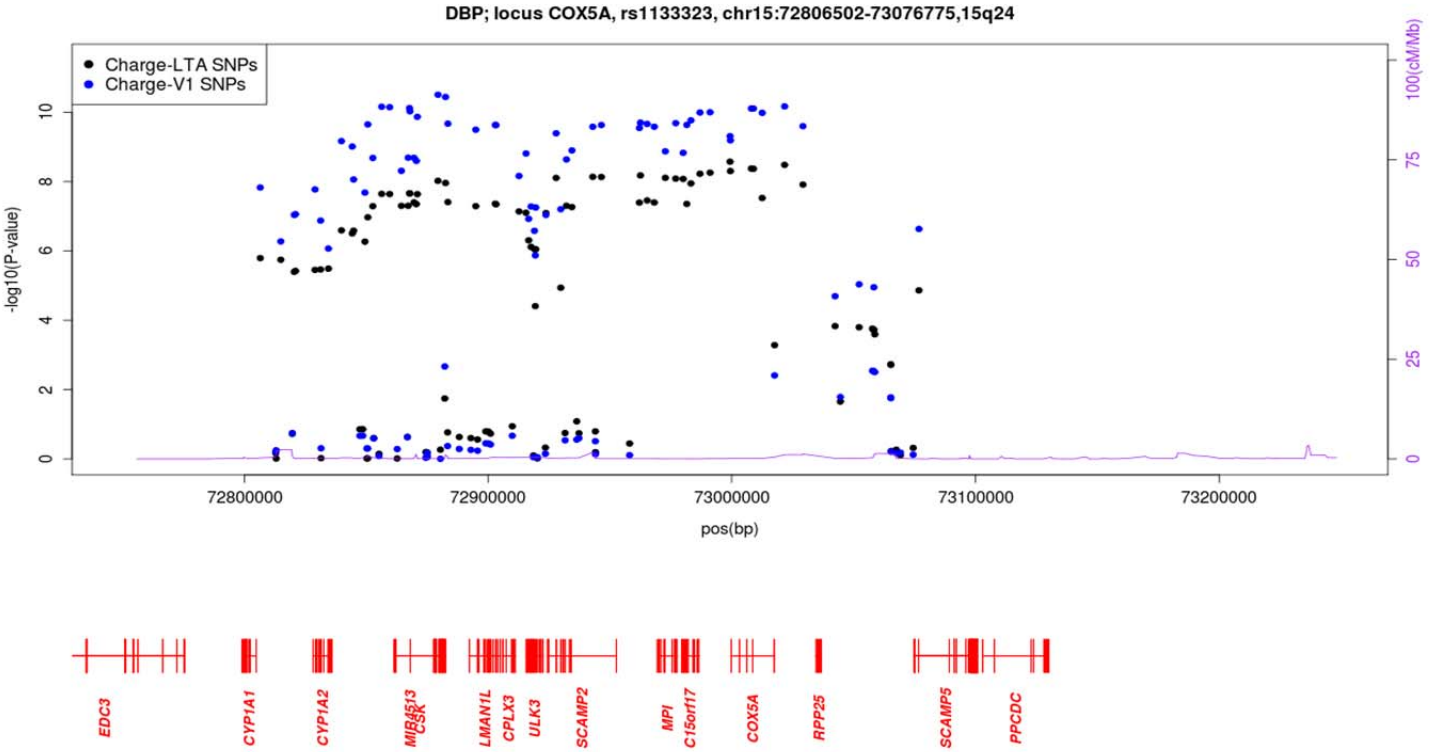
(b3)


SBP; locus COX5A, rs11072518, chr15:72820453-73029208,15q24
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
72800000
72900000
73000000
73100000
73200000
pos(bp)
CYP1A1
CYP1A2
MIR4513
CSK
LMAN1L
CPLX3
ULK3
SCAMP2
MPI
C15orf17
COX5A
RPP25
SCAMP5
PPCDC

(b4)

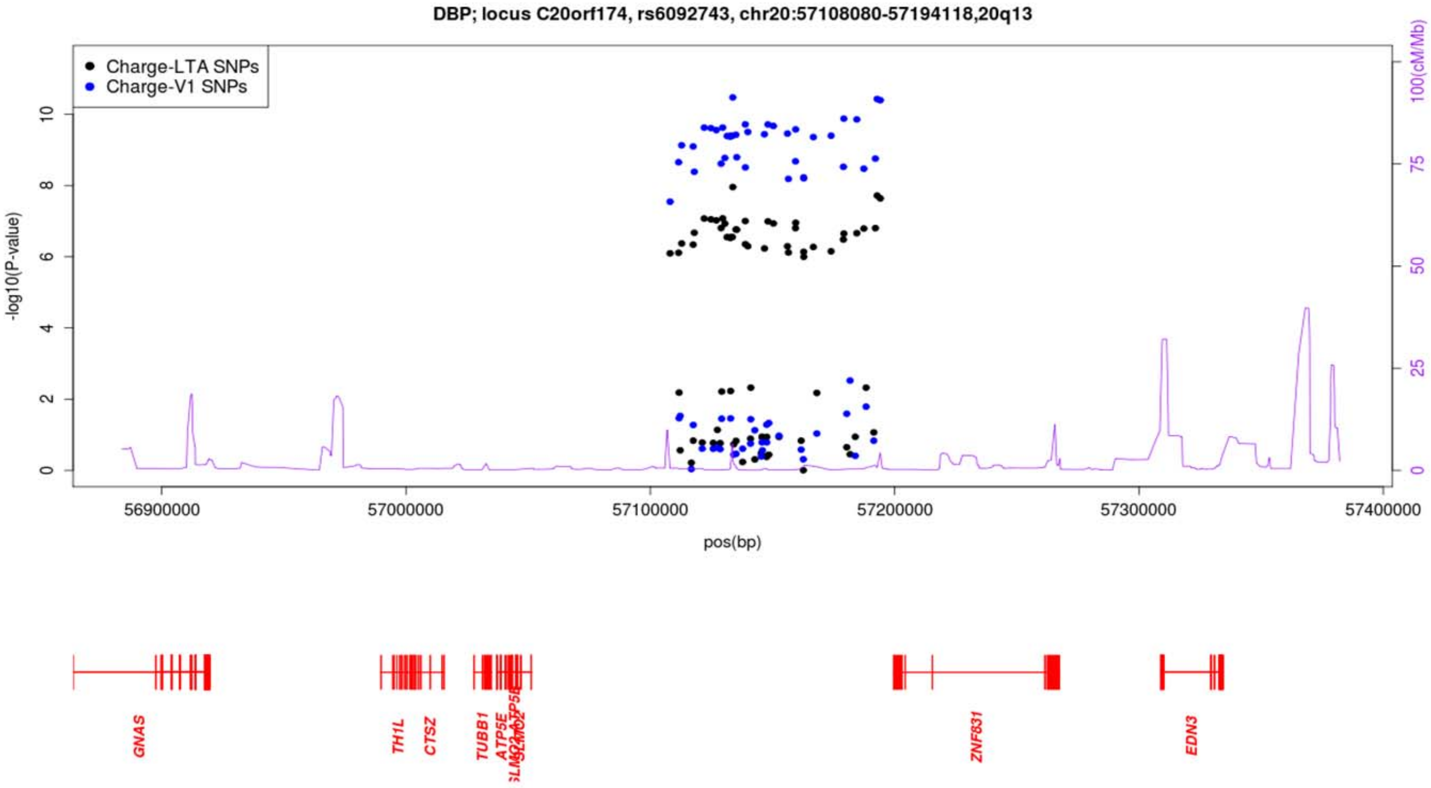

SBP; locus C20orf174, rs6092743, chr20:57112829-57194118,20q13
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
56900000
57000000
57100000
57200000
57300000
57400000
pos(bp)
GNAS
TH1L
CTSZ
TUBB1
ATP5E
SLMO2-ATP5E
SLMO2
ZNF831
EDN3

(b5)



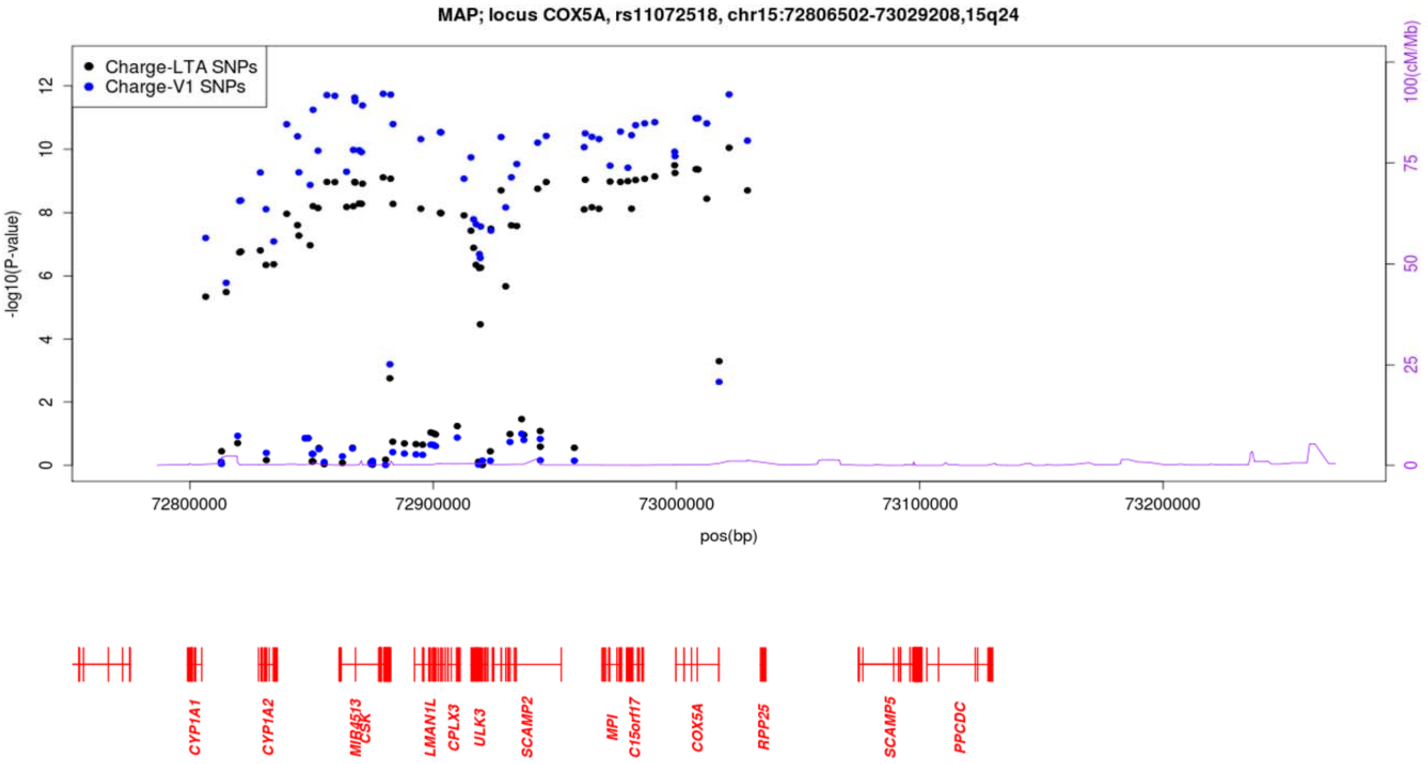
DBP; locus COX5A, rs1133323, chr15:72806502-73076775,15q24
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
72800000
72900000
73000000
73100000
73200000
pos(bp)
EDC3
CYP1A1
CYP1A2
MIR4513
CSK
LMAN1L
CPLX3
ULK3
SCAMP2
MPI
C15orf17
COX5A
RPP25
SCAMP5
PPCDC

(b6)

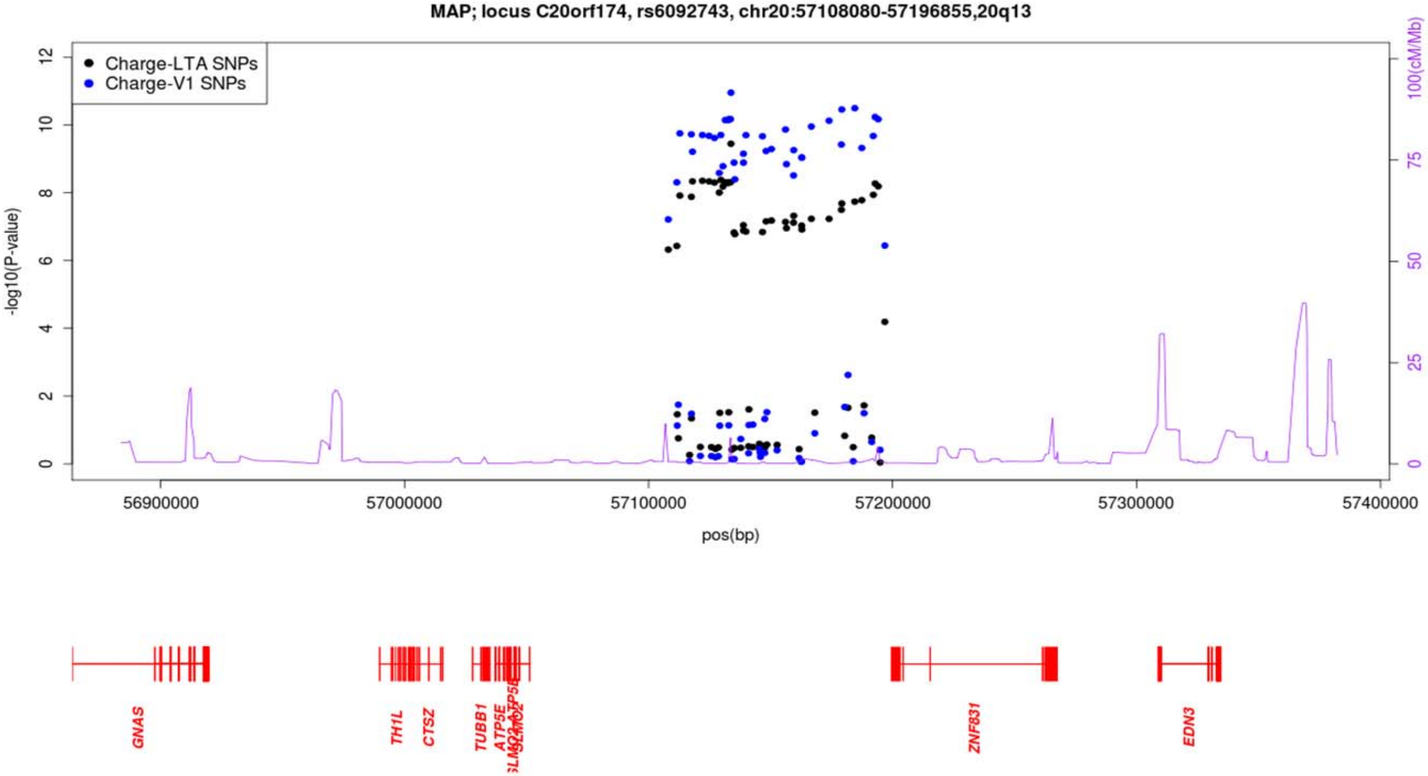


DBP; locus C20orf174, rs6092743, chr20:57108080-57194118,20q13
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
25
50
75
56900000
57000000
57100000
57200000
57300000
57400000
pos(bp)
GNAS
TH1L
CTSZ
TUBB1
ATP5E
SLMO2
ATP5E
SLMO2
ZNF831
EDN3

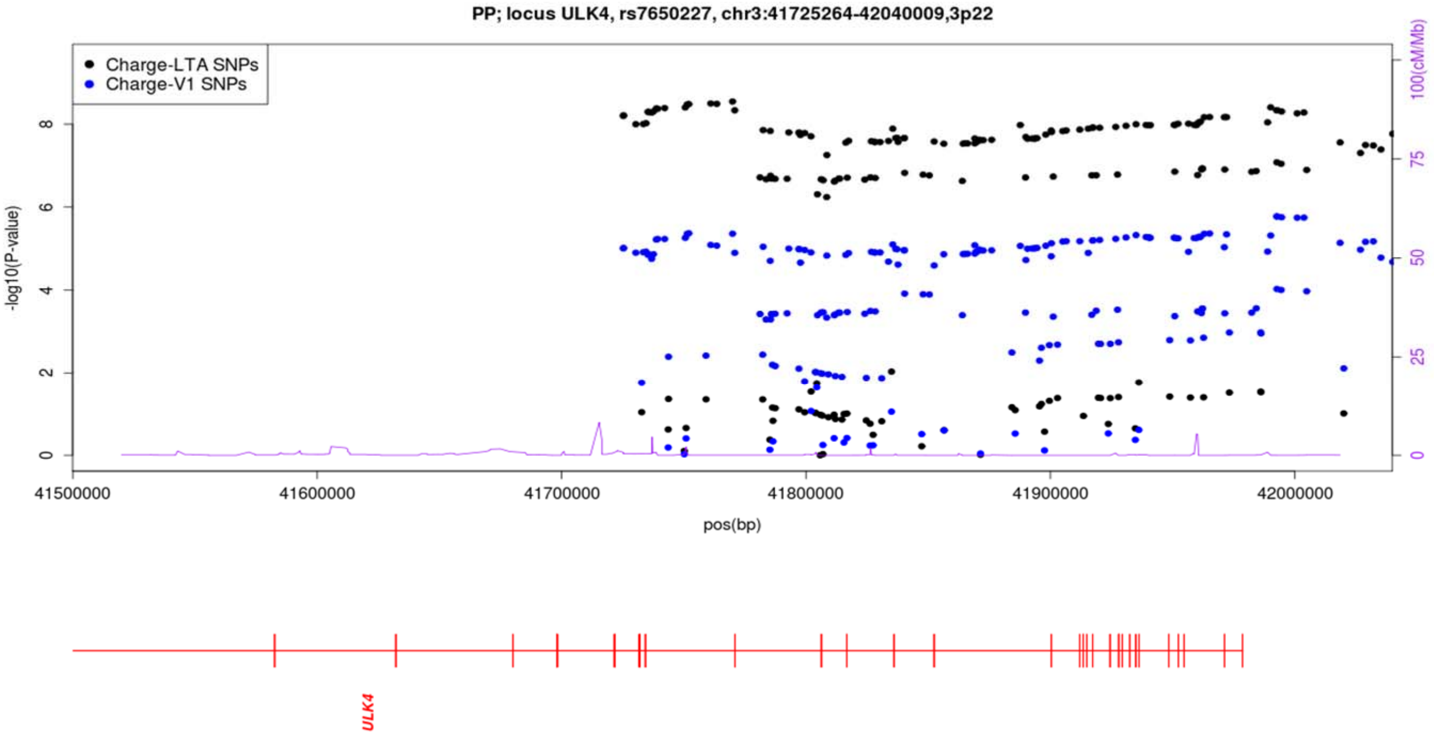
(b7)


MAP; locus COX5A, rs11072518, chr15:72806502-73029208,15q24
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
pos(bp)
72800000
72900000
73000000
73100000
73200000
CYP1A1
CYP1A2
MIR4513
CSK
LMAN1L
CPLX3
ULK3
SCAMP2
MPI
C15orf17
COX5A
RPP25
SCAMP5
PPCDC

(b8)


MAP; locus C20orf174, rs6092743, chr20:57108080-57196855,20q13
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
75
pos(bp)
56900000
57000000
57100000
57200000
57300000
57400000
GNAS
TH1L
CTSZ
TUBB1
ATP5E
SLMO2-ATP5E
SLMO2
ZNF831
EDN3

(c1)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6
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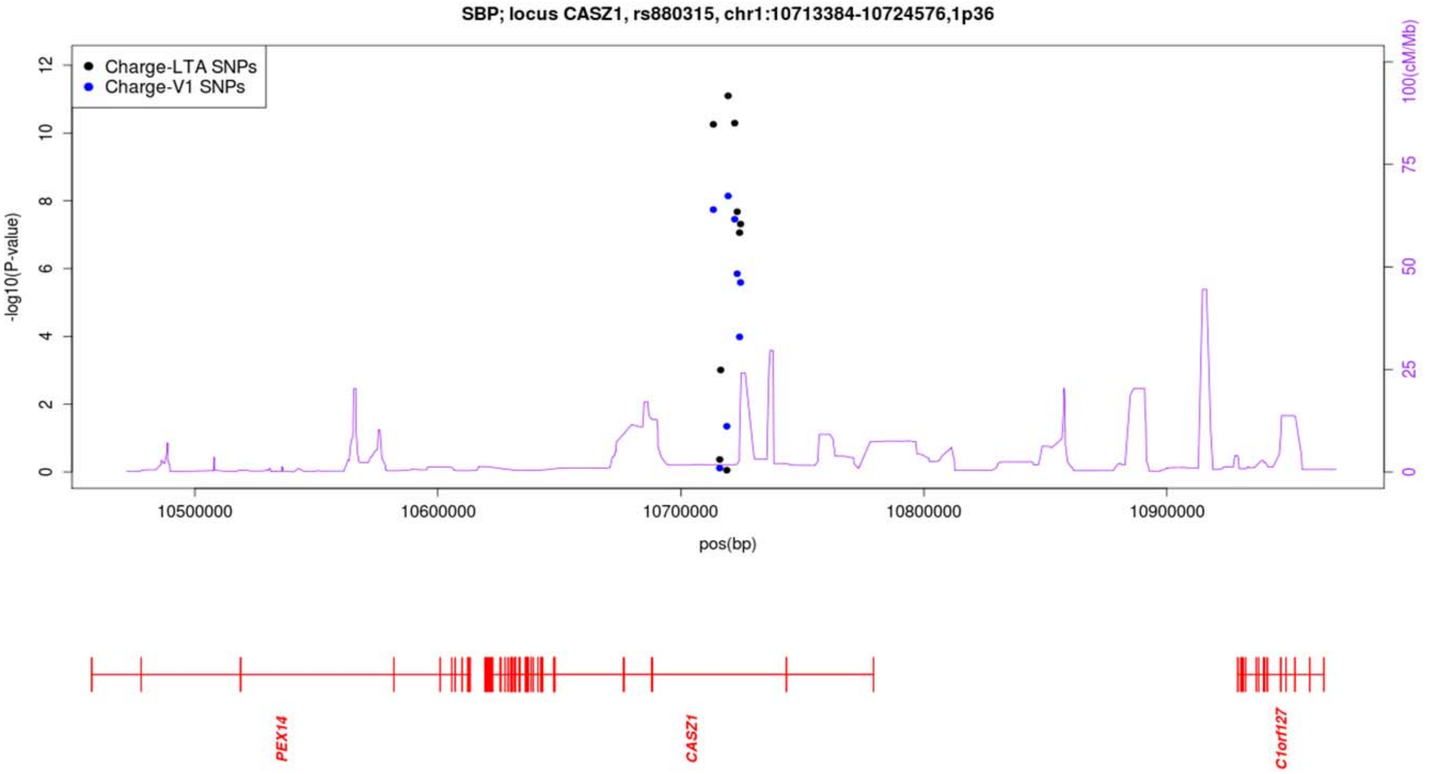
ULK4

(d1)


SBP; locus CASZ1, rs880315, chr1:10713384-10724576,1p36
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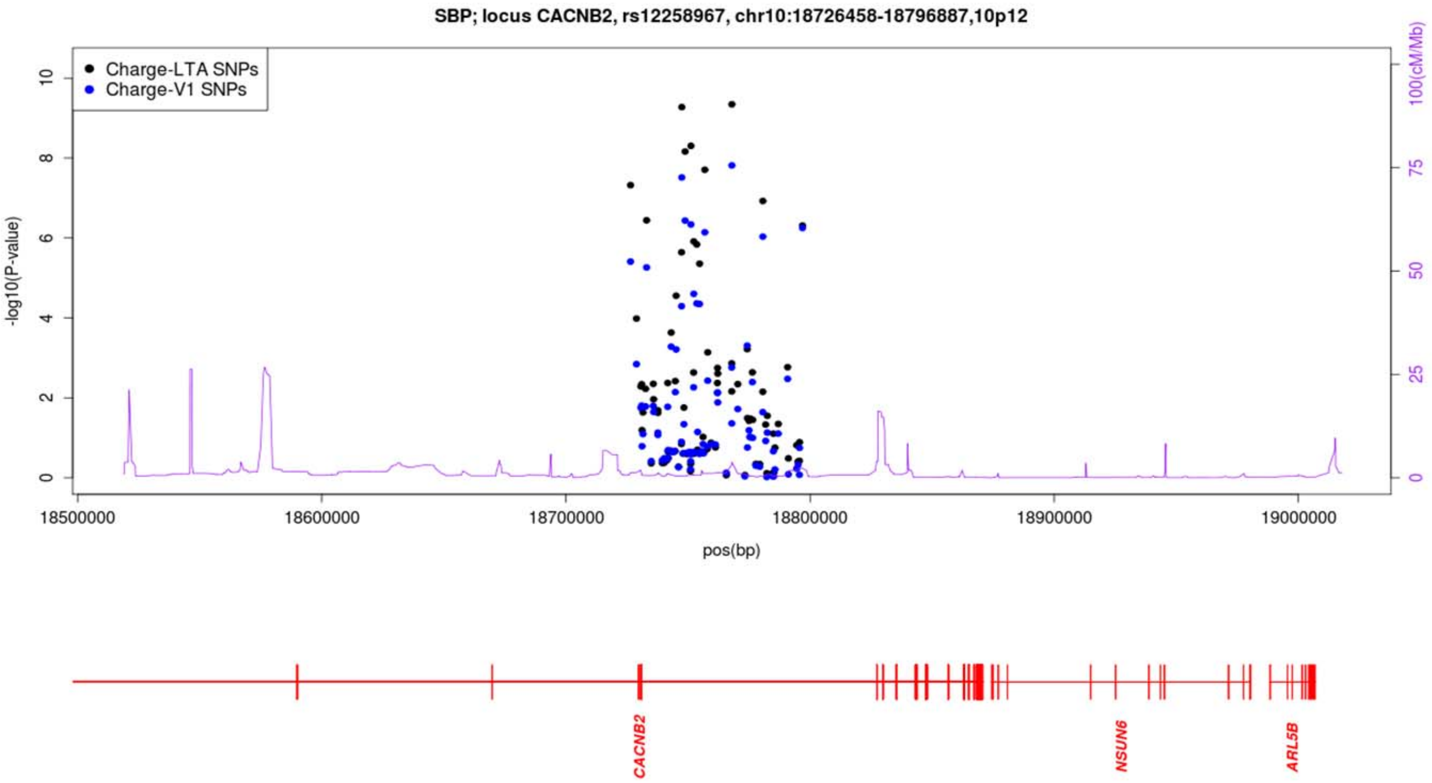
CASZ1
C1orf127

(d2)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100(cM/Mb)
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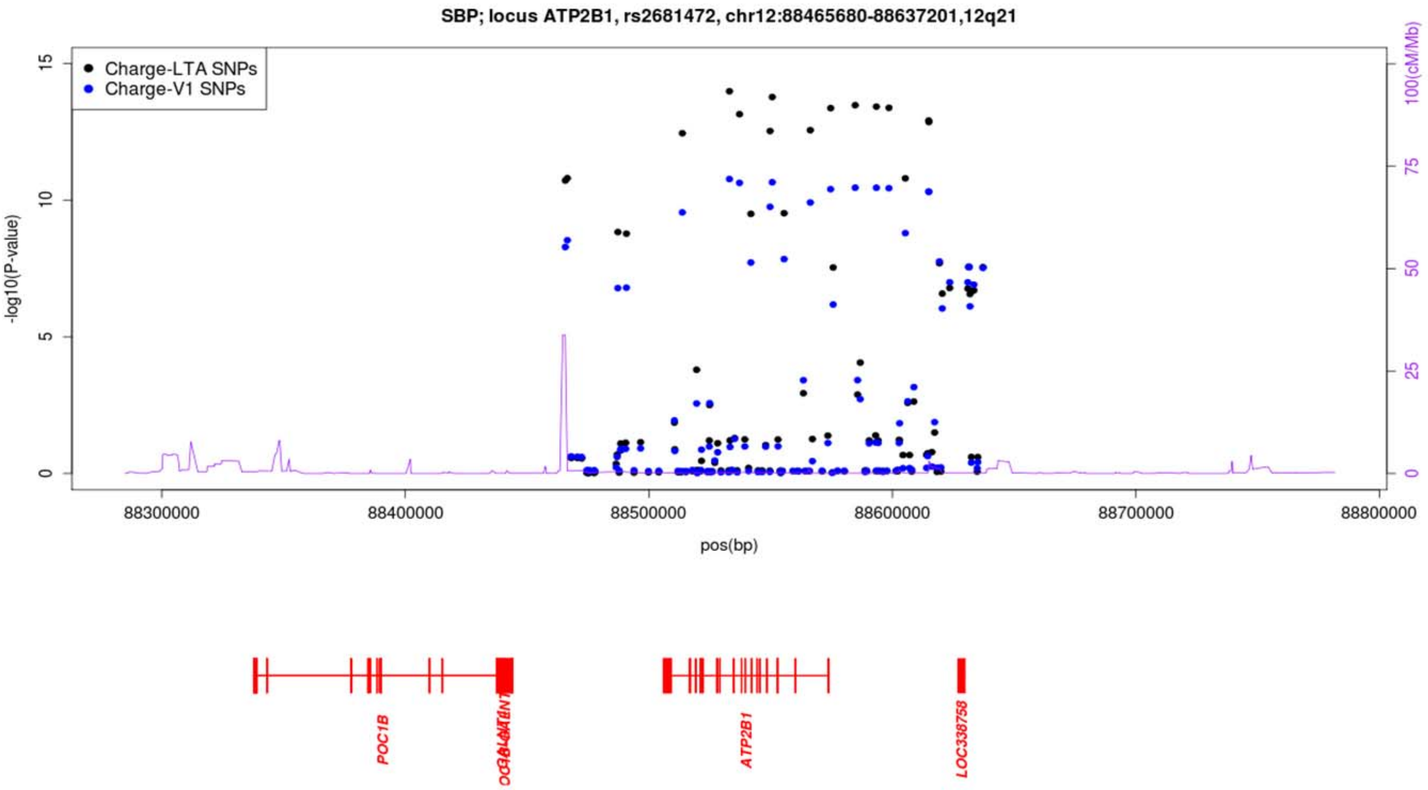
NSUN6
ARL5B

(d3)


SBP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21
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Charge-V1 SNPs
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10
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100(cM/Mb)
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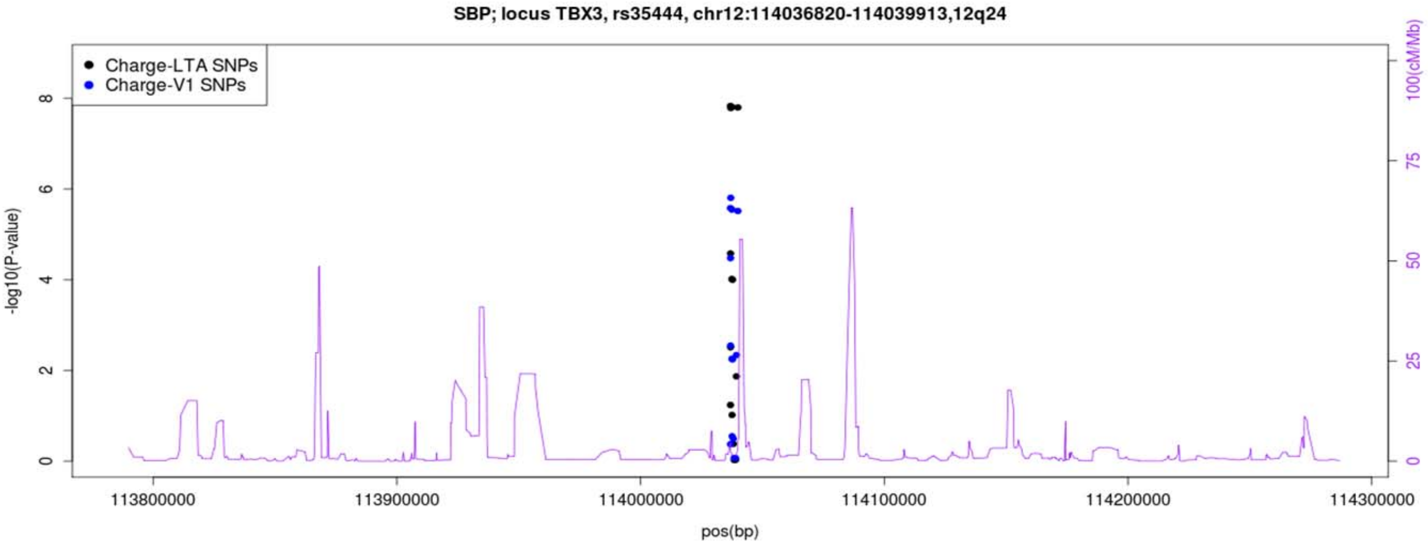
ATP2B1
LOC338758

(d4)


SBP; locus TBX3, rs35444, chr12:114036820-114039913,12q24
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6
8
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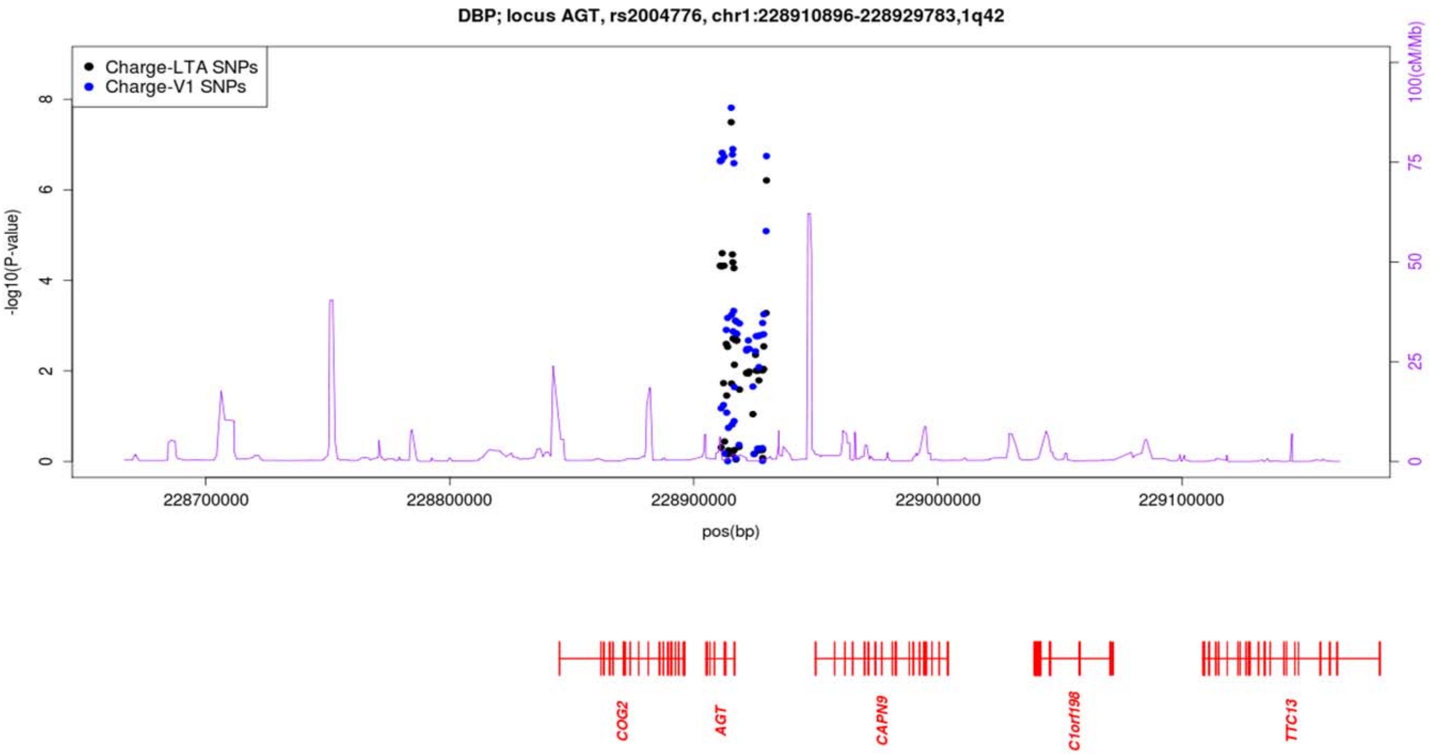
pos(bp)

(d5)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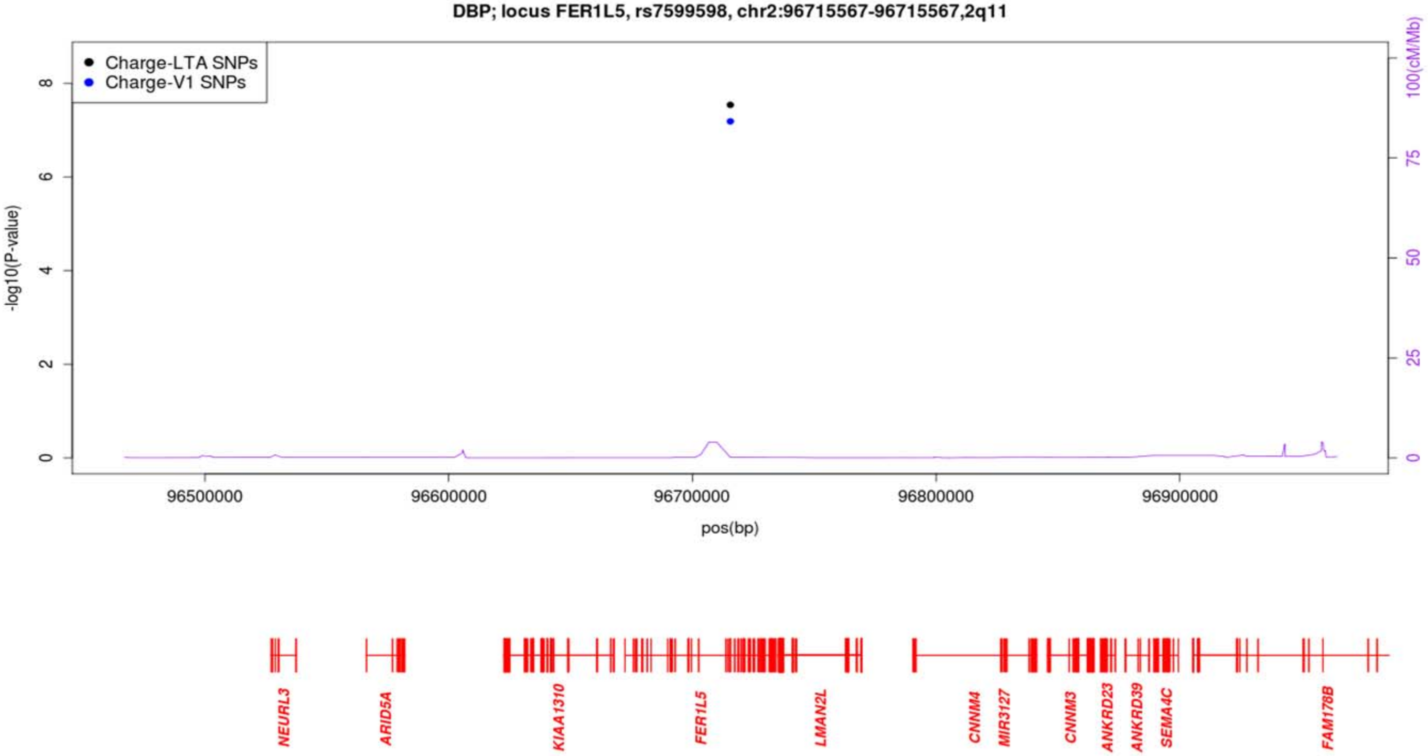
(d6)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6
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ANKRD39
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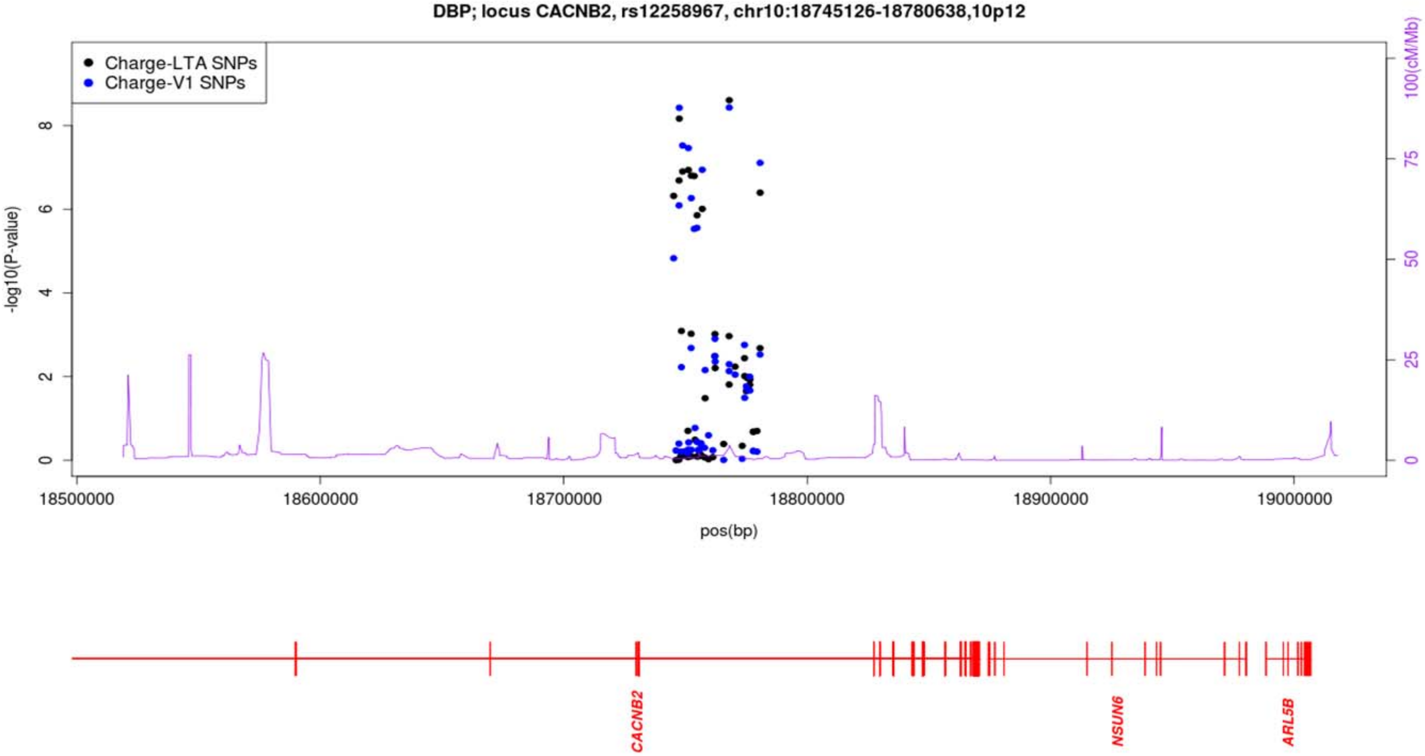
(d7)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4
6
8
100(cM/Mb)
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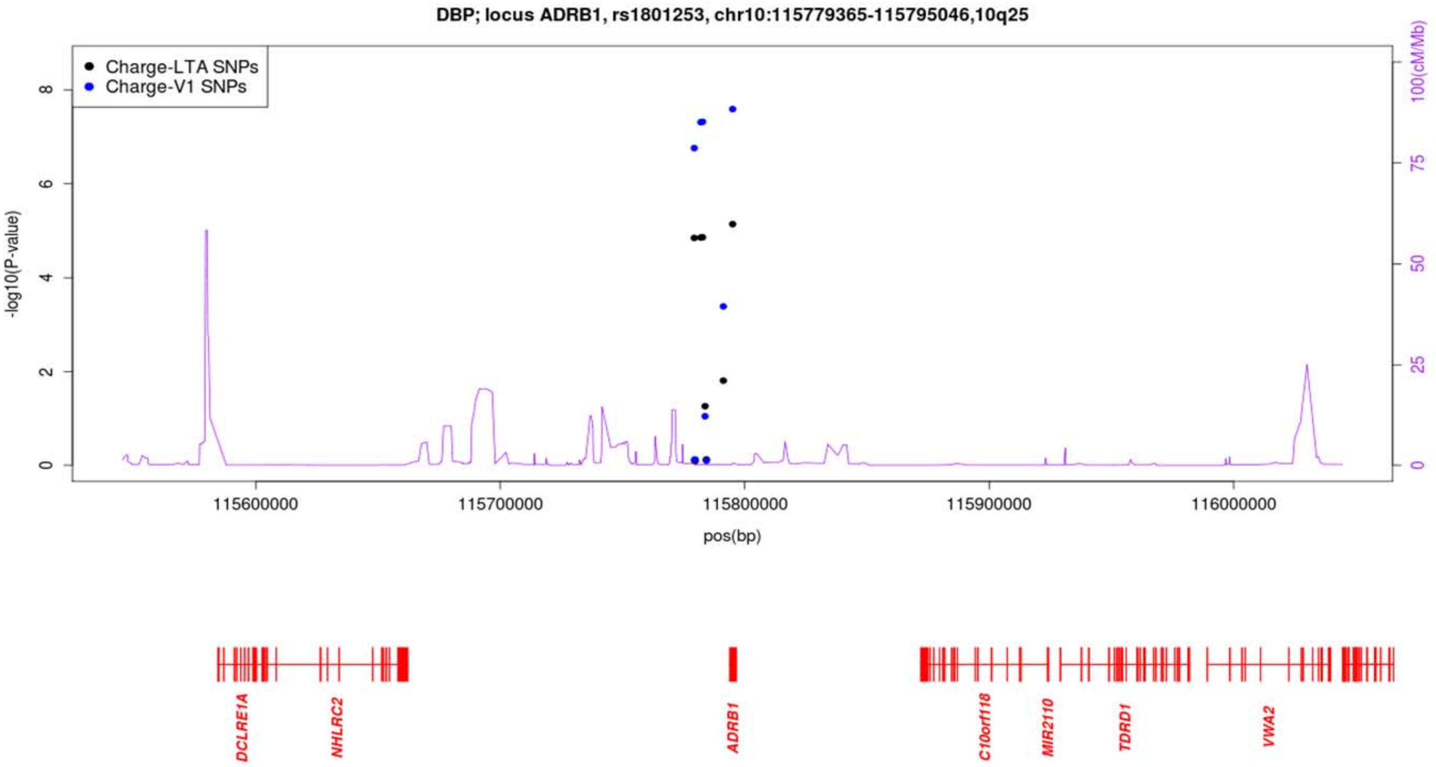
ARL5B

(d8)



DBP; locus ADRB1, rs1801253, chr10:115779365-115795046,10q25
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Charge-V1 SNPs
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4
6
8
100(cM/Mb)
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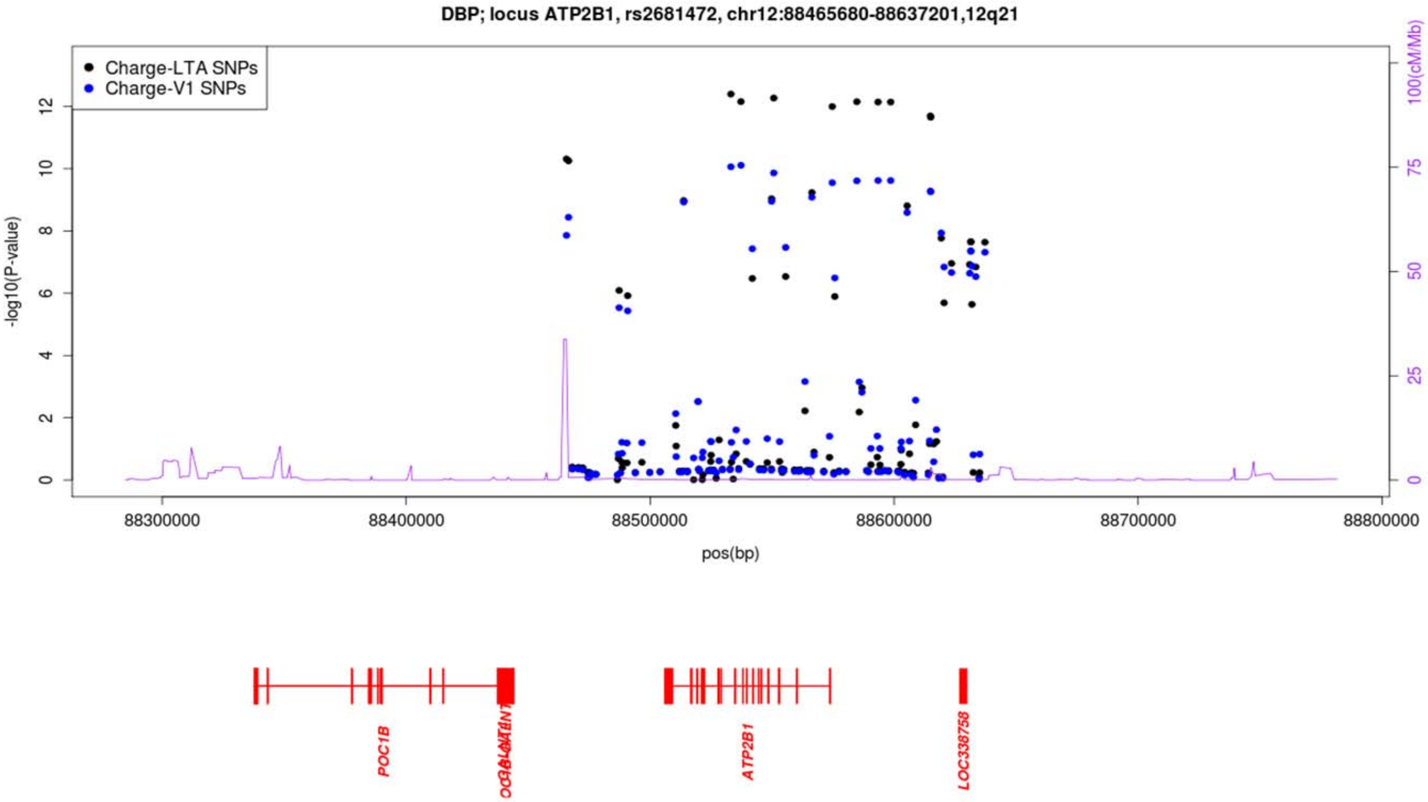
ADRB1
C10orf118
MIR2110
TDRD1
VWA2

(d9)


DBP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21
Charge-LTA SNPs
Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
12
100(cM/Mb)
0
25
50
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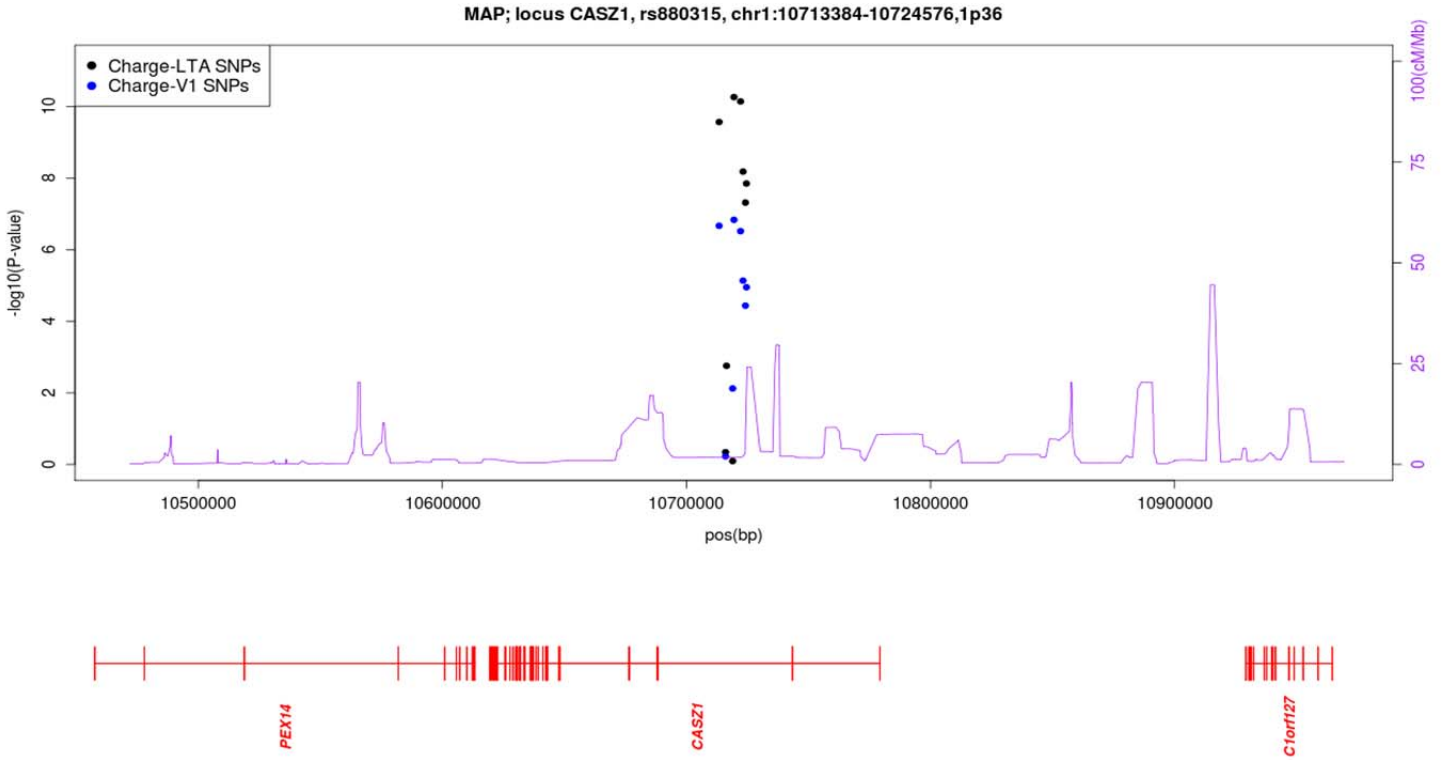
pos(bp)
POC1B
ATP2B1
LOC338758

(d10)



MAP; locus CASZ1, rs880315, chr1:10713384-10724576,1p36
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2
4
6
8
10
100(cM/Mb)
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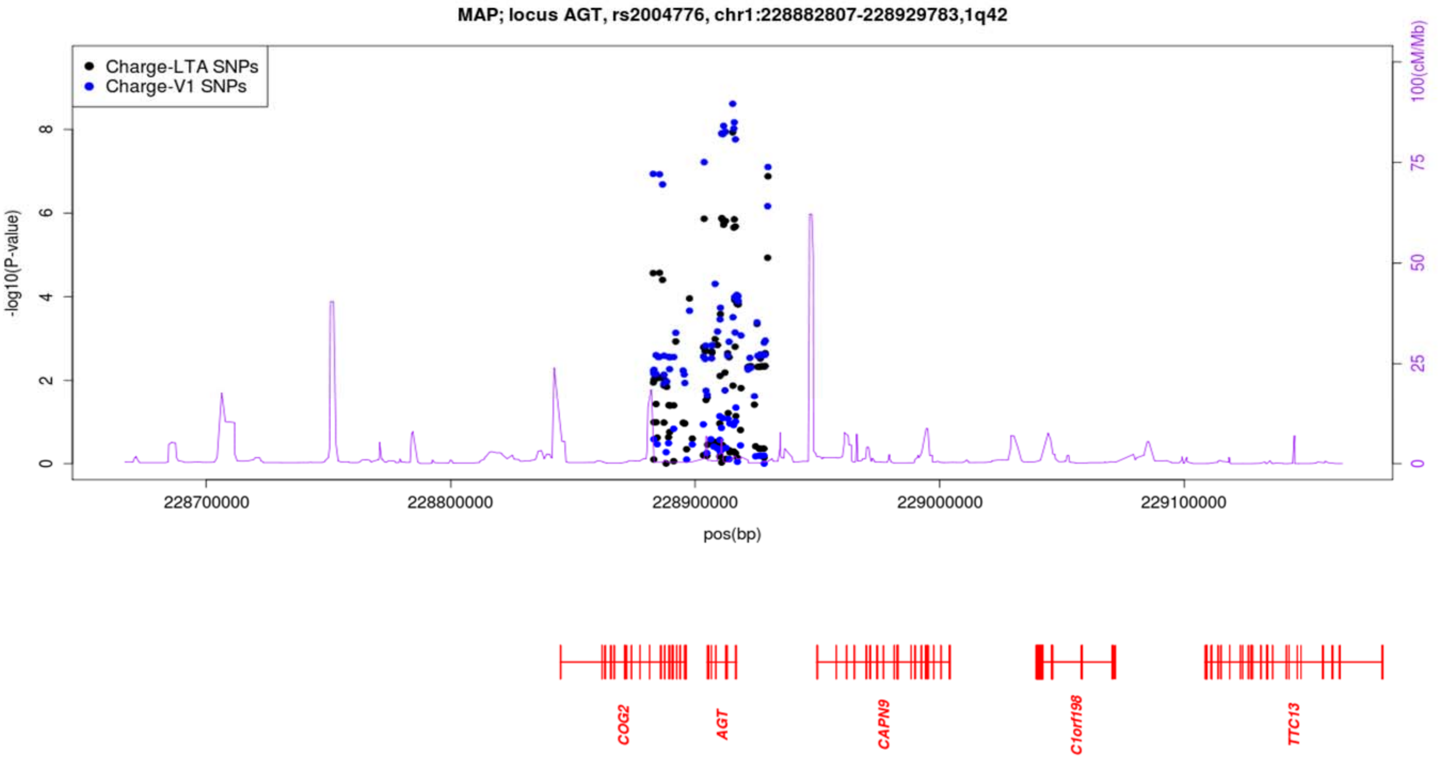
C1orf127

(d11)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Charge-V1 SNPs
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6
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100(cM/Mb)
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AGT
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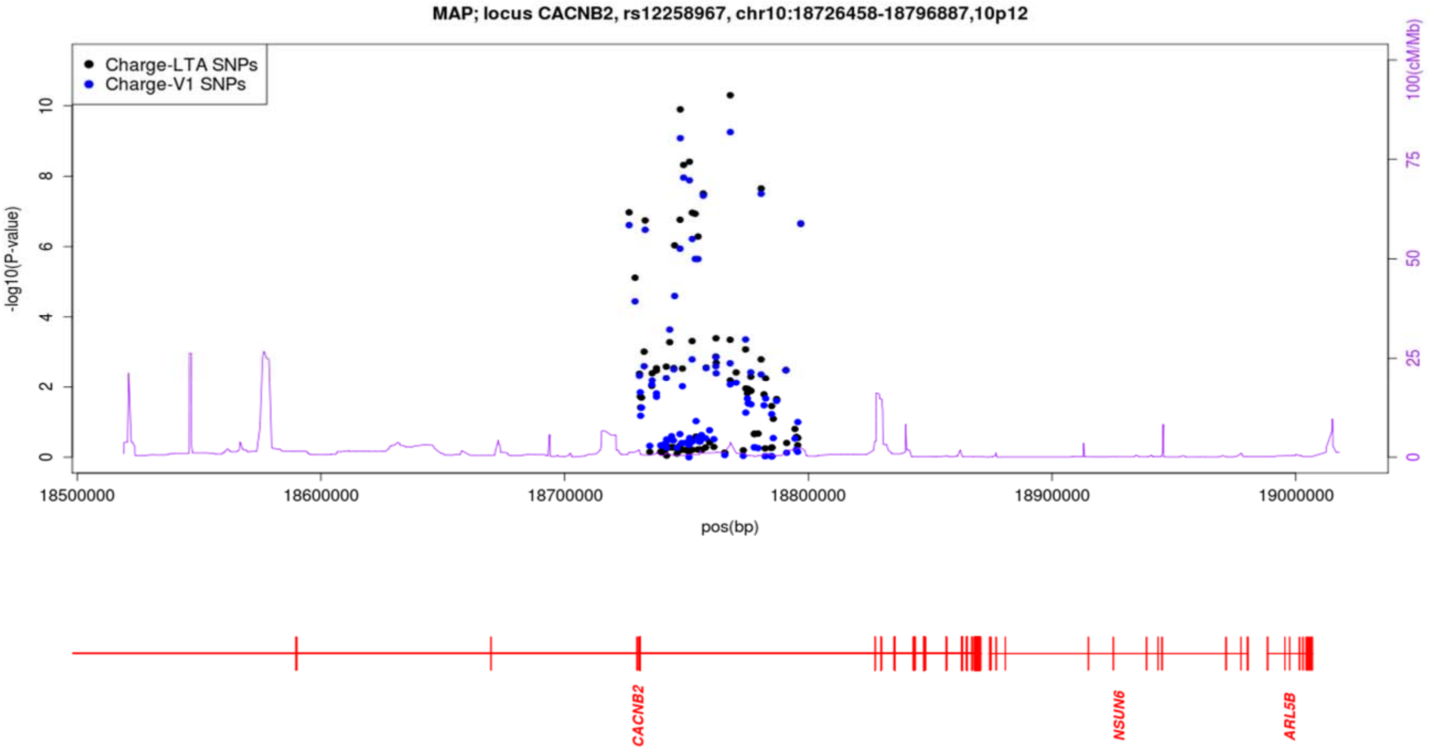
TTC13

(d12)


MAP; locus CACNB2, rs12258967, chr10:18726458-18796887,10p12
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● Charge-V1 SNPs
-log10(P-value)
0
2
4
6
8
10
100(cM/Mb)
0
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50
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18600000
18700000
18800000
18900000
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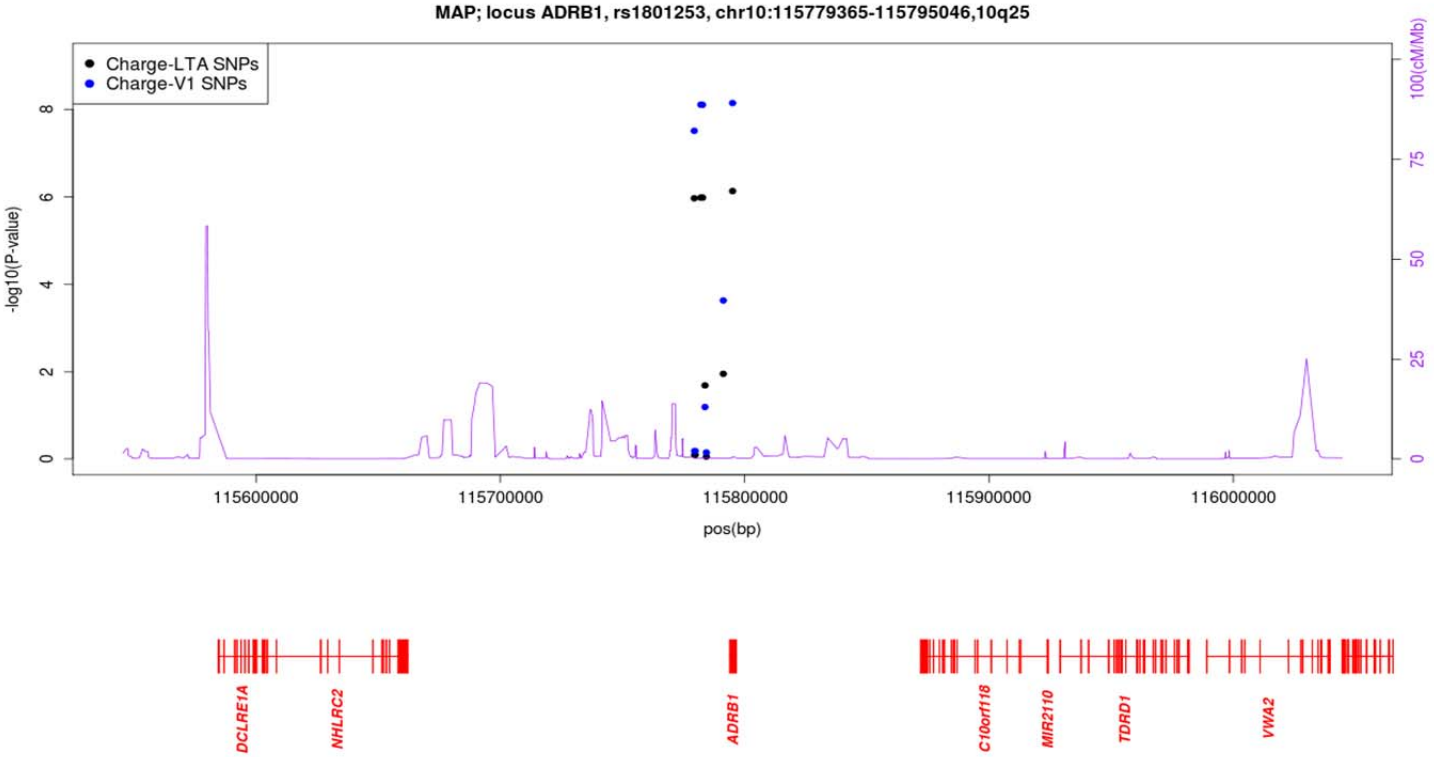
pos(bp)
CACNB2
NSUN6
ARL5B

(d13)


MAP; locus ADRB1, rs1801253, chr10:115779365-115795046,10q25
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
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2
4
6
8
100(cM/Mb)
0
25
50
75
115600000
115700000
115800000
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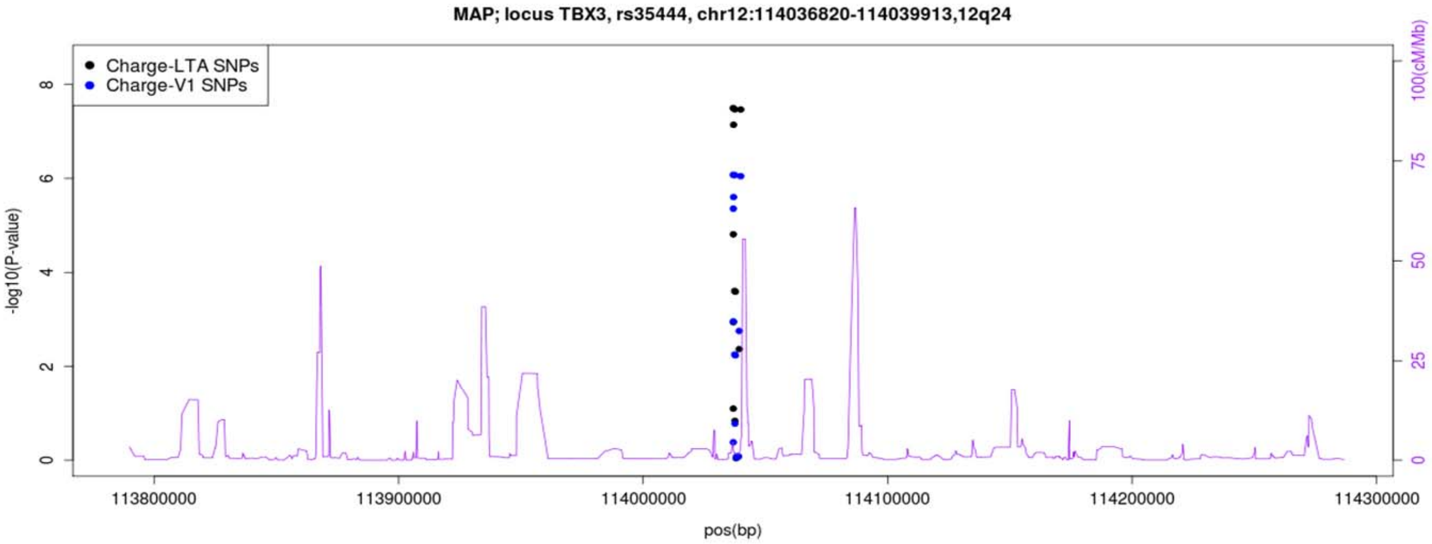
DCLRE1A
NHLRC2
ADRB1
C10orf118
MIR2110
TDRD1
VWA2

(d14)


MAP; locus TBX3, rs35444, chr12:114036820-114039913,12q24
● Charge-LTA SNPs
● Charge-V1 SNPs
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2
4
6
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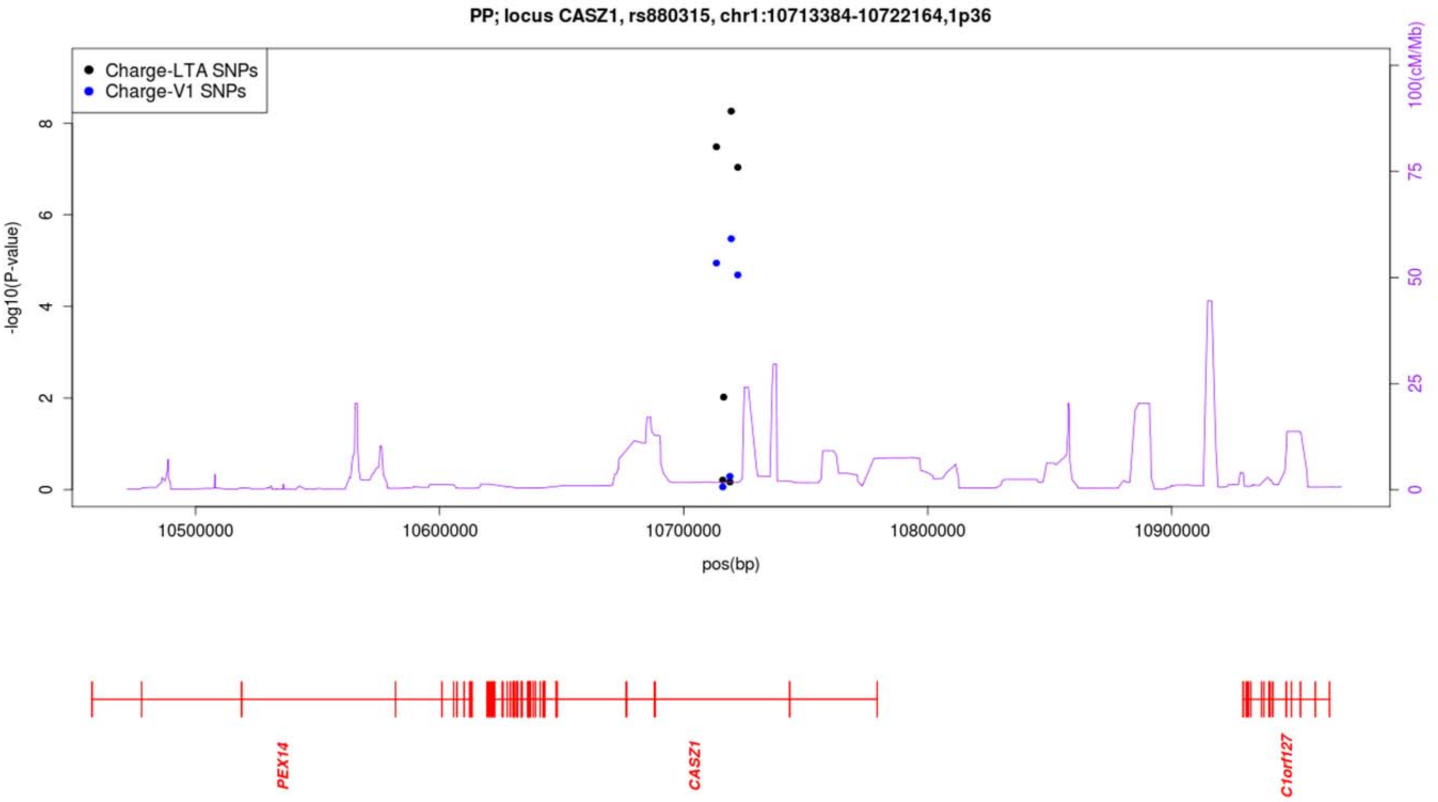
pos(bp)

(d15)


PP; locus CASZ1, rs880315, chr1:10713384-10722164,1p36
● Charge-LTA SNPs
● Charge-V1 SNPs
-log10(P-value)
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4
6
8
100(cM/Mb)
0
25
50
75
10500000
10600000
10700000
10800000
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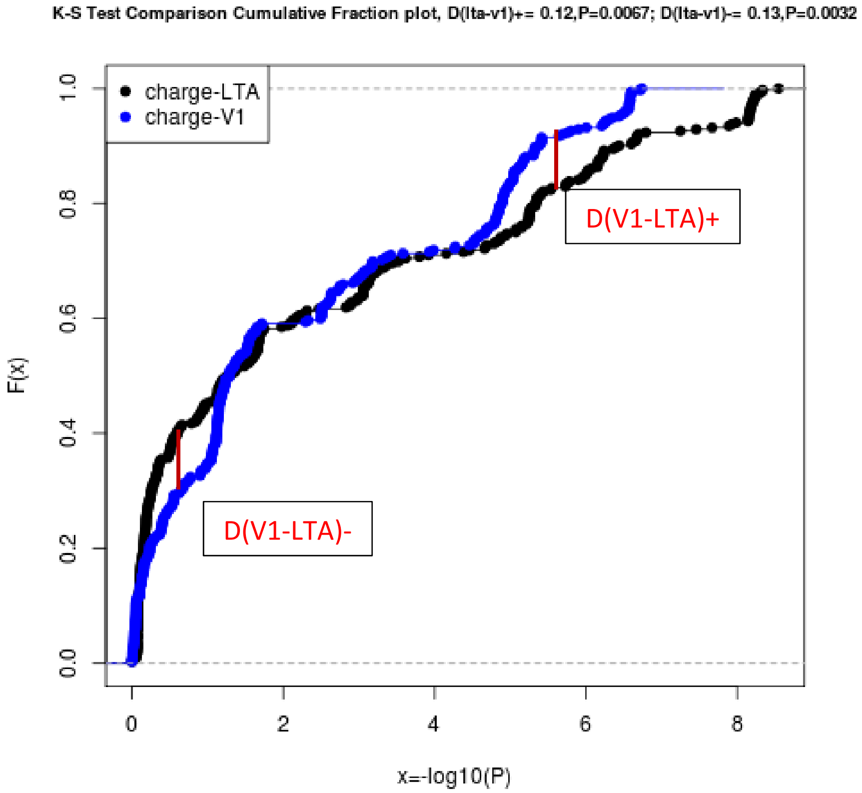
pos(bp)
PEX14
CASZ1
C1orf127

Figure S8. K-S test comparison cumulative fraction plot, where x-axis is the –log10(*P*) values and y-axis is the cumulative fraction.



To identify regions in which the enrichment of V1 is larger than LTA or LTA larger than V1 significantly, we used the Kolmogorov-Smirnov (K-S) statistics to compare the –log10(*P* values) within each region meeting criteria for genome-wide significance (*P* value < $5x10^{-8}$). Regions with at least one marker with *P* value<$5x10^{-8}$ in either LTA or V1 analysis were selected for enrichment analysis. Regions were defined as the lead SNP and by the LD-pruned list of SNPs in the region (r^2 >0.3). Since the KS-test uses the maximum vertical deviation between the two cumulative fraction curves as the statistic D, we used a one-tailed hypothesis test to test whether the positive vertical deviation derived from D(cdf(V1(X))-cdf(LTA(X)))+ was significant or whether the negative vertical deviation derived from D(cdf(V1(X))-cdf(LTA(X)))- was significant, where X is the –log10(P value).

Since the statistics based on different test directions are independent, for each region, two tests were conducted, one testing whether the LTA analysis yielded smaller *P* values than the V1 analysis, and vice versa. To test the structure and the strength of the K-S statistics, for each of the two tests, 10000 times permutation test was conducted by randomly shuffling the attributes of V1 and LTA and calculating new statistics repeatedly. From 10000 iterations, the permutation p-value was obtained by calculating the percentage of times when the original p-value from our data was smaller than the p-value of the new re-sampling data. Since the number of markers which selected for each region may influence the power of the K-S non-parametric test, regions with more markers may have a greater likelihood of being detected compared to regions with fewer markers. To overcome this issue, bootstrapping was used by randomly selecting *n* markers from the N=2.5 million whole-genome markers to do the K-S test of LTA and V1 10000 times, where *n* corresponds to the original number of markers we used for test in each region before. These 10000 test statistics were used as the baseline distribution, to test against whether regions with lower P values of association in the LTA or V1 analyses were truly significant compared to the distribution of the whole-genome-level baseline test statistics. Regions with true enrichment differences between LTA and V1 were identified as those with larger test statistics compared to the whole-genome-level distribution.

Two sample K-S statistics, where x is –log10(Pvalue):

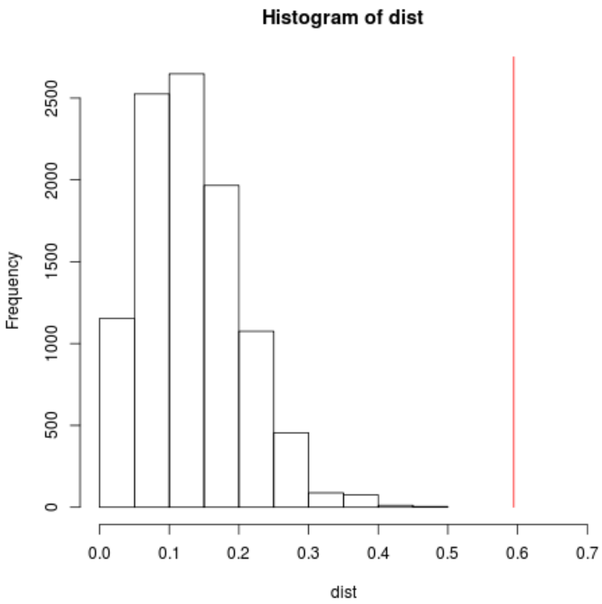
Dv1,LTA + = sup x (F1,v1(x) − F2,LTA(x)) +:

The maximum vertical positive deviation between the cdf of V1 and LTA. Deviation at each point X will be taken into account only if cdf(V1(X))-cdf(LTA(X)) is positive. This statistics means to test whether LTA has larger P-value than V1 in general.

Dv1,LTA - = sup x (F1,v1(x) − F2,LTA(x)) - :

The maximum vertical negative deviation between the cdf of V1 and LTA. Deviation at each point X will be taken into account only if cdf(V1(X))-cdf(LTA(X)) is negative. This statistics means to test whether V1 has larger P-value than LTA in general.

Figure S9. Distribution of the K-S test statistics (D-, H1: V1 analysis is more enriched) from 10000 times boot-strapping of the whole-genome markers, where the number of markers selected each time is correspondence to the number used for test in CYP1A2 region in DBP analysis. The red line is the original K-S test statistics (D-) in this CYP1A2 region.



For the Bootstrapping computing method:

1. For each selected region, we identified the number of markers (n) we used in our previous K-S test.

2. From the overall N=2.5 million genome-wide markers in our LTA or V1 data, we will (i) randomly select n markers from the N complete marker pool as our test samples, or (ii) considered the 'region' to be markers in near side instead of from different far-away sites, thus we could also randomly select one marker as the position start and then select the following n markers around this one marker as our test samples.

3. Used the sample we selected in 2 to do the K-S test. Then report the test statistics.

4. Repeated step2 to step3 many times(at least 100 times, depend on the computing speed)

5. Calculated the percentage when the simulated statistics is larger than the original K-S statistics.

Suppose the genome-wide markers are the baseline, when we randomly selected the markers from them to do the test, the test statistics should be not large (in other words, should be not significant) compared to the test statistics we got from the selected region we identified as the potential change region. Therefore, the percentage when the simulated test statistics is larger than our original K-S test statistics can be seen as the bootstrapping *P* value. If the *P* value was small enough, then we can say the region we identified is truly the one with enrichment change.

Table S1:Sample sizes available for the LTA analyses and Visit 1 analyses.

Cohort	LTA Sample Size	Visit1 Sample Size Available
AGES	526	3,219
ARIC	7,310	8,778
CARDIA	1,671	1,595
CHS	3,159	3,295
FHS	3,895	8,096
MESA	2,414	2,414
RS1	4,710	4,838
RS2	1,535	1,535
WGHS	21,409	21,670
Total	**46,629**	**55,440**

Table S2: Cohort summaries across all visit included in the analyses

		Year	*N*	Age, years (sd)	BMI, kg/m2 (sd)	SBP, mmHg (sd)	DBP, mmHg (sd)	Anti-hypertensive therapy (%)
AGES	Visit 1 (Reykjavik Study)	1987-1995	530	66.01 (7.0)	26.2 (3.9)	141.4 (18.8)	82.1 (8.7)	24%
AGES	Visit 2 (AGES)	2002-2005	530	78.49 (5.9)	26.5 (4.3)	143.4 (21.2)	73.1 (9.8)	65%
ARIC	Visit 1	1986-1990	8,778	54.3 (5.7)	27.0 (4.9)	118.5 (17.0)	71.7 (10.0)	26%
ARIC	Visit 2	1990-1993	7,844	57.2 (5.7)	27.4 (5.0)	119.9 (17.8)	71.3 (9.9)	28%
ARIC	Visit 3	1993-1996	7,214	60.3 (5.6)	28.0 (5.3)	122.9 (18.0)	70.8 (10.0)	33%
ARIC	Visit 4	1996-1999	6,582	63.1 (5.6)	28.4 (5.3)	126.1 (18.4)	70.0 (9.9)	40%
CARDIA	Visit 4	1993-1994	1,595	32.6 (3.3)	25.6 (5.1)	106.3 (11.4)	67.8 (9.5)	0.88%
CARDIA	Visit 5	1996-1997	1,571	35.6 (3.4)	26.1 (5.4)	107.2 (11.3)	70.4 (9.4)	1.34%
CARDIA	Visit 6	2001-2002	1,601	40.7 (3.4)	27.2 (5.9)	110.2 (13.4)	72.5 (10.3)	4.06%
CARDIA	Visit 7	2006-2007	1,563	45.8 (3.4)	27.9 (5.9)	113.4 (13.6)	69.9 (10.6)	11.34%
CHS	Visit 0	1989-90	3,153	72.2 (5.2)	26.3 (4.4)	134.9 (20.9)	70.3 (11.4)	35%
CHS	Visit 1	1990-91	3,056	73.1 (5.2)	-	132.2 (20.4)	69.3 (10.3)	37%
CHS	Visit 2	1992-93	2,991	74.1 (5.2)	-	133.4 (20.2)	69.5 (10.4)	39%
CHS	Visit 3	1993-94	2,838	75.0 (5.1)	26.4 (4.5)	135.3 (20.9)	70.8 (10.9)	41%
FHS-offspring	Visit 23	1992-1996	579	80.0 (4.4)	26.7 (4.6)	148.1 (23.5)	72.9 (11.3)	49%
FHS-offspring	Visit 24	1995-1998	525	82.0 (4.2)	26.4 (4.5)	146.8 (21.7)	73.2 (10.7)	51%
FHS-offspring	Visit 25	1997-1999	486	83.8 (4.1)	26.2 (4.6)	146.9 (21.9)	71.8 (11.7)	55%
FHS-offspring	Visit 26	2000-2001	389	85.6 (4.0)	26.2 (4.7)	146.6 (22.6)	71.2 (11.2)	60%
FHS-offspring	Visit 20	1986-1990	598	74.4 (4.5)	26.8 (4.6)	150.3 (22.6)	78.8 (10.7)	43%
FHS-offspring	Visit 21	1988-1992	606	76.4 (4.6)	27.1 (4.5)	149.8 (22.3)	77.1 (10.7)	48%
FHS-offspring	Visit 22	1990-1994	588	78.2 (4.4)	26.9 (4.7)	147.8 (21.3)	74.6 (11.1)	47%
FHS	Visit 4	1987-1991	3,108	50.7 (9.8)	26.8 (4.9)	127.4 (20.0)	79.7 (10.6)	15%
FHS	Visit 5	1991-1995	3,104	54.4 (9.8)	27.4 (4.9)	127.4 (20.0)	75.4 (10.3)	17%
FHS	Visit 6	1995-1998	2,975	58.3 (9.7)	27.9 (5.1)	130.6 (20.4)	76.8 (10.0)	26%
FHS	Visit 7	1998-2001	2,954	61.0 (9.5)	28.1 (5.3)	130.1 (20.4)	75.7 (10.1)	32%
MESA	Exam 1	2000-2002	2,414	62.7	27.7 (5.0)	123.5 (20.5)	70.2 (10.0)	33%
MESA	Exam 2	2002-2004	2,383	64.2	27.1 (5.1)	121.1 (19.2)	68.8 (9.6)	39%
MESA	Exam 3	2004-2005	2,302	65.5	27.7 (5.2)	120.0 (19.6)	68 (10.9)	42%
MESA	Exam 4	2005-2007	2,219	66.9	27.8 (5.2)	120.5 (19.3)	68.02 (9.7)	45%
RS1	Visit 1	1990-1993	4,838	67.9	26.3 (3.6)	140.4 (22.8)	74.9 (11.7)	22%
RS1	Visit 2	1994-1995	4,678	70.0	26.4 (3.7)	144.1 (23.4)	78.3 (12.3)	30%
RS1	Visit 3	1997-1999	3,562	72.6	26.8 (3.9)	146.0 (22.4)	76.4 (11.7)	26%
RS1	Visit 4	2002-2004	2,691	75.5	27.4 (4.1)	156.7 (23.2)	81.2 (11.7)	37%
RS2	Visit 1	2001-2001	1,535	63.7	27.2 (4.1)	143.4 (21.6)	79.7 (11.1)	21%
RS2	Visit 2	2004-2006	1,535	67.9	27.8 (4.1)	148.1 (21.4)	81.2 (11.2)	30%
WGHS	Visit 1	1992-1994	21,670	54.7	25.9 (4.9)	124.8 (15.4)	77.3 (9.7)	13%
WGHS	Visit 2	1996-1998	19,410	58.2	26.5 (5.1)	127.3 (16.7)	76.8 (9.8)	23%
WGHS	Visit 3	2003-2005	18,625	65.2	26.9 (5.4)	128.4 (14.7)	76.1 (8.9)	43%

Table S3: Genomic control inflation factors (λ_{GC}).

LTA

LTA- SBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.014	1.052	1.009	1.061	1.034	1.002	1.093	0.996	1.015	1.074

LTA - DBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.005	1.046	1.034	1.051	1.036	1.014	1.065	1.006	1.012	1.088

LTA - PP

ARIC	CHS	FHS	RS1	RS2	AGES	WGHS	MESA	CARDIA	Meta-analysis
1.041	1.023	1.026	1.037	1.017	1.015	1.071	0.996	1.031	1.055

LTA - MAP

ARIC	CHS	FHS	RS1	RS2	AGES	WGHS	MESA	CARDIA	Meta-analysis
1.048	1.031	1.022	1.039	1.006	1.019	1.101	0.996	1.008	1.095

Visit 1

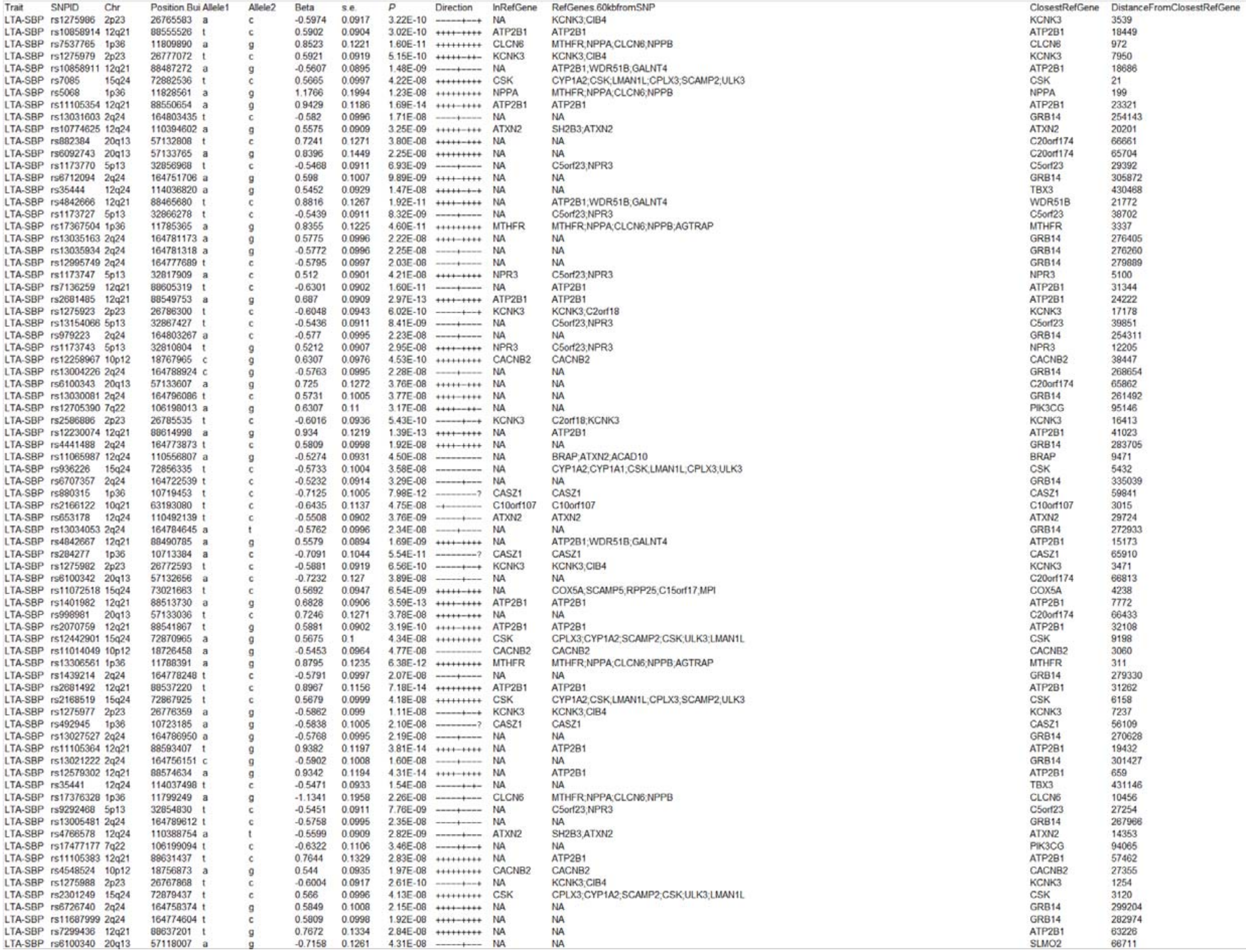
Visit 1 - SBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.014	1.052	1.009	1.061	1.034	1.002	1.093	0.996	1.025	1.076

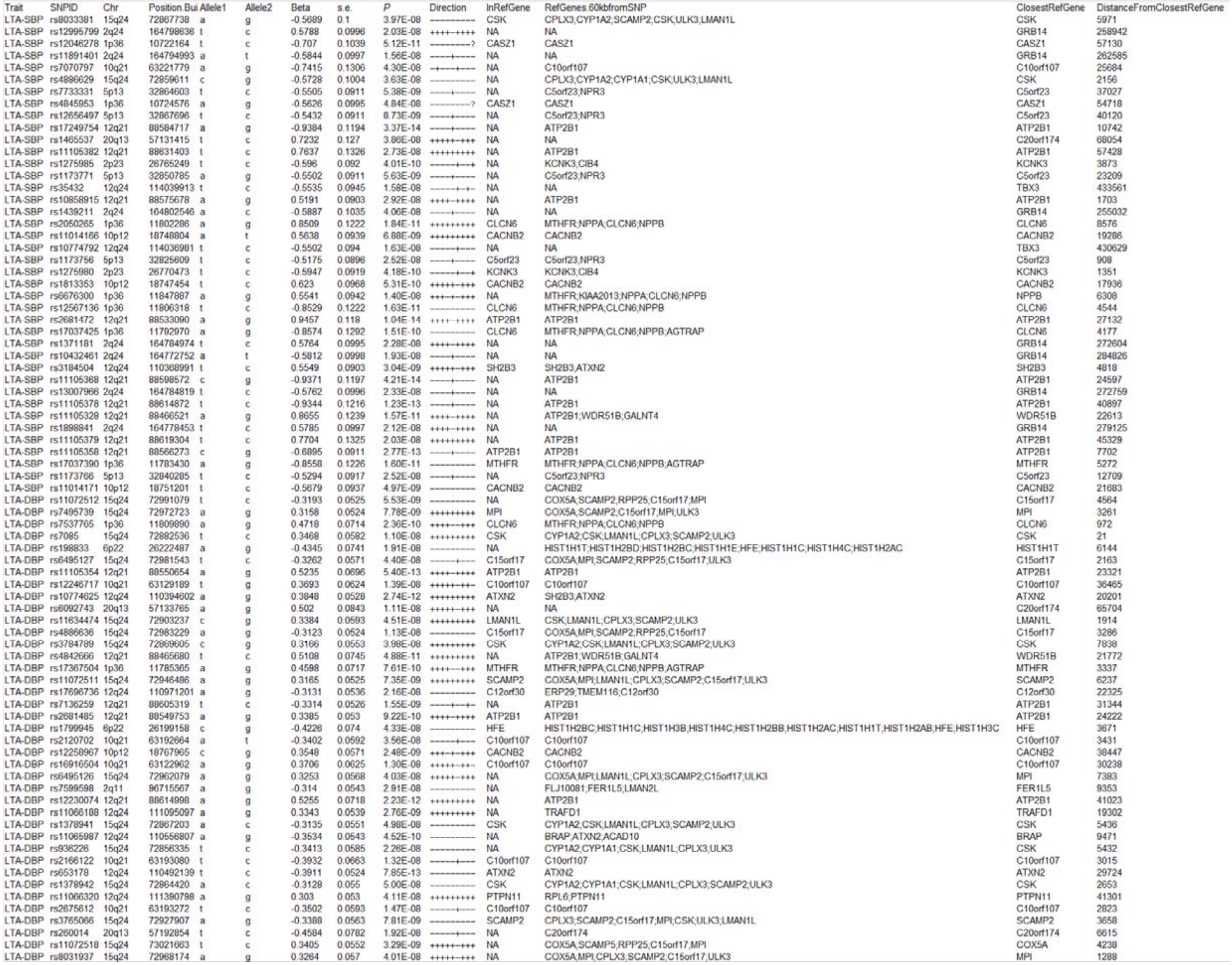
Visit 1 - DBP

AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	Meta-analysis
1.005	1.046	1.034	1.051	1.036	1.014	1.065	1.006	1.025	1.066

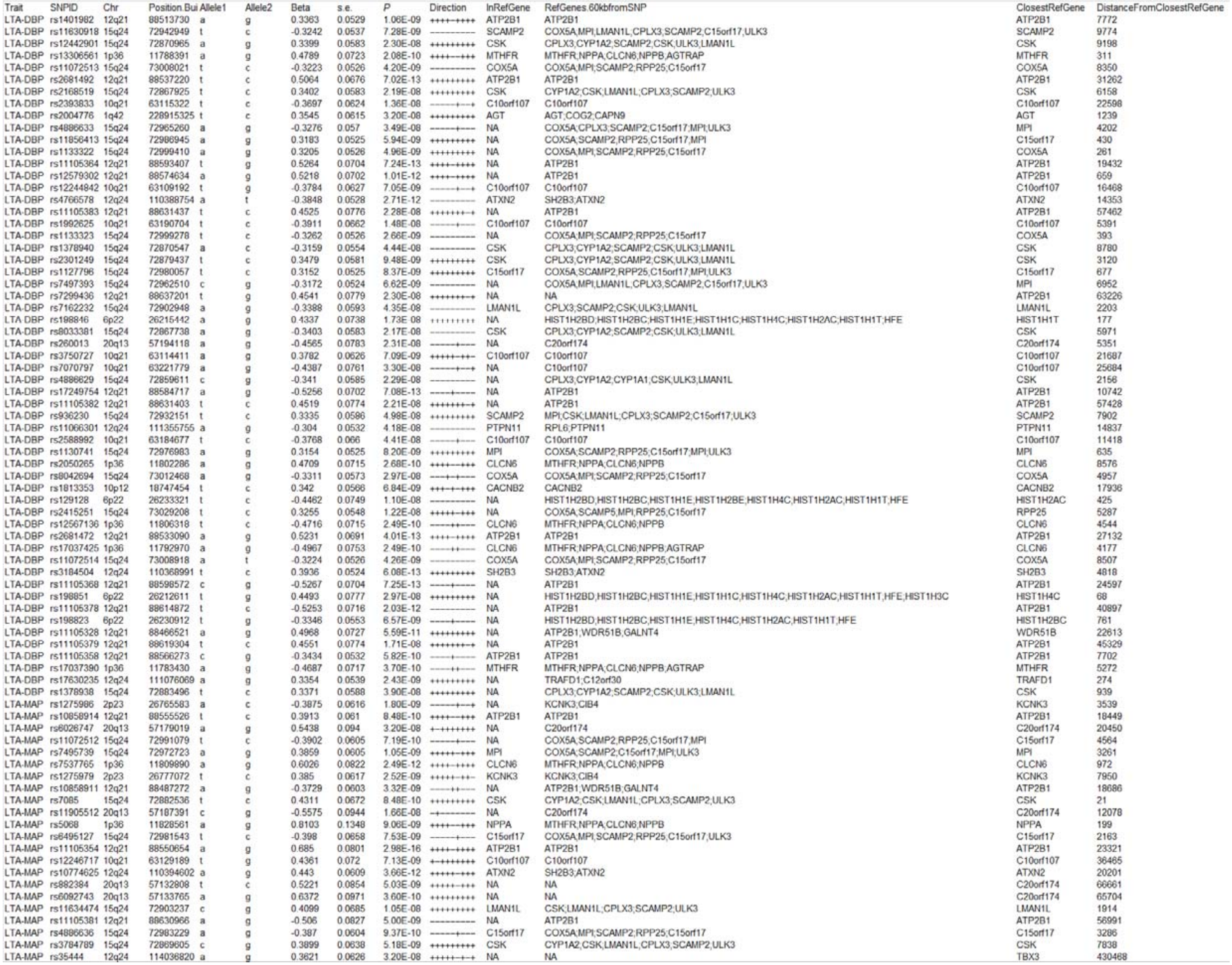
Table S4: All trait-SNPs with *P* value < 5x10-8 in the LTA analyses (LTA *P* value <5x10-8, Total 488 SNPs, 117 SBP, 96 DBP, 155 MAP, and 120 PP SNPs).



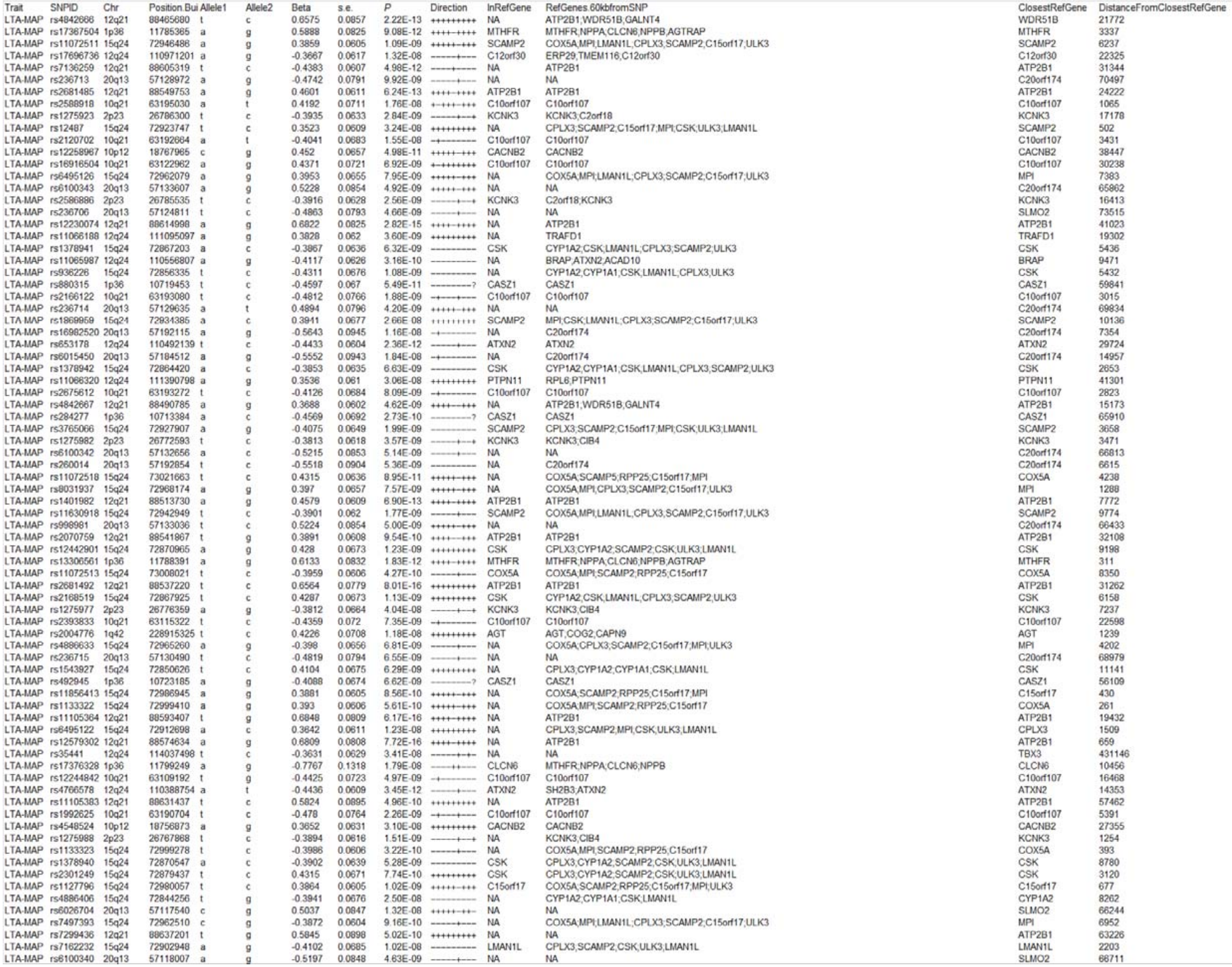
Trait	SNPID	Chr	Position Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-SBP	rs1275986	2p23	26765583	a	c	-0.5974	0.0917	3.22E-10	------+-+	NA	KCNK3;CIB4	KCNK3	3539
LTA-SBP	rs10858914	12q21	88555526	t	c	0.5902	0.0904	3.02E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	18449
LTA-SBP	rs7537765	1p36	11809890	a	g	0.8523	0.1221	1.60E-11	+++++++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA-SBP	rs1275979	2p23	26777072	t	c	0.5921	0.0919	5.15E-10	+++++-++-	KCNK3	KCNK3;CIB4	KCNK3	7950
LTA-SBP	rs10858911	12q21	88487272	a	g	-0.5607	0.0895	1.48E-09	----+----	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	18686
LTA-SBP	rs7085	15q24	72882536	t	c	0.5665	0.0997	4.22E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-SBP	rs5068	1p36	11828561	a	g	1.1766	0.1994	1.23E-08	+++++++++	NPPA	MTHFR;NPPA;CLCN6;NPPB	NPPA	199
LTA-SBP	rs11105354	12q21	88550654	a	g	0.9429	0.1186	1.69E-14	++++-++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-SBP	rs13031603	2q24	164803435	t	c	-0.582	0.0996	1.71E-08	----+----	NA	NA	GRB14	254143
LTA-SBP	rs10774625	12q24	110394602	a	g	0.5575	0.0909	3.25E-09	+++++-+++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LTA-SBP	rs882384	20q13	57132808	t	c	0.7241	0.1271	3.80E-08	+++++-+++	NA	NA	C20orf174	66661
LTA-SBP	rs6092743	20q13	57133765	a	g	0.8396	0.1449	2.25E-08	+++++++++	NA	NA	C20orf174	65704
LTA-SBP	rs1173770	5p13	32856968	t	c	-0.5468	0.0911	6.93E-09	----+----	NA	C5orf23;NPR3	C5orf23	29392
LTA-SBP	rs6712094	2q24	164751706	a	g	0.598	0.1007	9.89E-09	++++-++++	NA	NA	GRB14	305872
LTA-SBP	rs35444	12q24	114036820	a	g	0.5452	0.0929	1.47E-08	+++++-+-+	NA	NA	TBX3	430468
LTA-SBP	rs4842666	12q21	88465680	t	c	0.8816	0.1267	1.92E-11	++++-++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-SBP	rs1173727	5p13	32866278	t	c	-0.5439	0.0911	8.32E-09	----+----	NA	C5orf23;NPR3	C5orf23	38702
LTA-SBP	rs17367504	1p36	11785365	a	g	0.8355	0.1225	4.60E-11	+++++++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	3337
LTA-SBP	rs13035163	2q24	164781173	a	g	0.5775	0.0996	2.22E-08	++++-++++	NA	NA	GRB14	276405
LTA-SBP	rs13035934	2q24	164781318	a	g	-0.5772	0.0996	2.25E-08	----+----	NA	NA	GRB14	276260
LTA-SBP	rs12995749	2q24	164777689	t	c	-0.5795	0.0997	2.03E-08	----+----	NA	NA	GRB14	279889
LTA-SBP	rs1173747	5p13	32817909	a	c	0.512	0.0901	4.21E-08	++++-++++	NPR3	C5orf23;NPR3	NPR3	5100
LTA-SBP	rs7136259	12q21	88605319	t	c	-0.6301	0.0902	1.60E-11	----+----	NA	ATP2B1	ATP2B1	31344
LTA-SBP	rs2681485	12q21	88549753	a	g	0.687	0.0909	2.97E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-SBP	rs1275923	2p23	26786300	t	c	-0.6048	0.0943	6.02E-10	------+-+	KCNK3	KCNK3;C2orf18	KCNK3	17178
LTA-SBP	rs13154066	5p13	32867427	t	c	-0.5436	0.0911	8.41E-09	----+----	NA	C5orf23;NPR3	C5orf23	39851
LTA-SBP	rs979223	2q24	164803267	a	c	-0.577	0.0995	2.23E-08	----+----	NA	NA	GRB14	254311
LTA-SBP	rs1173743	5p13	32810804	t	g	0.5212	0.0907	2.95E-08	++++-++++	NPR3	C5orf23;NPR3	NPR3	12205
LTA-SBP	rs12258967	10p12	18767965	c	g	0.6307	0.0976	4.53E-10	+++++++++	CACNB2	CACNB2	CACNB2	38447
LTA-SBP	rs13004226	2q24	164788924	c	g	-0.5763	0.0995	2.28E-08	----+----	NA	NA	GRB14	268654
LTA-SBP	rs6100343	20q13	57133607	a	g	0.725	0.1272	3.76E-08	+++++-+++	NA	NA	C20orf174	65862
LTA-SBP	rs13030081	2q24	164796086	t	c	0.5731	0.1005	3.77E-08	++++-++++	NA	NA	GRB14	261492
LTA-SBP	rs12705390	7q22	106198013	a	g	0.6307	0.11	3.17E-08	++++--++-	NA	NA	PIK3CG	95146
LTA-SBP	rs2586886	2p23	26785535	t	c	-0.6016	0.0936	5.43E-10	------+-+	KCNK3	C2orf18;KCNK3	KCNK3	16413
LTA-SBP	rs12230074	12q21	88614998	a	g	0.934	0.1219	1.39E-13	++++-++++	NA	ATP2B1	ATP2B1	41023
LTA-SBP	rs4441488	2q24	164773873	t	c	0.5809	0.0998	1.92E-08	++++-++++	NA	NA	GRB14	283705
LTA-SBP	rs11065987	12q24	110556807	a	g	-0.5274	0.0931	4.50E-08	---------	NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-SBP	rs936226	15q24	72856335	t	c	-0.5733	0.1004	3.58E-08	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-SBP	rs6707357	2q24	164722539	t	c	-0.5232	0.0914	3.29E-08	-----+---	NA	NA	GRB14	335039
LTA-SBP	rs880315	1p36	10719453	t	c	-0.7125	0.1005	7.98E-12	--------?	CASZ1	CASZ1	CASZ1	59841
LTA-SBP	rs2166122	10q21	63193080	t	c	-0.6435	0.1137	4.75E-08	-+-------	C10orf107	C10orf107	C10orf107	3015
LTA-SBP	rs653178	12q24	110492139	t	c	-0.5508	0.0902	3.76E-09	-----+---	ATXN2	ATXN2	ATXN2	29724
LTA-SBP	rs13034053	2q24	164784645	a	t	-0.5762	0.0996	2.34E-08	----+----	NA	NA	GRB14	272933
LTA-SBP	rs4842667	12q21	88490785	a	g	0.5579	0.0894	1.69E-09	++++-++++	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	15173
LTA-SBP	rs284277	1p36	10713384	a	c	-0.7091	0.1044	5.54E-11	--------?	CASZ1	CASZ1	CASZ1	65910
LTA-SBP	rs1275982	2p23	26772593	t	c	-0.5881	0.0919	6.56E-10	------+-+	KCNK3	KCNK3;CIB4	KCNK3	3471
LTA-SBP	rs6100342	20q13	57132656	a	c	-0.7232	0.127	3.89E-08	-----+---	NA	NA	C20orf174	66813
LTA-SBP	rs11072518	15q24	73021663	t	c	0.5692	0.0947	6.54E-09	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
LTA-SBP	rs1401982	12q21	88513730	a	g	0.6828	0.0906	3.59E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	7772
LTA-SBP	rs998981	20q13	57133036	t	c	0.7246	0.1271	3.78E-08	+++++-+++	NA	NA	C20orf174	66433
LTA-SBP	rs2070759	12q21	88541867	t	g	0.5881	0.0902	3.19E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	32108
LTA-SBP	rs12442901	15q24	72870965	a	g	0.5675	0.1	4.34E-08	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	9198
LTA-SBP	rs11014049	10p12	18726458	a	g	-0.5453	0.0964	4.77E-08	---------	CACNB2	CACNB2	CACNB2	3060
LTA-SBP	rs13306561	1p36	11788391	a	g	0.8795	0.1235	6.38E-12	+++++++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	311
LTA-SBP	rs1439214	2q24	164778248	t	c	-0.5791	0.0997	2.07E-08	----+----	NA	NA	GRB14	279330
LTA-SBP	rs2681492	12q21	88537220	t	c	0.8967	0.1156	7.18E-14	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-SBP	rs2168519	15q24	72867925	t	c	0.5679	0.0999	4.18E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
LTA-SBP	rs1275977	2p23	26776359	a	g	-0.5862	0.099	1.11E-08	------+-+	KCNK3	KCNK3;CIB4	KCNK3	7237
LTA-SBP	rs492945	1p36	10723185	a	g	-0.5838	0.1005	2.10E-08	--------?	CASZ1	CASZ1	CASZ1	56109
LTA-SBP	rs13027527	2q24	164786950	a	g	-0.5768	0.0995	2.19E-08	----+----	NA	NA	GRB14	270628
LTA-SBP	rs11105364	12q21	88593407	t	g	0.9382	0.1197	3.81E-14	++++-++++	NA	ATP2B1	ATP2B1	19432
LTA-SBP	rs13021222	2q24	164756151	c	g	-0.5902	0.1008	1.60E-08	----+----	NA	NA	GRB14	301427
LTA-SBP	rs12579302	12q21	88574634	a	g	0.9342	0.1194	4.31E-14	++++-++++	NA	ATP2B1	ATP2B1	659
LTA-SBP	rs35441	12q24	114037498	t	c	-0.5471	0.0933	1.54E-08	-----+-+-	NA	NA	TBX3	431146
LTA-SBP	rs17376328	1p36	11799249	a	g	-1.1341	0.1958	2.26E-08	-----+---	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	10456
LTA-SBP	rs9292468	5p13	32854830	t	c	-0.5451	0.0911	7.76E-09	----+----	NA	C5orf23;NPR3	C5orf23	27254
LTA-SBP	rs13005481	2q24	164789612	t	c	-0.5758	0.0995	2.35E-08	----+----	NA	NA	GRB14	267966
LTA-SBP	rs4766578	12q24	110388754	a	t	-0.5599	0.0909	2.82E-09	-----+---	ATXN2	SH2B3;ATXN2	ATXN2	14353
LTA-SBP	rs17477177	7q22	106199094	t	c	-0.6322	0.1106	3.46E-08	-----++-+	NA	NA	PIK3CG	94065
LTA-SBP	rs11105383	12q21	88631437	t	c	0.7644	0.1329	2.83E-08	+++++++++	NA	ATP2B1	ATP2B1	57462
LTA-SBP	rs4548524	10p12	18756873	a	g	0.544	0.0935	1.97E-08	+++++++++	CACNB2	CACNB2	CACNB2	27355
LTA-SBP	rs1275988	2p23	26767868	t	c	-0.6004	0.0917	2.61E-10	------+-+	NA	KCNK3;CIB4	KCNK3	1254
LTA-SBP	rs2301249	15q24	72879437	t	c	0.566	0.0996	4.13E-08	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-SBP	rs6726740	2q24	164758374	t	g	0.5849	0.1008	2.15E-08	++++-++++	NA	NA	GRB14	299204
LTA-SBP	rs11687999	2q24	164774604	t	c	0.5809	0.0998	1.92E-08	++++-++++	NA	NA	GRB14	282974
LTA-SBP	rs7299436	12q21	88637201	t	g	0.7672	0.1334	2.84E-08	+++++++++	NA	NA	ATP2B1	63226
LTA-SBP	rs6100340	20q13	57118007	a	g	-0.7158	0.1261	4.31E-08	-----+---	NA	NA	SLMO2	66711



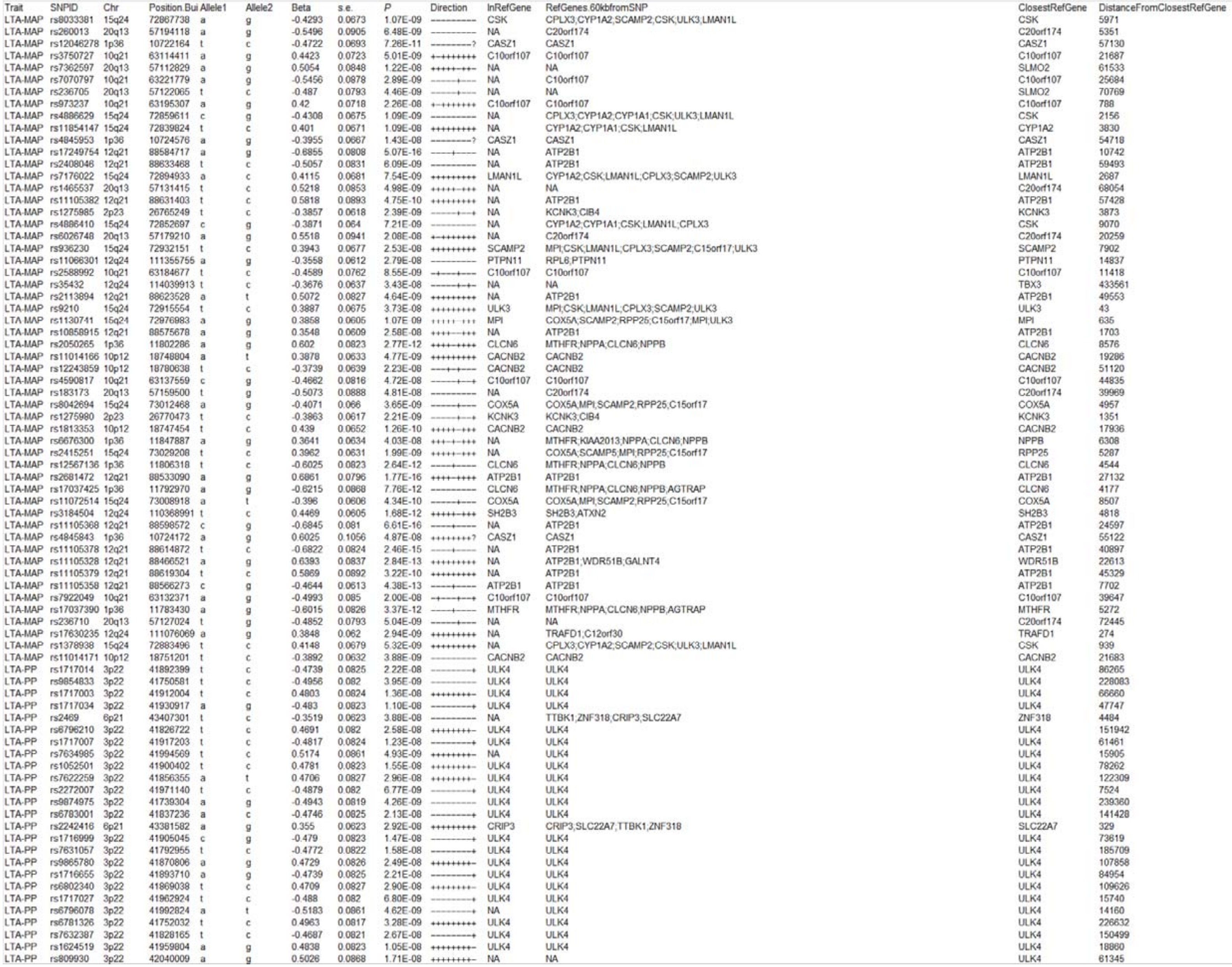
Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	P	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-SBP	rs8033381	15q24	72867738	a	g	-0.5689	0.1	3.97E-08	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-SBP	rs12995799	2q24	164798636	t	c	0.5788	0.0996	2.03E-08	++++-++++	NA	NA	GRB14	258942
LTA-SBP	rs12046278	1p36	10722164	t	c	-0.707	0.1039	5.12E-11	--------?	CASZ1	CASZ1	CASZ1	57130
LTA-SBP	rs11891401	2q24	164794993	a	t	-0.5844	0.0997	1.56E-08	----+----	NA	NA	GRB14	262585
LTA-SBP	rs7070797	10q21	63221779	a	g	-0.7415	0.1306	4.30E-08	-+---+---	NA	C10orf107	C10orf107	25684
LTA-SBP	rs4886629	15q24	72859611	c	g	-0.5728	0.1004	3.63E-08	---------	NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L	CSK	2156
LTA-SBP	rs7733331	5p13	32864603	t	c	-0.5505	0.0911	5.38E-09	----+----	NA	C5orf23;NPR3	C5orf23	37027
LTA-SBP	rs4845953	1p36	10724576	a	g	-0.5626	0.0995	4.84E-08	--------?	CASZ1	CASZ1	CASZ1	54718
LTA-SBP	rs12656497	5p13	32867696	t	c	-0.5432	0.0911	8.73E-09	----+----	NA	C5orf23;NPR3	C5orf23	40120
LTA-SBP	rs17249754	12q21	88584717	a	g	-0.9384	0.1194	3.37E-14	----+----	NA	ATP2B1	ATP2B1	10742
LTA-SBP	rs1465537	20q13	57131415	t	c	0.7232	0.127	3.86E-08	+++++-+++	NA	NA	C20orf174	68054
LTA-SBP	rs11105382	12q21	88631403	t	c	0.7637	0.1326	2.73E-08	+++++++++	NA	ATP2B1	ATP2B1	57428
LTA-SBP	rs1275985	2p23	26765249	t	c	-0.596	0.092	4.01E-10	-----+--+	NA	KCNK3;CIB4	KCNK3	3873
LTA-SBP	rs1173771	5p13	32850785	a	g	-0.5502	0.0911	5.63E-09	----+----	NA	C5orf23;NPR3	C5orf23	23209
LTA-SBP	rs35432	12q24	114039913	t	c	-0.5535	0.0945	1.58E-08	-----+-+-	NA	NA	TBX3	433561
LTA-SBP	rs10858915	12q21	88575678	a	g	0.5191	0.0903	2.92E-08	++++-++++	NA	ATP2B1	ATP2B1	1703
LTA-SBP	rs1439211	2q24	164802546	a	c	-0.5887	0.1035	4.06E-08	----+----	NA	NA	GRB14	255032
LTA-SBP	rs2050265	1p36	11802286	a	g	0.8509	0.1222	1.84E-11	+++++++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	8576
LTA-SBP	rs11014166	10p12	18748804	a	t	0.5638	0.0939	6.88E-09	+++++++++	CACNB2	CACNB2	CACNB2	19286
LTA-SBP	rs10774792	12q24	114036981	t	c	-0.5502	0.094	1.63E-08	-----+---	NA	NA	TBX3	430629
LTA-SBP	rs1173756	5p13	32825609	t	c	-0.5175	0.0896	2.52E-08	----+----	C5orf23	C5orf23;NPR3	C5orf23	908
LTA-SBP	rs1275980	2p23	26770473	t	c	-0.5947	0.0919	4.18E-10	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	1351
LTA-SBP	rs1813353	10p12	18747454	t	c	0.623	0.0968	5.31E-10	+++++-+++	CACNB2	CACNB2	CACNB2	17936
LTA-SBP	rs6676300	1p36	11847887	a	g	0.5541	0.0942	1.40E-08	+++-+-+++	NA	MTHFR;KIAA2013;NPPA;CLCN6;NPPB	NPPB	6308
LTA-SBP	rs12567136	1p36	11806318	t	c	-0.8529	0.1222	1.63E-11	---------	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA-SBP	rs2681472	12q21	88533090	a	g	0.9457	0.118	1.04E-14	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
LTA-SBP	rs17037425	1p36	11792970	a	g	-0.8574	0.1292	1.51E-10	---------	CLCN6	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	4177
LTA-SBP	rs1371181	2q24	164784974	t	c	0.5764	0.0995	2.28E-08	++++-++++	NA	NA	GRB14	272604
LTA-SBP	rs10432461	2q24	164772752	a	t	-0.5812	0.0998	1.93E-08	----+----	NA	NA	GRB14	284826
LTA-SBP	rs3184504	12q24	110368991	t	c	0.5549	0.0903	3.04E-09	+++++-+++	SH2B3	SH2B3;ATXN2	SH2B3	4818
LTA-SBP	rs11105368	12q21	88598572	c	g	-0.9371	0.1197	4.21E-14	----+----	NA	ATP2B1	ATP2B1	24597
LTA-SBP	rs13007966	2q24	164784819	t	c	-0.5762	0.0996	2.33E-08	----+----	NA	NA	GRB14	272759
LTA-SBP	rs11105378	12q21	88614872	t	c	-0.9344	0.1216	1.23E-13	----+----	NA	ATP2B1	ATP2B1	40897
LTA-SBP	rs11105328	12q21	88466521	a	g	0.8655	0.1239	1.57E-11	++++-++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	22613
LTA-SBP	rs1898841	2q24	164778453	t	c	0.5785	0.0997	2.12E-08	++++-++++	NA	NA	GRB14	279125
LTA-SBP	rs11105379	12q21	88619304	t	c	0.7704	0.1325	2.03E-08	+++++++++	NA	ATP2B1	ATP2B1	45329
LTA-SBP	rs11105358	12q21	88566273	c	g	-0.6895	0.0911	2.77E-13	----+----	ATP2B1	ATP2B1	ATP2B1	7702
LTA-SBP	rs17037390	1p36	11783430	a	g	-0.8558	0.1226	1.60E-11	---------	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	5272
LTA-SBP	rs1173766	5p13	32840285	t	c	-0.5294	0.0917	2.52E-08	----+----	NA	C5orf23;NPR3	C5orf23	12709
LTA-SBP	rs11014171	10p12	18751201	t	c	-0.5679	0.0937	4.97E-09	---------	CACNB2	CACNB2	CACNB2	21683
LTA-DBP	rs11072512	15q24	72991079	t	c	-0.3193	0.0525	5.53E-09	---------	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	4564
LTA-DBP	rs7495739	15q24	72972723	a	g	0.3158	0.0524	7.78E-09	+++++++++	MPI	COX5A;SCAMP2;C15orf17;MPI;ULK3	MPI	3261
LTA-DBP	rs7537765	1p36	11809890	a	g	0.4718	0.0714	2.36E-10	++++--+++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA-DBP	rs7085	15q24	72882536	t	c	0.3468	0.0582	1.10E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-DBP	rs198833	6p22	26222487	a	g	-0.4345	0.0741	1.91E-08	---------	NA	HIST1H1T;HIST1H2BD;HIST1H2BC;HIST1H1E;HFE;HIST1H1C;HIST1H4C;HIST1H2AC	HIST1H1T	6144
LTA-DBP	rs6495127	15q24	72981543	t	c	-0.3262	0.0571	4.40E-08	-----+---	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17;ULK3	C15orf17	2163
LTA-DBP	rs11105354	12q21	88550654	a	g	0.5235	0.0696	5.40E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-DBP	rs12246717	10q21	63129189	t	g	0.3693	0.0624	1.39E-08	+++++-++-	C10orf107	C10orf107	C10orf107	36465
LTA-DBP	rs10774625	12q24	110394602	a	g	0.3848	0.0528	2.74E-12	+++++++++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LTA-DBP	rs6092743	20q13	57133765	a	g	0.502	0.0843	1.11E-08	+++++-+++	NA	NA	C20orf174	65704
LTA-DBP	rs11634474	15q24	72903237	c	g	0.3384	0.0593	4.51E-08	+++++++++	LMAN1L	CSK;LMAN1L;CPLX3;SCAMP2;ULK3	LMAN1L	1914
LTA-DBP	rs4886636	15q24	72983229	a	g	-0.3123	0.0524	1.13E-08	---------	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17	C15orf17	3286
LTA-DBP	rs3784789	15q24	72869605	c	g	0.3166	0.0553	3.98E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	7838
LTA-DBP	rs4842666	12q21	88465680	t	c	0.5108	0.0745	4.88E-11	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-DBP	rs17367504	1p36	11785365	a	g	0.4598	0.0717	7.61E-10	++++--+++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	3337
LTA-DBP	rs11072511	15q24	72946486	a	g	0.3165	0.0525	7.35E-09	+++++++++	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	6237
LTA-DBP	rs17696736	12q24	110971201	a	g	-0.3131	0.0536	2.16E-08	---------	C12orf30	ERP29;TMEM116;C12orf30	C12orf30	22325
LTA-DBP	rs7136259	12q21	88605319	t	c	-0.3314	0.0526	1.55E-09	----+--+-	NA	ATP2B1	ATP2B1	31344
LTA-DBP	rs2681485	12q21	88549753	a	g	0.3385	0.053	9.22E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-DBP	rs1799945	6p22	26199158	c	g	-0.4226	0.074	4.33E-08	---------	HFE	HIST1H2BC;HIST1H1C;HIST1H3B;HIST1H4C;HIST1H2BB;HIST1H2AC;HIST1H1T;HIST1H2AB;HFE;HIST1H3C	HFE	3671
LTA-DBP	rs2120702	10q21	63192664	a	t	-0.3402	0.0592	3.56E-08	-----+---	C10orf107	C10orf107	C10orf107	3431
LTA-DBP	rs12258967	10p12	18767965	c	g	0.3548	0.0571	2.48E-09	+++-+-+++	CACNB2	CACNB2	CACNB2	38447
LTA-DBP	rs16916504	10q21	63122962	a	g	0.3706	0.0625	1.30E-08	+++++-++-	C10orf107	C10orf107	C10orf107	30238
LTA-DBP	rs6495126	15q24	72962079	a	g	0.3253	0.0568	4.03E-08	+++++-+++	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	7383
LTA-DBP	rs7599598	2q11	96715567	a	g	-0.314	0.0543	2.91E-08	---------	NA	FLJ10081;FER1L5;LMAN2L	FER1L5	9353
LTA-DBP	rs12230074	12q21	88614998	a	g	0.5255	0.0718	2.23E-12	+++++++++	NA	ATP2B1	ATP2B1	41023
LTA-DBP	rs11066188	12q24	111095097	a	g	0.3343	0.0539	2.76E-09	+++++++++	NA	TRAFD1	TRAFD1	19302
LTA-DBP	rs1378941	15q24	72867203	a	c	-0.3135	0.0551	4.98E-08	---------	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	5436
LTA-DBP	rs11065987	12q24	110556807	a	g	-0.3534	0.0543	4.52E-10	---------	NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-DBP	rs936226	15q24	72856335	t	c	-0.3413	0.0585	2.26E-08	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-DBP	rs2166122	10q21	63193080	t	c	-0.3932	0.0663	1.32E-08	-----+---	C10orf107	C10orf107	C10orf107	3015
LTA-DBP	rs653178	12q24	110492139	t	c	-0.3911	0.0524	7.85E-13	---------	ATXN2	ATXN2	ATXN2	29724
LTA-DBP	rs1378942	15q24	72864420	a	c	-0.3128	0.055	5.00E-08	---------	CSK	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	2653
LTA-DBP	rs11066320	12q24	111390798	a	g	0.303	0.053	4.11E-08	+++++++++	PTPN11	RPL6;PTPN11	PTPN11	41301
LTA-DBP	rs2675612	10q21	63193272	t	c	-0.3502	0.0593	1.47E-08	-----+---	C10orf107	C10orf107	C10orf107	2823
LTA-DBP	rs3765066	15q24	72927907	a	g	-0.3388	0.0563	7.81E-09	---------	SCAMP2	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	3658
LTA-DBP	rs260014	20q13	57192854	t	c	-0.4584	0.0782	1.92E-08	-----+---	NA	C20orf174	C20orf174	6615
LTA-DBP	rs11072518	15q24	73021663	t	c	0.3405	0.0552	3.29E-09	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
LTA-DBP	rs8031937	15q24	72968174	a	g	0.3264	0.057	4.01E-08	+++++-+++	NA	COX5A;MPI;CPLX3;SCAMP2;C15orf17;ULK3	MPI	1288



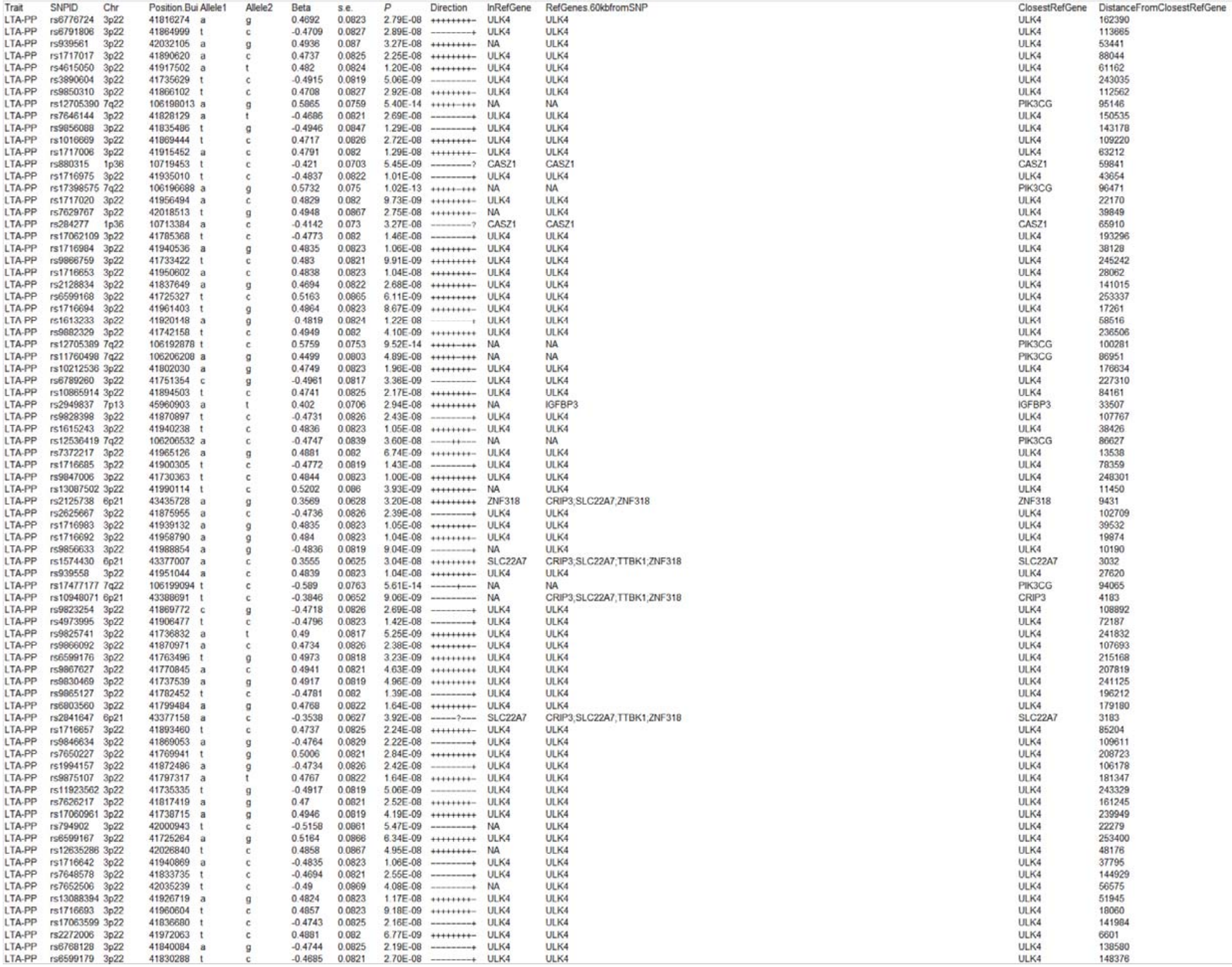
Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	P	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-DBP	rs1401982	12q21	88513730	a	g	0.3363	0.0529	1.06E-09	++++-++++	ATP2B1	ATP2B1	ATP2B1	7772
LTA-DBP	rs11630918	15q24	72942949	t	c	-0.3242	0.0537	7.28E-09	---------	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	9774
LTA-DBP	rs12442901	15q24	72870965	a	g	0.3399	0.0583	2.30E-08	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	9198
LTA-DBP	rs13306561	1p36	11788391	a	g	0.4789	0.0723	2.08E-10	++++--+++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	311
LTA-DBP	rs11072513	15q24	73008021	t	c	-0.3223	0.0526	4.20E-09	---------	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8350
LTA-DBP	rs2681492	12q21	88537220	t	c	0.5064	0.0676	7.02E-13	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-DBP	rs2168519	15q24	72867925	t	c	0.3402	0.0583	2.19E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
LTA-DBP	rs2393833	10q21	63115322	t	c	-0.3697	0.0624	1.36E-08	-----+--+	C10orf107	C10orf107	C10orf107	22598
LTA-DBP	rs2004776	1q42	228915325	t	c	0.3545	0.0615	3.20E-08	+++++++++	AGT	AGT;COG2;CAPN9	AGT	1239
LTA-DBP	rs4886633	15q24	72965260	a	g	-0.3276	0.057	3.49E-08	-----+---	NA	COX5A;CPLX3;SCAMP2;C15orf17;MPI;ULK3	MPI	4202
LTA-DBP	rs11856413	15q24	72986945	a	g	0.3183	0.0525	5.94E-09	+++++++++	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	430
LTA-DBP	rs1133322	15q24	72999410	a	g	0.3205	0.0526	4.96E-09	+++++++++	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	261
LTA-DBP	rs11105364	12q21	88593407	t	g	0.5264	0.0704	7.24E-13	++++-++++	NA	ATP2B1	ATP2B1	19432
LTA-DBP	rs12579302	12q21	88574634	a	g	0.5218	0.0702	1.01E-12	++++-++++	NA	ATP2B1	ATP2B1	659
LTA-DBP	rs12244842	10q21	63109192	t	g	-0.3784	0.0627	7.05E-09	-----+--+	C10orf107	C10orf107	C10orf107	16468
LTA-DBP	rs4766578	12q24	110388754	a	t	-0.3848	0.0528	2.71E-12	---------	ATXN2	SH2B3;ATXN2	ATXN2	14353
LTA-DBP	rs11105383	12q21	88631437	t	c	0.4525	0.0776	2.28E-08	+++++++-+	NA	ATP2B1	ATP2B1	57462
LTA-DBP	rs1992625	10q21	63190704	t	c	-0.3911	0.0662	1.48E-08	-----+---	C10orf107	C10orf107	C10orf107	5391
LTA-DBP	rs1133323	15q24	72999278	t	c	-0.3262	0.0526	2.66E-09	---------	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	393
LTA-DBP	rs1378940	15q24	72870547	a	c	-0.3159	0.0554	4.44E-08	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	8780
LTA-DBP	rs2301249	15q24	72879437	t	c	0.3479	0.0581	9.48E-09	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-DBP	rs1127796	15q24	72980057	t	c	0.3152	0.0525	8.37E-09	+++++++++	C15orf17	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	C15orf17	677
LTA-DBP	rs7497393	15q24	72962510	c	g	-0.3172	0.0524	6.62E-09	---------	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	6952
LTA-DBP	rs7299436	12q21	88637201	t	g	0.4541	0.0779	2.30E-08	+++++++-+	NA	NA	ATP2B1	63226
LTA-DBP	rs7162232	15q24	72902948	a	g	-0.3388	0.0593	4.35E-08	---------	LMAN1L	CPLX3;SCAMP2;CSK;ULK3;LMAN1L	LMAN1L	2203
LTA-DBP	rs198846	6p22	26215442	a	g	0.4337	0.0738	1.73E-08	+++++++++	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H1C;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H1T	177
LTA-DBP	rs8033381	15q24	72867738	a	g	-0.3403	0.0583	2.17E-08	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-DBP	rs260013	20q13	57194118	a	g	-0.4565	0.0783	2.31E-08	-----+---	NA	C20orf174	C20orf174	5351
LTA-DBP	rs3750727	10q21	63114411	a	g	0.3782	0.0626	7.09E-09	+++++-++-	C10orf107	C10orf107	C10orf107	21687
LTA-DBP	rs7070797	10q21	63221779	a	g	-0.4387	0.0761	3.30E-08	-----+--+	NA	C10orf107	C10orf107	25684
LTA-DBP	rs4886629	15q24	72859611	c	g	-0.341	0.0585	2.29E-08	---------	NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L	CSK	2156
LTA-DBP	rs17249754	12q21	88584717	a	g	-0.5256	0.0702	7.08E-13	----+----	NA	ATP2B1	ATP2B1	10742
LTA-DBP	rs11105382	12q21	88631403	t	c	0.4519	0.0774	2.21E-08	+++++++-+	NA	ATP2B1	ATP2B1	57428
LTA-DBP	rs936230	15q24	72932151	t	c	0.3335	0.0586	4.98E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	7902
LTA-DBP	rs11066301	12q24	111355755	a	g	-0.304	0.0532	4.18E-08	---------	PTPN11	RPL6;PTPN11	PTPN11	14837
LTA-DBP	rs2588992	10q21	63184677	t	c	-0.3768	0.066	4.41E-08	-----+---	C10orf107	C10orf107	C10orf107	11418
LTA-DBP	rs1130741	15q24	72976983	a	g	0.3154	0.0525	8.20E-09	+++++++++	MPI	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	MPI	635
LTA-DBP	rs2050265	1p36	11802286	a	g	0.4709	0.0715	2.68E-10	++++--+++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	8576
LTA-DBP	rs8042694	15q24	73012468	a	g	-0.3311	0.0573	2.97E-08	---+-+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	4957
LTA-DBP	rs1813353	10p12	18747454	t	c	0.342	0.0566	6.84E-09	+++-+-+++	CACNB2	CACNB2	CACNB2	17936
LTA-DBP	rs129128	6p22	26233321	t	c	-0.4462	0.0749	1.10E-08	---------	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H2BE;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H2AC	425
LTA-DBP	rs2415251	15q24	73029208	t	c	0.3255	0.0548	1.22E-08	+++++-+++	NA	COX5A;SCAMP5;MPI;RPP25;C15orf17	RPP25	5287
LTA-DBP	rs12567136	1p36	11806318	t	c	-0.4716	0.0715	2.49E-10	----++---	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA-DBP	rs2681472	12q21	88533090	a	g	0.5231	0.0691	4.01E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
LTA-DBP	rs17037425	1p36	11792970	a	g	-0.4967	0.0753	2.49E-10	----++---	CLCN6	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	4177
LTA-DBP	rs11072514	15q24	73008918	a	t	-0.3224	0.0526	4.26E-09	---------	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8507
LTA-DBP	rs3184504	12q24	110368991	t	c	0.3936	0.0524	6.08E-13	+++++++++	SH2B3	SH2B3;ATXN2	SH2B3	4818
LTA-DBP	rs11105368	12q21	88598572	c	g	-0.5267	0.0704	7.25E-13	----+----	NA	ATP2B1	ATP2B1	24597
LTA-DBP	rs198851	6p22	26212611	t	g	0.4493	0.0777	2.97E-08	+++++++++	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H1C;HIST1H4C;HIST1H2AC;HIST1H1T;HFE;HIST1H3C	HIST1H4C	68
LTA-DBP	rs11105378	12q21	88614872	t	c	-0.5253	0.0716	2.03E-12	---------	NA	ATP2B1	ATP2B1	40897
LTA-DBP	rs198823	6p22	26230912	t	g	-0.3346	0.0553	6.57E-09	----+----	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H2BC	761
LTA-DBP	rs11105328	12q21	88466521	a	g	0.4968	0.0727	5.59E-11	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	22613
LTA-DBP	rs11105379	12q21	88619304	t	c	0.4551	0.0774	1.71E-08	+++++++-+	NA	ATP2B1	ATP2B1	45329
LTA-DBP	rs11105358	12q21	88566273	c	g	-0.3434	0.0532	5.82E-10	----+----	ATP2B1	ATP2B1	ATP2B1	7702
LTA-DBP	rs17037390	1p36	11783430	a	g	-0.4687	0.0717	3.70E-10	----++---	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	5272
LTA-DBP	rs17630235	12q24	111076069	a	g	0.3354	0.0539	2.43E-09	+++++++++	NA	TRAFD1;C12orf30	TRAFD1	274
LTA-DBP	rs1378938	15q24	72883496	t	c	0.3371	0.0588	3.90E-08	+++++++++	NA	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	939
LTA-MAP	rs1275986	2p23	26765583	a	c	-0.3875	0.0616	1.80E-09	-----+--+	NA	KCNK3;CIB4	KCNK3	3539
LTA-MAP	rs10858914	12q21	88555526	t	c	0.3913	0.061	8.48E-10	++++--+++	ATP2B1	ATP2B1	ATP2B1	18449
LTA-MAP	rs6026747	20q13	57179019	a	g	0.5438	0.094	3.20E-08	+-+++++++	NA	C20orf174	C20orf174	20450
LTA-MAP	rs11072512	15q24	72991079	t	c	-0.3902	0.0605	7.19E-10	-----+---	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	4564
LTA-MAP	rs7495739	15q24	72972723	a	g	0.3859	0.0605	1.05E-09	+++++-+++	MPI	COX5A;SCAMP2;C15orf17;MPI;ULK3	MPI	3261
LTA-MAP	rs7537765	1p36	11809890	a	g	0.6026	0.0822	2.49E-12	++++-++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA-MAP	rs1275979	2p23	26777072	t	c	0.385	0.0617	2.52E-09	+++++-++-	KCNK3	KCNK3;CIB4	KCNK3	7950
LTA-MAP	rs10858911	12q21	88487272	a	g	-0.3729	0.0603	3.32E-09	----++---	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	18686
LTA-MAP	rs7085	15q24	72882536	t	c	0.4311	0.0672	8.48E-10	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-MAP	rs11905512	20q13	57187391	c	g	-0.5575	0.0944	1.66E-08	-+-------	NA	C20orf174	C20orf174	12078
LTA-MAP	rs5068	1p36	11828561	a	g	0.8103	0.1348	9.06E-09	++++--+++	NPPA	MTHFR;NPPA;CLCN6;NPPB	NPPA	199
LTA-MAP	rs6495127	15q24	72981543	t	c	-0.398	0.0658	7.53E-09	-----+---	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17;ULK3	C15orf17	2163
LTA-MAP	rs11105354	12q21	88550654	a	g	0.685	0.0801	2.98E-16	++++-++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-MAP	rs12246717	10q21	63129189	t	g	0.4361	0.072	7.13E-09	+-+++++++	C10orf107	C10orf107	C10orf107	36465
LTA-MAP	rs10774625	12q24	110394602	a	g	0.443	0.0609	3.66E-12	+++++-+++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LTA-MAP	rs882384	20q13	57132808	t	c	0.5221	0.0854	5.03E-09	+++++-+++	NA	NA	C20orf174	66661
LTA-MAP	rs6092743	20q13	57133765	a	g	0.6372	0.0971	3.60E-10	+++++++++	NA	NA	C20orf174	65704
LTA-MAP	rs11634474	15q24	72903237	c	g	0.4099	0.0685	1.05E-08	+++++++++	LMAN1L	CSK;LMAN1L;CPLX3;SCAMP2;ULK3	LMAN1L	1914
LTA-MAP	rs11105381	12q21	88630966	a	g	-0.506	0.0827	5.00E-09	---------	NA	ATP2B1	ATP2B1	56991
LTA-MAP	rs4886636	15q24	72983229	a	g	-0.387	0.0604	9.37E-10	-----+---	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17	C15orf17	3286
LTA-MAP	rs3784789	15q24	72869605	c	g	0.3899	0.0638	5.18E-09	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	7838
LTA-MAP	rs35444	12q24	114036820	a	g	0.3621	0.0626	3.20E-08	+++++-+-+	NA	NA	TBX3	430468



Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-MAP	rs4842666	12q21	88465680	t	c	0.6575	0.0857	2.22E-13	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-MAP	rs17367504	1p36	11785365	a	g	0.5888	0.0825	9.08E-12	++++-++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	3337
LTA-MAP	rs11072511	15q24	72946486	a	g	0.3859	0.0605	1.09E-09	+++++-+++	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	6237
LTA-MAP	rs17696736	12q24	110971201	a	g	-0.3667	0.0617	1.32E-08	-----+---	C12orf30	ERP29;TMEM116;C12orf30	C12orf30	22325
LTA-MAP	rs7136259	12q21	88605319	t	c	-0.4383	0.0607	4.98E-12	----+----	NA	ATP2B1	ATP2B1	31344
LTA-MAP	rs236713	20q13	57128972	a	g	-0.4742	0.0791	9.92E-09	-----+---	NA	NA	C20orf174	70497
LTA-MAP	rs2681485	12q21	88549753	a	g	0.4601	0.0611	6.24E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-MAP	rs2588918	10q21	63195030	a	t	0.4192	0.0711	1.76E-08	+-+++-+++	C10orf107	C10orf107	C10orf107	1065
LTA-MAP	rs1275923	2p23	26786300	t	c	-0.3935	0.0633	2.84E-09	-----+--+	KCNK3	KCNK3;C2orf18	KCNK3	17178
LTA-MAP	rs12487	15q24	72923747	t	c	0.3523	0.0609	3.24E-08	+++++++++	NA	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	502
LTA-MAP	rs2120702	10q21	63192664	a	t	-0.4041	0.0683	1.55E-08	-+-------	C10orf107	C10orf107	C10orf107	3431
LTA-MAP	rs12258967	10p12	18767965	c	g	0.452	0.0657	4.98E-11	+++++-+++	CACNB2	CACNB2	CACNB2	38447
LTA-MAP	rs16916504	10q21	63122962	a	g	0.4371	0.0721	6.92E-09	+-+++++++	C10orf107	C10orf107	C10orf107	30238
LTA-MAP	rs6495126	15q24	72962079	a	g	0.3953	0.0655	7.95E-09	+++++-+++	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	7383
LTA-MAP	rs6100343	20q13	57133607	a	g	0.5228	0.0854	4.92E-09	+++++-+++	NA	NA	C20orf174	65862
LTA-MAP	rs2586886	2p23	26785535	t	c	-0.3916	0.0628	2.56E-09	-----+--+	KCNK3	C2orf18;KCNK3	KCNK3	16413
LTA-MAP	rs236706	20q13	57124811	t	c	-0.4863	0.0793	4.66E-09	-----+---	NA	NA	SLMO2	73515
LTA-MAP	rs12230074	12q21	88614998	a	g	0.6822	0.0825	2.82E-15	++++-++++	NA	ATP2B1	ATP2B1	41023
LTA-MAP	rs11066188	12q24	111095097	a	g	0.3828	0.062	3.60E-09	+++++++++	NA	TRAFD1	TRAFD1	19302
LTA-MAP	rs1378941	15q24	72867203	a	c	-0.3867	0.0636	6.32E-09	---------	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	5436
LTA-MAP	rs11065987	12q24	110556807	a	g	-0.4117	0.0626	3.16E-10	---------	NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-MAP	rs936226	15q24	72856335	t	c	-0.4311	0.0676	1.08E-09	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-MAP	rs880315	1p36	10719453	t	c	-0.4597	0.067	5.49E-11	--------?	CASZ1	CASZ1	CASZ1	59841
LTA-MAP	rs2166122	10q21	63193080	t	c	-0.4812	0.0766	1.88E-09	-+---+---	C10orf107	C10orf107	C10orf107	3015
LTA-MAP	rs236714	20q13	57129635	a	t	0.4894	0.0796	4.20E-09	+++++-+++	NA	NA	C20orf174	69834
LTA-MAP	rs1869959	15q24	72934385	a	c	0.3941	0.0677	2.66E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	10136
LTA-MAP	rs16982520	20q13	57192115	a	g	-0.5643	0.0945	1.16E-08	-+-------	NA	C20orf174	C20orf174	7354
LTA-MAP	rs653178	12q24	110492139	t	c	-0.4433	0.0604	2.36E-12	-----+---	ATXN2	ATXN2	ATXN2	29724
LTA-MAP	rs6015450	20q13	57184512	a	g	-0.5552	0.0943	1.84E-08	-+-------	NA	C20orf174	C20orf174	14957
LTA-MAP	rs1378942	15q24	72864420	a	c	-0.3853	0.0635	6.63E-09	---------	CSK	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	2653
LTA-MAP	rs11066320	12q24	111390798	a	g	0.3536	0.061	3.06E-08	+++++++++	PTPN11	RPL6;PTPN11	PTPN11	41301
LTA-MAP	rs2675612	10q21	63193272	t	c	-0.4126	0.0684	8.09E-09	-+-------	C10orf107	C10orf107	C10orf107	2823
LTA-MAP	rs4842667	12q21	88490785	a	g	0.3688	0.0602	4.62E-09	++++--+++	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	15173
LTA-MAP	rs284277	1p36	10713384	a	c	-0.4569	0.0692	2.73E-10	--------?	CASZ1	CASZ1	CASZ1	65910
LTA-MAP	rs3765066	15q24	72927907	a	g	-0.4075	0.0649	1.99E-09	---------	SCAMP2	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	3658
LTA-MAP	rs1275982	2p23	26772593	t	c	-0.3813	0.0618	3.57E-09	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	3471
LTA-MAP	rs6100342	20q13	57132656	a	c	-0.5215	0.0853	5.14E-09	-----+---	NA	NA	C20orf174	66813
LTA-MAP	rs260014	20q13	57192854	t	c	-0.5518	0.0904	5.36E-09	---------	NA	C20orf174	C20orf174	6615
LTA-MAP	rs11072518	15q24	73021663	t	c	0.4315	0.0636	8.95E-11	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
LTA-MAP	rs8031937	15q24	72968174	a	g	0.397	0.0657	7.57E-09	+++++-+++	NA	COX5A;MPI;CPLX3;SCAMP2;C15orf17;ULK3	MPI	1288
LTA-MAP	rs1401982	12q21	88513730	a	g	0.4579	0.0609	6.90E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	7772
LTA-MAP	rs11630918	15q24	72942949	t	c	-0.3901	0.062	1.77E-09	-----+---	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	9774
LTA-MAP	rs998981	20q13	57133036	t	c	0.5224	0.0854	5.00E-09	+++++-+++	NA	NA	C20orf174	66433
LTA-MAP	rs2070759	12q21	88541867	t	g	0.3891	0.0608	9.54E-10	++++--+++	ATP2B1	ATP2B1	ATP2B1	32108
LTA-MAP	rs12442901	15q24	72870965	a	g	0.428	0.0673	1.23E-09	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	9198
LTA-MAP	rs13306561	1p36	11788391	a	g	0.6133	0.0832	1.83E-12	++++-++++	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	311
LTA-MAP	rs11072513	15q24	73008021	t	c	-0.3959	0.0606	4.27E-10	-----+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8350
LTA-MAP	rs2681492	12q21	88537220	t	c	0.6564	0.0779	8.01E-16	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-MAP	rs2168519	15q24	72867925	t	c	0.4287	0.0673	1.13E-09	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
LTA-MAP	rs1275977	2p23	26776359	a	g	-0.3812	0.0664	4.04E-08	-----+--+	KCNK3	KCNK3;CIB4	KCNK3	7237
LTA-MAP	rs2393833	10q21	63115322	t	c	-0.4359	0.072	7.35E-09	-+-------	C10orf107	C10orf107	C10orf107	22598
LTA-MAP	rs2004776	1q42	228915325	t	c	0.4226	0.0708	1.18E-08	+++++++++	AGT	AGT;COG2;CAPN9	AGT	1239
LTA-MAP	rs4886633	15q24	72965260	a	g	-0.398	0.0656	6.81E-09	-----+---	NA	COX5A;CPLX3;SCAMP2;C15orf17;MPI;ULK3	MPI	4202
LTA-MAP	rs236715	20q13	57130490	t	c	-0.4819	0.0794	6.55E-09	-----+---	NA	NA	C20orf174	68979
LTA-MAP	rs1543927	15q24	72850626	t	c	0.4104	0.0675	6.29E-09	+++++++++	NA	CPLX3;CYP1A2;CYP1A1;CSK;LMAN1L	CSK	11141
LTA-MAP	rs492945	1p36	10723185	a	g	-0.4088	0.0674	6.62E-09	--------?	CASZ1	CASZ1	CASZ1	56109
LTA-MAP	rs11856413	15q24	72986945	a	g	0.3881	0.0605	8.56E-10	+++++-+++	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	430
LTA-MAP	rs1133322	15q24	72999410	a	g	0.393	0.0606	5.61E-10	+++++-+++	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	261
LTA-MAP	rs11105364	12q21	88593407	t	g	0.6848	0.0809	6.17E-16	++++-++++	NA	ATP2B1	ATP2B1	19432
LTA-MAP	rs6495122	15q24	72912698	a	c	0.3642	0.0611	1.23E-08	+++++++++	NA	CPLX3;SCAMP2;MPI;CSK;ULK3;LMAN1L	CPLX3	1509
LTA-MAP	rs12579302	12q21	88574634	a	g	0.6809	0.0808	7.72E-16	++++-++++	NA	ATP2B1	ATP2B1	659
LTA-MAP	rs35441	12q24	114037498	t	c	-0.3631	0.0629	3.41E-08	-----+-+-	NA	NA	TBX3	431146
LTA-MAP	rs17376328	1p36	11799249	a	g	-0.7767	0.1318	1.79E-08	----++---	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	10456
LTA-MAP	rs12244842	10q21	63109192	t	g	-0.4425	0.0723	4.97E-09	-+-------	C10orf107	C10orf107	C10orf107	16468
LTA-MAP	rs4766578	12q24	110388754	a	t	-0.4436	0.0609	3.45E-12	-----+---	ATXN2	SH2B3;ATXN2	ATXN2	14353
LTA-MAP	rs11105383	12q21	88631437	t	c	0.5824	0.0895	4.96E-10	+++++++++	NA	ATP2B1	ATP2B1	57462
LTA-MAP	rs1992625	10q21	63190704	t	c	-0.478	0.0764	2.26E-09	-+---+---	C10orf107	C10orf107	C10orf107	5391
LTA-MAP	rs4548524	10p12	18756873	a	g	0.3652	0.0631	3.10E-08	+++++++++	CACNB2	CACNB2	CACNB2	27355
LTA-MAP	rs1275988	2p23	26767868	t	c	-0.3894	0.0616	1.51E-09	-----+--+	NA	KCNK3;CIB4	KCNK3	1254
LTA-MAP	rs1133323	15q24	72999278	t	c	-0.3986	0.0606	3.22E-10	-----+---	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	393
LTA-MAP	rs1378940	15q24	72870547	a	c	-0.3902	0.0639	5.28E-09	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	8780
LTA-MAP	rs2301249	15q24	72879437	t	c	0.4315	0.0671	7.74E-10	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-MAP	rs1127796	15q24	72980057	t	c	0.3864	0.0605	1.02E-09	+++++-+++	C15orf17	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	C15orf17	677
LTA-MAP	rs4886406	15q24	72844256	t	g	-0.3941	0.0676	2.50E-08	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L	CYP1A2	8262
LTA-MAP	rs6026704	20q13	57117540	c	g	0.5037	0.0847	1.32E-08	+++++-++-	NA	NA	SLMO2	66244
LTA-MAP	rs7497393	15q24	72962510	c	g	-0.3872	0.0604	9.16E-10	-----+---	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	6952
LTA-MAP	rs7299436	12q21	88637201	t	g	0.5845	0.0898	5.02E-10	+++++++++	NA	NA	ATP2B1	63226
LTA-MAP	rs7162232	15q24	72902948	a	g	-0.4102	0.0685	1.02E-08	---------	LMAN1L	CPLX3;SCAMP2;CSK;ULK3;LMAN1L	LMAN1L	2203
LTA-MAP	rs6100340	20q13	57118007	a	g	-0.5197	0.0848	4.63E-09	-----+---	NA	NA	SLMO2	66711



Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-MAP	rs8033381	15q24	72867738	a	g	-0.4293	0.0673	1.07E-09	---------	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-MAP	rs260013	20q13	57194118	a	g	-0.5496	0.0905	6.48E-09	---------	NA	C20orf174	C20orf174	5351
LTA-MAP	rs12046278	1p36	10722164	t	c	-0.4722	0.0693	7.26E-11	--------?	CASZ1	CASZ1	CASZ1	57130
LTA-MAP	rs3750727	10q21	63114411	a	g	0.4423	0.0723	5.01E-09	+-+++++++	C10orf107	C10orf107	C10orf107	21687
LTA-MAP	rs7362597	20q13	57112829	a	g	0.5054	0.0848	1.22E-08	+++++-++-	NA	NA	SLMO2	61533
LTA-MAP	rs7070797	10q21	63221779	a	g	-0.5456	0.0878	2.89E-09	-----+---	NA	C10orf107	C10orf107	25684
LTA-MAP	rs236705	20q13	57122065	t	c	-0.487	0.0793	4.46E-09	-----+---	NA	NA	SLMO2	70769
LTA-MAP	rs973237	10q21	63195307	a	g	0.42	0.0718	2.26E-08	+-+++++++	C10orf107	C10orf107	C10orf107	788
LTA-MAP	rs4886629	15q24	72859611	c	g	-0.4308	0.0675	1.09E-09	---------	NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L	CSK	2156
LTA-MAP	rs11854147	15q24	72839824	t	c	0.401	0.0671	1.09E-08	+++++++++	NA	CYP1A2;CYP1A1;CSK;LMAN1L	CYP1A2	3830
LTA-MAP	rs4845953	1p36	10724576	a	g	-0.3955	0.0667	1.43E-08	--------?	CASZ1	CASZ1	CASZ1	54718
LTA-MAP	rs17249754	12q21	88584717	a	g	-0.6855	0.0808	5.07E-16	----+----	NA	ATP2B1	ATP2B1	10742
LTA-MAP	rs2408046	12q21	88633468	t	c	-0.5057	0.0831	6.09E-09	---------	NA	ATP2B1	ATP2B1	59493
LTA-MAP	rs7176022	15q24	72894933	a	c	0.4115	0.0681	7.54E-09	+++++++++	LMAN1L	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	LMAN1L	2687
LTA-MAP	rs1465537	20q13	57131415	t	c	0.5218	0.0853	4.98E-09	+++++-+++	NA	NA	C20orf174	68054
LTA-MAP	rs11105382	12q21	88631403	t	c	0.5818	0.0893	4.75E-10	+++++++++	NA	ATP2B1	ATP2B1	57428
LTA-MAP	rs1275985	2p23	26765249	t	c	-0.3857	0.0618	2.39E-09	------+-+	NA	KCNK3;CIB4	KCNK3	3873
LTA-MAP	rs4886410	15q24	72852697	c	g	-0.3871	0.064	7.21E-09	---------	NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3	CSK	9070
LTA-MAP	rs6026748	20q13	57179210	a	g	0.5518	0.0941	2.08E-08	+-+++++++	NA	C20orf174	C20orf174	20259
LTA-MAP	rs936230	15q24	72932151	t	c	0.3943	0.0677	2.53E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	7902
LTA-MAP	rs11066301	12q24	111355755	a	g	-0.3558	0.0612	2.79E-08	---------	PTPN11	RPL6;PTPN11	PTPN11	14837
LTA-MAP	rs2588992	10q21	63184677	t	c	-0.4589	0.0762	8.55E-09	-+---+---	C10orf107	C10orf107	C10orf107	11418
LTA-MAP	rs35432	12q24	114039913	t	c	-0.3676	0.0637	3.43E-08	-----+-+-	NA	NA	TBX3	433561
LTA-MAP	rs2113894	12q21	88623528	a	t	0.5072	0.0827	4.64E-09	+++++++++	NA	ATP2B1	ATP2B1	49553
LTA-MAP	rs9210	15q24	72915554	t	c	0.3887	0.0675	3.73E-08	+++++++++	ULK3	MPI;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	ULK3	43
LTA-MAP	rs1130741	15q24	72976983	a	g	0.3858	0.0605	1.07E-09	+++++-+++	MPI	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	MPI	635
LTA-MAP	rs10858915	12q21	88575678	a	g	0.3548	0.0609	2.58E-08	++++--+++	NA	ATP2B1	ATP2B1	1703
LTA-MAP	rs2050265	1p36	11802286	a	g	0.602	0.0823	2.77E-12	++++-++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	8576
LTA-MAP	rs11014166	10p12	18748804	a	t	0.3878	0.0633	4.77E-09	+++++++++	CACNB2	CACNB2	CACNB2	19286
LTA-MAP	rs12243859	10p12	18780638	t	c	-0.3739	0.0639	2.23E-08	---+-+---	CACNB2	CACNB2	CACNB2	51120
LTA-MAP	rs4590817	10q21	63137559	c	g	-0.4662	0.0816	4.72E-08	------+-+	C10orf107	C10orf107	C10orf107	44835
LTA-MAP	rs183173	20q13	57159500	t	g	-0.5073	0.0888	4.81E-08	---------	NA	C20orf174	C20orf174	39969
LTA-MAP	rs8042694	15q24	73012468	a	g	-0.4071	0.066	3.65E-09	-----+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	4957
LTA-MAP	rs1275980	2p23	26770473	t	c	-0.3863	0.0617	2.21E-09	------+-+	KCNK3	KCNK3;CIB4	KCNK3	1351
LTA-MAP	rs1813353	10p12	18747454	t	c	0.439	0.0652	1.26E-10	+++++-+++	CACNB2	CACNB2	CACNB2	17936
LTA-MAP	rs6676300	1p36	11847887	a	g	0.3641	0.0634	4.03E-08	+++-+-+++	NA	MTHFR;KIAA2013;NPPA;CLCN6;NPPB	NPPB	6308
LTA-MAP	rs2415251	15q24	73029208	t	c	0.3962	0.0631	1.99E-09	+++++-+++	NA	COX5A;SCAMP5;MPI;RPP25;C15orf17	RPP25	5287
LTA-MAP	rs12567136	1p36	11806318	t	c	-0.6025	0.0823	2.64E-12	----+----	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA-MAP	rs2681472	12q21	88533090	a	g	0.6861	0.0796	1.77E-16	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
LTA-MAP	rs17037425	1p36	11792970	a	g	-0.6215	0.0868	7.76E-12	---------	CLCN6	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	4177
LTA-MAP	rs11072514	15q24	73008918	a	t	-0.396	0.0606	4.34E-10	-----+---	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8507
LTA-MAP	rs3184504	12q24	110368991	t	c	0.4469	0.0605	1.68E-12	+++++-+++	SH2B3	SH2B3;ATXN2	SH2B3	4818
LTA-MAP	rs11105368	12q21	88598572	c	g	-0.6845	0.081	6.61E-16	----+----	NA	ATP2B1	ATP2B1	24597
LTA-MAP	rs4845843	1p36	10724172	a	g	0.6025	0.1056	4.87E-08	++++++++?	CASZ1	CASZ1	CASZ1	55122
LTA-MAP	rs11105378	12q21	88614872	t	c	-0.6822	0.0824	2.46E-15	----+----	NA	ATP2B1	ATP2B1	40897
LTA-MAP	rs11105328	12q21	88466521	a	g	0.6393	0.0837	2.84E-13	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	22613
LTA-MAP	rs11105379	12q21	88619304	t	c	0.5869	0.0892	3.22E-10	+++++++++	NA	ATP2B1	ATP2B1	45329
LTA-MAP	rs11105358	12q21	88566273	c	g	-0.4644	0.0613	4.38E-13	----+----	ATP2B1	ATP2B1	ATP2B1	7702
LTA-MAP	rs7922049	10q21	63132371	a	g	-0.4993	0.085	2.00E-08	-+---+--+	C10orf107	C10orf107	C10orf107	39647
LTA-MAP	rs17037390	1p36	11783430	a	g	-0.6015	0.0826	3.37E-12	----+----	MTHFR	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHFR	5272
LTA-MAP	rs236710	20q13	57127024	t	g	-0.4852	0.0793	5.04E-09	-----+---	NA	NA	C20orf174	72445
LTA-MAP	rs17630235	12q24	111076069	a	g	0.3848	0.062	2.94E-09	+++++++++	NA	TRAFD1;C12orf30	TRAFD1	274
LTA-MAP	rs1378938	15q24	72883496	t	c	0.4148	0.0679	5.32E-09	+++++++++	NA	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	939
LTA-MAP	rs11014171	10p12	18751201	t	c	-0.3892	0.0632	3.88E-09	---------	CACNB2	CACNB2	CACNB2	21683
LTA-PP	rs1717014	3p22	41892399	t	c	-0.4739	0.0825	2.22E-08	--------+	ULK4	ULK4	ULK4	86265
LTA-PP	rs9854833	3p22	41750581	t	c	-0.4956	0.082	3.95E-09	---------	ULK4	ULK4	ULK4	228083
LTA-PP	rs1717003	3p22	41912004	t	c	0.4803	0.0824	1.36E-08	++++++++-	ULK4	ULK4	ULK4	66660
LTA-PP	rs1717034	3p22	41930917	a	g	-0.483	0.0823	1.10E-08	--------+	ULK4	ULK4	ULK4	47747
LTA-PP	rs2469	6p21	43407301	t	c	-0.3519	0.0623	3.88E-08	---------	NA	TTBK1;ZNF318;CRIP3;SLC22A7	ZNF318	4484
LTA-PP	rs6796210	3p22	41826722	t	c	0.4691	0.082	2.58E-08	++++++++-	ULK4	ULK4	ULK4	151942
LTA-PP	rs1717007	3p22	41917203	t	c	-0.4817	0.0824	1.23E-08	--------+	ULK4	ULK4	ULK4	61461
LTA-PP	rs7634985	3p22	41994569	t	c	0.5174	0.0861	4.93E-09	++++++++-	NA	ULK4	ULK4	15905
LTA-PP	rs1052501	3p22	41900402	t	c	0.4781	0.0823	1.55E-08	++++++++-	ULK4	ULK4	ULK4	78262
LTA-PP	rs7622259	3p22	41856355	a	t	0.4706	0.0827	2.96E-08	++++++++-	ULK4	ULK4	ULK4	122309
LTA-PP	rs2272007	3p22	41971140	t	c	-0.4879	0.082	6.77E-09	--------+	ULK4	ULK4	ULK4	7524
LTA-PP	rs9874975	3p22	41739304	a	g	-0.4943	0.0819	4.26E-09	---------	ULK4	ULK4	ULK4	239360
LTA-PP	rs6783001	3p22	41837236	a	c	-0.4746	0.0825	2.13E-08	--------+	ULK4	ULK4	ULK4	141428
LTA-PP	rs2242416	6p21	43381582	a	g	0.355	0.0623	2.92E-08	+++++++++	CRIP3	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	329
LTA-PP	rs1716999	3p22	41905045	c	g	-0.479	0.0823	1.47E-08	--------+	ULK4	ULK4	ULK4	73619
LTA-PP	rs7631057	3p22	41792955	t	c	-0.4772	0.0822	1.58E-08	--------+	ULK4	ULK4	ULK4	185709
LTA-PP	rs9865780	3p22	41870806	a	g	0.4729	0.0826	2.49E-08	++++++++-	ULK4	ULK4	ULK4	107858
LTA-PP	rs1716655	3p22	41893710	a	g	-0.4739	0.0825	2.21E-08	--------+	ULK4	ULK4	ULK4	84954
LTA-PP	rs6802340	3p22	41869038	t	c	0.4709	0.0827	2.90E-08	++++++++-	ULK4	ULK4	ULK4	109626
LTA-PP	rs1717027	3p22	41962924	t	c	-0.488	0.082	6.80E-09	--------+	ULK4	ULK4	ULK4	15740
LTA-PP	rs6796078	3p22	41992824	a	t	-0.5183	0.0861	4.62E-09	--------+	NA	ULK4	ULK4	14160
LTA-PP	rs6781326	3p22	41752032	t	c	0.4963	0.0817	3.28E-09	+++++++++	ULK4	ULK4	ULK4	226632
LTA-PP	rs7632387	3p22	41828165	t	c	-0.4687	0.0821	2.67E-08	--------+	ULK4	ULK4	ULK4	150499
LTA-PP	rs1624519	3p22	41959804	a	g	0.4838	0.0823	1.05E-08	++++++++-	ULK4	ULK4	ULK4	18860
LTA-PP	rs809930	3p22	42040009	a	g	0.5026	0.0868	1.71E-08	++++++++-	NA	NA	ULK4	61345



Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-PP	rs6776724	3p22	41816274	a	g	0.4692	0.0823	2.79E-08	++++++++-	ULK4	ULK4	ULK4	162390
LTA-PP	rs6791806	3p22	41864999	t	c	-0.4709	0.0827	2.89E-08	--------+	ULK4	ULK4	ULK4	113665
LTA-PP	rs939561	3p22	42032105	a	g	0.4936	0.087	3.27E-08	++++++++-	NA	ULK4	ULK4	53441
LTA-PP	rs1717017	3p22	41890620	a	c	0.4737	0.0825	2.25E-08	++++++++-	ULK4	ULK4	ULK4	88044
LTA-PP	rs4615050	3p22	41917502	a	t	0.482	0.0824	1.20E-08	++++++++-	ULK4	ULK4	ULK4	61162
LTA-PP	rs3890604	3p22	41735629	t	c	-0.4915	0.0819	5.06E-09	---------	ULK4	ULK4	ULK4	243035
LTA-PP	rs9850310	3p22	41866102	t	c	0.4708	0.0827	2.92E-08	++++++++-	ULK4	ULK4	ULK4	112562
LTA-PP	rs12705390	7q22	106198013	a	g	0.5865	0.0759	5.40E-14	+++++-+++	NA	NA	PIK3CG	95146
LTA-PP	rs7646144	3p22	41828129	a	t	-0.4686	0.0821	2.69E-08	--------+	ULK4	ULK4	ULK4	150535
LTA-PP	rs9856088	3p22	41835486	t	g	-0.4946	0.0847	1.29E-08	--------+	ULK4	ULK4	ULK4	143178
LTA-PP	rs1016669	3p22	41869444	t	c	0.4717	0.0826	2.72E-08	++++++++-	ULK4	ULK4	ULK4	109220
LTA-PP	rs1717006	3p22	41915452	a	c	0.4791	0.082	1.29E-08	++++++++-	ULK4	ULK4	ULK4	63212
LTA-PP	rs880315	1p36	10719453	t	c	-0.421	0.0703	5.45E-09	--------?	CASZ1	CASZ1	CASZ1	59841
LTA-PP	rs1716975	3p22	41935010	t	c	-0.4837	0.0822	1.01E-08	--------+	ULK4	ULK4	ULK4	43654
LTA-PP	rs17398575	7q22	106196688	a	g	0.5732	0.075	1.02E-13	+++++-+++	NA	NA	PIK3CG	96471
LTA-PP	rs1717020	3p22	41956494	a	c	0.4829	0.082	9.73E-09	++++++++-	ULK4	ULK4	ULK4	22170
LTA-PP	rs7629767	3p22	42018513	t	g	0.4948	0.0867	2.75E-08	++++++++-	NA	ULK4	ULK4	39849
LTA-PP	rs284277	1p36	10713384	a	c	-0.4142	0.073	3.27E-08	--------?	CASZ1	CASZ1	CASZ1	65910
LTA-PP	rs17062109	3p22	41785368	t	c	-0.4773	0.082	1.46E-08	--------+	ULK4	ULK4	ULK4	193296
LTA-PP	rs1716984	3p22	41940536	a	g	0.4835	0.0823	1.06E-08	++++++++-	ULK4	ULK4	ULK4	38128
LTA-PP	rs9866759	3p22	41733422	t	c	0.483	0.0821	9.91E-09	+++++++++	ULK4	ULK4	ULK4	245242
LTA-PP	rs1716653	3p22	41950602	a	c	0.4838	0.0823	1.04E-08	++++++++-	ULK4	ULK4	ULK4	28062
LTA-PP	rs2128834	3p22	41837649	a	g	0.4694	0.0822	2.68E-08	++++++++-	ULK4	ULK4	ULK4	141015
LTA-PP	rs6599168	3p22	41725327	t	c	0.5163	0.0865	6.11E-09	+++++++++	ULK4	ULK4	ULK4	253337
LTA-PP	rs1716694	3p22	41961403	t	g	0.4864	0.0823	8.67E-09	++++++++-	ULK4	ULK4	ULK4	17261
LTA-PP	rs1613233	3p22	41920148	a	g	-0.4819	0.0824	1.22E-08	--------+	ULK4	ULK4	ULK4	58516
LTA-PP	rs9882329	3p22	41742158	t	c	0.4949	0.082	4.10E-09	+++++++++	ULK4	ULK4	ULK4	236506
LTA-PP	rs12705389	7q22	106192878	t	c	0.5759	0.0753	9.52E-14	+++++-+++	NA	NA	PIK3CG	100281
LTA-PP	rs11760498	7q22	106206208	a	g	0.4499	0.0803	4.89E-08	+++++-+++	NA	NA	PIK3CG	86951
LTA-PP	rs10212536	3p22	41802030	a	g	0.4749	0.0823	1.96E-08	++++++++-	ULK4	ULK4	ULK4	176634
LTA-PP	rs6789260	3p22	41751354	c	g	-0.4961	0.0817	3.36E-09	---------	ULK4	ULK4	ULK4	227310
LTA-PP	rs10865914	3p22	41894503	t	c	0.4741	0.0825	2.17E-08	++++++++-	ULK4	ULK4	ULK4	84161
LTA-PP	rs2949837	7p13	45960903	a	t	0.402	0.0706	2.94E-08	+++++++++	NA	IGFBP3	IGFBP3	33507
LTA-PP	rs9828398	3p22	41870897	t	c	-0.4731	0.0826	2.43E-08	--------+	ULK4	ULK4	ULK4	107767
LTA-PP	rs1615243	3p22	41940238	t	c	0.4836	0.0823	1.05E-08	++++++++-	ULK4	ULK4	ULK4	38426
LTA-PP	rs12536419	7q22	106206532	a	c	-0.4747	0.0839	3.60E-08	----++---	NA	NA	PIK3CG	86627
LTA-PP	rs7372217	3p22	41965126	a	g	0.4881	0.082	6.74E-09	++++++++-	ULK4	ULK4	ULK4	13538
LTA-PP	rs1716685	3p22	41900305	t	c	-0.4772	0.0819	1.43E-08	--------+	ULK4	ULK4	ULK4	78359
LTA-PP	rs9847006	3p22	41730363	t	c	0.4844	0.0823	1.00E-08	+++++++++	ULK4	ULK4	ULK4	248301
LTA-PP	rs13087502	3p22	41990114	t	c	0.5202	0.086	3.93E-09	++++++++-	NA	ULK4	ULK4	11450
LTA-PP	rs2125738	6p21	43435728	a	g	0.3569	0.0628	3.20E-08	+++++++++	ZNF318	CRIP3;SLC22A7;ZNF318	ZNF318	9431
LTA-PP	rs2625667	3p22	41875955	a	c	-0.4736	0.0826	2.39E-08	--------+	ULK4	ULK4	ULK4	102709
LTA-PP	rs1716983	3p22	41939132	a	g	0.4835	0.0823	1.05E-08	++++++++-	ULK4	ULK4	ULK4	39532
LTA-PP	rs1716692	3p22	41958790	a	g	0.484	0.0823	1.04E-08	++++++++-	ULK4	ULK4	ULK4	19874
LTA-PP	rs9856633	3p22	41988854	a	g	-0.4836	0.0819	9.04E-09	--------+	NA	ULK4	ULK4	10190
LTA-PP	rs1574430	6p21	43377007	a	c	0.3555	0.0625	3.04E-08	+++++++++	SLC22A7	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	3032
LTA-PP	rs939558	3p22	41951044	a	c	0.4839	0.0823	1.04E-08	++++++++-	ULK4	ULK4	ULK4	27620
LTA-PP	rs17477177	7q22	106199094	t	c	-0.589	0.0763	5.61E-14	-----+---	NA	NA	PIK3CG	94065
LTA-PP	rs10948071	6p21	43388691	t	c	-0.3846	0.0652	9.06E-09	---------	NA	CRIP3;SLC22A7;TTBK1;ZNF318	CRIP3	4183
LTA-PP	rs9823254	3p22	41869772	c	g	-0.4718	0.0826	2.69E-08	--------+	ULK4	ULK4	ULK4	108892
LTA-PP	rs4973995	3p22	41906477	t	c	-0.4796	0.0823	1.42E-08	--------+	ULK4	ULK4	ULK4	72187
LTA-PP	rs9825741	3p22	41736832	a	t	0.49	0.0817	5.25E-09	+++++++++	ULK4	ULK4	ULK4	241832
LTA-PP	rs9866092	3p22	41870971	a	c	0.4734	0.0826	2.38E-08	++++++++-	ULK4	ULK4	ULK4	107693
LTA-PP	rs6599176	3p22	41763496	t	g	0.4973	0.0818	3.23E-09	+++++++++	ULK4	ULK4	ULK4	215168
LTA-PP	rs9867627	3p22	41770845	a	c	0.4941	0.0821	4.63E-09	+++++++++	ULK4	ULK4	ULK4	207819
LTA-PP	rs9830469	3p22	41737539	a	g	0.4917	0.0819	4.96E-09	+++++++++	ULK4	ULK4	ULK4	241125
LTA-PP	rs9865127	3p22	41782452	t	c	-0.4781	0.082	1.39E-08	--------+	ULK4	ULK4	ULK4	196212
LTA-PP	rs6803560	3p22	41799484	a	g	0.4768	0.0822	1.64E-08	++++++++-	ULK4	ULK4	ULK4	179180
LTA-PP	rs2841647	6p21	43377158	a	c	-0.3538	0.0627	3.92E-08	-----?---	SLC22A7	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	3183
LTA-PP	rs1716657	3p22	41893460	t	c	0.4737	0.0825	2.24E-08	++++++++-	ULK4	ULK4	ULK4	85204
LTA-PP	rs9846634	3p22	41869053	a	g	-0.4764	0.0829	2.22E-08	--------+	ULK4	ULK4	ULK4	109611
LTA-PP	rs7650227	3p22	41769941	t	g	0.5006	0.0821	2.84E-09	+++++++++	ULK4	ULK4	ULK4	208723
LTA-PP	rs1994157	3p22	41872486	a	g	-0.4734	0.0826	2.42E-08	--------+	ULK4	ULK4	ULK4	106178
LTA-PP	rs9875107	3p22	41797317	a	t	0.4767	0.0822	1.64E-08	++++++++-	ULK4	ULK4	ULK4	181347
LTA-PP	rs11923562	3p22	41735335	t	g	-0.4917	0.0819	5.06E-09	---------	ULK4	ULK4	ULK4	243329
LTA-PP	rs7626217	3p22	41817419	a	g	0.47	0.0821	2.52E-08	++++++++-	ULK4	ULK4	ULK4	161245
LTA-PP	rs17060961	3p22	41738715	a	g	0.4946	0.0819	4.19E-09	+++++++++	ULK4	ULK4	ULK4	239949
LTA-PP	rs794902	3p22	42000943	t	c	-0.5158	0.0861	5.47E-09	--------+	NA	ULK4	ULK4	22279
LTA-PP	rs6599167	3p22	41725264	a	g	0.5164	0.0866	6.34E-09	+++++++++	ULK4	ULK4	ULK4	253400
LTA-PP	rs12635286	3p22	42026840	t	c	0.4858	0.0867	4.95E-08	++++++++-	NA	ULK4	ULK4	48176
LTA-PP	rs1716642	3p22	41940869	a	c	-0.4835	0.0823	1.06E-08	--------+	ULK4	ULK4	ULK4	37795
LTA-PP	rs7648578	3p22	41833735	t	c	-0.4694	0.0821	2.55E-08	--------+	ULK4	ULK4	ULK4	144929
LTA-PP	rs7652506	3p22	42035239	t	c	-0.49	0.0869	4.08E-08	--------+	NA	ULK4	ULK4	56575
LTA-PP	rs13088394	3p22	41926719	a	g	0.4824	0.0823	1.17E-08	++++++++-	ULK4	ULK4	ULK4	51945
LTA-PP	rs1716693	3p22	41960604	t	c	0.4857	0.0823	9.18E-09	++++++++-	ULK4	ULK4	ULK4	18060
LTA-PP	rs17063599	3p22	41836680	t	c	-0.4743	0.0825	2.16E-08	--------+	ULK4	ULK4	ULK4	141984
LTA-PP	rs2272006	3p22	41972063	t	c	0.4881	0.082	6.77E-09	++++++++-	ULK4	ULK4	ULK4	6601
LTA-PP	rs6768128	3p22	41840084	a	g	-0.4744	0.0825	2.19E-08	--------+	ULK4	ULK4	ULK4	138580
LTA-PP	rs6599179	3p22	41830288	t	c	-0.4685	0.0821	2.70E-08	--------+	ULK4	ULK4	ULK4	148376

Trait	SNPID	Chr	Position.Bui	Allele1	Allele2	Beta	s.e.	*P*	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-PP	rs9842261	3p22	41797712	a	g	-0.4745	0.0821	1.83E-08	--------+	ULK4	ULK4	ULK4	180952
LTA-PP	rs9820192	3p22	41864285	a	g	-0.4706	0.0827	2.96E-08	--------+	ULK4	ULK4	ULK4	114379
LTA-PP	rs6793520	3p22	41840293	c	g	0.4748	0.0826	2.15E-08	++++++++-	ULK4	ULK4	ULK4	138371
LTA-PP	rs9876960	3p22	41960816	t	c	0.4856	0.0823	9.17E-09	++++++++-	ULK4	ULK4	ULK4	17848
LTA-PP	rs1716683	3p22	41898078	a	g	-0.4769	0.0824	1.78E-08	--------+	ULK4	ULK4	ULK4	80586
LTA-PP	rs6599175	3p22	41761013	t	c	0.4966	0.0816	3.18E-09	+++++++++	ULK4	ULK4	ULK4	217651
LTA-PP	rs13325965	3p22	41889946	t	g	-0.4752	0.0825	2.04E-08	--------+	ULK4	ULK4	ULK4	88718
LTA-PP	rs9852303	3p22	41734529	t	c	-0.483	0.0819	9.49E-09	---------	ULK4	ULK4	ULK4	244135
LTA-PP	rs794899	3p22	42003726	t	c	-0.5166	0.0861	5.22E-09	--------+	NA	ULK4	ULK4	25062
LTA-PP	rs13225723	7q22	106203703	a	g	0.6031	0.0827	1.26E-12	+++++-+++	NA	NA	PIK3CG	89456
LTA-PP	rs9815354	3p22	41887655	a	g	-0.5025	0.0855	1.05E-08	--------+	ULK4	ULK4	ULK4	91009
LTA-PP	rs13084436	3p22	41992541	a	t	0.5181	0.0861	4.63E-09	++++++++-	NA	ULK4	ULK4	13877
LTA-PP	rs704964	3p22	42028903	a	g	0.4921	0.0866	3.18E-08	++++++++-	NA	ULK4	ULK4	50239
LTA-PP	rs9857175	3p22	41797058	t	g	0.4772	0.0822	1.59E-08	++++++++-	ULK4	ULK4	ULK4	181606
LTA-PP	rs3934103	3p22	41952218	t	c	0.4848	0.0823	9.77E-09	++++++++-	ULK4	ULK4	ULK4	26446
LTA-PP	rs3774372	3p22	41852418	t	c	0.4718	0.0825	2.62E-08	++++++++-	ULK4	ULK4	ULK4	126246

"Direction" corresponds to order of cohorts as listed in Supplementary Table 3.

Table S5: eQTL analysis results for the index SNP in each of the 39 loci identified in the analysis of LTA BP traits and for which eQTL data was available.

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Whole blood (CHARGE)	2.19E-72	1	11788391	3990477	MTHFR,C1orf167	cis	17.99	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	LCL (MuTHER)	1.91E-16	1	11788391	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Whole blood (PaxGene) in Japanese	1.20E-09	1	11788391	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Skin (MuTHER)	2.36E-06	1	11788391	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Subc adipose (MuTHER)	5.98E-06	1	11788391	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Whole blood (CHARGE)	2.21E-78	1	11802286	3990477	MTHFR,C1orf167	cis	18.74	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Whole blood (CHARGE)	2.64E-78	1	11806318	3990477	MTHFR,C1orf167	cis	18.73	T	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Whole blood (CHARGE)	3.23E-78	1	11809890	3990477	MTHFR,C1orf167	cis	18.72	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	LCL (MuTHER)	5.77E-19	1	11806318	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	LCL (MuTHER)	8.49E-19	1	11802286	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	LCL (MuTHER)	2.10E-18	1	11809890	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Monocytes	3.57E-14	1	11806318		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Monocytes	1.14E-13	1	11809890		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs17037429	Monocytes	2.33E-13	1	11796374		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	PaxGeneWholeBlood(Mehta)	8.44E-10	1	11809890	ILMN_1731434	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Whole blood (PaxGene) in Japanese	1.20E-09	1	11806318	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Whole blood (PaxGene) in Japanese	1.20E-09	1	11802286	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs3753584	Whole blood (PaxGene) in Japanese	1.20E-09	1	11787173	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	PaxGeneWholeBlood(Mehta)	1.44E-09	1	11806318	ILMN_1731434	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Whole blood (PaxGene) in Japanese	2.16E-09	1	11809890	A_23_P400081	MTHFR	cis	0.62			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	SchadtLiver	1.37E-07	1	11809890		CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Skin (MuTHER)	1.44E-07	1	11806318	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Skin (MuTHER)	1.50E-07	1	11802286	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Skin (MuTHER)	3.50E-07	1	11809890	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Subc adipose (MuTHER)	5.39E-07	1	11806318	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Subc adipose (MuTHER)	6.63E-07	1	11802286	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Subc adipose (MuTHER)	8.64E-07	1	11809890	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Liver(Greenawalt)	1.02E-06	1	11809890	10023816366	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Lymph	1.67E-06	1	11809890	GI_12025672-A	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Dendritic cells after Mycobacetrium tube	2.41E-06	1	11806318		MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Whole blood (CHARGE)	7.04E-83	1	11783430	3990477	MTHFR,C1orf167	cis	19.29	A	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Whole blood (CHARGE)	2.88E-79	1	11785365	3990477	MTHFR,C1orf167	cis	18.85	G	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	LCL (MuTHER)	5.45E-18	1	11783430	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	LCL (MuTHER)	7.40E-18	1	11785365	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Whole blood (PaxGene) in Japanese	1.20E-09	1	11783430	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Whole blood (PaxGene) in Japanese	1.20E-09	1	11785365	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Subc adipose (MuTHER)	2.66E-07	1	11783430	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17037390	Skin (MuTHER)	5.16E-07	1	11783430	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Subc adipose (MuTHER)	6.16E-07	1	11785365	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Skin (MuTHER)	7.50E-07	1	11785365	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Liver (ScanDB)	9.54E-07	1	11785365		GPR116	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Lymph	1.54E-05	1	11785365	GI_12025672-A	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	omental	7.21E-05	1	11785365	10025934633	HSS00048903	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs17367504	Blood(Fehrmann et al)	1.50E-27;1.9(	1	11785365	3990477;3850136	MTHFR;AL953897.6;C	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	LCL (MuTHER)	6.00E-24	1	11818262	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Whole blood (PaxGene) in Japanese	1.20E-09	1	11818262	A_23_P400081	MTHFR	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Skin (MuTHER)	3.72E-09	1	11818262	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Subc adipose (MuTHER)	1.56E-07	1	11818262	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-1kg)	0.947	rs17037452	Whole blood (CHARGE)	1.66E-07	1	11818262	60437	PLOD1	cis	-5.23	G	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Whole blood (CHARGE)	7.97E-95	1	11792970	3990477	MTHFR,C1orf167	cis	20.66	A	1	11769609
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	LCL (MuTHER)	5.98E-20	1	11792970	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Whole blood (PaxGene) in Japanese	1.20E-09	1	11792970	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Skin (MuTHER)	1.03E-08	1	11792970	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Subc adipose (MuTHER)	2.22E-08	1	11792970	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.853	rs17037425	Liver(UChicago)	0.00017275	1	11792970	A_24_P302374	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	LCL (MuTHER)	2.97E-24	1	11786736	ILMN_1734830	MTHFR	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	LCL (MuTHER)	5.44E-24	1	11815237	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	LCL (MuTHER)	5.56E-24	1	11819189	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	PaxGeneWholeBlood(Mehta)	1.64E-11	1	11815237	ILMN_1731434	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Whole blood (PaxGene) in Japanese	7.49E-10	1	11819189	A_23_P400081	MTHFR	cis	0.64			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Whole blood (PaxGene) in Japanese	1.20E-09	1	11815237	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Whole blood (PaxGene) in Japanese	1.20E-09	1	11786736	A_23_P400081	MTHFR	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Skin (MuTHER)	2.04E-09	1	11786736	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	RNAseq(HapMapLCL)+DeepSage(blood)	3.48E-09	1	11896602	ENST0000037659	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Skin (MuTHER)	3.56E-09	1	11819189	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Skin (MuTHER)	3.63E-09	1	11815237	ILMN_1734830	MTHFR	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Whole blood (CHARGE)	1.32E-07	1	11819189	60437	PLOD1	cis	-5.28	C	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Whole blood (CHARGE)	1.46E-07	1	11786736	60437	PLOD1	cis	-5.26	A	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Subc adipose (MuTHER)	1.65E-07	1	11815237	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Subc adipose (MuTHER)	1.75E-07	1	11819189	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Whole blood (CHARGE)	3.42E-07	1	11815237	60437	PLOD1	cis	-5.10	T	1	11958130
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Subc adipose (MuTHER)	4.13E-07	1	11786736	ILMN_1741594	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Lung	2.34E-06	1	11786736	100146210_TGI_a	Unknown	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs7553194	Monocytes (CD14+)	1.45E-05	1	11786736	TiKVCul2UleSz47	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Monocytes (CD14+)	5.10E-05	1	11815237	TiKVCul2UleSz47	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Lymph	0.00104498	1	11815237	GI_12025672-A	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2075538	Monocytes	1.43E-34;1.2	1	11819189		MTHFR;CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.713	rs2236797	Blood(Fehrmann et al)	4.70E-45;2.3	1	11815237	3990477;Human_	MTHFR;AL953897.6;	cis				
rs2004776	DBP/MAP	AGT	COG2;AGT;CAPN9	2	IndexSNP		rs2004776	Cerebellum (ScanDB)	2.19E-09	1	228915325		AGT	cis				
rs2004776	DBP/MAP	AGT	COG2;AGT;CAPN9	2	LDproxy(CEU-H3)	0.754	rs1326888	Cerebellum (ScanDB)	5.13E-10	1	228929783		AGT	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Lung	2.17E-09	2	96715567	100134941_TGI_a	CNNM4	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Whole blood (CHARGE)	5.38E-08	2	96715567	1190673	LMAN2L	cis	-5.44	A	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Blood(Fehrmann et al)	1.70E-04	2	96715567	1190673	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Bcells (CD19+)	0.0008951	2	96715567	fQbX2EuV1lEh.la	ARID5A	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	IndexSNP		rs7599598	Lymph	0.00281896	2	96715567	GI_13540593-S	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.806	rs7582249	Whole blood (CHARGE)	2.20E-09	2	96827256	1190673	LMAN2L	cis	5.98	A	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.806	rs7582249	Skin (MuTHER)	5.64E-06	2	96827256	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs6727384	Whole blood (Battle)	4.91E-46	2	97400324		CNNM4	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Whole blood (CHARGE)	2.52E-09	2	96787353	1190673	LMAN2L	cis	5.96	C	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Whole blood (CHARGE)	3.01E-09	2	96823647	1190673	LMAN2L	cis	5.93	G	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs6727384	Whole blood (CHARGE)	3.03E-09	2	96764051	1190673	LMAN2L	cis	5.93	G	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Blood(Fehrmann et al)	5.10E-06	2	96823647	1190673	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Skin (MuTHER)	5.41E-06	2	96823647	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs6727384	Skin (MuTHER)	5.63E-06	2	96764051	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Skin (MuTHER)	5.79E-06	2	96787353	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	Cerebellum (all samples)	1.79E-05	2	96823647	10025902983	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Lymph	0.00232082	2	96787353	GI_13540593-S	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs968470	Prefrontal cortex (all samples)	3.50E-02	2	96787353	10025902983	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.791	rs7608661	omental	7.82E-09;2.21	2	96823647	10023820566;100	CNNM4;LMAN2L;AN	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.771	rs994430	Whole blood (CHARGE)	2.78E-09	2	96802728	1190673	LMAN2L	cis	5.94	T	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.771	rs994430	Skin (MuTHER)	5.66E-06	2	96802728	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs6730773	Lung	1.74E-09	2	96805370	100141976_TGI_a	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs1318597	Whole blood (CHARGE)	2.40E-09	2	96826822	1190673	LMAN2L	cis	5.97	C	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs6730773	Whole blood (CHARGE)	3.04E-09	2	96805370	1190673	LMAN2L	cis	5.93	G	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs7586317	Whole blood (CHARGE)	3.21E-09	2	96811558	1190673	LMAN2L	cis	5.92	A	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs1318597	Skin (MuTHER)	5.64E-06	2	96826822	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs7586317	Skin (MuTHER)	5.66E-06	2	96811558	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757	rs6730773	Skin (MuTHER)	5.67E-06	2	96805370	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.735	rs6576984	Whole blood (CHARGE)	1.39E-08	2	96818432	1190673	LMAN2L	cis	5.68	T	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.735	rs6576984	Skin (MuTHER)	6.41E-06	2	96818432	ILMN_1755221	LMAN2L	cis				
rs7650227	PP	ULK4	ULK4	4	IndexSNP		rs7650227	Intestine (normal ileum)	2.98E-05	3	41794937		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1615243	Whole blood (Battle)	2.92E-190	3	41965234		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	omental	4.79E-21	3	41900402	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Prefrontal cortex (all samples)	1.05E-19	3	41952218	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Parietal lobe (ScanDB)	5.85E-17	3	41952218		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Parietal lobe (ScanDB)	6.48E-17	3	41940869		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Parietal lobe (ScanDB)	6.48E-17	3	41940869		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Parietal lobe (ScanDB)	7.20E-17	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856633	Parietal lobe (ScanDB)	7.20E-17	3	41988854		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	Parietal lobe (ScanDB)	7.21E-17	3	41956494		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717024	Parietal lobe (ScanDB)	7.21E-17	3	41959892		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Parietal lobe (ScanDB)	2.54E-16	3	41802030		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Parietal lobe (ScanDB)	2.54E-16	3	42000386		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs13325965	Parietal lobe (ScanDB)	2.54E-16	3	41889946		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs17062109	Parietal lobe (ScanDB)	2.54E-16	3	41785368		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716685	Parietal lobe (ScanDB)	2.54E-16	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Parietal lobe (ScanDB)	2.54E-16	3	41905223		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717006	Parietal lobe (ScanDB)	2.54E-16	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717017	Parietal lobe (ScanDB)	2.54E-16	3	41890620		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Parietal lobe (ScanDB)	2.54E-16	3	41826722		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Parietal lobe (ScanDB)	2.54E-16	3	41799560		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	Parietal lobe (ScanDB)	2.54E-16	3	41833735		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9839399	Parietal lobe (ScanDB)	2.54E-16	3	41903048		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1016669	Parietal lobe (ScanDB)	2.55E-16	3	41869444		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128834	Parietal lobe (ScanDB)	2.55E-16	3	41837649		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	Parietal lobe (ScanDB)	2.55E-16	3	41852418		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6791806	Parietal lobe (ScanDB)	2.55E-16	3	41864999		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Parietal lobe (ScanDB)	2.55E-16	3	41859754		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Parietal lobe (ScanDB)	2.73E-16	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Parietal lobe (ScanDB)	2.80E-16	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9854833	Parietal lobe (ScanDB)	4.38E-16	3	41750581		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9854833	Cerebellum (ScanDB)	8.69E-16	3	41750581		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Parietal lobe (ScanDB)	1.21E-15	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Cerebellum (ScanDB)	1.31E-15	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Visual cortex (Huntington's)	1.39E-15	3	41900402	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Cerebellum (ScanDB)	1.39E-15	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3890604	Parietal lobe (ScanDB)	1.52E-15	3	41735629		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Parietal lobe (ScanDB)	1.52E-15	3	41736832		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Parietal lobe (ScanDB)	1.52E-15	3	41734529		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Parietal lobe (ScanDB)	1.58E-15	3	41730363		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Cerebellum (ScanDB)	2.00E-15	3	41950394		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs13325965	Cerebellum (ScanDB)	2.00E-15	3	41889946		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716685	Cerebellum (ScanDB)	2.00E-15	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Cerebellum (ScanDB)	2.00E-15	3	41905223		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717006	Cerebellum (ScanDB)	2.00E-15	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717017	Cerebellum (ScanDB)	2.00E-15	3	41890620		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128834	Cerebellum (ScanDB)	2.00E-15	3	41837649		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Cerebellum (ScanDB)	2.00E-15	3	41826722		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	Cerebellum (ScanDB)	2.00E-15	3	41833735		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9839399	Cerebellum (ScanDB)	2.00E-15	3	41903048		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1016669	Cerebellum (ScanDB)	2.01E-15	3	41869444		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	Cerebellum (ScanDB)	2.01E-15	3	41852418		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6791806	Cerebellum (ScanDB)	2.01E-15	3	41864999		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Cerebellum (ScanDB)	2.01E-15	3	41859754		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (ScanDB)	2.04E-15	3	41802030		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Cerebellum (ScanDB)	2.04E-15	3	41799560		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs17062109	Cerebellum (ScanDB)	2.05E-15	3	41785368		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Cerebellum (ScanDB)	2.20E-15	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Cerebellum (ScanDB)	2.71E-15	3	41730363		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3890604	Cerebellum (ScanDB)	2.78E-15	3	41735629		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Cerebellum (ScanDB)	2.78E-15	3	41734529		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Cerebellum (ScanDB)	2.79E-15	3	41736832		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Cerebellum (ScanDB)	2.97E-15	3	41940869		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Cerebellum (ScanDB)	3.44E-15	3	41952218		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	Cerebellum (ScanDB)	5.61E-15	3	41956494		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717024	Cerebellum (ScanDB)	5.61E-15	3	41959892		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Cerebellum (ScanDB)	5.61E-15	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856633	Cerebellum (ScanDB)	5.61E-15	3	41988854		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	Peripheral artery plaque	9.06E-14	3	41833735	100160459_TGI_a	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Lung	9.75E-14	3	41799560	100149945_TGI_a	ULK4	trans				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Visual cortex (all samples)	4.32E-13	3	41952218	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Liver (ScanDB)	5.57E-13	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Liver (ScanDB)	6.22E-13	3	41975390		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Liver (ScanDB)	7.34E-13	3	41734529		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Liver (ScanDB)	9.19E-13	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3934103	Liver (ScanDB)	9.88E-13	3	41952218		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	Liver (ScanDB)	1.47E-12	3	41935010		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717017	Liver (ScanDB)	3.08E-12	3	41890620		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Liver (ScanDB)	3.08E-12	3	41826722		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Peripheral artery plaque	3.91E-12	3	41736832	100149945_TGI_a	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599179	Liver (ScanDB)	4.02E-12	3	41830288		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Liver(Greenawalt)	7.81E-12	3	41900402	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	Hippocampus (CA1, n=61; Kim et al.)	1.06E-11	3	41981490	232206_at	ULK4	cis	0.00			
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Liver (ScanDB)	1.24E-11	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Liver (ScanDB)	1.25E-11	3	41799560		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856633	ER+ breast tumor cells	1.31E-11	3	41988854		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	Normal dendritic cells (before Mycobacte	1.77E-11	3	41935010		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	ER+ breast tumor cells	1.95E-11	3	41852418		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716685	ER+ breast tumor cells	2.66E-11	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717006	ER+ breast tumor cells	2.66E-11	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	ER+ breast tumor cells	2.66E-11	3	41956494		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	ER+ breast tumor cells	2.66E-11	3	41971140		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7648578	ER+ breast tumor cells	2.66E-11	3	41833735		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717024	ER+ breast tumor cells	2.87E-11	3	41959892		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	RNAseq(HapMapLCL)+DeepSage(blood)	4.77E-11	3	41851718	ENST0000030183	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs13325965	ER+ breast tumor cells	5.17E-11	3	41889946		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9856088	Liver (ScanDB)	5.62E-11	3	41835486		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717020	BcellsTransformed_HapMapCEU	5.99E-11	3	41956494	2670619 in 26704	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128834	ER+ breast tumor cells	9.91E-11	3	41837649		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Liver (ScanDB)	1.02E-10	3	41802030		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs17062109	ER+ breast tumor cells	1.09E-10	3	41785368		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	ER+ breast tumor cells	1.15E-10	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Liver (ScanDB)	3.48E-10	3	41905223		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9842261	ER+ breast tumor cells	3.95E-10	3	41797712		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	ER+ breast tumor cells	7.44E-10	3	41761013		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599176	ER+ breast tumor cells	7.44E-10	3	41763496		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	ER+ breast tumor cells	7.44E-10	3	41736832		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Liver (ScanDB)	9.63E-10	3	41770845		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Liver (ScanDB)	6.65E-09	3	41859754		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Prefrontal cortex (Alzheimer's)	7.60E-09	3	41802030	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	LCL	2.70E-08	3	41971140	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	LCL	3.90E-08	3	41900402	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1994157	Liver (ScanDB)	4.07E-08	3	41872486		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	LCL	7.90E-08	3	41935010	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (Huntington's)	9.93E-07	3	41802030	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Cerebellum (normal samples)	1.1088E-05	3	41734529	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1125203	Intestine (normal ileum)	2.98E-05	3	41760895		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Intestine (normal ileum)	2.98E-05	3	41786009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9874975	Intestine (normal ileum)	2.98E-05	3	41764300		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs7632387	Intestine (normal ileum)	3.61E-05	3	41853161		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Prefrontal cortex (Huntington's)	3.85E-05	3	41900402	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Intestine (normal ileum)	4.60E-05	3	41925398		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1717000	Intestine (normal ileum)	4.60E-05	3	41930219		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599179	Intestine (normal ileum)	4.60E-05	3	41855284		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6796210	Intestine (normal ileum)	4.60E-05	3	41851718		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9857175	Intestine (normal ileum)	4.60E-05	3	41822054		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1994157	Intestine (normal ileum)	5.68E-05	3	41897482		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Visual cortex (all samples)	5.95E-05	3	41734529	10023829862	AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1615243	Intestine (normal ileum)	6.89E-05	3	41965234		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716984	Intestine (normal ileum)	6.89E-05	3	41965532		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2272007	Intestine (normal ileum)	6.89E-05	3	41996136		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs2128835	Intestine (normal ileum)	7.22E-05	3	41862873		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1716975	Prefrontal cortex (normal samples)	1.83E-03	3	41935010	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Lung	<2E-16	3	41730363	100125684_TGI_	Unknown	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	omental	6.93E-17;4.7	3	41802030	10023809218;100	ULK4;AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.953	rs6599167	Visual cortex (Alzheimer's)	3.11E-08	3	41725264	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs10510731	Lung	1.40E-14	3	41828314	100160459_TGI_	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs4299460	Lung	1.47E-14	3	41927449	100311290_TGI_	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17214945	ER+ breast tumor cells	2.69E-11	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17214987	ER+ breast tumor cells	2.69E-11	3	41785485		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17218264	ER+ breast tumor cells	2.69E-11	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17283929	ER+ breast tumor cells	2.69E-11	3	41916902		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17218103	Liver (ScanDB)	5.14E-11	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17218264	Parietal lobe (ScanDB)	7.13E-11	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17215183	Parietal lobe (ScanDB)	1.21E-10	3	41787338		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17214945	Parietal lobe (ScanDB)	1.24E-10	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17215589	Parietal lobe (ScanDB)	1.27E-10	3	41806207		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17218103	Parietal lobe (ScanDB)	1.36E-10	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17214945	Cerebellum (ScanDB)	3.47E-10	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17283677	ER+ breast tumor cells	3.55E-10	3	41901152		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17215183	Cerebellum (ScanDB)	4.01E-10	3	41787338		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17215589	Cerebellum (ScanDB)	4.05E-10	3	41806207		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17218103	Cerebellum (ScanDB)	4.20E-10	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs17218264	Cerebellum (ScanDB)	4.54E-10	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.861	rs10510731	Liver (ScanDB)	4.74E-10	3	41828314		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs794894	Parietal lobe (ScanDB)	1.63E-16	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs7634985	Parietal lobe (ScanDB)	1.73E-16	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs13087502	Parietal lobe (ScanDB)	1.78E-16	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs794894	Cerebellum (ScanDB)	1.45E-13	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs7634985	Cerebellum (ScanDB)	1.56E-13	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs13087502	Cerebellum (ScanDB)	1.61E-13	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.857	rs13087502	ER+ breast tumor cells	1.55E-10	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs809930	Parietal lobe (ScanDB)	5.10E-15	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7652506	Parietal lobe (ScanDB)	6.85E-15	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs939561	Parietal lobe (ScanDB)	7.69E-15	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7629767	Parietal lobe (ScanDB)	7.83E-15	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	SubCutAdipose(Greenawalt)	1.06E-14	3	41982343	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs939561	Cerebellum (ScanDB)	5.72E-12	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7629767	Cerebellum (ScanDB)	6.08E-12	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs809930	Cerebellum (ScanDB)	6.19E-12	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7652506	Cerebellum (ScanDB)	7.19E-12	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs7652506	ER+ breast tumor cells	1.07E-11	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	ER+ breast tumor cells	2.69E-11	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284313	ER+ breast tumor cells	2.69E-11	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284472	ER+ breast tumor cells	2.69E-11	3	41971308		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284313	Parietal lobe (ScanDB)	7.62E-11	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Parietal lobe (ScanDB)	7.64E-11	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284472	Parietal lobe (ScanDB)	7.64E-11	3	41971308		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs809930	ER+ breast tumor cells	9.77E-11	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Liver (ScanDB)	1.11E-10	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284313	Cerebellum (ScanDB)	4.41E-10	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Cerebellum (ScanDB)	4.42E-10	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs17284472	Cerebellum (ScanDB)	4.42E-10	3	41971308		ULK4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Stomach	8.32E-10	3	41982343	100311290	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.812	rs10510732	Cerebellum (Alzheimer's)	5.26E-02	3	41982343	10023829862	AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.762	rs794899	LCL	1.30E-07	3	42003726	231149_s_at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Parietal lobe (ScanDB)	7.75E-15	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Cerebellum (ScanDB)	6.72E-12	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Liver (ScanDB)	1.85E-08	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Liver(Greenawalt)	1.76E-07	3	42026840	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.761	rs12635286	Cerebellum (Alzheimer's)	2.92E-05	3	42026840	10025919071	CTNNB1	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2	0.967	rs12656497	Lung	1.67E-07	5	32867696	100142475_TGI_a	NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2	0.84	rs1173766	Lung	7.02E-08	5	32840285	100303568_TGI_a	NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-H3)	0.784	rs1173756	Lung	1.91E-08	5	32825609	100145622_TGI_a	NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-1kg)	0.781	rs1173743	Primary PHA-stimulated T cells (GenCord	5.68E-07	5	32775047		ENSG00000056097.1	cis	0.36			
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Cerebellum	5.54E-21	6	26230912	ILMN_2075334	HIST1H4C	cis				
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Whole blood (CHARGE)	1.30E-15	6	26230912	2970019	HIST1H4H	cis	-7.99	G	6	26393396
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Temporal cortex	2.59E-13	6	26230912	ILMN_2075334	HIST1H4C	cis				
rs198823	DBP	NA	HIST1H1E;HIST1H1T;HIST1H2BD;HIST1H2BC;HFE;H	6	IndexSNP		rs198823	Liver(UChicago)	0.02226068	6	26230912	A_23_P395374	HIST1H4D	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	IndexSNP		rs10948071	Whole blood (CHARGE)	6.44E-09	6	43388691	7050040	ZNF318	cis	-5.81	C	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	IndexSNP		rs10948071	LCL (MuTHER)	1.82E-06	6	43388691	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	IndexSNP		rs10948071	Skin (MuTHER)	2.56E-05	6	43388691	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Whole blood (Battle)	4.88E-53	6	43273604		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	Whole blood (CHARGE)	2.71E-16	6	43377007	50193	ZNF318	cis	-8.19	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Whole blood (CHARGE)	2.83E-16	6	43381582	50193	ZNF318	cis	-8.18	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Whole blood (CHARGE)	4.13E-16	6	43407301	50193	ZNF318	cis	-8.13	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	Intestine (normal ileum)	5.70E-14	6	43269029		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2841648	Intestine (normal ileum)	5.70E-14	6	43269179		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Intestine (normal ileum)	1.37E-13	6	43273604		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Blood(Fehrmann et al)	5.90E-06	6	43381582	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Blood(Fehrmann et al)	5.90E-06	6	43407301	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Skin (MuTHER)	1.11E-05	6	43407301	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2841648	Skin (MuTHER)	1.46E-05	6	43377157	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	Skin (MuTHER)	1.46E-05	6	43377007	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Skin (MuTHER)	1.97E-05	6	43381582	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2841648	LCL (MuTHER)	2.12E-05	6	43377157	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs1574430	LCL (MuTHER)	2.13E-05	6	43377007	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	LCL (MuTHER)	2.27E-05	6	43381582	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	LCL (MuTHER)	2.74E-05	6	43407301	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Lymph	0.00015064	6	43407301	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Liver(UChicago)	0.00071416	6	43381582	A_23_P156562	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Liver(Greenawalt)	1.75E-06;2.2	6	43407301	10025906643;100	SLC22A7;SLC22A7	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	Whole blood (CHARGE)	1.78E-18	6	43435728	50193	ZNF318	cis	-8.77	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125737	Whole blood (CHARGE)	1.53E-16	6	43435514	50193	ZNF318	cis	-8.25	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs4714677	Whole blood (CHARGE)	1.53E-16	6	43435017	50193	ZNF318	cis	-8.25	G	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9369407	Whole blood (CHARGE)	1.53E-16	6	43435353	50193	ZNF318	cis	-8.25	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	Whole blood (CHARGE)	1.53E-16	6	43428388	50193	ZNF318	cis	-8.25	T	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2841642	Whole blood (CHARGE)	1.66E-16	6	43410263	50193	ZNF318	cis	-8.24	G	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	Intestine (normal ileum)	5.70E-14	6	43276390		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	Monocytes	4.97E-12	6	43435728		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	Blood(Fehrmann et al)	2.50E-06	6	43428388	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	Skin (MuTHER)	1.29E-05	6	43384368	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125737	LCL (MuTHER)	1.59E-05	6	43435514	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9369407	LCL (MuTHER)	1.59E-05	6	43435353	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs4714677	LCL (MuTHER)	1.59E-05	6	43435017	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2841642	LCL (MuTHER)	1.63E-05	6	43410263	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	LCL (MuTHER)	1.63E-05	6	43428388	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	LCL (MuTHER)	1.97E-05	6	43435728	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	LCL (MuTHER)	2.39E-05	6	43384368	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9369407	Skin (MuTHER)	2.98E-05	6	43435353	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125737	Skin (MuTHER)	2.98E-05	6	43435514	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs4714677	Skin (MuTHER)	2.98E-05	6	43435017	ILMN_1694711	MAD2L1BP	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2841642	Skin (MuTHER)	3.15E-05	6	43410263	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs9381237	Skin (MuTHER)	3.15E-05	6	43428388	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2125738	Skin (MuTHER)	3.27E-05	6	43435728	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965	rs2254303	Lymph	0.00025613	6	43384368	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931	rs9369408	Whole blood (CHARGE)	1.72E-16	6	43440164	50193	ZNF318	cis	-8.24	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931	rs9369408	Skin (MuTHER)	6.63E-06	6	43440164	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931	rs9369408	LCL (MuTHER)	1.72E-05	6	43440164	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892	rs2396002	LCL (MuTHER)	5.60E-07	6	43367990	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892	rs2396002	Whole blood (CHARGE)	5.68E-07	6	43367990	7050040	ZNF318	cis	-5.00	C	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892	rs2396002	Skin (MuTHER)	8.40E-06	6	43367990	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828	rs2841647	Whole blood (CHARGE)	3.05E-16	6	43377157	50193	ZNF318	cis	-8.17	C	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828	rs2841647	Skin (MuTHER)	1.15E-05	6	43377158	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828	rs2841647	LCL (MuTHER)	2.68E-05	6	43377158	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Liver(Greenawalt)	1.26E-28	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	Monocytes	1.18E-26	6	43368638		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Visual cortex (all samples)	2.69E-25	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	omental	4.72E-23	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	SubCutAdipose(Greenawalt)	6.30E-19	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	Whole blood (CHARGE)	5.81E-18	6	43368638	7050040	ZNF318	cis	-8.64	C	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs16896398	Whole blood (CHARGE)	8.93E-18	6	43370682	7050040	ZNF318	cis	-8.59	T	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Whole blood (CHARGE)	1.55E-17	6	43387699	7050040	ZNF318	cis	-8.52	A	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Prefrontal cortex (normal samples)	8.53E-17	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Whole blood (PAX) in breast cancer survi	6.97E-11	6	43387699	6200307	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Intestine (normal ileum)	5.10E-10	6	43279721		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Cerebellum (Huntington's)	8.76E-10	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Liver(Schroder)	1.82E-09	6	43387699		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Lymph	3.44E-08	6	43387699	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	LCL (MuTHER)	1.72E-05	6	43368638	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Tcells	1.83E-05	6	43387699		PTK7	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs6901866	Skin (MuTHER)	2.15E-05	6	43368638	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	LCL (MuTHER)	2.20E-05	6	43387699	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Skin (MuTHER)	2.97E-05	6	43387699	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748	rs4398731	Blood(Fehrmann et al)	5.10E-20;1.0	6	43387699	50193;7210484	ZNF318;RP3-330M21	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	Whole blood (CHARGE)	1.75E-17	6	43407036	7050040	ZNF318	cis	-8.51	G	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	Intestine (normal ileum)	4.60E-10	6	43299058		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	LCL (MuTHER)	1.75E-05	6	43407036	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715	rs2279087	Skin (MuTHER)	2.70E-05	6	43407036	ILMN_1694711	MAD2L1BP	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1	rs2393833	Liver (ScanDB)	8.10E-07	10	63115322		SGTA	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1	rs12246717	Liver (ScanDB)	9.54E-07	10	63129189		SERPIND1	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1	rs2393833	Blood	0.0000286	10	63115322	HSG00268758	LOC219790	cis				
rs7070797	SBP	NA	C10orf107	9	LDproxy(CEU-Rel2	0.786	rs10509158	Adipose	0.0000037	10	63177675	HSG00269025	NM_173554	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.778	rs2588918	EndometrialTumor	0.00379818	10	63195030		C10orf107	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.734	rs973237	Liver (ScanDB)	5.92E-07	10	63195307		FUCA1	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.734	rs973237	Prefrontal cortex (Alzheimer's)	9.15E-05	10	63195307	10025902662	C10orf107	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP		rs2681472	Whole blood (CHARGE)	1.83E-15	12	88533090	7320717	WDR51B	cis	7.95	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP		rs2681472	Liver (ScanDB)	3.74E-07	12	88533090		LOC100131662	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP		rs2681472	Blood(Fehrmann et al)	2.20E-08;2.2	12	88533090	6650035;7320717	;WDR51B;ATP2B1	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs11105368	Whole blood (CHARGE)	3.56E-15	12	88598572	7320717	WDR51B	cis	7.87	C	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs11105364	Whole blood (CHARGE)	3.80E-15	12	88593407	7320717	WDR51B	cis	7.86	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs11105354	Whole blood (CHARGE)	3.82E-15	12	88550654	7320717	WDR51B	cis	7.86	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs17249754	Whole blood (CHARGE)	4.81E-15	12	88584717	7320717	WDR51B	cis	7.83	A	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1	rs12579302	Whole blood (CHARGE)	5.09E-15	12	88574634	7320717	WDR51B	cis	7.82	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	1	rs12230074	Whole blood (CHARGE)	5.11E-15	12	88614998	7320717	WDR51B	cis	7.82	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	1	rs11105378	Whole blood (CHARGE)	7.12E-15	12	88614872	7320717	WDR51B	cis	7.78	T	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92	rs2681492	Whole blood (CHARGE)	7.76E-13	12	88537220	7320717	WDR51B	cis	7.17	C	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92	rs2681492	Liver (ScanDB)	3.15E-07	12	88537220		LOC100131662	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92	rs2681492	Blood(Fehrmann et al)	2.10E-08;5.9	12	88537220	6650035;7320717	;WDR51B;ATP2B1	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	0.915	rs4842666	Whole blood (CHARGE)	3.74E-07	12	88465680	7160609	WDR51B	cis	-5.08	C	12	88337954
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	0.915	rs4842666	Monocytes (CD14+)	4.35E-05	12	88465680	9N1yRYl6R8pJ.S	GALNT4	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-H3)	0.805	rs11105328	Monocytes (CD14+)	5.41E-05	12	88466521	9N1yRYl6R8pJ.S	GALNT4	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Liver(Greenawalt)	4.63E-26	12	110368991	10023848139	AL049919	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs4766578	Whole blood (CHARGE)	5.62E-20	12	110388754	6560301	SH2B3	cis	9.15	T	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Whole blood (CHARGE)	5.02E-19	12	110368991	6560301	SH2B3	cis	8.91	T	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Visual cortex (Huntington's)	1.75E-12	12	110368991	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Prefrontal cortex (normal samples)	7.00E-11	12	110368991	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Whole blood (CHARGE)	2.00E-07	12	110368991	7570673	UPP1	trans	5.20	T	7	48114477
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Blood(Fehrmann et al)	3.50E-07	12	110368991	6560301	SH2B3;ATXN2	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Blood	0.0002037	12	110368991	HSG00276844	FLJ21127	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs10774625	Whole blood (CHARGE)	8.15E-20	12	110394602	6560301	SH2B3	cis	9.11	A	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Whole blood (CHARGE)	1.68E-19	12	110492139	6560301	SH2B3	cis	9.03	C	12	110373489
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs10774625	Whole blood (CHARGE)	3.56E-08	12	110394602	2070170	UBE2L6	trans	5.51	A	11	57075756
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Cerebellum (all samples)	9.56E-08	12	110492139	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Whole blood (CHARGE)	4.37E-07	12	110492139	7570673	UPP1	trans	5.05	C	7	48114477
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-Rel2	1	rs653178	Blood(Fehrmann et al)	2.20E-07;9.8	12	110492139	6560301;840253	SH2B3;ATXN2;ALDH2	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Liver(Greenawalt)	4.63E-26	12	110368991	10023848139	AL049919	cis				
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs4766578	Whole blood (CHARGE)	5.62E-20	12	110388754	6560301	SH2B3	cis	9.15	T	12	110373489
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Whole blood (CHARGE)	5.02E-19	12	110368991	6560301	SH2B3	cis	8.91	T	12	110373489
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Visual cortex (Huntington's)	1.75E-12	12	110368991	10023848139	AL049919	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Prefrontal cortex (normal samples)	7.00E-11	12	110368991	10023848139	AL049919	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Whole blood (CHARGE)	2.00E-07	12	110368991	7570673	UPP1	trans	5.20	T	7	48114477
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Blood(Fehrmann et al)	3.50E-07	12	110368991	6560301	SH2B3;ATXN2	cis				
rs4766578	SBP	SH2B3	ATXN2;SH2B3	11	LDproxy(CEU-1kg)	0.967	rs3184504	Blood	0.0002037	12	110368991	HSG00276844	FLJ21127	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Whole blood (CHARGE)	1.57E-34	15	73021663	4480132	ULK3	cis	12.26	T	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	omental	1.11E-13	15	73021663	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Subc adipose (MuTHER)	8.68E-09	15	73021663	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Lymph	8.12E-08	15	73021663	GI_4505234-S	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	LCL (MuTHER)	5.27E-07	15	73021663	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Skin (MuTHER)	7.69E-07	15	73021663	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Bcells (CD19+)	3.32E-06	15	73021663	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Prefrontal cortex (Alzheimer's)	3.32E-04	15	73021663	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Monocytes (CD14+)	0.000374	15	73021663	r_tdN3VF1vV3q	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Blood(Fehrmann et al)	1.90E-27;7.9	15	73021663	3170239;4480132	CSK;ULK3;COX5A;SC	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Whole blood (CHARGE)	5.55E-45	15	72927907	4480132	ULK3	cis	14.07	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	LCL in asthmatics (Liang 1kg)	1.06E-23	15	72927907	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Subc adipose (MuTHER)	1.16E-09	15	72927907	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Skin (MuTHER)	1.15E-08	15	72927907	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Lung	1.32E-07	15	72927907	100151075_TGI_	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Bcells (CD19+)	4.65E-07	15	72927907	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	LCL (MuTHER)	4.26E-06	15	72927907	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Whole blood (CHARGE)	2.10E-47	15	73012468	4480132	ULK3	cis	14.46	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Subc adipose (MuTHER)	3.46E-12	15	73012468	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	LCL (MuTHER)	4.95E-08	15	73012468	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Skin (MuTHER)	6.16E-07	15	73012468	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Lymph	1.02E-05	15	73012468	GI_4505234-S	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Cerebellum (all samples)	9.88E-05	15	73012468	10025904895	C15orf17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Monocytes	4.69E-54	15	72962079		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Whole blood (CHARGE)	4.20E-48	15	72968174	4480132	ULK3	cis	14.57	A	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Whole blood (CHARGE)	4.69E-48	15	72962079	4480132	ULK3	cis	14.57	A	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Whole blood (CHARGE)	5.76E-48	15	72981543	4480132	ULK3	cis	14.55	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	LCL in asthmatics (Liang 1kg)	4.58E-23	15	72968174	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	LCL in asthmatics (Liang 1kg)	5.33E-23	15	72962079	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs7497201	LCL in asthmatics (Liang 1kg)	2.74E-22	15	72977743	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Subc adipose (MuTHER)	2.11E-12	15	72968174	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Subc adipose (MuTHER)	2.18E-12	15	72962079	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Subc adipose (MuTHER)	2.66E-12	15	72981543	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Whole blood (Battle)	3.91E-11	15	75194490		COX5A	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Cerebellum (all samples)	3.89E-10	15	72962079	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Visual cortex (normal samples)	2.40E-08	15	72962079	10025927424	ULK3	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	LCL (MuTHER)	1.36E-07	15	72981543	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	LCL (MuTHER)	2.10E-07	15	72968174	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	LCL (MuTHER)	3.69E-07	15	72962079	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Lymph	7.22E-07	15	72962079	GI_4505234-S	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Skin (MuTHER)	1.01E-06	15	72981543	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Skin (MuTHER)	1.52E-06	15	72968174	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Skin (MuTHER)	3.23E-06	15	72962079	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs7497201	Bcells (CD19+)	3.92E-06	15	72977743	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Bcells (CD19+)	4.00E-06	15	72981543	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Blood	0.00000646	15	72962079	HSG00291325	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Bcells (CD19+)	6.61E-06	15	72968174	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	SchadtLiver	8.60E-06	15	72962079		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Bcells (CD19+)	8.77E-06	15	72962079	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Monocytes (CD14+)	7.18E-05	15	72962079	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Monocytes (CD14+)	7.50E-05	15	72981543	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs8031937	Monocytes (CD14+)	0.000101	15	72968174	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs7497201	Monocytes (CD14+)	0.000152	15	72977743	Wu17hRSKTiKhB	C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Adipose	0.0001963	15	72962079	HSG00291325	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Induced sputum (COPD cases)	0.00037621	15	72962079	224805_s_at	C15orf17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Blood(Fehrmann et al)	2.00E-28;3.0	15	72962079	3170239;4480132	CSK;ULK3;C15orf17;C	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.751	rs11636952	LCL in asthmatics (Liang 1kg)	2.98E-23	15	72901375	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.751	rs11636952	Bcells (CD19+)	1.06E-08	15	72901375	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Monocytes	8.25E-26	15	72999278		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Whole blood (CHARGE)	5.97E-21	15	72999278	4480132	ULK3	cis	-9.39	T	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	LCL (MuTHER)	3.18E-08	15	72999278	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Skin (MuTHER)	1.30E-05	15	72999278	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Subc adipose (MuTHER)	2.40E-05	15	72999278	ILMN_2364535	SNUPN	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.75	rs1133323	Bcells (CD19+)	3.86E-05	15	72999278	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.735	rs4886633	Whole blood (CHARGE)	3.99E-48	15	72965260	4480132	ULK3	cis	14.58	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.735	rs4886633	LCL in asthmatics (Liang 1kg)	5.73E-23	15	72965260	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Monocytes	3.21E-35	15	72864420		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Whole blood (CHARGE)	6.15E-35	15	72870547	4480132	ULK3	cis	12.33	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Whole blood (CHARGE)	3.65E-34	15	72869605	4480132	ULK3	cis	12.19	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	Whole blood (CHARGE)	4.77E-34	15	72867203	4480132	ULK3	cis	12.17	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	Whole blood (CHARGE)	6.23E-34	15	72852697	4480132	ULK3	cis	12.14	G	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Whole blood (CHARGE)	5.71E-33	15	72864420	4480132	ULK3	cis	11.96	C	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Whole blood (Battle)	1.79E-27	15	75083494		CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Bcells (CD19+)	1.33E-08	15	72870547	ubt12tlW7_Z_FO	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Skin (MuTHER)	1.37E-08	15	72870547	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Skin (MuTHER)	1.75E-08	15	72869605	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	Skin (MuTHER)	2.59E-08	15	72867203	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Skin (MuTHER)	3.12E-08	15	72864420	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	Skin (MuTHER)	3.16E-08	15	72852697	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Subc adipose (MuTHER)	4.43E-08	15	72869605	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	Subc adipose (MuTHER)	4.62E-08	15	72867203	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	Subc adipose (MuTHER)	4.72E-08	15	72870547	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Subc adipose (MuTHER)	6.30E-08	15	72864420	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	Subc adipose (MuTHER)	7.48E-08	15	72852697	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	Whole blood (DeepSAGESeq)	1.48E-06	15	75082552	15_75095325	None:15_75095325	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs4886410	LCL (MuTHER)	3.79E-06	15	72852697	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378940	LCL (MuTHER)	4.06E-06	15	72870547	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs1378941	LCL (MuTHER)	4.16E-06	15	72867203	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733	rs3784789	LCL (MuTHER)	4.43E-06	15	72869605	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	LCL (MuTHER)	4.49E-06	15	72864420	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Lung	3.02E-05	15	72864420	100132373_TGI_a	CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.733	rs1378942	Blood(Fehrmann et al)	2.00E-45;3.2	15	72864420	3170239;4480132	CSK;ULK3;COX5A	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.719	rs12591513	LCL in asthmatics (Liang 1kg)	1.92E-22	15	72889767	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	Whole blood (CHARGE)	6.50E-29	15	72844800	4480132	ULK3	cis	11.16	A	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	Skin (MuTHER)	7.34E-08	15	72844800	ILMN_1679495	ULK3	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	Subc adipose (MuTHER)	8.91E-08	15	72844800	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.701	rs4886606	LCL (MuTHER)	6.38E-06	15	72844800	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Monocytes	8.25E-26	15	72999278		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Whole blood (CHARGE)	5.97E-21	15	72999278	4480132	ULK3	cis	-9.39	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	LCL (MuTHER)	3.18E-08	15	72999278	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Skin (MuTHER)	1.30E-05	15	72999278	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Subc adipose (MuTHER)	2.40E-05	15	72999278	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Bcells (CD19+)	3.86E-05	15	72999278	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	Whole blood (Battle)	7.31E-79	15	75183935		SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Monocytes	8.85E-27	15	72999410		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11857695	LCL in asthmatics (Liang 1kg)	3.41E-21	15	72952804	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs12911254	LCL in asthmatics (Liang 1kg)	3.41E-21	15	72953388	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	LCL in asthmatics (Liang 1kg)	5.92E-21	15	72970988	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11633472	LCL in asthmatics (Liang 1kg)	5.99E-21	15	72971137	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Whole blood (CHARGE)	6.01E-21	15	72999410	4480132	ULK3	cis	-9.39	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	Whole blood (CHARGE)	6.51E-21	15	73008021	4480132	ULK3	cis	-9.38	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Whole blood (CHARGE)	7.20E-21	15	73008918	4480132	ULK3	cis	-9.37	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	1	rs12909335	LCL in asthmatics (Liang 1kg)	2.70E-20	15	73001842	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	LCL in asthmatics (Liang 1kg)	4.20E-20	15	73008021	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs12912839	LCL in asthmatics (Liang 1kg)	1.09E-19	15	73008298	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	LCL in asthmatics (Liang 1kg)	1.10E-19	15	73008918	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs62029167	LCL in asthmatics (Liang 1kg)	2.14E-19	15	73015403	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs12901190	LCL in asthmatics (Liang 1kg)	4.25E-19	15	73018505	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Hippocampus (CA1, n=61; Kim et al.)	5.88E-11	15	75212357	229426_at	COX5A	cis	0.00			
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	LCL (MuTHER)	3.12E-09	15	72999410	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	LCL (MuTHER)	2.97E-08	15	73008021	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	LCL (MuTHER)	3.03E-08	15	73008918	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Skin (MuTHER)	1.37E-05	15	73008918	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	Skin (MuTHER)	1.39E-05	15	73008021	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs11072513	Subc adipose (MuTHER)	1.98E-05	15	73008021	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Subc adipose (MuTHER)	2.04E-05	15	73008918	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Subc adipose (MuTHER)	2.19E-05	15	72999410	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Skin (MuTHER)	3.02E-05	15	72999410	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Bcells (CD19+)	3.21E-05	15	72999410	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11633472	Bcells (CD19+)	3.86E-05	15	72971137	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	Bcells (CD19+)	3.86E-05	15	72970988	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Monocytes (CD14+)	0.0001945	15	72999410	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	LCL in asthmatics (Liang 1kg)	1.02E-20	15	72986945	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Whole blood (CHARGE)	3.32E-20	15	72986945	4480132	ULK3	cis	-9.21	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Liver(Greenawalt)	1.34E-18	15	72986945	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	LCL (MuTHER)	3.91E-08	15	72986945	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Lymph	4.27E-06	15	72986945	GI_4505234-S	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Skin (MuTHER)	1.33E-05	15	72986945	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Prefrontal cortex (all samples)	1.3997E-05	15	72986945	10026392220	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Subc adipose (MuTHER)	3.12E-05	15	72986945	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Bcells (CD19+)	3.86E-05	15	72986945	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Induced sputum (COPD cases)	0.00015722	15	72986945	224805_s_at	C15orf17	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rs11856413	Blood(Fehrmann et al)	2.20E-21;2.20	15	72986945	3170239;50341;4	CSK;SCAMP2;ULK3;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Whole blood (Battle)	4.09E-124	15	75189930		MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	Monocytes	3.25E-29	15	72972723		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	LCL in asthmatics (Liang 1kg)	5.96E-29	15	72972723	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	LCL in asthmatics (Liang 1kg)	1.45E-28	15	72976983	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	LCL in asthmatics (Liang 1kg)	3.40E-28	15	72991079	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	LCL in asthmatics (Liang 1kg)	3.40E-28	15	72983229	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Monocytes	6.08E-27	15	72980057		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Whole blood (CHARGE)	1.49E-22	15	72983229	4480132	ULK3	cis	-9.77	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Whole blood (CHARGE)	5.14E-22	15	72976983	4480132	ULK3	cis	-9.65	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	Whole blood (CHARGE)	5.40E-22	15	72972723	4480132	ULK3	cis	-9.64	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	Whole blood (CHARGE)	5.71E-22	15	72962510	4480132	ULK3	cis	-9.63	C	15	72915933

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Whole blood (CHARGE)	1.00E-21	15	72980057	4480132	ULK3	cis	-9.58	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	Whole blood (CHARGE)	1.61E-21	15	72946486	4480132	ULK3	cis	-9.53	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	LCL in asthmatics (Liang 1kg)	3.92E-21	15	72999278	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Whole blood (CHARGE)	7.79E-21	15	72991079	4480132	ULK3	cis	-9.36	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	LCL in asthmatics (Liang 1kg)	5.64E-20	15	72946486	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	SubCutAdipose(Greenawalt)	7.68E-11	15	72983229	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	LCL (MuTHER)	3.00E-09	15	72983229	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	LCL (MuTHER)	3.10E-09	15	72991079	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	LCL (MuTHER)	4.61E-09	15	72980057	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	LCL (MuTHER)	4.89E-09	15	72976983	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	LCL (MuTHER)	5.54E-09	15	72972723	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	LCL (MuTHER)	6.47E-09	15	72946486	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	LCL (MuTHER)	8.74E-08	15	72962510	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	RNAseq(HapMapLCL)+DeepSage(blood)	2.76E-07	15	75185670	ENST0000037969	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	Subc adipose (MuTHER)	1.49E-05	15	72962510	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	Subc adipose (MuTHER)	1.53E-05	15	72946486	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Subc adipose (MuTHER)	1.94E-05	15	72983229	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7495739	Subc adipose (MuTHER)	2.20E-05	15	72972723	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Subc adipose (MuTHER)	2.25E-05	15	72976983	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs7497393	Skin (MuTHER)	2.44E-05	15	72962510	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Subc adipose (MuTHER)	2.49E-05	15	72980057	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Induced sputum (COPD cases)	2.56E-05	15	72983229	224805_s_at	C15orf17	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Subc adipose (MuTHER)	2.61E-05	15	72991079	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Skin (MuTHER)	3.01E-05	15	72991079	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Bcells (CD19+)	3.21E-05	15	72991079	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Bcells (CD19+)	3.21E-05	15	72980057	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Bcells (CD19+)	3.35E-05	15	72983229	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Bcells (CD19+)	4.67E-05	15	72976983	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Monocytes (CD14+)	0.000135	15	72983229	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072511	Bcells (CD19+)	0.0001942	15	72946486	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs11072512	Monocytes (CD14+)	0.0001945	15	72991079	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1127796	Monocytes (CD14+)	0.0001945	15	72980057	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Visual cortex (all samples)	2.80E-04	15	72983229	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs1130741	Monocytes (CD14+)	0.0003045	15	72976983	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Liver(UChicago)	0.000119825;	15	72983229	A_23_P60579;A_	MPI;SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967	rs4886636	Blood(Fehrmann et al)	1.60E-19;1.1	15	72983229	3170239;50341;	CSK;SCAMP2;ULK3;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs12902515	LCL in asthmatics (Liang 1kg)	4.40E-20	15	72948051	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Whole blood (CHARGE)	1.49E-19	15	73029208	4480132	ULK3	cis	-9.05	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs4886641	LCL in asthmatics (Liang 1kg)	2.23E-19	15	73015708	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs11639413	LCL in asthmatics (Liang 1kg)	2.55E-19	15	73030347	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	LCL in asthmatics (Liang 1kg)	2.58E-19	15	73029208	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	omental	3.08E-19	15	73029208	10025911367	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415249	LCL in asthmatics (Liang 1kg)	4.75E-19	15	73029093	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	LCL (MuTHER)	4.19E-08	15	73029208	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Subc adipose (MuTHER)	2.09E-05	15	73029208	ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Skin (MuTHER)	2.46E-05	15	73029208	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966	rs2415251	Bcells (CD19+)	3.17E-05	15	73029208	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11854704	LCL in asthmatics (Liang 1kg)	4.96E-28	15	73008068	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Whole blood (CHARGE)	1.26E-22	15	72942949	4480132	ULK3	cis	-9.79	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	LCL in asthmatics (Liang 1kg)	1.94E-20	15	72942949	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	LCL (MuTHER)	6.46E-08	15	72942949	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Lung	2.86E-06	15	72942949	100161886_TGI_	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Skin (MuTHER)	4.23E-06	15	72942949	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Subc adipose (MuTHER)	3.77E-05	15	72942949	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965	rs11630918	Bcells (CD19+)	5.10E-05	15	72942949	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs12913293	LCL in asthmatics (Liang 1kg)	5.44E-29	15	72971511	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs8025447	LCL in asthmatics (Liang 1kg)	1.59E-28	15	72979275	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs12907898	LCL in asthmatics (Liang 1kg)	3.26E-28	15	72994925	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs12904897	LCL in asthmatics (Liang 1kg)	3.85E-28	15	73004739	202472_at	MPI	cis				

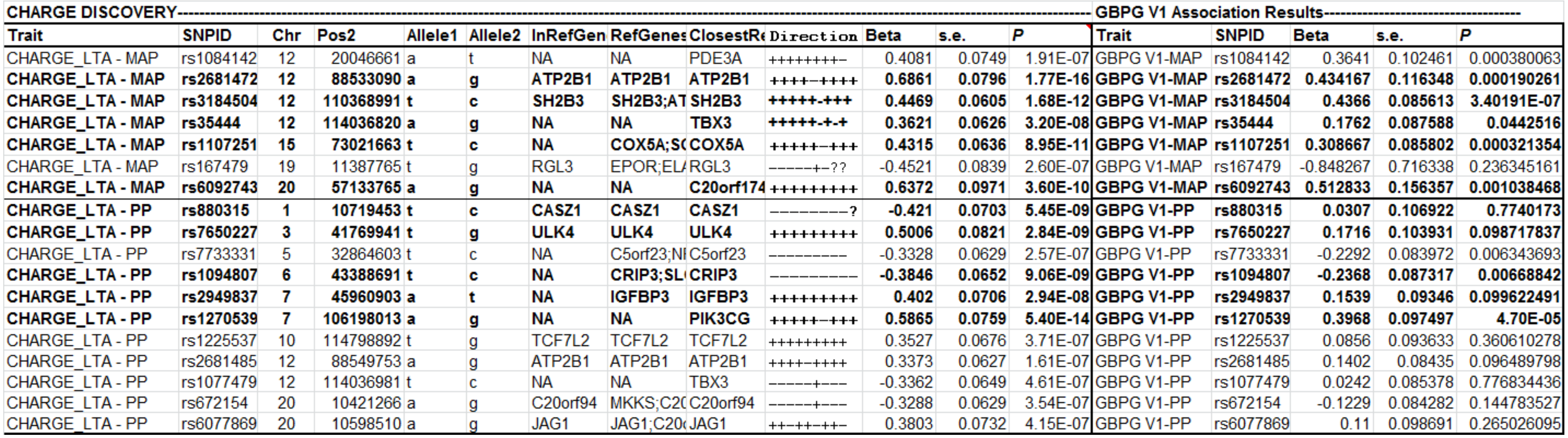
IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index	eSNPid	Tissue	eSNP *P* value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932	rs59945415	LCL in asthmatics (Liang 1kg)	8.04E-28	15	73015480	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Monocytes	5.36E-26	15	72923747		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Whole blood (CHARGE)	3.69E-24	15	72923747	4480132	ULK3	cis	-10.14	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	LCL in asthmatics (Liang 1kg)	9.19E-21	15	72923747	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	LCL (MuTHER)	2.37E-07	15	72923747	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Skin (MuTHER)	3.95E-06	15	72923747	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.931	rs12487	Subc adipose (MuTHER)	4.58E-05	15	72923747	ILMN_1695271	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.9	rs4480762	LCL in asthmatics (Liang 1kg)	9.19E-21	15	72926479	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Whole blood (CHARGE)	3.44E-23	15	72912698	4480132	ULK3	cis	-9.92	C	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	LCL in asthmatics (Liang 1kg)	4.34E-20	15	72912698	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Cerebellum (Alzheimer's)	7.49E-10	15	72912698	10025927424	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Bcells (CD19+)	3.92E-07	15	72912698	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Lymph	4.47E-07	15	72912698	GI_39930360-S	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	LCL (MuTHER)	6.72E-07	15	72912698	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Skin (MuTHER)	5.50E-06	15	72912698	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Subc adipose (MuTHER)	3.13E-05	15	72912698	ILMN_1695271	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Monocytes (CD14+)	9.64E-05	15	72912698	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Blood	0.0002728	15	72912698	HSG00290189	ARID3B	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Lung	<2E-16	15	72912698	100312245_TGI_	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Blood(Fehrmann et al)	1.00E-25;1.5	15	72912698	3170239;4480132	CSK;ULK3;SCAMP2;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.832	rs34063670	LCL in asthmatics (Liang 1kg)	1.28E-18	15	73034209	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.832	rs11636892	LCL in asthmatics (Liang 1kg)	2.81E-18	15	73053102	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.808	rs12917376	LCL in asthmatics (Liang 1kg)	1.61E-22	15	72903220	202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.801	rs56338926	LCL in asthmatics (Liang 1kg)	1.23E-18	15	73046388	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.801	rs35556055	LCL in asthmatics (Liang 1kg)	2.88E-18	15	73040467	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.801	rs35556055	Bcells (CD19+)	0.0001316	15	73040467	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	Whole blood (CHARGE)	3.19E-20	15	72916647	4480132	ULK3	cis	-9.21	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	LCL in asthmatics (Liang 1kg)	3.77E-20	15	72916647	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	LCL (MuTHER)	3.57E-07	15	72916647	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.799	rs2290573	Skin (MuTHER)	8.85E-06	15	72916647	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.798	rs11630087	LCL in asthmatics (Liang 1kg)	1.82E-18	15	73048726	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.798	rs62029217	LCL in asthmatics (Liang 1kg)	3.24E-18	15	73048952	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.771	rs12912343	LCL in asthmatics (Liang 1kg)	1.30E-18	15	73038094	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.767	rs4886413	LCL in asthmatics (Liang 1kg)	3.29E-18	15	73049363	218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Whole blood (CHARGE)	1.57E-34	15	73021663	4480132	ULK3	cis	12.26	T	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	omental	1.11E-13	15	73021663	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Subc adipose (MuTHER)	8.68E-09	15	73021663	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Lymph	8.12E-08	15	73021663	GI_4505234-S	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	LCL (MuTHER)	5.27E-07	15	73021663	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Skin (MuTHER)	7.69E-07	15	73021663	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Bcells (CD19+)	3.32E-06	15	73021663	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Prefrontal cortex (Alzheimer's)	3.32E-04	15	73021663	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Monocytes (CD14+)	0.000374	15	73021663	r_tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Blood(Fehrmann et al)	1.90E-27;7.9	15	73021663	3170239;4480132	CSK;ULK3;COX5A;SC	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Whole blood (CHARGE)	2.42E-29	15	72917626	4480132	ULK3	cis	11.25	A	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	LCL (MuTHER)	1.67E-07	15	72917626	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Subc adipose (MuTHER)	1.58E-06	15	72917626	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Bcells (CD19+)	5.64E-06	15	72917626	ubt12tlW7_Z_FO	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	rs2290572	Skin (MuTHER)	1.83E-05	15	72917626	ILMN_1679495	ULK3	cis				
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs6026704	Whole blood (CHARGE)	1.59E-08	20	57117540	4220259	CTSZ	cis	5.65	C	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs7362597	Whole blood (CHARGE)	1.60E-08	20	57112829	4220259	CTSZ	cis	5.65	A	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs6100342	Whole blood (CHARGE)	2.28E-08	20	57132656	4220259	CTSZ	cis	5.59	C	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs882384	Whole blood (CHARGE)	2.28E-08	20	57132808	4220259	CTSZ	cis	5.59	T	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs998981	Whole blood (CHARGE)	2.44E-08	20	57133036	4220259	CTSZ	cis	5.58	T	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	1	rs6100343	Whole blood (CHARGE)	2.70E-08	20	57133607	4220259	CTSZ	cis	5.56	A	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	0.915	rs1465537	Whole blood (CHARGE)	2.37E-08	20	57131415	4220259	CTSZ	cis	5.58	T	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14	LDproxy(CEU-1kg)	0.85	rs6100340	Whole blood (CHARGE)	2.53E-08	20	57118007	4220259	CTSZ	cis	5.57	G	20	57003893

Table S6: PUUMA cohort characteristics.

N	Age, years (sd)	BMI, kg/m2 (sd)	SBP, mmHg (sd)	DBP, mmHg (sd)	Anti-hypertensive therapy (%)	SBP, mmHg, adjusted for antihypertensive therapy (sd)	DBP, mmHg, adjusted for antihypertensive therapy (sd)
5,605	57.35 (9.02)	26.07 (3.38)	133.92 (16.61)	74.92 (9.95)	33.52%	138.95 (19.88)	78.27 (11.42)

Table S7: LTA discovery analysis summary for loci with SNP association(s) *P* value < 5x10-7, and association results in GBPG Visit 1 BP analyses.A1

CHARGE DISCOVERY---													GBPG V1 Association Results---				
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGenes	ClosestRe	Direction	Beta	s.e.	*P*	Trait	SNPID	Beta	s.e.	*P*
CHARGE_LTA - DBP	rs1204627	1	10722164	t	c	CASZ1	CASZ1	CASZ1	--------?	-0.3223	0.0597	2.29E-07	GBPG V1-DBP	rs1204627	-0.2799	0.0934	0.002726
CHARGE_LTA - DBP	**rs1330656**	**1**	**11788391**	**a**	**g**	**MTHFR**	**MTHFR;N**	**MTHFR**	**++++--+++**	**0.4789**	**0.0723**	**2.08E-10**	**GBPG V1-DBP**	**rs1330656**	**0.4529**	**0.1083**	**0.00002905**
CHARGE_LTA - DBP	**rs2004776**	**1**	**228915325**	**t**	**c**	**AGT**	**AGT;COG**	**AGT**	**+++++++++**	**0.3545**	**0.0615**	**3.20E-08**	**GBPG V1-DBP**	**rs2004776**	**0.1014**	**0.091**	**0.2656**
CHARGE_LTA - DBP	rs1275988	2	26767868	t	c		KCNK3;CI	KCNK3	-----+--+	-0.2814	0.0534	4.25E-07	GBPG V1-DBP	rs1275988	-0.1123	0.0775	0.1473
CHARGE_LTA - DBP	**rs7599598**	**2**	**96715567**	**a**	**g**		**FLJ10081;**	**FER1L5**	**---------**	**-0.314**	**0.0543**	**2.91E-08**	**GBPG V1-DBP**	**rs7599598**	**-0.0403**	**0.0799**	**0.6139**
CHARGE_LTA - DBP	rs1528293	3	170637205	a	t	MDS1	MDS1	MDS1	+++++++++	0.2738	0.0522	4.96E-07	GBPG V1-DBP	rs1528293	0.2427	0.0769	0.00161
CHARGE_LTA - DBP	rs1952650	5	157746045	a	t			EBF1	++++-++++	0.2862	0.0523	1.58E-07	GBPG V1-DBP	rs1952650	0.2984	0.0765	0.00009565
CHARGE_LTA - DBP	**rs198823**	**6**	**26230912**	**t**	**g**		**HIST1H2E**	**HIST1H2E**	**----+----**	**-0.3346**	**0.0553**	**6.57E-09**	**GBPG V1-DBP**	**rs198823**	**-0.1705**	**0.0801**	**0.03331**
CHARGE_LTA - DBP	**rs1225896**	**10**	**18767965**	**c**	**g**	**CACNB2**	**CACNB2**	**CACNB2**	**+++-+-+++**	**0.3548**	**0.0571**	**2.48E-09**	**GBPG V1-DBP**	**rs1225896**	**0.2836**	**0.0834**	**0.0006716**
CHARGE_LTA - DBP	**rs1224484**	**10**	**63109192**	**t**	**g**	**C10orf107**	**C10orf107**	**C10orf107**	**-----+--+**	**-0.3784**	**0.0627**	**7.05E-09**	**GBPG V1-DBP**	**rs1224484**	**-0.432**	**0.0901**	**0.000001618**
CHARGE_LTA - DBP	rs1084142	12	20046661	a	t			PDE3A	+++++++++	0.3604	0.0651	1.09E-07	GBPG V1-DBP	rs1084142	0.3446	0.0941	0.0002492
CHARGE_LTA - DBP	**rs2681472**	**12**	**88533090**	**a**	**g**	**ATP2B1**	**ATP2B1**	**ATP2B1**	**++++-++++**	**0.5231**	**0.0691**	**4.01E-13**	**GBPG V1-DBP**	**rs2681472**	**0.336**	**0.1065**	**0.001608**
CHARGE_LTA - DBP	**rs3184504**	**12**	**110368991**	**t**	**c**	**SH2B3**	**SH2B3;AT**	**SH2B3**	**+++++++++**	**0.3936**	**0.0524**	**6.08E-13**	**GBPG V1-DBP**	**rs3184504**	**0.4265**	**0.0789**	**6.361E-08**
CHARGE_LTA - DBP	**rs1133323**	**15**	**72999278**	**t**	**c**		**COX5A;M**	**COX5A**	**---------**	**-0.3262**	**0.0526**	**2.66E-09**	**GBPG V1-DBP**	**rs1133323**	**-0.2747**	**0.0763**	**0.000321**
CHARGE_LTA - DBP	rs167479	19	11387765	t	g	RGL3	EPOR;EL	RGL3	-------??	-0.3913	0.0729	2.67E-07	GBPG V1-DBP	rs167479	-0.942	0.597	0.1146
CHARGE_LTA - DBP	**rs6092743**	**20**	**57133765**	**a**	**g**			**C20orf174**	**+++++-+++**	**0.502**	**0.0843**	**1.11E-08**	**GBPG V1-DBP**	**rs6092743**	**0.3393**	**0.1436**	**0.01814**
CHARGE_LTA - SBP	**rs880315**	**1**	**10719453**	**t**	**c**	**CASZ1**	**CASZ1**	**CASZ1**	**--------?**	**-0.7125**	**0.1005**	**7.98E-12**	**GBPG V1-SBP**	**rs880315**	**-0.2245**	**0.1504**	**0.1355**
CHARGE_LTA - SBP	**rs1330656**	**1**	**11788391**	**a**	**g**	**MTHFR**	**MTHFR;N**	**MTHFR**	**+++++++++**	**0.8795**	**0.1235**	**6.38E-12**	**GBPG V1-SBP**	**rs1330656**	**0.7349**	**0.1646**	**0.000007978**
CHARGE_LTA - SBP	rs2004776	1	228915325	t	c	AGT	AGT;COG	AGT	+-+++++++	0.5488	0.1049	4.45E-07	GBPG V1-SBP	rs2004776	0.1419	0.1395	0.3091
CHARGE_LTA - SBP	**rs1275988**	**2**	**26767868**	**t**	**c**	**NA**	**KCNK3;C**	**KCNK3**	**-----+--+**	**-0.6004**	**0.0917**	**2.61E-10**	**GBPG V1-SBP**	**rs1275988**	**-0.2554**	**0.1175**	**0.02977**
CHARGE_LTA - SBP	**rs6712094**	**2**	**164751706**	**a**	**g**	**NA**	**NA**	**GRB14**	**++++-++++**	**0.598**	**0.1007**	**9.89E-09**	**GBPG V1-SBP**	**rs6712094**	**0.4239**	**0.1298**	**0.001095**
CHARGE_LTA - SBP	rs9823197	3	11478133	a	t	ATG7	ATG7	ATG7	-----+-+-	-0.4884	0.0915	2.58E-07	GBPG V1-SBP	rs9823197	-0.2888	0.1168	0.01344
CHARGE_LTA - SBP	**rs7733331**	**5**	**32864603**	**t**	**c**	**NA**	**C5orf23;N**	**C5orf23**	**----+----**	**-0.5505**	**0.0911**	**5.38E-09**	**GBPG V1-SBP**	**rs7733331**	**-0.4965**	**0.118**	**0.00002564**
CHARGE_LTA - SBP	rs1253434	7	27242452	a	g	NA	HOXA13;H	EVX1	-----+--?	-1.5903	0.292	1.48E-07	GBPG V1-SBP	rs1253434	-0.6512	0.3214	0.04273
CHARGE_LTA - SBP	**rs1270539**	**7**	**106198013**	**a**	**g**	**NA**	**NA**	**PIK3CG**	**++++--++-**	**0.6307**	**0.11**	**3.17E-08**	**GBPG V1-SBP**	**rs1270539**	**0.4007**	**0.1371**	**0.003466**
CHARGE_LTA - SBP	rs1267714	8	11488146	c	g	NA	BLK	BLK	---------	-0.5272	0.0988	2.60E-07	GBPG V1-SBP	rs1267714	-0.1581	0.1218	0.194
CHARGE_LTA - SBP	**rs1225896**	**10**	**18767965**	**c**	**g**	**CACNB2**	**CACNB2**	**CACNB2**	**+++++++++**	**0.6307**	**0.0976**	**4.53E-10**	**GBPG V1-SBP**	**rs1225896**	**0.3876**	**0.1268**	**0.002244**
CHARGE_LTA - SBP	**rs7070797**	**10**	**63221779**	**a**	**g**	**NA**	**C10orf107**	**C10orf107**	**-+---+---**	**-0.7415**	**0.1306**	**4.30E-08**	**GBPG V1-SBP**	**rs7070797**	**-0.6611**	**0.174**	**0.0001443**
CHARGE_LTA - SBP	rs1926032	10	104819459	t	c	CNNM2	NT5C2;CN	CNNM2	-----+---	-0.9087	0.1715	3.15E-07	GBPG V1-SBP	rs1926032	-1.0971	0.2137	2.826E-07
CHARGE_LTA - SBP	**rs2681472**	**12**	**88533090**	**a**	**g**	**ATP2B1**	**ATP2B1**	**ATP2B1**	**++++-++++**	**0.9457**	**0.118**	**1.04E-14**	**GBPG V1-SBP**	**rs2681472**	**0.6305**	**0.1646**	**0.0001282**
CHARGE_LTA - SBP	**rs4766578**	**12**	**110388754**	**a**	**t**	**ATXN2**	**SH2B3;AT**	**ATXN2**	**-----+---**	**-0.5599**	**0.0909**	**2.82E-09**	**GBPG V1-SBP**	**rs4766578**	**-0.4787**	**0.1201**	**0.00006713**
CHARGE_LTA - SBP	**rs35444**	**12**	**114036820**	**a**	**g**	**NA**	**+++++-+-**	**TBX3**	**+++++-+-+**	**0.5452**	**0.0929**	**1.47E-08**	**GBPG V1-SBP**	**rs35444**	**0.1568**	**0.1226**	**0.2009**
CHARGE_LTA - SBP	**rs1107251**	**15**	**73021663**	**t**	**c**	**NA**	**COX5A;S**	**COX5A**	**+++++-+++**	**0.5692**	**0.0947**	**6.54E-09**	**GBPG V1-SBP**	**rs1107251**	**0.3548**	**0.12**	**0.003102**
CHARGE_LTA - SBP	**rs6092743**	**20**	**57133765**	**a**	**g**	**NA**	**NA**	**C20orf174**	**+++++++++**	**0.8396**	**0.1449**	**2.25E-08**	**GBPG V1-SBP**	**rs6092743**	**0.8599**	**0.2202**	**0.00009393**
CHARGE_LTA - MAP	**rs880315**	**1**	**10719453**	**t**	**c**	**CASZ1**	**CASZ1**	**CASZ1**	**--------?**	**-0.4597**	**0.067**	**5.49E-11**	**GBPG V1-MAP**	**rs880315**	**-0.244967**	**0.108505**	**0.023966954**
CHARGE_LTA - MAP	**rs1330656**	**1**	**11788391**	**a**	**g**	**MTHFR**	**MTHFR;N**	**MTHFR**	**++++-++++**	**0.6133**	**0.0832**	**1.83E-12**	**GBPG V1-MAP**	**rs1330656**	**0.5469**	**0.11748**	**3.23559E-06**
CHARGE_LTA - MAP	**rs2004776**	**1**	**228915325**	**t**	**c**	**AGT**	**AGT;COG**	**AGT**	**+++++++++**	**0.4226**	**0.0708**	**1.18E-08**	**GBPG V1-MAP**	**rs2004776**	**0.1149**	**0.099071**	**0.246143016**
CHARGE_LTA - MAP	**rs1275988**	**2**	**26767868**	**t**	**c**	**NA**	**KCNK3;C**	**KCNK3**	**-----+--+**	**-0.3894**	**0.0616**	**1.51E-09**	**GBPG V1-MAP**	**rs1275988**	**-0.16**	**0.083983**	**0.056759651**
CHARGE_LTA - MAP	rs6712094	2	164751706	a	g	NA	NA	GRB14	++++-++++	0.385	0.0677	5.42E-08	GBPG V1-MAP	rs6712094	0.2713	0.092326	0.003297944
CHARGE_LTA - MAP	rs1528293	3	170637205	a	t	MDS1	MDS1	MDS1	+++++++++	0.3361	0.0602	9.29E-08	GBPG V1-MAP	rs1528293	0.279367	0.083395	0.000808377
CHARGE_LTA - MAP	rs7728845	5	122933582	a	g	CSNK1G3	CSNK1G3	CSNK1G3	+++++++++	0.3766	0.0712	4.34E-07	GBPG V1-MAP	rs7728845	0.3521	0.099069	0.000379275
CHARGE_LTA - MAP	rs198846	6	26215442	a	g	NA	HIST1H2B	HIST1H1T	+++++++++	0.4829	0.085	5.69E-08	GBPG V1-MAP	rs198846	0.5286	0.120456	1.1423E-05
CHARGE_LTA - MAP	rs7794193	7	27261226	a	g	NA	HOXA13;E	EVX1	-----+-+-	-0.914	0.1724	4.03E-07	GBPG V1-MAP	rs7794193	-0.296533	0.205208	0.148447395
CHARGE_LTA - MAP	**rs1225896**	**10**	**18767965**	**c**	**g**	**CACNB2**	**CACNB2**	**CACNB2**	**+++++-+++**	**0.452**	**0.0657**	**4.98E-11**	**GBPG V1-MAP**	**rs1225896**	**0.318267**	**0.090482**	**0.000435732**
CHARGE_LTA - MAP	**rs2166122**	**10**	**63193080**	**t**	**c**	**C10orf107**	**C10orf107**	**C10orf107**	**-+---+---**	**-0.4812**	**0.0766**	**1.88E-09**	**GBPG V1-MAP**	**rs2166122**	**-0.439133**	**0.101765**	**1.5948E-05**



CHARGE DISCOVERY--													GBPG V1 Association Results------------------				
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGenes	ClosestR	Direction	Beta	s.e.	*P*	Trait	SNPID	Beta	s.e.	*P*
CHARGE_LTA - MAP	rs1084142	12	20046661	a	t	NA	NA	PDE3A	++++++++-	0.4081	0.0749	1.91E-07	GBPG V1-MAP	rs1084142	0.3641	0.102461	0.000380063
CHARGE_LTA - MAP	**rs2681472**	**12**	**88533090**	**a**	**g**	**ATP2B1**	**ATP2B1**	**ATP2B1**	**++++-++++**	**0.6861**	**0.0796**	**1.77E-16**	**GBPG V1-MAP**	**rs2681472**	**0.434167**	**0.116348**	**0.000190261**
CHARGE_LTA - MAP	**rs3184504**	**12**	**110368991**	**t**	**c**	**SH2B3**	**SH2B3;AT**	**SH2B3**	**+++++-+++**	**0.4469**	**0.0605**	**1.68E-12**	**GBPG V1-MAP**	**rs3184504**	**0.4366**	**0.085613**	**3.40191E-07**
CHARGE_LTA - MAP	**rs35444**	**12**	**114036820**	**a**	**g**	**NA**	**NA**	**TBX3**	**+++++-+-+**	**0.3621**	**0.0626**	**3.20E-08**	**GBPG V1-MAP**	**rs35444**	**0.1762**	**0.087588**	**0.0442516**
CHARGE_LTA - MAP	**rs1107251**	**15**	**73021663**	**t**	**c**	**NA**	**COX5A;S**	**COX5A**	**+++++-+++**	**0.4315**	**0.0636**	**8.95E-11**	**GBPG V1-MAP**	**rs1107251**	**0.308667**	**0.085802**	**0.000321354**
CHARGE_LTA - MAP	rs167479	19	11387765	t	g	RGL3	EPOR;EL	RGL3	-----+-??	-0.4521	0.0839	2.60E-07	GBPG V1-MAP	rs167479	-0.848267	0.716338	0.236345161
CHARGE_LTA - MAP	**rs6092743**	**20**	**57133765**	**a**	**g**	**NA**	**NA**	**C20orf174**	**+++++++++**	**0.6372**	**0.0971**	**3.60E-10**	**GBPG V1-MAP**	**rs6092743**	**0.512833**	**0.156357**	**0.001038468**
CHARGE_LTA - PP	**rs880315**	**1**	**10719453**	**t**	**c**	**CASZ1**	**CASZ1**	**CASZ1**	**--------?**	**-0.421**	**0.0703**	**5.45E-09**	**GBPG V1-PP**	**rs880315**	**0.0307**	**0.106922**	**0.7740173**
CHARGE_LTA - PP	**rs7650227**	**3**	**41769941**	**t**	**g**	**ULK4**	**ULK4**	**ULK4**	**+++++++++**	**0.5006**	**0.0821**	**2.84E-09**	**GBPG V1-PP**	**rs7650227**	**0.1716**	**0.103931**	**0.098717837**
CHARGE_LTA - PP	rs7733331	5	32864603	t	c	NA	C5orf23;N	C5orf23	---------	-0.3328	0.0629	2.57E-07	GBPG V1-PP	rs7733331	-0.2292	0.083972	0.006343693
CHARGE_LTA - PP	**rs1094807**	**6**	**43388691**	**t**	**c**	**NA**	**CRIP3;SL**	**CRIP3**	**---------**	**-0.3846**	**0.0652**	**9.06E-09**	**GBPG V1-PP**	**rs1094807**	**-0.2368**	**0.087317**	**0.00668842**
CHARGE_LTA - PP	**rs2949837**	**7**	**45960903**	**a**	**t**	**NA**	**IGFBP3**	**IGFBP3**	**+++++++++**	**0.402**	**0.0706**	**2.94E-08**	**GBPG V1-PP**	**rs2949837**	**0.1539**	**0.09346**	**0.099622491**
CHARGE_LTA - PP	**rs1270539**	**7**	**106198013**	**a**	**g**	**NA**	**NA**	**PIK3CG**	**+++++-+++**	**0.5865**	**0.0759**	**5.40E-14**	**GBPG V1-PP**	**rs1270539**	**0.3968**	**0.097497**	**4.70E-05**
CHARGE_LTA - PP	rs1225537	10	114798892	t	g	TCF7L2	TCF7L2	TCF7L2	+++++++++	0.3527	0.0676	3.71E-07	GBPG V1-PP	rs1225537	0.0856	0.093633	0.360610278
CHARGE_LTA - PP	rs2681485	12	88549753	a	g	ATP2B1	ATP2B1	ATP2B1	++++-++++	0.3373	0.0627	1.61E-07	GBPG V1-PP	rs2681485	0.1402	0.08435	0.096489798
CHARGE_LTA - PP	rs1077479	12	114036981	t	c	NA	NA	TBX3	-----+---	-0.3362	0.0649	4.61E-07	GBPG V1-PP	rs1077479	0.0242	0.085378	0.776834436
CHARGE_LTA - PP	rs672154	20	10421266	a	g	C20orf94	MKKS;C20	C20orf94	-----+---	-0.3288	0.0629	3.54E-07	GBPG V1-PP	rs672154	-0.1229	0.084282	0.144783527
CHARGE_LTA - PP	rs6077869	20	10598510	a	g	JAG1	JAG1;C20	JAG1	++-++-++-	0.3803	0.0732	4.15E-07	GBPG V1-PP	rs6077869	0.11	0.098691	0.265026095

Rows in **bold** show LTA analysis *P* values < $5x10^{-8}$.

Table S8: Summary of number of SNPs and loci identified by LTA

Number of significant SNPs

	P value < 5×10^{-8}	
	#LTA SNPs	#V1 SNPs
SBP	117	122
DBP	96	126
MAP	155	153
PP	120	1
Total	488	402

Number of significant Loci

	P value < 5×10^{-8}	
	#LTA loci	#V1 loci
SBP	13	8
DBP	10	9
MAP	11	9
PP	5	1
Total	39	27

Table S9: Distribution of LTA *P* values as compared to the corresponding V1 BP trait analysis *P* values

SBP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	40013	2480814	
LTA SNP (pGC<5e-8)	101	16	Chisquare test *P* value < 2.2e-16

DBP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	29775	2491052	
LTA SNP (pGC<5e-8)	64	32	Chisquare test *P* value < 2.2e-16

MAP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	32885	2487942	
LTA SNP (pGC<5e-8)	123	32	Chisquare test *P* value < 2.2e-16

PP (delta distribution)	Extreme values* (right tail+left tail)	Non-Extreme values (central)	
Total SNP distributed as normal	36139	2484688	
LTA SNP (pGC<5e-8)	120	0	Chisquare test *P* value < 2.2e-16

*Extreme values are defined as values that are larger than 'mean+3*sd' or smaller than 'mean-3*sd'

Table S10: Power simulations for the application of LTA to SBP.

a: Correlation between the 4 visits for SBP residual adjusted for BMI, age, and age*age and gender in ARIC.

	SBP V1	**SBP V2**	**SBP V3**	**SBP V4**
SBP V1	1.00	0.73	0.65	0.60
SBP V2	0.73	1.00	0.72	0.64
SBP V3	0.65	0.72	1.00	0.70
SBP V4	0.60	0.64	0.70	1.00

b1: Power Estimates. Sample size N = 1000 and testing at alpha=0.05. The true effect size is 0.1. Monte Carlo size 10,000.

q	**0.05**	**0.10**	**0.20**	**0.30**	**0.40**
Visit 1	0.16	0.27	0.43	0.52	0.59
LTA	0.19	0.33	0.52	0.63	0.70
GEE (4 visits)	0.20	0.34	0.52	0.64	0.70

b2: Power Estimates, Null Hypothesis. Sample size N = 1000 and testing at alpha=0.05. The true effect size is 0. Monte Carlo size 10,000.

q	**0.05**	**0.10**	**0.20**	**0.30**	**0.40**
Visit 1	0.050	0.048	0.048	0.050	0.047
LTA	0.053	0.051	0.052	0.048	0.048
GEE (4 visits)	0.059	0.052	0.051	0.051	0.050

c: Sample size N = 10000 and testing at alpha = 5x10-8. The true effect size is 0.05. Monte Carlo size 5,000.

	0.05	**0.1**	**0.2**	**0.3**	**0.4**
Visit 1	0	0.001	0.005	0.011	0.023
LTA	0	0.002	0.015	0.039	0.070
GEE (4 visits)	0	0.002	0.015	0.039	0.071

Table S11: Enrichment analysis results

Stronger results in LTA versus V1 analysis	**Summary of lead SNPs and LTA and V1 results**										**Tested Region**			Pvalue of Kolmogorov–Smirnov statistics with 10000 permutation		Pvalue of 10000 times Bootstrapping compared to the statistics from the	
	trait	**SNPID**	**Allele1**	**Chr**	**Position**	**InRefGene**	**RefGenes.60kbfrom**	**ClosestRefGene**	**LTA P value**	**V1 P value**	**Position Start**	**Position End**	**# SNPs**	**D-.*P*value**	**D+.*P*value**	**D-.*P*value**	**D+.*P*value**
LTA	SBP	rs13306561	a	1p36	11788391	MTHFR	MTHFR;NPPA;CLCN	MTHFR	6.38E-12	1.11E-07	11775103	11847887	102	0.4522	**1.00E-04**	0.3983	**<0.0001**
LTA	SBP	rs1275988	t	2p23	26767868	NA	KCNK3;CIB4	KCNK3	2.61E-10	1.38E-05	26765249	26786300	10	1	**<0.0001**	1	**<0.0001**
LTA	SBP	rs6712094	a	2q24	164751706	NA	NA	GRB14	9.89E-09	5.22E-07	164722539	164839114	175	0.6859	**2.00E-04**	0.7081	**<0.0001**
LTA	SBP	rs7733331	t	5p13	32864603	NA	C5orf23;NPR3	C5orf23	5.38E-09	0.000141351	32810804	32867696	43	1	**0.0016**	1	**4.00E-04**
LTA	SBP	rs12705390	a	7q22	106198013	NA	NA	PIK3CG	3.17E-08	2.63E-05	106192878	106199094	20	0.956	**4.00E-04**	0.9823	**1.00E-04**
LTA	SBP	rs7070797	a	10q21	63221779	NA	C10orf107	C10orf107	4.30E-08	1.17E-06	63190704	63221779	48	0.7187	**0.0024**	0.7434	**1.00E-04**
LTA	DBP	rs13306561	a	1p36	11788391	MTHFR	MTHFR;NPPA;CLCN	MTHFR	2.08E-10	1.28E-07	11783430	11828561	83	0.7217	**<0.0001**	0.7821	**<0.0001**
LTA	DBP	rs1952650	a	5q33	157746045	NA	NA	EBF1	1.58E-07	2.16E-05	157746045	157746045	82	0.3685	**<0.0001**	0.3102	**<0.0001**
LTA	DBP	rs198823	t	6p22	26230912	NA	HIST1H2BD;HIST1H2	HIST1H2BC	6.57E-09	4.52E-06	26150218	26233321	155	0.8544	**<0.0001**	0.8949	**<0.0001**
LTA	DBP	rs3184504	t	12q24	110368991	SH2B3	SH2B3;ATXN2	SH2B3	6.08E-13	1.26E-08	110368991	111390798	277	0.9517	**<0.0001**	0.9721	**<0.0001**
LTA	MAP	rs880315	t	1p36	10719453	CASZ1	CASZ1	CASZ1	5.49E-11	1.47E-07	10713384	10724576	9	0.856	**0.0081**	0.9464	**0.0042**
LTA	MAP	rs13306561	a	1p36	11788391	MTHFR	MTHFR;NPPA;CLCN	MTHFR	1.83E-12	1.48E-08	11775103	11847887	104	0.7774	**1.00E-04**	0.8154	**<0.0001**
LTA	MAP	rs1275988	t	2p23	26767868	NA	KCNK3;CIB4	KCNK3	1.51E-09	7.06E-06	26765249	26786300	10	1	**3.00E-04**	1	**<0.0001**
LTA	MAP	rs2681472	a	12q21	88533090	ATP2B1	ATP2B1	ATP2B1	1.77E-16	1.70E-12	88465680	88637201	132	0.3985	**<0.0001**	0.3285	**<0.0001**
LTA	PP	rs10948071	t	6p21	43388691	NA	CRIP3;SLC22A7;TTE	CRIP3	9.06E-09	0.000111242	43367990	43440164	49	0.9211	**<0.0001**	0.9491	**<0.0001**
LTA	PP	rs2949837	a	7p13	45960903	NA	IGFBP3	IGFBP3	2.94E-08	6.88E-06	45929639	45960903	49	1	**<0.0001**	1	**<0.0001**
LTA	PP	rs12705390	a	7q22	106198013	NA	NA	PIK3CG	5.40E-14	1.20E-06	106192878	106206532	24	0.612	**5.00E-04**	0.7028	**<0.0001**
V1	SBP	rs2004776	t	1q42	228915325	AGT	AGT;COG2;CAPN9	AGT	4.45E-07	4.63E-08	228903667	228916422	76	**0.0061**	0.9914	**4.00E-04**	1
V1	SBP	rs4766578	a	12q24	110388754	ATXN2	SH2B3;ATXN2	ATXN2	2.82E-09	1.18E-09	110368991	110556807	201	**<0.0001**	0.7427	**<0.0001**	0.7695
V1	SBP	rs11072518	t	15q24	73021663	NA	COX5A;SCAMP5;RP	COX5A	6.54E-09	2.93E-11	72820453	73029208	90	**<0.0001**	0.7609	**<0.0001**	0.8024
V1	SBP	rs6092743	a	20q13	57133765	NA	NA	C20orf174	2.25E-08	2.18E-09	57112829	57194118	67	**1.00E-04**	0.9868	**<0.0001**	0.9975
V1	DBP	rs2004776	t	1q42	228915325	AGT	AGT;COG2;CAPN9	AGT	3.20E-08	1.53E-08	228915325	228915982	50	**0.0057**	0.9252	**0.001**	0.9622
V1	DBP	rs12258967	c	10p12	18767965	CACNB2	CACNB2	CACNB2	2.48E-09	3.71E-09	18747454	18780638	51	**0.0195**	0.7355	**0.0048**	0.7591
V1	DBP	rs1133323	t	15q24	72999278	NA	COX5A;MPI;SCAMP2	COX5A	2.66E-09	4.89E-10	72806502	73029208	109	**<0.0001**	0.3275	**<0.0001**	0.2717
V1	DBP	rs6092743	a	20q13	57133765	NA	NA	C20orf174	1.11E-08	3.37E-11	57108080	57194118	71	**<0.0001**	0.7041	**<0.0001**	0.7368
V1	MAP	rs2004776	t	1q42	228915325	AGT	AGT;COG2;CAPN9	AGT	1.18E-08	2.45E-09	228882807	228929783	105	**0.0336**	0.9726	**0.0078**	0.9898
V1	MAP	rs12258967	c	10p12	18767965	CACNB2	CACNB2	CACNB2	4.98E-11	5.57E-10	18726458	18780638	91	0.0843	0.4946	**0.0355**	0.4722
V1	MAP	rs11072518	t	15q24	73021663	NA	COX5A;SCAMP5;RP	COX5A	8.95E-11	1.86E-12	72806502	73029208	95	**<0.0001**	0.5105	**<0.0001**	0.4795
Mixed effect	DBP	rs12244842	t	10q21	63109192	C10orf107	C10orf107	C10orf107	7.05E-09	6.15E-08	63109192	63221779	158	**0.0348**	**<0.0001**	**0.0101**	**<0.0001**
Mixed effect	MAP	rs2166122	t	10q21	63193080	C10orf107	C10orf107	C10orf107	1.88E-09	4.76E-08	63109192	63221779	142	0.0565	**<0.0001**	**0.0184**	**<0.0001**
Mixed effect	MAP	rs3184504	t	12q24	110368991	SH2B3	SH2B3;ATXN2	SH2B3	1.68E-12	3.71E-10	110368991	111390798	316	**<0.0001**	0.06	**<0.0001**	**0.0192**
Mixed effect	MAP	rs6092743	a	20q13	57133765	NA	NA	C20orf174	3.60E-10	1.12E-11	57108080	57194118	73	**<0.0001**	0.0924	**<0.0001**	**0.0439**
Mixed effect	PP	rs7650227	t	3p22	41769941	ULK4	ULK4	ULK4	2.84E-09	4.38E-06	41725264	42040009	201	**0.0042**	**<0.0001**	**8.00E-04**	**<0.0001**
No difference	SBP	rs880315	t	1p36	10719453	CASZ1	CASZ1	CASZ1	7.98E-12	7.20E-09	10713384	10724576	9	0.8669	0.2722	0.9464	0.3158
No difference	SBP	rs12258967	c	10p12	18767965	CACNB2	CACNB2	CACNB2	4.53E-10	1.53E-08	18726458	18780638	91	0.9551	0.2148	0.9822	0.1264
No difference	SBP	rs2681472	a	12q21	88533090	ATP2B1	ATP2B1	ATP2B1	1.04E-14	1.69E-11	88465680	88637201	132	0.1781	0.2263	0.1116	0.1561
No difference	SBP	rs35444	a	12q24	114036820	NA	NA	TBX3	1.47E-08	2.63E-06	114036820	114039913	14	0.7564	0.3222	0.7963	0.2573
No difference	DBP	rs7599598	a	2q11	96715567	NA	FLJ10081;FER1L5;LI	FER1L5	2.91E-08	6.54E-08	96715567	rs7599598	1	1	0.4993	1	0.5046
No difference	DBP	rs1801253	c	10q25	115795046	ADRB1	ADRB1	ADRB1	7.22E-06	2.58E-08	115782052	115795046	9	0.1765	0.8999	0.112	0.9477
No difference	DBP	rs2681472	a	12q21	88533090	ATP2B1	ATP2B1	ATP2B1	4.01E-13	8.68E-11	88465680	88637201	132	0.1105	0.3348	0.0576	0.2681
No difference	MAP	rs1801253	c	10q25	115795046	ADRB1	ADRB1	ADRB1	7.32E-07	7.10E-09	115779365	115795046	9	0.1665	0.8955	0.1032	0.9494
No difference	MAP	rs35444	a	12q24	114036820	NA	NA	TBX3	3.20E-08	8.38E-07	114036820	114039913	14	0.7605	0.3228	0.7945	0.2617
No difference	PP	rs880315	t	1p36	10719453	CASZ1	CASZ1	CASZ1	5.45E-09	3.31E-06	10713384	10722164	6	0.8323	0.1492	0.8929	0.1943
No difference	PP	rs12631867	a	3p24	30437485	NA	NA	TGFBR2	0.023903474	9.25E-10	30437485	rs12631867	1	0.5002	1	0.5043	1

SUPPLEMENTAL COHORT DESCRIPTIONS

Cohort Descriptions

Discovery cohorts

The CHARGE Consortium[1] includes cohort studies that completed genome-wide genotyping and had extensive data on multiple phenotypes including blood pressure. Each study adopted collaboration guidelines and established a consensus on phenotype harmonization, covariate selection and an analytical plan for within-study genome-wide association and prospective meta-analysis of results across studies. Each study received institutional review board approval of its consent procedures, examination and surveillance components, data security measures, and DNA collection and its use for genetic research. All participants provided written informed consent.

In the current analysis, most of the participating cohorts were general population samples (AGES, ARIC, CHS, FHS, RS, MESA, CARDIA). Demographic information, blood pressure, height, and weight were directly measured in all participants, except for the Women's Genome Health Study as described. All studies with GWAS data used hidden Markov model approaches[2-4] and HapMap reference panels[5] to impute genotypes at unmeasured SNPs and excluded SNPs, so that a common set of ~2.5M HapMap SNPs were available across the discovery samples[4,6]. All studies with GWAS data used hidden Markov model approaches1-3 and HapMap reference panels4 to impute genotypes at unmeasured SNPs and excluded SNPs, so that a common set of ~2.5M HapMap SNPs were available across the discovery samples[4,6].

AGES Reykjavik

The Age Gene/Environment Susceptibility-Reykjavik (AGES- Reykjavik) Study cohort originally comprised a random sample of 30,795 men and women born in 1907-1935 and living in Reykjavik in 1967. A total of 19,381 people attended, resulting in 71% recruitment rate. The study sample was divided into six groups by birth year and birth date within month. One group was designated for longitudinal follow up and was examined in all stages. One group was designated a control group and was not included in examinations until 1991. Other groups were invited to participate in specific stages of the study. Between 2002 and 2006, the AGES-Reykjavik study re-examined 5764 survivors of the original cohort who had participated before in the Reykjavik Study.[7] The midlife data blood pressure measurement was taken from stage 3 of the Reykjavik Study (1974-1979), if available. Half of the cohort attended during this period. Otherwise an observation was selected closest in time to the stage 3 visit. Participants came in a fasting state to the clinic. The supine blood pressure was measured twice by a nurse using a mercury sphygmomanometer after a 5-min rest. Blood pressure was measured according to World Health Organization recommendations. Individuals with previous MI were excluded from the analyses (n=12). Successful genotyping was available for 3219 AGES participants who were eligible for this study. The AGES Reykjavik Study GWAS was approved by the National Bioethics Committee and the Data Protection Authority.

ARIC

The Atherosclerosis Risk In Communities Study (ARIC) study is a population-based prospective cohort study of cardiovascular disease sponsored by National Heart, Lung, and Blood Institute (NHLBI). ARIC included 15,792 individuals aged 45-64 years at baseline (1987-89), chosen by probability sampling from four US communities[8] Cohort members completed four clinic examinations, conducted three years apart between 1987 and 1998. The data used in this study are from all four visits. A detailed study protocol is available on the ARIC study website (http://www.cscc.unc.edu/aric). Clinic examinations included assessment of cardiovascular disease risk factors, a detailed medical and psychosocial history, and measurement of various clinical and laboratory variables. The physical examination included measurements of weight and height from which the body mass index (BMI) was calculated. Blood pressure was measured using a standardized Hawskley random-zero mercury column sphygmomanometer with participants in sitting position after a resting period of 5 minutes. The size of the cuff was chosen according to the arm circumference. For the first three visits, three sequential recordings for systolic and diastolic blood pressure were obtained and the mean of the last two measurements used in this analysis. At the fourth visit, two blood pressure measurements were taken and averaged. Blood pressure lowering medication use was recorded from the medication history. Outliers (>4SD from the mean) with respect to the systolic or diastolic blood pressure distribution were excluded from the analysis. For this investigation we limited the sample to individuals of European descent by self-report and in whom GWAS was carried out.

CARDIA

The Coronary Artery Risk Development in Young Adults (CARDIA) is a prospective multicenter study with 5115 adults Caucasian and African American participants of the age group 18-30 years, recruited from four centers at the baseline examination in 1985-1986. The recruitment was done from the total community in Birmingham, AL, from selected census tracts in Chicago, IL and Minneapolis, MN; and from the Kaiser Permanente health plan membership in Oakland, CA. The details of the study design for the CARDIA study have been previously published.[17] Eight examinations have been completed since initiation of the study, respectively in the years 0, 2, 5, 7, 10, 15, 20 and 25. Written informed consent was obtained from participants at each examination and all study protocols were approved by the institutional review boards of the participating institutions. At each examination, systolic and diastolic blood pressure was measured in triplicate on the right arm using a random-zero sphygmomanometer with the participant seated and following a 5-min. rest. The average of the second and third measurements was taken as the blood pressure value. Blood pressure medication use was obtained by questionnaire. Blood pressure data measured at year 7 through year 20 were used in this study. In addition, the sample was restricted to individuals of European descent by self-report and principal component analysis using genome-wide genotypes.

CHS

The CHS is a population-based cohort study of risk factors for cardiovascular disease in adults 65 years of age or older conducted across four field centers. The original predominantly white cohort of 5201 persons was recruited in 1989-1990 from random samples of the Medicare eligibility lists and an additional 687 African-Americans were enrolled in 1992-93 for a total sample of 5888. Details of the study design are summarized elsewhere[9]. A total of 1908 persons were excluded from the study sample due to 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). Participants with missing BMI (n=10) or BP measurements (n=8) were excluded. CHS participants completed standardized clinical examinations and questionnaires at study baseline and at nine annual follow-up visits. Research staff who received central training in blood pressure measurement assessed repeat right-arm seated systolic and diastolic blood pressure levels at baseline with a

Hawksley random-zero sphygmomanometer. Means of the repeated blood pressure measurements from the baseline examination were used for GWAS analyses. Because the other cohorts were predominantly white, African American participants were excluded from this analysis. 3,159 CHS subjects contributed to this analysis.

FHS

The Framingham Heart Study (FHS) began in 1948 with the recruitment of an original cohort of 5,209 men and women who were 28 to 62 years of age (mean age 44 years; 55 percent women) at entry. In 1971 enrollment of a second generation of study participants took place; this cohort consisted of 5,124 children and spouses of children of the original cohort. The mean age of the offspring cohort was 37 years; 52 percent were women. A third generation cohort The FHS began in 1948 with the recruitment of an original cohort of 5,209 men and women who were 28 to 62 years of age (mean age 44 years; 55 percent women) at entry. In 1971 enrollment of a second generation of study participants took place; this cohort consisted of 5,124 children and spouses of children of the original cohort. The mean age of the offspring cohort was 37 years; 52 percent were women.[10-12] At each clinic visit, a medical history was obtained with a focus on cardiovascular content, and participants underwent a physical examination including measurement of height and weight from which BMI was calculated. Systolic and diastolic blood pressures were measured twice by a physician on the left arm of the resting and seated participant using a mercury column sphygmomanometer. Pressures were recorded to the nearest even number. The means of two separate systolic and diastolic blood pressure readings at the first clinic examination of each cohort were used for GWAS analyses. For a subset of offspring cohort participants only one measurement was obtained. Individuals under 20 years of age, those who had a myocardial infarction, or congestive heart failure were excluded from the analyses because those conditions may affect blood pressure levels.

MESA

The Multi-Ethnic Study of Atherosclerosis investigation is a population-based study of 6,814 men and women age 45 to 85 years, without clinical cardiovascular disease, recruited from six United States communities (Baltimore, MD; Chicago, IL; Forsyth County, NC; Los Angeles County, CA; northern Manhattan, NY; and St. Paul, MN). The main objective of MESA is to determine the characteristics of subclinical cardiovascular disease and its progression. Sampling and recruitment procedures have been previously described in detail.[15] Adults with symptoms or history of medical or surgical treatment for cardiovascular disease were excluded. During the recruitment process, potential participants were asked about their race/ethnicity. Self-reported ethnicity was used to classify participants into groups.[16] After a 5-minute rest BP was measured three times at 1 minute intervals using a Dinamap PRO 100 automated oscillometric device (Critikon, Tampa, FL) with the subject in seated, and the average of the second and third BP measurements was recorded for each visit. Data from white participants, collected at MESA exams 1 through 4, was used in this analysis.

Rotterdam Study - RS1, RS2

The RS is a prospective population-based cohort study comprising 7,983 subjects aged 55 years or older. Participants completed an interview at home and at the research center, where participants were subsequently examined. Baseline data were collected between 1990 and 1993. In 1999, inhabitants who turned 55 years of age or moved into the study district since the start of the study were invited to participate in an extension of the RS (RES) of whom 3011 participated (67% response rate). The rationale and design of the RS have been described in detail elsewhere.[13] At the research center, we obtained two seated blood pressure measurements in the right brachial artery with a random zero sphygmomanometer. The mean of two consecutive measurements was used in association analyses. We excluded participants who were older than 85 years of age and those who had a history myocardial infarction or congestive heart failure, because of the impact of these conditions on blood pressure levels.

WGHS

The Women's Genome Health Study (WGHS)[14] is a prospective cohort of female North American health care professionals representing participants in the Women's Health Study (WHS) trial who provided a blood sample at baseline and consent for blood-based analyses. Participants in the WHS were 45 years or older at enrolment and free of cardiovascular disease, cancer or other major chronic illness. For the primary WHS endpoints of cardiovascular disease, full medical records were obtained for reported endpoints and reviewed by an endpoints committee of physicians unaware of assignment. The current data are derived from 23,294 WGHS participants for whom whole genome genotype information was available at the time of analysis and for whom self-reported European ancestry could be confirmed by multidimensional scaling analysis of 1,443 ancestry informative markers in PLINK v. 1.06. Baseline BP in the WGHS was ascertained by a self-reported questionnaire, an approach which has been validated in the WGHS demographic, namely female health care professionals. Questionnaires recorded systolic blood pressure in 9 categories (<110, 110-119, 120-129, 130- 139, 140-149, 150-159, 160-169, 170-179, ≥180 mmHg), and diastolic blood pressure in 7 categories (<65, 65-74, 75-84, 85-89, 90-94, 95-104, ≥105 mmHg). The midpoint of each category was used for analysis. Hypertension was defined as a history of physician-diagnosed HTN and ongoing HTN treatment, or SBP ≥ 140 or DBP ≥ 90 mmHg. To account for treatment effects, 10 and 5 mmHg were added to the measured systolic and diastolic blood pressures respectively, if a participant was taking antihypertensive medication.

Replication Cohorts

The replication cohorts in this analysis were used to test the reproducibility of novel discovered loci which were identified by the use of the LTA method. The replication cohorts all provided single-visit BP traits. All participants provided written informed consent and studies were approved by their local Institutional Review Boards or Research Ethics Committees.

Global BP Gen (GBPG)

Single-visit BP traits were previously analyzed in 17 cohorts, and the results of the meta-analysis have been previously reported.[18] Adjustment was performed for the use of anti-hypertensive medications using similar methods as we used in the discovery analysis. The same covariates were included in the individual cohort analyses, including age, age-squared, body mass index, and gender, as in the LTA discovery analyses.

Peking University – University of Michigan Study of Atherosclerosis (PUUMA) Beijing Shijensheng Cohort

The Peking University – University of Michigan Study of Atherosclerosis (PUUMA) is based upon the enrollment of individuals at two hospitals in the Peking University Health Science system: PKU First Hospital and PKU Third Hospital. There were several sources of samples, including the cardiac catheterization laboratories of the hospitals and a community-based enrollment in Beijing Shijengsheng district. The single-visit BP analyses reported in this study were based upon the community based enrollment of 5,065 unrelated individuals (confirmed by exome wide genotypes) which represents a population sample of Han Chinese from Beijing. Blood pressure was recorded using the Omron 7100 machine three times at 2-minute interval in a seated position. The average of three readings was used for the analysis. Genotyping was performed using the Illumina Exome Plus chip with additional custom content based upon sequencing of additional individuals of Asian ancestry and candidate SNPs identified in prior BP association studies. QC was performed as described elsewhere (manuscript in preparation). Association analyses were implemented in PLINK, and genomic control was applied to the final association statistics.

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<u>Reproducibility studies with single-visit BP traits:</u>

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SUPPLEMENTAL REFERENCES

1. Psaty, B.M. *et al.* Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: Design of prospective meta-analyses of genome-wide association studies from 5 cohorts. *Circ Cardiovasc Genet* **2**, 73-80 (2009).
2. Servin, B. & Stephens, M. Imputation-based analysis of association studies: candidate regions and quantitative traits. *PLoS Genet* **3**, e114 (2007).
3. Marchini, J. & Howie, B. Genotype imputation for genome-wide association studies. *Nat Rev Genet* **11**, 499-511.
4. Li, Y., Willer, C., Sanna, S. & Abecasis, G. Genotype imputation. *Annu Rev Genomics Hum Genet* **10**, 387-406 (2009).
5. International HapMap, C. The International HapMap Project. *Nature* **426**, 789-96 (2003).
6. Guan, Y. & Stephens, M. Practical issues in imputation-based association mapping. *PLoS Genet* **4**, e1000279 (2008).
7. Harris, T.B. *et al.* Age, Gene/Environment Susceptibility-Reykjavik Study: multidisciplinary applied phenomics. *Am J Epidemiol* **165**, 1076-87 (2007).
8. The Atherosclerosis Risk in Communities (ARIC) Study: design and objectives. The ARIC investigators. *Am J Epidemiol* **129**, 687-702 (1989).
9. Fried, L.P. *et al.* The Cardiovascular Health Study: design and rationale. *Ann Epidemiol* **1**, 263-76 (1991).
10. Dawber, T.R., Meadors, G.F. & Moore, F.E., Jr. Epidemiological approaches to heart disease: the Framingham Study. *Am J Public Health Nations Health* **41**, 279-81 (1951).
11. Feinleib, M., Kannel, W.B., Garrison, R.J., McNamara, P.M. & Castelli, W.P. The Framingham Offspring Study. Design and preliminary data. *Prev Med* **4**, 518-25 (1975).
12. Splansky, G.L. *et al.* The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. *Am J Epidemiol* **165**, 1328-35 (2007).
13. Hofman, A. *et al.* The Rotterdam Study: objectives and design update. *Eur J Epidemiol* **22**, 819-29 (2007).
14. Ridker, P.M. *et al.* Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy american women. *Clin Chem* **54**, 249-55 (2008).
15. Kramer, H. *et al.* Racial/ethnic differences in hypertension and hypertension treatment and control in the multi-ethnic study of atherosclerosis (MESA). *Am J Hypertens* **17**, 963-70 (2004).
16. Bild, D.E. *et al.* Multi-ethnic study of atherosclerosis: objectives and design. *Am J Epidemiol* **156**, 871-81 (2002).
17. Friedman, G.D. *et al.* CARDIA: study design, recruitment, and some characteristics of the examined subjects. *J Clin Epidemiol* **41**, 1105-16 (1988).
18. Newton-Cheh, C. *et al.* Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet* (2009).
19. Johnson, A.D. *et al.* SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. *Bioinformatics.* **24**, 2938-2939 (2008).
20. Goring, H.H. *et al.* Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. *Nat.Genet.* **39**, 1208-1216 (2007).
21. Idaghdour, Y. *et al.* Geographical genomics of human leukocyte gene expression variation in southern Morocco. *Nat Genet* **42**, 62-67.

22. Heap, G.A. *et al.* Complex nature of SNP genotype effects on gene expression in primary human leucocytes. *BMC Med Genomics* **2**, 1 (2009).
23. The Genotype-Tissue Expression (GTEx) project. *Nat.Genet.* **45**, 580-585 (2013).
24. Battle, A. *et al.* Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. *Genome Res.* **24**, 14-24 (2014).
25. Benton, M.C. *et al.* Mapping eQTLs in the Norfolk Island genetic isolate identifies candidate genes for CVD risk traits. *Am.J.Hum.Genet.* **93**, 1087-1099 (2013).
26. Emilsson, V. *et al.* Genetics of gene expression and its effect on disease. *Nature* **452**, 423-428 (2008).
27. Fehrmann, R.S. *et al.* Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. *PLoS Genet* **7**, e1002197.
28. Landmark-Hoyvik, H. *et al.* Genome-wide association study in breast cancer survivors reveals SNPs associated with gene expression of genes belonging to MHC class I and II. *Genomics* **102**, 278-287 (2013).
29. Mehta, D. *et al.* Impact of common regulatory single-nucleotide variants on gene expression profiles in whole blood. *Eur.J.Hum.Genet.* **21**, 48-54 (2013).
30. Sasayama, D. *et al.* Identification of single nucleotide polymorphisms regulating peripheral blood mRNA expression with genome-wide significance: an eQTL study in the Japanese population. *PLoS.One.* **8**, e54967 (2013).
31. van Eijk, K.R. *et al.* Genetic analysis of DNA methylation and gene expression levels in whole blood of healthy human subjects. *BMC.Genomics* **13**, 636 (2012).
32. Westra, H.J. *et al.* Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nat.Genet.* **45**, 1238-1243 (2013).
33. Zhernakova, D.V. *et al.* DeepSAGE Reveals Genetic Variants Associated with Alternative Polyadenylation and Expression of Coding and Non-coding Transcripts. *PLoS.Genet.* **9**, e1003594 (2013).
34. Dixon, A.L. *et al.* A genome-wide association study of global gene expression. *Nat Genet* **39**, 1202-1207 (2007).
35. Liang, L. *et al.* A cross-platform analysis of 14,177 expression quantitative trait loci derived from lymphoblastoid cell lines. *Genome Res.* (2013).
36. Stranger, B.E. *et al.* Patterns of cis regulatory variation in diverse human populations. *PLoS Genet.* **8**, e1002639 (2012).
37. Kwan, T. *et al.* Genome-wide analysis of transcript isoform variation in humans. *Nat.Genet.* **40**, 225-231 (2008).
38. Cusanovich, D.A. *et al.* The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. *Hum.Mol.Genet.* **21**, 2111-2123 (2012).
39. Dimas, A.S. *et al.* Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science* **325**, 1246-1250 (2009).
40. Grundberg, E. *et al.* Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nat.Genet.* **44**, 1084-1089 (2012).
41. Gutierrez-Arcelus, M. *et al.* Passive and active DNA methylation and the interplay with genetic variation in gene regulation. *Elife.* **2**, e00523 (2013).
42. Mangravite, L.M. *et al.* A statin-dependent QTL for GATM expression is associated with statin-induced myopathy. *Nature* **502**, 377-380 (2013).
43. Fairfax, B.P. *et al.* Genetics of gene expression in primary immune cells identifies cell type-specific master regulators and roles of HLA alleles. *Nat.Genet.* **44**, 502-510 (2012).

44. Murphy, A. *et al.* Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. *Hum Mol Genet* **19**, 4745-4757.
45. Heinzen, E.L. *et al.* Tissue-specific genetic control of splicing: implications for the study of complex traits. *PLoS Biol* **6**, e1 (2008).
46. Zeller, T. *et al.* Genetics and beyond--the transcriptome of human monocytes and disease susceptibility. *PLoS One* **5**, e10693.
47. Barreiro, L.B. *et al.* Deciphering the genetic architecture of variation in the immune response to Mycobacterium tuberculosis infection. *Proc.Natl.Acad.Sci.U.S.A* **109**, 1204-1209 (2012).
48. Huang, R.S. *et al.* Population differences in microRNA expression and biological implications. *RNA.Biol.* **8**, 692-701 (2011).
49. Degner, J.F. *et al.* DNase I sensitivity QTLs are a major determinant of human expression variation. *Nature* **482**, 390-394 (2012).
50. Greenawalt, D.M. *et al.* A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. *Genome Res* **21**, 1008-1016.
51. Kompass, K.S. & Witte, J.S. Co-regulatory expression quantitative trait loci mapping: method and application to endometrial cancer. *BMC.Med.Genomics* **4**, 6 (2011).
52. Li, Q. *et al.* Integrative eQTL-based analyses reveal the biology of breast cancer risk loci. *Cell* **152**, 633-641 (2013).
53. Webster, J.A. *et al.* Genetic control of human brain transcript expression in Alzheimer disease. *Am J Hum Genet* **84**, 445-458 (2009).
54. Zou, F. *et al.* Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. *PLoS Genet* **8**, e1002707.
55. Colantuoni, C. *et al.* Temporal dynamics and genetic control of transcription in the human prefrontal cortex. *Nature* **478**, 519-523.
56. Kim, S., Cho, H., Lee, D. & Webster, M.J. Association between SNPs and gene expression in multiple regions of the human brain. *Transl.Psychiatry* **2**, e113 (2012).
57. Liu, C. *et al.* Whole-genome association mapping of gene expression in the human prefrontal cortex. *Mol Psychiatry* **15**, 779-784.
58. Gamazon, E.R. *et al.* Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. *Mol.Psychiatry* **18**, 340-346 (2013).
59. Gibbs, J.R. *et al.* Abundant quantitative trait loci exist for DNA methylation and gene expression in human brain. *PLoS Genet* **6**, e1000952.
60. Zhang, B. *et al.* Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. *Cell* **153**, 707-720 (2013).
61. Innocenti, F. *et al.* Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. *PLoS Genet* **7**, e1002078.
62. Schadt, E.E. *et al.* Mapping the genetic architecture of gene expression in human liver. *PLoS Biol* **6**, e107 (2008).
63. Schroder, A. *et al.* Genomics of ADME gene expression: mapping expression quantitative trait loci relevant for absorption, distribution, metabolism and excretion of drugs in human liver. *Pharmacogenomics.J.* **13**, 12-20 (2013).
64. Grundberg, E. *et al.* Population genomics in a disease targeted primary cell model. *Genome Res.* **19**, 1942-1952 (2009).
65. Kabakchiev, B. & Silverberg, M.S. Expression quantitative trait loci analysis identifies associations between genotype and gene expression in human intestine. *Gastroenterology* **144**, 1488-96, 1496 (2013).

66. Keildson, S. *et al.* Skeletal Muscle Expression of Phosphofructokinase is Influenced by Genetic Variation and Associated with Insulin Sensitivity. *Diabetes* (2013).
67. Quigley, D.A. *et al.* The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogen-receptor positive tumors. *Mol.Oncol.* (2013).
68. Gao, C. *et al.* HEFT: eQTL analysis of many thousands of expressed genes while simultaneously controlling for hidden factors. *Bioinformatics.* (2013).
69. Hao, K. *et al.* Lung eQTLs to help reveal the molecular underpinnings of asthma. *PLoS.Genet.* **8**, e1003029 (2012).
70. Ding, J. *et al.* Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. *Am.J.Hum.Genet.* **87**, 779-789 (2010).
71. Qiu, W. *et al.* Genetics of sputum gene expression in chronic obstructive pulmonary disease. *PLoS.One.* **6**, e24395 (2011).
72. Lin, H. *et al.* Gene expression and genetic variation in human atria. *Heart Rhythm.* (2013).
73. Rantalainen, M. *et al.* MicroRNA expression in abdominal and gluteal adipose tissue is associated with mRNA expression levels and partly genetically driven. *PLoS One* **6**, e27338 (2011).