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

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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 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.

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#### Introduction

Blood pressure (BP) is a quantitative trait that varies both within subjects, according to diurnal patterns and longerterm 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.<sup>1</sup> 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.<sup>2-5</sup> 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."<sup>6</sup> 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 communitybased cohorts in which BP traits have been measured at multiple visits over several years of follow-up.<sup>7</sup> 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,<sup>7</sup> 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.<sup>5</sup> 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, agesquared, 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.<sup>4</sup>

#### 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.<sup>2,4,5</sup>

#### 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<sup>8</sup> with linear regression under an additive genetic model. In the FHS, family structure was modeled with a linear mixed-effects model implemented in R.<sup>9</sup> Regression coefficients and corresponding SEs for each SNP and trait were metaanalyzed by inverse-variance-weighted meta-analysis to provide the primary findings. Genomic control<sup>10</sup> 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  $5.0 \times 10^{-8}$ . For loci where variants showed significant associations, we examined the linkage-disequilibrium (LD) patterns with SNAP;<sup>11</sup> 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 ×  $10^{-8}$ ), 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 × 10<sup>-8</sup>) 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 × 10<sup>-8</sup> 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<sup>2</sup> > 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,<sup>11</sup> 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.<sup>12–60</sup> 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.<sup>12</sup>

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.<sup>14</sup> All GTex results had associations with  $p < 8.4 \times 10^{-7}$ .

Table 1. Sum	mary of	Discovery C	ohorts, Samp	le Sizes, and	Visits for the	LTA Analyses	i 		
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 <sup>2</sup> (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 inversevariance-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 ( $\lambda_{GC}$ ) 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<sup>5</sup>—and 5,605 Han Chinese individuals from PUUMA. Clinical summaries have been previously published for the GBPG Consortium. <sup>5</sup> 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 metaanalysis and demonstrated significant association between chromosomal region 2p23 (KCNK3 [MIM 603220]) and



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 < p0.10) 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 ×  $10^{-7}$ ) 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

#### 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.

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  $5 \times 10^{-7}$ , 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. S	ummary	of LT/	A Discovery Ar	alyses for L	oci with SNP-Tr	rait Association p Values $<$ 5 $ imes$ 10 <sup>-8</sup>			
SNP ID	Allele	Chr	Position	In Gene	Closest Gene	Genes in LD Block	Beta	SE	p Value
LTA DBP									
rs13306561	а	1	11,788,391	MTHFR	MTHFR	NPPA-AS1, CLCN6, MTHFR, NPPA	0.48	0.07	$2.08\times10^{-10}$
rs2004776	t	1	228,915,325	AGT	AGT	AGT	0.35	0.06	$3.20 \times 10^{-8}$
rs7599598 <sup>a</sup>	а	2	96,715,567	FER1L5	FER1L5	FER1L5	-0.31	0.05	$2.91 \times 10^{-8}$
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	$6.57 \times 10^{-9}$
rs12258967	с	10	18,767,965	CACNB2	CACNB2	CACNB2	0.35	0.06	$2.48 \times 10^{-9}$
rs12244842	t	10	63,109,192	C10orf107	C10orf107	C10orf107	-0.38	0.06	$7.05 \times 10^{-9}$
rs2681472	а	12	88,533,090	ATP2B1	ATP2B1	ATP2B1, LOC338758	0.52	0.07	$4.01 \times 10^{-13}$
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	$6.08 \times 10^{-13}$
rs1133323	t	15	72,999,278	NA	COX5A	CSK, CPLX3, COX5A, SCAMP2, C15orf17, MPI, ULK3, LMAN1L, MIR4513	-0.33	0.05	$2.66 \times 10^{-9}$
rs6092743	а	20	57,133,765	NA	C20orf174	NA	0.50	0.08	$1.11\times10^{-8}$
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	$7.98 \times 10^{-12}$
rs13306561	а	1	11,788,391	MTHFR	MTHFR	NPPB, NPPA-AS1, CLCN6, MTHFR, NPPA	0.88	0.12	$6.38 \times 10^{-12}$
rs1275988ª	t	2	26,767,868	NA	KCNK3	KCNK3	-0.60	0.09	$2.61 \times 10^{-10}$
rs6712094	а	2	164,751,706	NA	GRB14	NA	0.60	0.10	$9.89 \times 10^{-9}$
rs7733331	t	5	32,864,603	NA	C5orf23	NPR3	-0.55	0.09	$5.38 \times 10^{-9}$
rs12705390	а	7	106,198,013	NA	PIK3CG	NA	0.63	0.11	$3.17 \times 10^{-8}$
rs12258967	с	10	18,767,965	CACNB2	CACNB2	CACNB2	0.63	0.10	$4.53 \times 10^{-10}$
rs7070797	а	10	63,221,779	NA	C10orf107	C10orf107	-0.74	0.13	$4.30 \times 10^{-8}$
rs2681472	а	12	88,533,090	ATP2B1	ATP2B1	ATP2B1, LOC338758	0.95	0.12	$1.04\times10^{-14}$
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	$2.82 \times 10^{-9}$
rs35444	а	12	114,036,820	NA	TBX3	NA	0.55	0.09	$1.47 \times 10^{-8}$
rs11072518	t	15	73,021,663	NA	COX5A	CSK, CPLX3, COX5A, SCAMP2, C15orf17, CYP1A2, MPI, ULK3, LMAN1L, MIR4513	0.57	0.09	$6.54 \times 10^{-9}$
rs6092743	а	20	57,133,765	NA	C20orf174	NA	0.84	0.14	$2.25 \times 10^{-8}$
LTA MAP									
rs880315	t	1	10,719,453	CASZ1	CASZ1	CASZ1	-0.46	0.07	$5.49 \times 10^{-11}$
rs13306561	а	1	11,788,391	MTHFR	MTHFR	NPPB, NPPA-AS1, CLCN6, MTHFR, NPPA	0.61	0.08	$1.83 \times 10^{-12}$
rs2004776	t	1	228,915,325	AGT	AGT	AGT	0.42	0.07	$1.18 \times 10^{-8}$
rs1275988 <sup>a</sup>	t	2	26,767,868	NA	KCNK3	KCNK3	-0.39	0.06	$1.51 \times 10^{-9}$
rs12258967	с	10	18,767,965	CACNB2	CACNB2	CACNB2	0.45	0.07	$4.98 \times 10^{-11}$
rs2166122	t	10	63,193,080	C10orf107	C10orf107	C10orf107	-0.48	0.08	$1.88 \times 10^{-9}$
rs2681472	а	12	88,533,090	ATP2B1	ATP2B1	ATP2B1, LOC338758	0.69	0.08	$1.77 \times 10^{-16}$
								(Cont	inued on next pag

Table 2. Co	ontinued								
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	$1.68 \times 10^{-12}$
rs35444	а	12	114,036,820	NA	TBX3	NA	0.36	0.06	$3.20\times10^{-8}$
rs11072518	t	15	73,021,663	NA	COX5A	CSK, CPLX3, COX5A, SCAMP2, C15orf17, CYP1A2, MPI, ULK3, LMAN1L, MIR4513	0.43	0.06	$8.95 \times 10^{-11}$
rs6092743	а	20	57,133,765	NA	C20orf174	NA	0.64	0.10	$3.60\times10^{-10}$
LTA PP									
rs880315	t	1	10,719,453	CASZ1	CASZ1	CASZ1	-0.42	0.07	$5.45 \times 10^{-9}$
rs7650227	t	3	41,769,941	ULK4	ULK4	ULK4	0.50	0.08	$2.84 \times 10^{-9}$
rs10948071 <sup>a</sup>	t	6	43,388,691	NA	CRIP3	CRIP3, SLC22A7, ZNF318	-0.38	0.07	$9.06 \times 10^{-9}$
rs2949837 <sup>a</sup>	а	7	45,960,903	NA	IGFBP3	NA	0.40	0.07	$2.94\times10^{-8}$
rs12705390	а	7	106,198,013	NA	PIK3CG	NA	0.59	0.08	$5.40 \times 10^{-14}$

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.

<sup>a</sup>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 andCRIP3) 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.<sup>61</sup> 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.<sup>62</sup> 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.<sup>63</sup> 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.<sup>64–67</sup>

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

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

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 metaanalysis 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.<sup>68</sup> 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.<sup>64,69</sup> Although single "casual" BP measurements in

Table 4.	Reproducibi	lity-Analy	sis Assoc	iation F	Results in the <b>C</b>	BPG Con	sortiun	n and PUUMA	V1 BP Ana	lyses	
		Classet	GBPG ( Associa	Consort Ition Re	ium V1 BP esults	PUUMA Associa	V1 BP tion Re	esults	Meta-ana and PUU	lysis of GBP MA V1 BP As	G Consortium sociation Results
Trait	SNP ID	Gene	Beta	SE	p Value	Beta	SE	p Value	Beta	SE	p Value
V1 DBP	rs7599598	FER1L5	-0.04	0.08	$6.14 \times 10^{-1}$	0.001	0.21	$9.95 \times 10^{-1}$	-0.03	0.07	$6.40 \times 10^{-1}$
V1 SBP	rs1275988 <sup>a</sup>	KCNK3	-0.26	0.12	$2.98 \times 10^{-2}$	-0.79	0.39	$4.54 \times 10^{-2}$	-0.30	0.11	$7.93 \times 10^{-3}$
V1 MAP	rs1275988 <sup>a</sup>	KCNK3	-0.16	0.08	$5.68 \times 10^{-2}$	-0.72	0.27	$7.85 \times 10^{-3}$	-0.21	0.08	$9.08 \times 10^{-3}$
V1 PP	rs10948071 <sup>a</sup>	CRIP3	-0.24	0.09	$6.69 \times 10^{-3}$	-0.25	0.27	$3.56 \times 10^{-1}$	-0.24	0.08	$4.17 \times 10^{-3}$
V1 PP	rs2949837	IGFBP3	0.15	0.09	$9.96 \times 10^{-2}$	0.34	0.26	$1.94 \times 10^{-1}$	0.17	0.09	$4.68 \times 10^{-2}$

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. <sup>a</sup>Loci meeting a Bonferroni-corrected replication threshold.

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

(Continued on next page)

Table 5.	Continued													
				Clocort	LTA BP Res	ults in Dis	scovery Si	amples	V1 BP Resu	lts in LTA l	Discovery 5	amples	LTA-V1 Differe	nces
SNP ID	Allele	ĥ	Position	Gene	Trait	Beta	SE	p Value	Trait	Beta	SE	p Value	∆ Beta	∆ p Value
rs2166122	t	10	63,193,080	C100rf107	LTA MAP	-0.48	0.08	$1.88 \times 10^{-9}$	V1 MAP	-0.50	0.09	$4.76 \times 10^{-8}$	$-2.38 \times 10^{-2}$	$-4.57 \times 10^{-8}$
rs2681472	ŋ	12	88,533,090	ATP2B1	LTA MAP	0.69	0.08	$1.77 \times 10^{-16}$	V1 MAP	0.70	0.09	$1.70 \times 10^{-12}$	$9.17 \times 10^{-3}$	$-1.70 \times 10^{-12}$
rs3184504	t	12	110,368,991	SH2B3	LTA MAP	0.45	0.06	$1.68 \times 10^{-12}$	V1 MAP	0.47	0.07	$3.71 \times 10^{-10}$	$2.50 \times 10^{-2}$	$-3.69 \times 10^{-10}$
rs35444	IJ	12	114,036,820	TBX3	LTA MAP	0.36	0.06	$3.20 \times 10^{-8}$	V1 MAP	0.38	0.08	$8.38 \times 10^{-7}$	$2.16 \times 10^{-2}$	$-8.06 \times 10^{-7}$
rs11072518	8 t	15	73,021,663	COX5A	LTA MAP	0.43	0.06	$8.95 \times 10^{-11}$	V1 MAP	0.55	0.07	$1.86 \times 10^{-12}$	$1.15 \times 10^{-1}$	$8.76 \times 10^{-11}$
rs6092743	ъ	20	57,133,765	C20orf174	LTA MAP	0.64	0.10	$3.60 \times 10^{-10}$	V1 MAP	0.81	0.11	$1.12 \times 10^{-11}$	$1.69 \times 10^{-1}$	$3.49 \times 10^{-10}$
rs880315	t	1	10,719,453	CASZ1	LTA PP	-0.42	0.07	$5.45 \times 10^{-9}$	V1 PP	-0.38	0.08	$3.31 \times 10^{-6}$	$4.46 \times 10^{-2}$	$-3.31 \times 10^{-6}$
rs7650227	t	ε	41,769,941	ULK4	LTA PP	0.50	0.08	$2.84 \times 10^{-9}$	V1 PP	0.43	0.09	$4.38 \times 10^{-6}$	$-6.71 \times 10^{-2}$	$-4.38 \times 10^{-6}$
rs1094807	1 t	9	43,388,691	CRIP3	LTA PP	-0.38	0.07	$9.06 \times 10^{-9}$	V1 PP	-0.29	0.07	$1.11 \times 10^{-4}$	$9.49 \times 10^{-2}$	$-1.11 \times 10^{-4}$
rs2949837	а	7	45,960,903	IGFBP3	LTA PP	0.40	0.07	$2.94 \times 10^{-8}$	V1 PP	0.36	0.08	$6.88 \times 10^{-6}$	$-3.79 \times 10^{-2}$	$-6.85 \times 10^{-6}$
rs12705390	0 a	7	106, 198,013	PIK3CG	LTA PP	0.59	0.08	$5.40 \times 10^{-14}$	V1 PP	0.43	0.09	$1.20 \times 10^{-6}$	$-1.59 \times 10^{-1}$	$-1.20 \times 10^{-6}$
Abbreviatio	ins are as follo	ows: BP,	blood pressure; C	Jhr, chromoson	ne; DBP, diasto	olic blood p	ressure; M	AP, mean arterial p	ressure; LTA, lo	ing-term av€	srage; PP, pı	ulse pressure; SBP, sy	/stolic blood pressu	re; and V1, visit 1.

a population predict CVD,<sup>70</sup> 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.<sup>71</sup> 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.<sup>61,72–75</sup> 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<sup>2</sup>) 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 hypothesisdriven 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)<sup>2</sup> 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.<sup>76</sup> 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.<sup>77</sup> 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<sup>78</sup>



**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  $\pm$  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.<sup>79</sup> 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.<sup>80</sup> Serum levels of IGFBP3 are associated with measures of aortic stiffness, of which PP is an indicator,<sup>81</sup> and a GWAS of circulating IGFBP3 amounts in plasma showed an association with IGFBP3 SNPs we identified.<sup>82</sup> Circulating amounts of IGFBP3 are also related to SBP.<sup>83</sup> 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.<sup>66,67,84-90</sup> 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<sup>91</sup> 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.

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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

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The American Journal of Human Genetics, Volume 95 Supplemental Data

### Effects of Long-Term Averaging of Quantitative

### **Blood Pressure Traits on the Detection**

### of Genetic Associations

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#### 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: -logP 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<sup>-8</sup> are shown in red, and regions reaching P value < 5x10<sup>-7</sup> are shown in blue.



(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)



(c)



(d)



(e)

#### 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.

## SBP, MTHFR, 1p36



12

## SBP, KCNK3, 2p23



SBP; locus KCNK3, rs1275988, chr2:26765249-26786300,2p23

(a2)

# SBP, GRB14, 2q24



# SBP, C5orf23,5p13



(a4)

## SBP, PIK3CG, 7q22



(a5)

## SBP, PIK3CG, 7q22



(a6)

# SBP, PIK3CG, 7q22



(a7)
## SBP, C10orf107, 10q21



(a8)

## SBP, C10orf107, 10q21



## DBP, MTHFR, 1p36



(a10)

# DBP,EBF1,5q33



## DBP, HIST1H2BC, 6p22



(a12)

# DBP,C10orf107



(a13)

## DBP, SH2B3, 12q24



## MAP, MTHFR, 1p36



## MAP, KCNK3, 2p23



(a16)

## MAP, C10orf107,10q21



(a17)

## MAP, ATP2B1,12q21

MAP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21 100(cM/Mb) Charge-LTA SNPsCharge-V1 SNPs 15 75 -log10(P-value) 10 • 20 S 25 0 0 88300000 88400000 88500000 88600000 88700000 88800000 pos(bp)



- - -

## PP, CRIP3,6p21

PP; locus CRIP3, rs10948071, chr6:43367990-43472472,6p21 100(cM/Mb) Charge-LTA SNPsCharge-V1 SNPs ω . 75 9 -log10(P-value) 20 4 25 2 0 0 43300000 43200000 43400000 43500000 43600000 pos(bp) 

SLC22A7 CRIP3

ZNF318

C6ort108

CUL9

SRF

TTBK1

KLC4

PTK7

ABCC10 DLK2 TJAP1 C6ort154 YIPF3 POLR1C

XP05

#### PP, IGFBP3,7p13

PP; locus IGFBP3, rs2949837, chr7:45929639-45974635,7p13 100(cM/Mb) Charge-LTA SNPs
Charge-V1 SNPs α 75 9 -log10(P-value) 20 4 25 N 0 0 45800000 45900000 46100000 45700000 46000000 46200000 pos(bp)

 $\mathbb{H}$ 

IGFBP3

IGFBP1

SEPT7P2

## PP, IGFBP3,7p13

PP; locus IGFBP3, rs2949837, chr7:45929639-45974635,7p13





(a21)

## SBP,AGT,1q42



(b1)

## SBP, ATXN2, 12q24

SBP; locus ATXN2, rs4766578, chr12:110368991-111095097,12q24 100(cM/Mb) 9 Charge-LTA SNPs
Charge-V1 SNPs : :: ٠ . ω 75 ٠ • -log10(P-value) 9 20 4 :: . 25  $\sim$ 0 0 110300000 110200000 110400000 110500000 110600000 pos(bp)



(b2)

## SBP,COX5A,15q24

SBP; locus COX5A, rs11072518, chr15:72820453-73029208,15q24





# SBP, C20orf174,20q13







#### DBP, COX5A, 15q24

DBP; locus COX5A, rs1133323, chr15:72806502-73076775,15q24 100(cM/Mb) Charge-LTA SNPsCharge-V1 SNPs 9 75 8 -log10(P-value) 9 50 4 25 2 -0 0 72800000 73000000 72900000 73100000 73200000 pos(bp) ||||-|+╉  $\vdash$ ł

MPI C15ort17 COX5A RPP25

SCAMP5

PPCDC

CYP1A1

EDC3

CYP1A2

MIB4513

LMAN1L CPLX3 ULK3 SCAMP2

## DBP, C20orf174,20q13



EDN3

GNAS

THIL CTSZ

TUBB1 ATP5E

#### MAP, COX5A, 15q24



LMAN1L CPLX3 ULK3 SCAMP2

MPI C15or117

COX5A

RPP25

SCAMP5

PPCDC

CYP1A1

CYP1A2

MIB4513

(b7)

## MAP, C20orf174,20q13



40

EDN3

GNAS

THIL

TUBB1 AL POR

## PP,ULK4,3p22

PP; locus ULK4, rs7650227, chr3:41725264-42040009,3p22





(c1)

## SBP, CASZ1

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



(d1)

# SBP, CACNB2

SBP; locus CACNB2, rs12258967, chr10:18726458-18796887,10p12



CACNB2

**NSUNG** 

**ARL5B** 

# SBP, ATP2B1

SBP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21 100(cM/Mb) Charge-LTA SNPsCharge-V1 SNPs . -log10(P-value) •• •• pos(bp)



## SBP, TBX3

SBP; locus TBX3, rs35444, chr12:114036820-114039913,12q24



(d4)

## DBP, AGT

DBP; locus AGT, rs2004776, chr1:228910896-228929783,1q42





(d5)

#### DBP, FER1L5

DBP; locus FER1L5, rs7599598, chr2:96715567-96715567,2q11



FER1L5

LMAN2L

KIAA1310

NEURL3

ARID5A

CNNM3 ANKRD23 ANKRD39 SEMA4C

FAM178B

CNNM4 MIR3127

# DBP, CACNB2

DBP; locus CACNB2, rs12258967, chr10:18745126-18780638,10p12





(d7)

## DBP, ADRB1

DBP; locus ADRB1, rs1801253, chr10:115779365-115795046,10q25



(d8)

# DBP, ATP2B1

DBP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21 100(cM/Mb) Charge-LTA SNPs
Charge-V1 SNPs 12 9 75 -log10(P-value) œ 22 -9 : 4 25  $\sim$ 0 0 88300000 88400000 88500000 88600000 88700000 88800000 pos(bp)



(d9)

## MAP, CASZ1

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





(d10)

## MAP, AGT

MAP; locus AGT, rs2004776, chr1:228882807-228929783,1q42 100(cM/Mb) Charge-LTA SNPs
Charge-V1 SNPs œ - 12 -log10(P-value) 9 - 23 4 25 2 0 0 228700000 228800000 228900000 229000000 229100000 pos(bp)



(d11)

## MAP, CACNB2

MAP; locus CACNB2, rs12258967, chr10:18726458-18796887,10p12





(d12)

## MAP, ADRB1

MAP; locus ADRB1, rs1801253, chr10:115779365-115795046,10q25


# MAP, TBX3

MAP; locus TBX3, rs35444, chr12:114036820-114039913,12q24



# PP,CASZ1

PP; locus CASZ1, rs880315, chr1:10713384-10722164,1p36



CASZ1

PEX14

C1ort127

**Figure S8**. K-S test comparison cumulative fraction plot, where x-axis is the  $-\log 10(P)$  values and y-axis is the cumulative fraction.



K-S Test Comparison Cumulative Fraction plot, D(Ita-v1)+= 0.12,P=0.0067; D(Ita-v1)-= 0.13,P=0.0032

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  $-\log 10(P \text{ values})$  within each region meeting criteria for genome-wide significance ( $P \text{ value} < 5x10^{-8}$ ). Regions with at least one marker with  $P \text{ value} < 5x10^{-8}$  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  $-\log 10(P \text{ value})$ .

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.

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

				Age,	BMI,	SBP,	DBP,	Anti-hypertensive
		Year	N	years (sd)	kg/m2 (sd)	mmHg (sd)	mmHg (sd)	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 S2: Cohort summaries across all visit included in the analyses

### Table S3: Genomic control inflation factors ( $\lambda_{GC}$ ).

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

									Meta-
AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	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

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

### Visit 1 - DBP

									Meta-
AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	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</th>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	С	-0.5974	0.0917	3.22E-10	+	NA	KCNK3;CIB4	KCNK3	3539
LTA-SBP	rs10858914	12q21	88555526 t	С	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	с	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	с	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	С	-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	С	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	С	-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	С	0.8816	0.1267	1.92E-11	++++-++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-SBP	rs1173727	5p13	32866278 t	с	-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	С	-0.5795	0.0997	2.03E-08	+	NA	NA	GRB14	279889
LTA-SBP	rs1173747	5p13	32817909 a	С	0.512	0.0901	4.21E-08	++++-++++	NPR3	C5orf23;NPR3	NPR3	5100
LTA-SBP	rs7136259	12q21	88605319 t	С	-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	С	-0.6048	0.0943	6.02E-10	+	KCNK3	KCNK3;C2orf18	KCNK3	17178
LTA-SBP	rs13154066	5p13	32867427 t	С	-0.5436	0.0911	8.41E-09	+	NA	C5orf23;NPR3	C5orf23	39851
LTA-SBP	rs979223	2q24	164803267 a	С	-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	С	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	С	-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	С	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	С	-0.5733	0.1004	3.58E-08		NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-SBP	rs6707357	2q24	164722539 t	С	-0.5232	0.0914	3.29E-08	+	NA	NA	GRB14	335039
LTA-SBP	rs880315	1p36	10719453 t	С	-0.7125	0.1005	7.98E-12	?	CASZ1	CASZ1	CASZ1	59841
LTA-SBP	rs2166122	10q21	63193080 t	С	-0.6435	0.1137	4.75E-08	-+	C10orf107	C10orf107	C10orf107	3015
LTA-SBP	rs653178	12q24	110492139 t	с	-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	С	-0.7091	0.1044	5.54E-11	?	CASZ1	CASZ1	CASZ1	65910
LTA-SBP	rs1275982	2p23	26772593 t	С	-0.5881	0.0919	6.56E-10	+	KCNK3	KCNK3;CIB4	KCNK3	3471
LTA-SBP	rs6100342	20q13	57132656 a	С	-0.7232	0.127	3.89E-08	+	NA	NA	C20orf174	66813
LTA-SBP	rs11072518	15q24	73021663 t	С	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	С	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	MTHER	311
LTA-SBP	rs1439214	2q24	164778248 t	С	-0.5791	0.0997	2.07E-08	+	NA	NA	GRB14	279330
LTA-SBP	rs2681492	12q21	88537220 t	С	0.8967	0.1156	7.18E-14	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-SBP	rs2168519	15q24	72867925 t	с	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	с	-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	с	-0.5451	0.0911	7.76E-09	+	NA	C5orf23;NPR3	C5orf23	27254
LTA-SBP	rs13005481	2q24	164789612 t	с	-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	с	-0.6322	0.1106	3.46E-08	+	NA	NA	PIK3CG	94065
LTA-SBP	rs11105383	12q21	88631437 t	с	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	с	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

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I rait	SNPID C	Chr	Position.Bui Allele1	Allele2	Beta	s.e.	P	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA CDD	FS8033381 1	5q24	1286/738 a	g	-0.5689	0.1	3.97E-08		USK	OPLX3;GYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CDR14	5971
LTA CDD	1512995799 2	:q24	104/98030 t	c	0.5788	0.0996	2.03E-08	++++-++++	NA CAC71		GRB14	208942
LTA CDD	IS12040276 1	p30	10/22104 L	с •	-0.707	0.1039	0.12E-11 1.56E-00		CA5Z1		CRB14	323505
LTA ODD	1511091401 2	0a21	62221770 a		-0.3044	0.0997	1.000-00	+	NA	144 C10acf107	C10orf107	202000
LTA SED	rc4006620 1	5q24	72050611 c	y	0.5720	0.1300	2 62E 00	-++	NA		CIUCITU	2156
LTA ODD	154000029 1	0424 in12	22009011 0	y	-0.0720	0.0011	5.03E-00		NA	CEnt23, CETTAL, CSR, OER3, LWAINTE	CEorf22	2100
LTA CDD	15/133331 3	p15	10724576 0	C C	-0.0000	0.0011	4.94E.09		CAS71		C301123	5/02/
I TA SBP	re12656/07 5	p30 in13	32867696 t	y c	0.5020	0.0000	8 73E 00	;	NA	Chart(2)NER3	C5orf23	40120
	re17240754_1	2021	99594717 9	0	0.0204	0.1104	2 27E 14		NA		ATD2B1	10742
	re1465527 2	2421 0a12	67121/16 +	g	0.0004	0.1134	2 065 00		NA		C20orf174	69054
I TA SEP	re11105292 1	2021	99621402 t	c	0.7637	0.1226	2 73E 09		NA	ATD2B1	ATP2B1	57/29
	rc1276095 2	2421	26765240 +	c	0.7037	0.002	4.01E 10		NA		KONKS	2072
I TA SBD	re1173771 5	.p23	20703243 1	с а	0.5502	0.002	5.63E.00	+	NA	Contro, GDP4	C5orf23	22200
	re25422 1	2024	114020012 +	g	0.5502	0.0045	1 595 09		NA	NA NA	TEV2	122561
I TA SBP	re10959015_1	2924	99575679 a	0	0.5101	0.0043	2 02E 09	+-+-	NA	IAA	ATP2B1	1703
I TA-SBP	re1439211 2	2921	164802546 a	9	-0.5887	0.0303	4.06E-08		NA		GRB14	255032
I TA-SBP	rs2050265 1	n36	11802286 a	a	0.8509	0.1222	1.84E-11	********	CLCN6		CLCN6	8576
I TA-SBP	re11014166 1	0n12	18748804 a	9 t	0.5638	0.0030	6.88E-09	********	CACNB2	CACNE2	CACNB2	19286
I TA SBP	re10774702 1	2024	11/036981 +		0.5502	0.0000	1.63E.09		NA		TRY3	430629
I TA SDD	re1172756 5	2427 in12	22925600 +	6	0.5175	0.004	2.52E.09		CEorf22	CEAr#32:NDD3	C5orf22	909
ITA ODD	re1276090 2	1010 1022	26770472 +	0	0.5175	0.0030	4 19E 10		KCNK2	CONTROL A	KONK2	1251
I TA-SPP	re1813352 1	0n12	18747454 t	č	0.623	0.0969	5.31E-10	+	CACNB2	CACNB2	CACNB2	17936
I TA. SRD	rs6676300 4	n36	11847887 9	0	0.5541	0.0000	1 40 - 09	*********	NA	MTHER KIAA2013 NPPA CLONG NPPB	NPPR	6308
I TA-SPP	rs12567126 1	p36	11806318 t	9	-0.8520	0.1222	1.63E-11		CLCN6	MTHER NPPA CI CN6 NPPB	CL CN6	4544
ITA SPP	re2681472 4	2021	88533090 a	0	0.0028	0.1222	1.04E-14		ATP2B1	ATP2R1	ATP2B1	27132
I TA-SPP	rs17037425 1	n36	11792970 a	9	-0.8574	0.1292	1.51E-14		CLCN6	MTHER NPPA CLONG NPPB AGTRAP	CLCN6	4177
ITA SRP	rs1371181 2	n24	164784974 +	9	0.5764	0.0005	2 28 - 09	****	NA	NA	GRB14	272604
I TA-SPP	rs10432461 2	a24	164772752 a	t	-0.5812	0.0998	1 93E-09		NΔ	NΔ	GRB14	284826
I TA, SRP	rs3184504 4	2024	110368991 +	ċ	0.5540	0.0000	3.04E-00	*****	SH2B3	SH2B3:ATXN2	SH2B3	4818
I TA-SPP	rs11105369 1	2021	88598572 c	0	-0.9371	0 1197	4 21E-14		NA	ATP2R1	ATP2B1	24597
I TA-SBP	rs13007966 2	n24	164784819 t	с я	-0.5762	0.0996	2.33E-08		NA	NA	GRB14	272759
I TA SBP	re11105378 1	2021	9961/972 t	c	0.0702	0.0330	1 23E 13		NA	NTP2B1	ATP2B1	10997
I TA-SBP	re11105328_1	2021	88466521 a	0	0.8655	0.1230	1.57E-11	****	NA		WDR51B	22613
I TA SBP	rc18088/11 2	2921	164779453 t	y c	0.5785	0.1238	2 12E 08	++++	NA	NA N	GRB1/	270125
I TA-SBP	re11105379 1	2a21	88619304 t	c	0.7704	0.1325	2.03E-08	+++++++++	NA	ATP2B1	ATP2B1	45329
I TA SBP	re11105358 1	2021	88566273 c	0	0.6895	0.0011	2.03L=00		ATP2B1		ATP2B1	7702
I TA SED	re17027200 1	n26	11792420 2	9	0.0000	0.1226	1.60E 11		MTUED		MTUED	5272
I TA SBP	re1173766 5	p30 in13	32840285 t	y c	-0.5304	0.0017	2.52E-08		NA		C5orf23	12709
I TA SEP	re1101/171 1	0612	19751201 t	с с	0.5670	0.0017	4 07E 00		CACNE2	CACNE2	CACNE2	21692
	re11072512_1	5g24	72001070 +	c	0.2102	0.0537	5.52E-00		NA		C15orf17	4664
	re7/05730 1	5924	72072722 2	0	0.2159	0.0524	7 79E 00		MPI		MPI	3261
I TA-DBP	re7537765 1	n36	11809890 a	9	0.4718	0.0714	2 36E-10		CLCN6	MTHEP.NPPACICN8.NPPR	CLONE	972
I TA-DBP	rs7085 1	5024	72882536 t	9	0.3468	0.0582	1 10E-08		CSK	CYP142°CSK1MAN11 CPLX3 SCAMP211 K3	CSK	21
I TA-DBP	rs198833 6	in22	26222487 a	a	-0 4345	0.0741	1.91E-08		NA	HIST1H/JOH/EINWITE,OF LENGUENER LIJOTOO	HIST1H1T	6144
I TA-DBP	rs6495127 1	5a24	72981543 t	e e	-0.3262	0.0571	4 40E-08		C15orf17	COX54:MPI:SCAMP2:RPP25:C15orf17:ULK3	C15orf17	2163
I TA-DBP	rs11105354_1	2021	88550654 a	a	0.5235	0.0696	5 40E-13	****	ATP2B1		ATP2B1	23321
I TA-DBP	rs12246717_1	0g21	63129189 t	a	0.3693	0.0624	1.39E-08	+++++-++-	C10orf107	C10orf107	C10orf107	36465
I TA-DBP	rs10774625_1	2024	110394602 a	a	0 3848	0.0528	274E-12	++++++++++	ATXN2	SH2B3:ATXN2	ATXN2	20201
LTA-DBP	rs6092743 2	0a13	57133765 a	a	0.502	0.0843	1.11E-08	+++++-+++	NA	NA	C20orf174	65704
LTA-DBP	rs11634474 1	5a24	72903237 c	a	0.3384	0.0593	4.51E-08	+++++++++	LMAN1L	CSK:LMAN1L:CPLX3:SCAMP2:ULK3	LMAN1L	1914
LTA-DBP	rs4886636 1	5g24	72983229 a	q	-0.3123	0.0524	1.13E-08		C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17	C15orf17	3286
LTA-DBP	rs3784789 1	5a24	72869605 c	a	0.3166	0.0553	3.98E-08	+++++++++	CSK	CYP1A2:CSK:LMAN1L:CPLX3:SCAMP2:ULK3	CSK	7838
LTA-DBP	rs4842666 1	2q21	88465680 t	c	0.5108	0.0745	4.88E-11	+++++++++	NA	ATP2B1;WDR51B;GALNT4	WDR51B	21772
LTA-DBP	rs17367504 1	p36	11785365 a	a	0.4598	0.0717	7.61E-10	+++++++	MTHER	MTHFR:NPPA:CLCN6:NPPB:AGTRAP	MTHER	3337
LTA-DBP	rs11072511 1	5g24	72946486 a	q	0.3165	0.0525	7.35E-09	+++++++++	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	6237
LTA-DBP	rs17696736 1	2q24	110971201 a	g	-0.3131	0.0536	2.16E-08		C12orf30	ERP29;TMEM116;C12orf30	C12orf30	22325
LTA-DBP	rs7136259 1	2q21	88605319 t	č	-0.3314	0.0526	1.55E-09	++	NA	ATP2B1	ATP2B1	31344
LTA-DBP	rs2681485 1	2q21	88549753 a	g	0.3385	0.053	9.22E-10	++++-++++	ATP2B1	ATP2B1	ATP2B1	24222
LTA-DBP	rs1799945 6	ip22	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 1	0q21	63192664 a	ť	-0.3402	0.0592	3.56E-08		C10orf107	C10orf107	C10orf107	3431
LTA-DBP	rs12258967 1	0p12	18767965 c	g	0.3548	0.0571	2.48E-09	+++-++++	CACNB2	CACNB2	CACNB2	38447
LTA-DBP	rs16916504 1	0q21	63122962 a	g	0.3706	0.0625	1.30E-08	+++++-++	C10orf107	C10orf107	C10orf107	30238
LTA-DBP	rs6495126 1	5q24	72962079 a	g	0.3253	0.0568	4.03E-08	+++++-+++	NA	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	MPI	7383
LTA-DBP	rs7599598 2	q11	96715567 a	g	-0.314	0.0543	2.91E-08		NA	FLJ10081;FER1L5;LMAN2L	FER1L5	9353
LTA-DBP	rs12230074 1	2q21	88614998 a	g	0.5255	0.0718	2.23E-12	+++++++++	NA	ATP2B1	ATP2B1	41023
LTA-DBP	rs11066188 1	2q24	111095097 a	g	0.3343	0.0539	2.76E-09	+++++++++	NA	TRAFD1	TRAFD1	19302
LTA-DBP	rs1378941 1	5q24	72867203 a	с	-0.3135	0.0551	4.98E-08		CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	5436
LTA-DBP	rs11065987 1	2q24	110556807 a	g	-0.3534	0.0543	4.52E-10		NA	BRAP;ATXN2;ACAD10	BRAP	9471
LTA-DBP	rs936226 1	5q24	72856335 t	С	-0.3413	0.0585	2.26E-08		NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-DBP	rs2166122 1	0q21	63193080 t	с	-0.3932	0.0663	1.32E-08	+	C10orf107	C10orf107	C10orf107	3015
LTA-DBP	rs653178 1	2q24	110492139 t	с	-0.3911	0.0524	7.85E-13		ATXN2	ATXN2	ATXN2	29724
LTA-DBP	rs1378942 1	5q24	72864420 a	с	-0.3128	0.055	5.00E-08		CSK	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	2653
LTA-DBP	rs11066320 1	2q24	111390798 a	g	0.303	0.053	4.11E-08	+++++++++	PTPN11	RPL6;PTPN11	PTPN11	41301
LTA-DBP	rs2675612 1	0q21	63193272 t	с	-0.3502	0.0593	1.47E-08	+	C10orf107	C10orf107	C10orf107	2823
LTA-DBP	rs3765066 1	5q24	72927907 a	g	-0.3388	0.0563	7.81E-09		SCAMP2	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	3658
LTA-DBP	rs260014 2	0q13	57192854 t	с	-0.4584	0.0782	1.92E-08	+	NA	C20orf174	C20orf174	6615
I TA DBP	rs11072518 1	5q24	73021663 t	С	0.3405	0.0552	3.29E-09	+++++-+++	NA	COX5A;SCAMP5;RPP25;C15orf17;MPI	COX5A	4238
CIAODI												

	Trait	SNPID	Chr	Position.Bui Allele1	Allele2	Beta	s.e.	Р	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
Decke         Decke <th< td=""><td>LTA-DBP</td><td>rs1401982</td><td>12q21</td><td>88513730 a</td><td>g</td><td>0.3363</td><td>0.0529</td><td>1.06E-09</td><td>++++-++++</td><td>ATP2B1</td><td>ATP2B1 COVENIND!! MANULICELV2:SCAMP2:C45+rf471111/2</td><td>ATP2B1</td><td>7772</td></th<>	LTA-DBP	rs1401982	12q21	88513730 a	g	0.3363	0.0529	1.06E-09	++++-++++	ATP2B1	ATP2B1 COVENIND!! MANULICELV2:SCAMP2:C45+rf471111/2	ATP2B1	7772
Classe         Classe<		rs12442901	15q24	72870965 a	c a	0.3242	0.0583	2 30E-09		CSK	CONSA, MELLMAINTE, CEENS, SCAMEZ, CTSOTTI, JEENS CPLX3: CVP1A2: SCAMP2: CSK: ULK3: LMAN11	CSK	9198
LALDER         HUBBEN         COUNT         C         AUG         NUMBEN         COUNT         CO	LTA-DBP	rs13306561	1p36	11788391 a	g	0.4789	0.0723	2.08E-10	+++++++	MTHFR	MTHFR:NPPA;CLCN6;NPPB;AGTRAP	MTHER	311
Lobie         Constrained         Allogie	LTA-DBP	rs11072513	15q24	73008021 t	c	-0.3223	0.0526	4.20E-09		COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8350
LAD BUR STORM         Constrained State         <	LTA-DBP	rs2681492	12q21	88537220 t	с	0.5064	0.0676	7.02E-13	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
	LTA-DBP	rs2168519	15q24	72867925 t	С	0.3402	0.0583	2.19E-08	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	6158
11.000         100000         10000         10000         <	LTA-DBP	rs2393833	10q21 1q42	63115322 t 228015325 t	c	-0.3697	0.0624	1.36E-08	++	C100m107		C100m107	22598
LACK         PUBAL	LTA-DBP	rs4886633	15a24	72965260 a	a	-0.3276	0.057	3.49E-08	+	NA	COX5A:CPLX3:SCAMP2:C15orf17:MPI:ULK3	MPI	4202
LAGE         PUBDE         PUBDE         PUBDE         PUBDE <thlage< th="">         PUBDE         PUBDE         &lt;</thlage<>	LTA-DBP	rs11856413	15q24	72986945 a	g	0.3183	0.0525	5.94E-09	+++++++++	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	C15orf17	430
Label Price         Label Price <thlabel price<="" th=""> <thlabel price<="" th=""></thlabel></thlabel>	LTA-DBP	rs1133322	15q24	72999410 a	g	0.3205	0.0526	4.96E-09	+++++++++	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	261
LALUE         LALUE <th< td=""><td>LTA-DBP</td><td>rs11105364</td><td>12q21</td><td>88593407 t</td><td>g</td><td>0.5264</td><td>0.0704</td><td>7.24E-13</td><td>++++-++++</td><td>NA</td><td>ATP2B1</td><td>ATP2B1</td><td>19432</td></th<>	LTA-DBP	rs11105364	12q21	88593407 t	g	0.5264	0.0704	7.24E-13	++++-++++	NA	ATP2B1	ATP2B1	19432
LALEY         LALEY <th< td=""><td>LTA-DBP</td><td>rs12579302</td><td>12q21</td><td>88574634 a</td><td>g</td><td>0.5218</td><td>0.0702</td><td>1.01E-12</td><td>++++-++++</td><td>NA OA0</td><td>ATP2B1</td><td>ATP2B1</td><td>659</td></th<>	LTA-DBP	rs12579302	12q21	88574634 a	g	0.5218	0.0702	1.01E-12	++++-++++	NA OA0	ATP2B1	ATP2B1	659
LADE         LADE <thlade< th="">         LADE         LADE         <thl< td=""><td>LTA DBP</td><td>rs12244842</td><td>10q21 12q24</td><td>110399754 a</td><td>g t</td><td>-0.3784</td><td>0.0627</td><td>2 71E 12</td><td>+</td><td>C1000107</td><td>SH2R3-ATYN2</td><td>C10001107</td><td>10408</td></thl<></thlade<>	LTA DBP	rs12244842	10q21 12q24	110399754 a	g t	-0.3784	0.0627	2 71E 12	+	C1000107	SH2R3-ATYN2	C10001107	10408
Linder         Linder <thlinder< th=""> <thlinder< th=""> <thlinder< td="" th<=""><td>I TA-DBP</td><td>rs11105383</td><td>12q24</td><td>88631437 t</td><td>c</td><td>0.3040</td><td>0.0528</td><td>2.71E-12 2.28E-08</td><td>*****</td><td>NA</td><td>ATP2B1</td><td>ATP2B1</td><td>57462</td></thlinder<></thlinder<></thlinder<>	I TA-DBP	rs11105383	12q24	88631437 t	c	0.3040	0.0528	2.71E-12 2.28E-08	*****	NA	ATP2B1	ATP2B1	57462
LIADDP         Cipical Scient 2007         C         C         Size Control         CORR         Corr<         Corr         Corr         Corr         Corr<         Corr<         Corr	LTA-DBP	rs1992625	10g21	63190704 t	c	-0.3911	0.0662	1.48E-08	+	C10orf107	C10orf107	C10orf107	5391
Linker         High         Prop         Constraint         Constraint <thconstraint< th="">         Constraint</thconstraint<>	LTA-DBP	rs1133323	15q24	72999278 t	с	-0.3262	0.0526	2.66E-09		NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	393
LADB         LADB <thladb< th="">         LADB         LADB         <thl< td=""><td>LTA-DBP</td><td>rs1378940</td><td>15q24</td><td>72870547 a</td><td>С</td><td>-0.3159</td><td>0.0554</td><td>4.44E-08</td><td></td><td>CSK</td><td>CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L</td><td>CSK</td><td>8780</td></thl<></thladb<>	LTA-DBP	rs1378940	15q24	72870547 a	С	-0.3159	0.0554	4.44E-08		CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	8780
LADDE         LADDE <th< td=""><td>LTA-DBP</td><td>rs2301249</td><td>15q24</td><td>72879437 t</td><td>С</td><td>0.3479</td><td>0.0581</td><td>9.48E-09</td><td>+++++++++</td><td>CSK</td><td>CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L</td><td>CSK</td><td>3120</td></th<>	LTA-DBP	rs2301249	15q24	72879437 t	С	0.3479	0.0581	9.48E-09	+++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
Link Dep         Dirik Dep         Dirk Dep	LTA-DBP	rs1127796	15q24	72980057 t	с	0.3152	0.0525	8.37E-09	+++++++++++++++++++++++++++++++++++++++	C15orf17	COX5A;SCAMP2;RPP25;C15orf17;MPI;ULK3	C15orf17	677
Linksper         Cirksper		rc7200436	10q24 12q21	72902010 C 88637201 t	g	-0.3172	0.0524	2 30E-08		NA	COASA,MIPI,LMAINTE,CPEA3,SCAMP2,CT50117,UEK3	MPI ATP2B1	63226
Linder         Bisses         Bisses<	I TA-DBP	rs7162232	15024	72902948 a	9	-0.3388	0.0593	4.35E-08		I MAN1I	CPLX3:SCAMP2:CSK:ULK3:LMAN1L	I MAN1I	2203
LIADDP         Pattern         CSK         CPU-CACPPIA_SCAMP2CSCAMPLASHUKLAMANL         CSK         PPIAL           LIADDP         PABURA         0.017         2000         COMING         COMING        COMING	LTA-DBP	rs198846	6p22	26215442 a	q	0.4337	0.0738	1.73E-08	+++++++++++++++++++++++++++++++++++++++	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H1C;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H1T	177
LHADP         LHADP         RESURPT         Soft         Soft         Soft         Soft         Soft         Soft           LHADP         RESURPT         Soft         Soft         Soft         Construct         Construct <td>LTA-DBP</td> <td>rs8033381</td> <td>15q24</td> <td>72867738 a</td> <td>g</td> <td>-0.3403</td> <td>0.0583</td> <td>2.17E-08</td> <td></td> <td>CSK</td> <td>CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L</td> <td>CSK</td> <td>5971</td>	LTA-DBP	rs8033381	15q24	72867738 a	g	-0.3403	0.0583	2.17E-08		CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LHADP         International Status         Closential Status         Closentia Status         Closentia Status         Clos	LTA-DBP	rs260013	20q13	57194118 a	g	-0.4565	0.0783	2.31E-08	+	NA	C20orf174	C20orf174	5351
Link Link         Construction         Construction <td>LTA-DBP</td> <td>rs3750727</td> <td>10q21</td> <td>63114411 a</td> <td>g</td> <td>0.3782</td> <td>0.0626</td> <td>7.09E-09</td> <td>+++++-++-</td> <td>C10orf107</td> <td>C10off107</td> <td>C10orf107</td> <td>21687</td>	LTA-DBP	rs3750727	10q21	63114411 a	g	0.3782	0.0626	7.09E-09	+++++-++-	C10orf107	C10off107	C10orf107	21687
Link DB         Difference         Difference <thdifference< th="">         Differenc         Difference<!--</td--><td>LTA-DBP</td><td>rs/0/0/9/</td><td>10q21</td><td>63221779 a</td><td>g</td><td>-0.4387</td><td>0.0761</td><td>3.30E-08</td><td>+</td><td>NA</td><td>C100rf107</td><td>C10orf107</td><td>25684</td></thdifference<>	LTA-DBP	rs/0/0/9/	10q21	63221779 a	g	-0.4387	0.0761	3.30E-08	+	NA	C100rf107	C10orf107	25684
LADBP       millings2       124       0.0473       0.0473       0.2476       0.0473       0.2476       0.0473       0.0474       0.0473		rc17240754	15q24 12q21	72859611 C	g	-0.341	0.0585	2.29E-08		NA	CPLX3;CYP1A2;CYP1A1;CSK;ULK3;LMAN1L ATD2B1	ATD2D1	2156
Lik Abb P         PROVE ID         C         0.338         0.0388         4.962.66         MPC SCK (LMML (LSC) SCM (LML))         SCM (LPL)         MPC SCK (LMML (LSC) SCM (LML))         SCM (LPL)         MPC SCK (LMML (LSC) SCM (LML))         SCM (LML)         SCM (L	I TA-DBP	rs11105382	12021	88631403 t	y c	0.3230	0.0702	2 21E-08	+++++++++++++++++++++++++++++++++++++++	NA	ATP2B1	ATP2B1	57428
Lin AdB         mining	LTA-DBP	rs936230	15q24	72932151 t	c	0.3335	0.0586	4.98E-08	+++++++++++++++++++++++++++++++++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	7902
LAADP         ressesse         102-10         6184677         1         c         0.318         0.005         4416.9	LTA-DBP	rs11066301	12q24	111355755 a	g	-0.304	0.0532	4.18E-08		PTPN11	RPL6;PTPN11	PTPN11	14837
Lin Aber         miting         miting         miting         COXAS ADMINIST         Miting         COXAS ADMINIST         Miting         COXAS ADMINIST         Miting         COXAS ADMINIST         COXAS ADMINIST <thcoxas administ<="" th=""> <t< td=""><td>LTA-DBP</td><td>rs2588992</td><td>10q21</td><td>63184677 t</td><td>С</td><td>-0.3768</td><td>0.066</td><td>4.41E-08</td><td>+</td><td>C10orf107</td><td>C10orf107</td><td>C10orf107</td><td>11418</td></t<></thcoxas>	LTA-DBP	rs2588992	10q21	63184677 t	С	-0.3768	0.066	4.41E-08	+	C10orf107	C10orf107	C10orf107	11418
LALADE         Fight Solution         Instance         GL/MB         Bit PACHAGE         CL/MB         CL/MB         Bit PACHAGE         CL/MB	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         PION 333         PION 34         PION 344         PION 3444         PION 344	LTA-DBP	rs2050265	1p36	11802286 a	g	0.4709	0.0715	2.68E-10	+++++++	CLCN6	MTHER;NPPA;CLCN6;NPPB	CLCN6	85/6
LTADEP         P12922         P2292         P22922         P2292		rs1813353	10p12	19747454 t	y c	0.3311	0.0575	6.84E-09	+-+	CACNB2	COASA,MIEL,SCAMIEZ,REE23,CT30117 CACNE2	CACNB2	4957
LTADBP         P2412521         F524         7522208         1         C         0.0232         0.0471         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571         0.0571	I TA-DBP	rs129128	6p22	26233321 t	c	-0 4462	0.0300	1 10E-08		NA	HIST1H2BD HIST1H2BC HIST1H1E HIST1H2BE HIST1H4C HIST1H2AC HIST1H1T HEE	HIST1H2AC	425
LTADBP       rel357139       1580378       1       c       -0.4710       0.9715       -0.4867	LTA-DBP	rs2415251	15q24	73029208 t	с	0.3255	0.0548	1.22E-08	+++++-+++	NA	COX5A;SCAMP5;MPI;RPP25;C15orf17	RPP25	5287
LTA-DBP       re28142       122,12       8853000       a       g       0.521       0.091       4016-13       +	LTA-DBP	rs12567136	1p36	11806318 t	с	-0.4716	0.0715	2.49E-10	++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	4544
LTA.DB         rst703742 hg8         1722370         a         g         0.4877         CLONB         4177           LTA.DB         rst703741 hg24         1003891 a         1         0.223         248E-10	LTA-DBP	rs2681472	12q21	88533090 a	g	0.5231	0.0691	4.01E-13	++++-++++	ATP2B1	ATP2B1	ATP2B1	27132
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	LTA-DBP	rs1/03/425	1p36	11/929/0 a	g	-0.4967	0.0753	2.49E-10	++	CLCN6	MTHER;NPPA;CLCN6;NPPB;AGTRAP	CLCN6	41//
LTA.DBP       estilizable       2221       BSSB8572       c       0       9287       2487         LTA.DBP       estilizable       0222       BSSB8572       c       0       9287       0077       2276-08       MA       ATP281       4087         LTA.DBP       estilizable       0223       BSS14872       1       c       0.4525       0.0776       276-08       MA       ATP281       4087         LTA.DBP       estilizable       0.0436       0.0556       67:09       MA       HISTH2BD,HSTH1H2,HSTHH2AC,HSTHH1C,HSTH42C,HSTH1H2,HSTH42C,HSTH1H2,HSTH42C,HSTH1H2,HSTH42C,HSTH1H1,FE       MTP281       40867       761         LTA.DBP       estilizable       0.0468       0.027       5.55E-11       MA       ATP281       MA       MTP281       MA       417281       45329       2218       45329       2116       MTP281       7702       2117       772       2117       74       2123       772       74       2117       772       74       2117       774       2117       774       2117       774       2117       774       2117       774       2117       774       2117       774       2117       774       2117       774       2117       774       2117		rc2194504	15q24 12g24	73008918 a 110269001 t	t	-0.3224	0.0526	4.26E-09		CUX5A SU2D2	COX5A;MPI;SCAMP2;RPP25;C150IT17 SH2p2:ATVN2	CUX5A SU2D2	8507
TA-DEP         restRess         object         22212011         1         0         4483         0.777         2 97-08         ********         NA         HISTINEGC/HISTINEGC	I TA-DBP	rs11105368	12021	88598572 c	a	-0.5267	0.0324	7 25E-13		NA	ATP2B1	ATP2B1	24597
LTADEP rs1100378 1221       B8014972       c       -0.523       0.716       2.08-12	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 Dep rs198823       6.92       2823012       1       g       0.053       6.75-09	LTA-DBP	rs11105378	12q21	88614872 t	с	-0.5253	0.0716	2.03E-12		NA	ATP2B1	ATP2B1	40897
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	LTA-DBP	rs198823	6p22	26230912 t	g	-0.3346	0.0553	6.57E-09	+	NA	HIST1H2BD;HIST1H2BC;HIST1H1E;HIST1H4C;HIST1H2AC;HIST1H1T;HFE	HIST1H2BC	761
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	LTA-DBP	rs11105328	12q21	88466521 a	g	0.4968	0.0727	5.59E-11	+++++++++++++++++++++++++++++++++++++++	NA	ATP2B1;WDR51B;GALN14	WDR51B	22613
LTL 2016         S1103230         Los B         DOR 77         DOR 77 <thdor 77<="" th=""> <thdor 77<="" th="">         DOR 77</thdor></thdor>		rs11105379	12q21 12q21	88619304 t	c	0.4551	0.0774	1./1E-08	+++++++-+	NA ATD2D1	ATP2B1	ATP2B1	45329
LTA_DBP rs17830235 1924       111070695 a       a       0.0354       0.0539       2.43E.09       TRAFD1 C12430       TRAFD1 C24         LTA_DBP rs1783983 15924       17285346 c       0.3371       0.0583       3.90-068       4.90-068       3.90-068       4.90-068       3.90-068       4.90-068       3.90-068       4.90-068       3.90-068       4	LTA-DBP	rs17037390	1p36	11783430 a	9 a	-0.4687	0.0717	3.70E-10	++	MTHER	MTHER:NPPA:CLCN6:NPPB:AGTRAP	MTHER	5272
LTA.DPP rs178938       19624       7288496       t       c       0.3371       0.0588       3.900-08       ++++++       NA       CPLX3.CYP1A2_SCAMP2_CSK,ULK3,LMAN1L       CSK       939         LTA.MAP rs10287968       2.92765588       a       c       0.3913       0.0616       1.800-09       ++++++       ATP2B1       ATP2B1 <td>LTA-DBP</td> <td>rs17630235</td> <td>12q24</td> <td>111076069 a</td> <td>g</td> <td>0.3354</td> <td>0.0539</td> <td>2.43E-09</td> <td>+++++++++</td> <td>NA</td> <td>TRAFD1;C12orf30</td> <td>TRAFD1</td> <td>274</td>	LTA-DBP	rs17630235	12q24	111076069 a	g	0.3354	0.0539	2.43E-09	+++++++++	NA	TRAFD1;C12orf30	TRAFD1	274
$ \begin{array}{c} \mbox{LTA}MP \ rs1275986 \ 2p23 \ 2p375583 \ a \ c \ 0.3875 \ 0.0816 \ 180-09 \ + NA \ KCNK3 \ CNK3 \ 0.594 \ CDK3 \ 0.594 \ CDK3 \ 0.594 $	LTA-DBP	rs1378938	15q24	72883496 t	c	0.3371	0.0588	3.90E-08	+++++++++	NA	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	939
LIA-MAP       rs108b8014       1221       8850526       t       c       0.3913       0.061       8 48E-10       AIP281       AIP281       0449         LTA-MAP       rs108269747       2015       57175019       a       g       0.543       0.0605       7.19E-10       C20off74       2045         LTA-MAP       rs1072512       fs24       72991079       t       c       -0.3902       0.0605       7.19E-10       MPI       3261         LTA-MAP       rs7537765       fp38       11009890       a       g       0.6028       0.0822       2.49E-12       ++++++       MPI       C2X6ASCAMP2; C16off17, MPI, ULX3       MPI       3261         LTA-MAP       rs7537765       fp38       11009890       a       g       0.6028       0.822       2.49E-12       ++++++       CX6M       MRP; NPA; C1606, NPB       CLCN8       PC       CLN8       972         LTA-MAP       rs7085       15624       72882538       t       c       0.4311       0.672       8.48E-10       MA       ATP281       MPA       MTP2       MTAP       C3X6       CAMP2; NPB       CSK       C12oH174       C20oH174       12078         LTA-MAP       rs5068       15624       72882536 </td <td>LTA-MAP</td> <td>rs1275986</td> <td>2p23</td> <td>26765583 a</td> <td>с</td> <td>-0.3875</td> <td>0.0616</td> <td>1.80E-09</td> <td>+</td> <td>NA</td> <td>KCNK3;CIB4</td> <td>KCNK3</td> <td>3539</td>	LTA-MAP	rs1275986	2p23	26765583 a	с	-0.3875	0.0616	1.80E-09	+	NA	KCNK3;CIB4	KCNK3	3539
LTA-MAP       r5020747       20413       01438       0.0417       4.044<	LTA MAD	rs10858914	12q21	88555526 t	c	0.3913	0.061	8.48E-10	+++++++	ATP2B1	AIP2B1 C20ord174	ATP2B1 C20orf174	18449
LTA.MAP is7495739 1524       72972723 a       g       0.3859       0.0805       1.05E-09       ++++++       MPI       COX5A_SCAMP2_C15or17_MPI_ULK3       MPI       3281         LTA.MAP is7537765       1p36       11809890 a       g       0.6026       0.0822       2.49E-12       ++++++++       CLON6       MTHER_NPA_CLCN6N/NPPB       CLON6       972         LTA.MAP is70505       5124       7285776       2.677702 t       c       0.3359       0.0617       2.52E-09       ++++++       CLON6       MTHER_NPA_CLCN6N/NPPB       CLON6       972         LTA.MAP is70505       5124       72882772 a       g       0.3729       0.003       3.32E-09       ++++++       CSK       CNN3 SCAMP2_UK3       CSK       21         LTA.MAP is70505       5124       7288253 t       c       0.411       0.0672       ++++++       CSK       CVP142_CSK_UMAN1L_CPLX3_SCAMP2_ULK3       CSK       21         LTA.MAP is70515       124       728850654       a       g       0.685       0.685       0.686       -+++++       NPA       MTHER_NPA_CLCN6,NPB       NPA       199         LTA.MAP is7049512       124       7289143 t       c       0.0685       0.685       0.6861       CCOXA_NP2_CCN6,NPB       CT6or117 <t< td=""><td></td><td>rs11072512</td><td>20013 15a24</td><td>72991079 t</td><td>y c</td><td>-0.3902</td><td>0.094</td><td>7 19E-10</td><td>+-+++++++</td><td>NA</td><td>COX54:SC4MP2:RPP25:C15off17:MPI</td><td>C15orf17</td><td>4564</td></t<>		rs11072512	20013 15a24	72991079 t	y c	-0.3902	0.094	7 19E-10	+-+++++++	NA	COX54:SC4MP2:RPP25:C15off17:MPI	C15orf17	4564
LTA.MAP       rs7537765       transpondence       0.6022       0.4022       2.49E-12       +++++++       CLCN6       MTHERNPACLCN6,NPPB       CLCN6       972         LTA.MAP       rs7537765       transpondence       0.8022       2.49E-12       +++++++       CLCN6       MTHERNPACLCN6,NPPB       KCNK3       7950         LTA.MAP       rs7085       15024       72882536       t       c       0.311       0.0672       8.48E-10       +++++++       CLCN6       MTHERNPACLCN6,NPPB       KCNK3       7950         LTA.MAP       rs7085       15024       72882536       t       c       0.4311       0.0672       8.48E-10       ++++++       CSK       CYP1A2,CSKLMAN1L,CPLX3,SCAMP2,ULK3       CSK       21         LTA.MAP       rs5068       1p36       11828641       a       0       0.0610       7.38E-09       ++++++       CSK       CYP1A2,CSKLMAN1L,CPLX3,SCAMP2,ULK3       CSK       21         LTA.MAP       rs5068       1p36       11828641       s       0       0.685       0.8611       2.98E-16       +++++       NPPA       CLCN6,NPPB       CLCN6       NPPA       199         LTA.MAP       rs1054512 10241       8550654       a       g       0.4861       0.072 <t< td=""><td>I TA-MAP</td><td>rs7495739</td><td>15q24</td><td>72972723 a</td><td>a</td><td>0.3859</td><td>0.0605</td><td>1.05E-09</td><td>+++++-+++</td><td>MPI</td><td>COX5A:SCAMP2:C15orf17:MPI:ULK3</td><td>MPI</td><td>3261</td></t<>	I TA-MAP	rs7495739	15q24	72972723 a	a	0.3859	0.0605	1.05E-09	+++++-+++	MPI	COX5A:SCAMP2:C15orf17:MPI:ULK3	MPI	3261
LTA.MAP       rsf275979       2p2.3       2p2.77772       t       c       0.385       0.0877       2 52E-09       +++++++       KCNR3       CIMA3CIE4       ATP2B1       18868         LTA.MAP       rsf085911       12q21       8487272       a       g       -0.3729       0.0803       3.32E-09       -++++++++       ATP2B1       MARA       ATP2B1       MARA       CSK       21         LTA.MAP       rsf085911       12q24       72887536       t       c       0.4311       0.0672       8.48E-10       +++++++++       CSK       CYP1A2_CSKLMAN1L_CPLX3_SCAMP2_ULK3       C3K       21         LTA.MAP       rsf09561       a       g       -0.575       0.0944       1.68E-09       ++++++++++++++++       CSK       CYP1A2_CSKLMAN1L_CPLX3_SCAMP2_ULK3       C30       C30       200       110276       C30       C30       2163       C37       0.0944       1.68E-09       +++++++++++++++++++       ATP2B1       ATP2B1       ATP2B1       23321       C150r17       2163         LTA.MAP       rsf1246717       10q21       63129189       t       g       0.481       0.072       7.13E-09       ++++++       ATP2B1       ATP2B1       ATP2B1       23321       L1A+A447       S1713765       <	LTA-MAP	rs7537765	1p36	11809890 a	g	0.6026	0.0822	2.49E-12	++++-++++	CLCN6	MTHFR;NPPA;CLCN6;NPPB	CLCN6	972
LTA.MAP       rs10658911       1221       8847272       a       g       -0.3729       0.003       3.32E-09	LTA-MAP	rs1275979	2p23	26777072 t	С	0.385	0.0617	2.52E-09	+++++-++-	KCNK3	KCNK3;CIB4	KCNK3	7950
LTAMAP rs7085 15024 7288538 t c 0.4311 0.0672 8.48E:10 +++++++ CSK CYP1A2/CSKUMANIL/CPLX3;SCAMP2,ULK3 CSK 21 LTAMAP rs5068 1p36 11828661 a g 0.8103 0.134 9.06E:08 +++++++ CSK CYP1A2/CSKUMANIL/CPLX3;SCAMP2,ULK3 C150rf17 12163 LTAMAP rs109512 0124 72881543 t c 0.389 0.0685 7.58E:09 -++++++ NPA MTHFR,NPA,CLCA6,NPPB C150rf17,ULK3 C150rf17 2163 LTAMAP rs1017425 12248 110394002 a g 0.4861 0.072 7.13E:09 ++++++ ATP2B1 ATP2B1 ATP2B1 LTAMAP rs10174625 12244 110394002 a g 0.4861 0.072 7.13E:09 ++++++ ATP2B1 ATP2B1 ATP2B1 LTAMAP rs10274625 12244 110394002 a g 0.4861 0.072 7.13E:09 ++++++ ATP2B1 ATP2B1 LTAMAP rs10274625 12241 110394002 a g 0.4861 0.072 7.13E:09 ++++++ ATP2B1 ATP2B1 LTAMAP rs10274625 12241 110394002 a g 0.4861 0.072 7.13E:09 ++++++ ATP2B1 ATP2B1 LTAMAP rs10274625 12241 110394002 a g 0.4861 0.072 7.13E:09 +++++++ ATX2 SH2B3 ATX12 LTAMAP rs10274625 12241 110394002 a g 0.4861 0.072 7.13E:09 +++++++ ATX2 SH2B3 ATX12 LTAMAP rs10274625 12241 110394002 a g 0.4861 0.072 7.13E:09 +++++++ ATX12 SH2B3 ATX12 LTAMAP rs10274625 12241 110394002 a g 0.4861 0.072 7.13E:09 +++++++ NA NA LTAMAP rs1027462 013 57133765 a g 0.0872 0.0971 3.60E:10 +++++++ NA NA LTAMAP rs10311224 1224 129883298 a g 0.0385 1.08E:09 +++++++ NA NA LTAMAP rs10341224 1524 129883298 a g 0.0387 0.0864 9.37E:10 +++++++ LMAN1L CSKLMAN1L/CPLX3;SCAMP2,ULK3 LTAMAP rs105412 1224 88630966 a g 0.3899 0.0885 1.08E:09 +++++++ NA NA LTAMAP rs184789 1524 72886298 a g 0.3389 0.0889 5.18E:09 +++++++ NA NA LTAMAP rs184789 1524 72889805 c g 0.3899 0.088 5.18E:09 +++++++ NA NA LTAMAP rs3784789 1524 72889805 c g 0.3899 0.088 5.18E:09 +++++++ NA NA LTAMAP rs3784789 1524 72889805 c g 0.3899 0.0889 5.18E:09 +++++++ NA NA LTAMAP rs384789 1524 72889805 c g 0.3899 0.0889 5.18E:09 +++++++ NA NA LTAMAP rs384789 1524 72889805 c g 0.3899 0.0889 5.18E:09 +++++++ NA NA LTAMAP rs384789 1524 72889805 c g 0.3899 0.0889 5.18E:09 +++++++ NA LTAMAP rs384789 1524 72889805 c g 0.3899 0.0889 5.18E:09 +++++++ NA LTAMAP rs384789 1524 728898050 c g 0.3899 0.0889 5.18E:09	LTA-MAP	rs10858911	12q21	88487272 a	g	-0.3729	0.0603	3.32E-09	++	NA	ATP2B1;WDR51B;GALNT4	ATP2B1	18686
LTA-MAP       rs1900512 20013       5/187391       c       g       -0.5075       0.0944       1.006-09       +++++++       NA       C2001174       12078         LTA-MAP       rs50081       p.36       11822661       a       g       0.01548       p.06E-09       +++++++       NPPA       LTA-MAP       rs50081       p.36       11822661       a       g       0.01614       12078         LTA-MAP       rs50081       p.36       11822661       a       g       0.0650       ++++++       NPPA       LTA-MAP       Stap14251       C156r117       2163         LTA-MAP       rs1120561       a       g       0.685       0.0801       2.98E-16       ++++++       ATP2B1       23321         LTA-MAP       rs1120452       12024       10394602       a       g       0.4361       0.072       7.13E-09       +++++++       ATP2B1       C156r117       2163         LTA-MAP       rs102344       2013       57132706       a       g       0.4361       0.072       7.13E-09       ++++++       ATP2B1       C106r1107       C106r1107       C106r1107       C106r1107       C106r1107       C106r1107       C106r1107       C2001174       66661         LTA-MAP	LTA-MAP	rs/085	15q24	72882536 t	с	0.4311	0.0672	8.48E-10	+++++++++	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	21
LTA-MAP       rs0495127       fs24       T2891543       t       c       -0.38       rs0495127       fs24       T2891543       t       c       1036       1046       1046 </td <td></td> <td>re5069</td> <td>20013 1p26</td> <td>5/18/391 C 11929561 a</td> <td>g</td> <td>-0.5575</td> <td>0.0944</td> <td>1.00E-08</td> <td>-+</td> <td></td> <td></td> <td>C2000174</td> <td>12078</td>		re5069	20013 1p26	5/18/391 C 11929561 a	g	-0.5575	0.0944	1.00E-08	-+			C2000174	12078
LTA-MAP       rs11105354       12021       88550654       a       g       0.685       0.0801       2.98E-16       +++++++       ATP2B1       ATP2B1       23321         LTA-MAP       rs12246717       10021       63129189       g       0.481       0.072       7.13E-09       +++++++       ATP2B1       ATP2B1       C10or1107       20021         LTA-MAP       rs12246717       100394052       a       g       0.443       0.0609       36E-12       +++++++       ATD2B1       C10or1107       20021         LTA-MAP       rs182384       20013       57133765       a       g       0.635       0.0671       ++++++       ATN       NA       NA         LTA-MAP       rs182384       2013       57133765       a       g       0.635       0.0671       ++++++       ATN       NA       NA         LTA-MAP       rs182384       2013       57133765       a       g       0.687       0.0671       ++++++       NA       NA         LTA-MAP       rs1802344       150247       2703237       c       g       0.0671       0.0687       0.0687       0.0679       -+++++       NA       NA         LTA-MAP       rs1054474       150247<	LTA-MAP	rs6495127	15q24	72981543 t	C C	-0.398	0.0658	7.53E-09	+	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17;ULK3	C15orf17	2163
LTA-MAP       rs12246717       10q21       63129189       t       g       0.4361       0.072       7.13E-09       ++++++       C10orf107       C10orf107       30465         LTA-MAP       rs10774625       12q24       110394602       g       0.4361       0.072       7.13E-09       +++++++       ATNN2       SH283AT2N2       ATNN2       ATNN2       2001         LTA-MAP       rs6082344       2013       57132065       c       0.521       0.0854       5.03E-09       ++++++       ATNN2       SH283AT2N2       C20orf174       66661         LTA-MAP       rs6082743       2013       57132065       a       g       0.6372       0.0971       3.60E-10       ++++++       NA       NA         LTA-MAP       rs6082743       2013       57132065       a       g       0.6372       0.0971       3.60E-10       ++++++       NA       NA         LTA-MAP       rs6082743       2013       57132065       a       g       0.6372       0.0971       3.60E-10       +++++++       NA       NA       C20orf174       65704         LTA-MAP       rs6180666       g       0.0508       1.05E-08       ++++++++       LMAN1L       CSK_LIMAN1L/CPLX3,SCAMP2,ULK3       ATP2B1	LTA-MAP	rs11105354	12q21	88550654 a	g	0.685	0.0801	2.98E-16	++++-+++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-MAP       rs10774625       12q24       110394602       a       g       0.443       0.069       3.66E-12       +++++++       ATXN2       SH283ATXN2       ATXN2       20201         LTA-MAP       rs808234       20q13       57133765       a       g       0.6372       0.0971       3.60E-10       +++++++       NA       NA       C20nf174       66661         LTA-MAP       rs10834743       10q43       57133765       a       g       0.6372       0.0971       3.60E-10       +++++++       NA       NA       C20nf174       66661         LTA-MAP       rs10834743       15q24       72303237       c       g       0.057       0.0655       +++++++       NA       NA       C20nf174       65704         LTA-MAP       rs1083417105381       12q24       18030966       g       0.0527       506-9        NA       ATP2B1       ATP2B1       58991         LTA-MAP       rs4886638       15q24       72889229       a       g       0.387       0.064       9.37E-10        C15of17       CX5AMP12,CEVX3,SCAMP2,ULK3       C15of17       3286         LTA-MAP       rs4886638       15q24       728890566       g       0.386       181	LTA-MAP	rs12246717	10q21	63129189 t	g	0.4361	0.072	7.13E-09	+-++++++	C10orf107	C10orf107	C10orf107	36465
LTA.MAP rs828238 20q13       57132608 t       c       0.5221       0.0854       5.03E-09 +++++++ +       NA       NA       C2001174       66861         LTA.MAP rs8082343       20q13       57132608 t       57132608 t       0.627       0.0671       57132608 t       C2001174       65704         LTA.MAP rs1163411 2q24       12030237 c       g       0.4099       0.0855       1.05E-08 +++++++ HMAN1L       CSK.LMAN1L_CPLX3,SCAMP2,ULK3       LMAN1L       1914         LTA.MAP rs1105341 12q24       188030968 a       g       -0.50E 0        NA       ATP2B1       ATP2B1       56991         LTA.MAP rs1844789       15q24       72893229 a       g       -0.387       0.0614       9.37E-10        C156717       CX6AMP1;SCAMP2;ULK3       C150117       3286         LTA.MAP rs384789       15q24       72898209 c       g       0.389       0.888       518E-09       +++       C156717       CX6AMP1;CPLX3;SCAMP2;ULK3       C150117       3286         LTA.MAP rs384789       15q24       72889605 c       g       0.389       0.888       518E-09       +++++++       NA       NA       NA       SKLMAN1;CPLX3;SCAMP2;ULK3       C5K       7838         LTA.MAP rs35444       12q24       14038820 a<	LTA-MAP	rs10774625	12q24	110394602 a	g	0.443	0.0609	3.66E-12	+++++-+++	ATXN2	SH2B3;ATXN2	ATXN2	20201
LIA-MAP r500%2/43 2013 07133/r05 a g 0.0572 0.091 3.00E-10 +++++++ NA NA NA C200f174 65704 LTA-MAP r511105381 12q2 88630966 a g 0.068 10.6E-08 +++++++ LMAN1L CSK.LMAN1L;CPLX3;SCAMP2;ULK3 LMAN1L 1914 LTA-MAP r64806638 15q2 72983229 a g 0.367 0.0604 9.37E-10 NA ATP2B1 56991 LTA-MAP r5487478 15q2 72808206 c g 0.387 0.0604 9.37E-10 CSK.LMAN1L;CPLX3;SCAMP2;ULK3 C150117 2286 LTA-MAP r535444 12q2 114036820 a g 0.3621 0.062 3.20E-08 ++++++ NA NA NA TBX 3430468	LTA-MAP	rs882384	20q13	57132808 t	с	0.5221	0.0854	5.03E-09	+++++-+++	NA	NA	C20orf174	66661
LTA-MAP rs35444 12q2 114036820 a g 0.362 0.062 3.20E-08 ++++++ NA NA NA TBX 430468		rs6092743	20q13 15q24	5/133/65 a	g	0.6372	0.0971	3.60E-10	++++++++++		NA CSK/LMAN4L/CDLX2/SCAMD2/TILK2	C200f174	1014
LTA-MAP       rs4888638       15q24       72983229       a       g       -0.387       0.0604       9.37E-10      +-       C15orf17       C15orf17       3286         LTA-MAP       rs3784789       15q24       72869605 c       g       0.389       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	TA-MAP	rs11105381	12g24	88630966 a	y a	-0.506	0.0000	5.00E-08	+++++++++		ATP2B1	ATP2B1	56991
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 NA TBX3 430468	LTA-MAP	rs4886636	15q24	72983229 a	g g	-0.387	0.0604	9.37E-10	+	C15orf17	COX5A;MPI;SCAMP2;RPP25;C15orf17	C15orf17	3286
LTA-MAP rs35444 12q2 114036820 a g 0.3621 0.0626 3.20E-08 +++++ NA NA NA TBX3 430468	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	с	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	С	-0.4383	0.0607	4.98E-12	+	NA	ATP2B1	ATP2B1	31344
LIA-MAP	rs236713	20q13	5/1289/2 a	g	-0.4742	0.0791	9.92E-09	+	NA	NA	C20orf1/4	/049/
LTA-MAP	rs2681485	12q21	88549753 a	g	0.4601	0.0611	6.24E-13	++++-++++	ATP2B1	AIP2B1	ATP2B1	24222
LTA-MAP	rs2588918	10q21	63195030 a	t	0.4192	0.0/11	1.76E-08	+-+++-+++	C10orf107		C10orf107	1065
LTA-MAP	rs1275923	2p23	26786300 t	с	-0.3935	0.0633	2.84E-09	+	KCNK3		KCNK3	1/1/8
LTA-MAP	rs12487	15q24	72923747 t	c	0.3523	0.0609	3.24E-08	+++++++++	NA CLOT	CPEX3;SCAMP2;C150fT7;MPI;CSK;UEK3;LMAN1L	SCAMPZ	502
LTA-MAP	rs2120702	10q21	63192664 a	t	-0.4041	0.0683	1.55E-08	-+	C100ff107		C100ff107	3431
LTA-MAP	rs12258967	10p12	18767965 C	g	0.452	0.0657	4.98E-11	+++++	CACINB2		CACNB2	38447
LTA-MAP	rs16916504	10q21	63122962 a	g	0.4371	0.0721	6.92E-09	+-++++++	C100ff107		C100ff107	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	5/13360/ a	g	0.5228	0.0854	4.92E-09	+++++-+++	NA	NA	C200f174	65862
LTA-MAP	rs2586886	2p23	26785535 t	С	-0.3916	0.0628	2.56E-09	+	KCNK3	C20f18;KCNK3	KCNK3	16413
LTA-MAP	rs236706	20q13	5/124811 t	с	-0.4863	0.0793	4.66E-09	+	NA	NA NA	SLMO2	/3515
LTA-MAP	rs12230074	12q21	88614998 a	g	0.6822	0.0825	2.82E-15	++++-++++	NA	ATP2B1	ATP2B1	41023
LIA-MAP	rs11066188	12q24	111095097 a	g	0.3828	0.062	3.60E-09	+++++++++	NA	IRAFD1	TRAFD1	19302
LTA-MAP	rs1378941	15q24	72867203 a	С	-0.3867	0.0636	6.32E-09		CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	5436
LIA-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	с	-0.4311	0.0676	1.08E-09		NA	CYP1A2;CYP1A1;CSK;LMAN1L;CPLX3;ULK3	CSK	5432
LTA-MAP	rs880315	1p36	10719453 t	С	-0.4597	0.067	5.49E-11	?	CASZ1	CAS21	CASZ1	59841
LIA-MAP	rs2166122	10q21	63193080 t	с	-0.4812	0.0766	1.88E-09	-++	C10ort107	C10ort107	C10orf107	3015
LIA-MAP	rs236714	20q13	5/129635 a	t	0.4894	0.0796	4.20E-09	+++++-+++	NA		C200rf174	69834
LIA-MAP	rs1869959	15q24	72934385 a	С	0.3941	0.0677	2.66E-08	+++++++++	SCAMP2	MPI;CSK;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	10136
LTA-MAP	rs16982520	20q13	5/192115 a	g	-0.5643	0.0945	1.16E-08	-+	NA	G200f174	C20orf174	/354
LTA-MAP	rs653178	12q24	110492139 t	с	-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	с	-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	с	-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	с	-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	с	-0.3813	0.0618	3.57E-09	+	KCNK3	KCNK3;CIB4	KCNK3	3471
LTA-MAP	rs6100342	20q13	57132656 a	с	-0.5215	0.0853	5.14E-09		NA	NA	C20orf174	66813
LTA-MAP	rs260014	20q13	57192854 t	с	-0.5518	0.0904	5.36E-09		NA	C20orf174	C20orf174	6615
LTA-MAP	rs11072518	15q24	73021663 t	с	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	с	-0.3901	0.062	1.77E-09	+	SCAMP2	COX5A;MPI;LMAN1L;CPLX3;SCAMP2;C15orf17;ULK3	SCAMP2	9774
LTA-MAP	rs998981	20q13	57133036 t	с	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	с	-0.3959	0.0606	4.27E-10	+	COX5A	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	8350
LTA-MAP	rs2681492	12q21	88537220 t	с	0.6564	0.0779	8.01E-16	+++++++++	ATP2B1	ATP2B1	ATP2B1	31262
LTA-MAP	rs2168519	15q24	72867925 t	с	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	с	-0.4359	0.072	7.35E-09	-+	C10orf107	C10orf107	C10orf107	22598
LTA-MAP	rs2004776	1q42	228915325 t	с	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	с	-0.4819	0.0794	6.55E-09		NA	NA	C20orf174	68979
LTA-MAP	rs1543927	15q24	72850626 t	с	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	С	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	с	-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	с	0.5824	0.0895	4.96E-10	+++++++++	NA	ATP2B1	ATP2B1	57462
LTA-MAP	rs1992625	10q21	63190704 t	с	-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	с	-0.3894	0.0616	1.51E-09	+	NA	KCNK3;CIB4	KCNK3	1254
LTA-MAP	rs1133323	15q24	72999278 t	С	-0.3986	0.0606	3.22E-10	+	NA	COX5A;MPI;SCAMP2;RPP25;C15orf17	COX5A	393
LTA-MAP	rs1378940	15q24	72870547 a	с	-0.3902	0.0639	5.28E-09		CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	8780
LTA-MAP	rs2301249	15q24	72879437 t	с	0.4315	0.0671	7.74E-10	+++++++++++++++++++++++++++++++++++++++	CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	3120
LTA-MAP	rs1127796	15q24	72980057 t	с	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. <u>5</u> 197	0.0848	4.63E-09		NA	NA	SLMO2	66711
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Trait	SNPID (	Chr	Position.Bui Allele1	Allele2	Beta	s.e.	Р	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-MAP	rs8033381 1	15q24	72867738 a	g	-0.4293	0.0673	1.07E-09		CSK	CPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L	CSK	5971
LTA-MAP	rs260013 2	20q13	57194118 a	g	-0.5496	0.0905	6.48E-09		NA	C20orf174	C20orf174	5351
LTA-MAP	rs12046278 1	1p36	10722164 t	С	-0.4722	0.0693	7.26E-11	'	CASZ1	CAS21	CASZ1	57130
LTA-MAP	rs3750727 1	10q21	63114411 a	g	0.4423	0.0723	5.01E-09	+-++++++	C10orf107	C10orf107	C10orf107	21687
LTA-MAP	rs7362597 2	20q13	57112829 a	g	0.5054	0.0848	1.22E-08	++++-++-	NA	NA	SLMO2	61533
LTA-MAP	rs/0/0/9/ 1	10q21	63221779 a	g	-0.5456	0.0878	2.89E-09	+	NA	C10ort10/	C10orf107	25684
LTA-MAP	rs236705 2	20q13	5/122065 t	С	-0.487	0.0793	4.46E-09	+	NA OAO (AOZ	NA	SLMO2	70769
LTA-MAP	rs9/323/ 1	10q21	63195307 a	g	0.42	0.0718	2.26E-08	+-++++++	C100m107		C100m107	788
	rs4880029 1	15q24	72859611 C	g	-0.4308	0.0075	1.09E-09		NA	CYPLAS CYPLAS CONTACTORS (URAS)	CVD442	2150
	1511854147	15024	12839824 L	C	0.401	0.0071	1.09E-08	++++++++++	INA CAC71	CAP24	CARTA	3830
	154645955	12021	10/240/0 a	g	-0.3955	0.0007	1.43E-00	(	CASZI		ATD2D1	04/10
	rc2409046 1	12021	00004/11/ d	y c	-0.0000	0.0000	5.07E-10	+	NA		ATE2D1	50402
	152406040	15924	72004022 a	с с	-0.5057	0.0601	7.E4E 00		INA I MANI1I	ATE2D1 CVD4A2-CSV-LMAN4L-CDLV2-SCAMD2-LLV2		2607
	15/1/0022	15Q24	72894933 a	C	0.4115	0.0081	1.54E-09	+++++++++++++++++++++++++++++++++++++++		CTFTAZ,CSK,LWANTE,CFEA3,SCAMPZ,UEK3	C20orf174	2087
	151400007 2	12021	00601400 +	с с	0.0210	0.0000	4.96E-09	+++++-+++	NA		62001174 ATD2D1	67420
	1511105382	12021	00031403 L	C	0.0010	0.0893	4.75E-10	+++++++++++++++++++++++++++++++++++++++	NA	ATEZDI KONKO ODA	ATF2D1 KCNK2	07428
	1512/09600 2	2µ23 16a24	20700249 t	с а	-0.3037	0.0010	2.39E-09	+	NA	CVD145,CDP4	CEK	0070
	re6026749	20a12	57170210 a	y	0.5510	0.004	2.000 00		NA	C20odt74	C20orf174	20250
	150020746 2	20013 16a24	72022161 +	y c	0.0010	0.0941	2.000-00	+-+++++++	SCAMP2	O2001174 MDI-O2141 MANIT-ODI V2-SOAMD2-O15-cf17-ULK2	SCAMP2	20239
	15550250	12024	111252131 1	C	0.3543	0.0612	2.33E-00	+++++++++++++++++++++++++++++++++++++++	DTDN111		DTDN44	14027
	ro2600000 1	10:21	6210/677 +	g	0.3555	0.0012	2.732-00		C10orf107		C10orf107	11/10
	re25422 1	12024	11/020012 +	с с	0.4005	0.0627	2 42E 09	-++	NA		TRY2	122561
	re2113894 1	12021	88623528 a	+	0.5070	0.0037	4.64E-00		NA	ATP2B1	ATP2B1	40553
	re0210 1	15a24	72015554 t		0.3072	0.0675	2 72E 09	+++++++++++++++++++++++++++++++++++++++	LILK2	ATE201 MDE28K-LMAN41-CDLV2-SCAMD2-TILK2	HIK2	49000
	re1130741 1	15924	72076083 a	0	0.3858	0.0605	1.07E-00	********	MPI		MPI	40 635
	rs10858915 1	12a21	88575678 a	9	0.3548	0.0609	2.58E-09		NA	ΔTP2R1	ATP2B1	1703
I TA.MAP	rs2050265	1n36	11802286	9	0.602	0.0003	2 77 - 12	**********	CLONG	MTHER NPPA CLONG NPPB	CL CN6	8576
	rs11014166 1	10n12	18748804 a	9 t	0.3878	0.0633	4 77E-00		CACNB2	CACNR2	CACNB2	19286
	re12243859 1	10p12	18780638 t	ć	-0 3730	0.0033	2 23E-08		CACNB2	CACNB2	CACNB2	51120
	re/500917 1	10/21	63137550 c	0	0.4662	0.0816	4 72E 08		C10orf107	C10nf107	C10orf107	44935
	re183173	20a13	57159500 t	9	-0.5073	0.0010	4.81E-08		NA	C20orH74	C20orf174	30060
	re8042694 1	15a24	73012468 a	9	0.4071	0.066	3.65E.00		COY5A	COV511 MPI-SCAMP2-PPP25-C15orf17	COY5A	4957
I TA-MAP	re1275980	2023	26770473 t	9	-0.3863	0.0617	2 21E-09		KCNK3	KONKY, MI L, KI LO, STOOTT	KCNK3	1351
ΙΤΔ.ΜΔΡ	rs1813353 1	10n12	18747454 t	c c	0.439	0.0652	1 26E-10	*****	CACNB2	CACNR2	CACNB2	17936
I TA-MAP	rs6676300 1	1036	11847887 a	a	0.3641	0.0634	4.03E-08	***	NA		NPPR	6308
ΙΤΔ.ΜΔΡ	rs2415251 1	15a24	73029208 t	9	0.3962	0.0631	1.99E-09	+++++++++++++++++++++++++++++++++++++++	NA	COX64-SCAMP5-MP1-RCP25-C15orf17	RPP25	5287
I TA-MAP	rs12567136_1	1n36	11806318 t	c	-0.6025	0.0823	2.64E-12		CLCN6	MTHER NPPA CI CNS NPPB	CL CN6	4544
Ι ΤΔ.ΜΔΡ	rs2681472 1	12021	88533090 a	a	0.6861	0.0796	1 77E-16	****	ATP2B1		ATP2B1	27132
ΙΤΔ.ΜΔΡ	rs17037425 1	1n36	11792970 a	9	-0.6215	0.0868	7 76E-12		CLCN6		CLCN6	4177
Ι ΤΔ.ΜΔΡ	rs11072514 1	15024	73008918 a	9 t	-0.396	0.0606	4 34E-10		COX5A	COX5AMPI:SCAMP2:RP25:C15orf17	COX5A	8507
ΙΤΔ.ΜΔΡ	rs3184504 1	12024	110368991 t		0.4469	0.0605	1.68E-12	*****	SH2B3	SH2R3-ATXN2	SH2B3	4818
I TA-MAP	rs11105368_1	12021	88598572 c	a	-0.6845	0.081	6.61E-16		NA		ATP2B1	24597
I TA-MAP	rs4845843 1	1p36	10724172 a	9	0.6025	0 1056	4 87E-08		CAS71	CASZ1	CASZ1	55122
I TA-MAP	rs11105378 1	12021	88614872 t	9	-0.6822	0.0824	2 46E-15		NA	ATP2B1	ATP2B1	40897
I TA-MAP	rs11105328_1	12021	88466521 a	a	0.6393	0.0837	2.84E-13		NA	ATP2B1 WDR51B GAI NT4	WDR51B	22613
I TA-MAP	rs11105379_1	12021	88619304 t	9	0.5869	0.0892	3 22E-10	+++++++++	NA		ATP2B1	45329
I TA-MAP	rs11105358_1	12021	88566273 c	a	-0 4644	0.0613	4 38E-13		ATP2B1	ATP281	ATP2B1	7702
I TA-MAP	rs7922049 1	10a21	63132371 a	9	-0 4993	0.085	2 00E-08	-++	C10orf107	C10orf107	C10orf107	39647
LTA-MAP	rs17037390 1	1p36	11783430 a	a	-0.6015	0.0826	3.37E-12		MTHER	MTHER:NPPA:CLCN6:NPPB:AGTRAP	MTHER	5272
LTA-MAP	rs236710 2	20a13	57127024 t	a	-0.4852	0.0793	5.04E-09		NA	NA	C20orf174	72445
LTA-MAP	rs17630235 1	12g24	111076069 a	q	0.3848	0.062	2.94E-09	+++++++++	NA	TRAFD1;C12orf30	TRAFD1	274
LTA-MAP	rs1378938 1	15a24	72883496 t	č	0.4148	0.0679	5.32E-09	+++++++++++++++++++++++++++++++++++++++	NA	CPLX3:CYP1A2:SCAMP2:CSK:ULK3:LMAN1L	CSK	939
LTA-MAP	rs11014171 1	10p12	18751201 t	с	-0.3892	0.0632	3.88E-09		CACNB2	CACNB2	CACNB2	21683
LTA-PP	rs1717014 3	3p22	41892399 t	с	-0.4739	0.0825	2.22E-08	+	ULK4	ULK4	ULK4	86265
LTA-PP	rs9854833 3	3p22	41750581 t	с	-0.4956	0.082	3.95E-09		ULK4	ULK4	ULK4	228083
LTA-PP	rs1717003	3p22	41912004 t	С	0.4803	0.0824	1.36E-08	++++++++	ULK4	ULK4	ULK4	66660
LTA-PP	rs1717034 3	3p22	41930917 a	g	-0.483	0.0823	1.10E-08	+	ULK4	ULK4	ULK4	47747
LTA-PP	rs2469 6	6p21	43407301 t	с	-0.3519	0.0623	3.88E-08		NA	TTBK1;ZNF318;CRIP3;SLC22A7	ZNF318	4484
LTA-PP	rs6796210 3	3p22	41826722 t	с	0.4691	0.082	2.58E-08	+++++++	ULK4	ULK4	ULK4	151942
LTA-PP	rs1717007 3	3p22	41917203 t	с	-0.4817	0.0824	1.23E-08	+	ULK4	ULK4	ULK4	61461
LTA-PP	rs7634985 3	3p22	41994569 t	с	0.5174	0.0861	4.93E-09	+++++++	NA	ULK4	ULK4	15905
LTA-PP	rs1052501 3	3p22	41900402 t	с	0.4781	0.0823	1.55E-08	+++++++	ULK4	ULK4	ULK4	78262
LTA-PP	rs7622259 3	3p22	41856355 a	t	0.4706	0.0827	2.96E-08	+++++++	ULK4	ULK4	ULK4	122309
LTA-PP	rs2272007 3	3p22	41971140 t	с	-0.4879	0.082	6.77E-09	+	ULK4	ULK4	ULK4	7524
LTA-PP	rs9874975 3	3p22	41739304 a	g	-0.4943	0.0819	4.26E-09		ULK4	ULK4	ULK4	239360
LTA-PP	rs6783001 3	3p22	41837236 a	с	-0.4746	0.0825	2.13E-08	+	ULK4	ULK4	ULK4	141428
LTA-PP	rs2242416 6	6p21	43381582 a	g	0.355	0.0623	2.92E-08	+++++++++	CRIP3	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	329
LTA-PP	rs1716999 3	3p22	41905045 c	g	-0.479	0.0823	1.47E-08	+	ULK4	ULK4	ULK4	73619
LTA-PP	rs7631057 3	3p22	41792955 t	С	-0.4772	0.0822	1.58E-08	+	ULK4	ULK4	ULK4	185709
LTA-PP	rs9865780 3	3p22	41870806 a	g	0.4729	0.0826	2.49E-08	+++++++	ULK4	ULK4	ULK4	107858
LTA-PP	rs1716655 3	3p22	41893710 a	g	-0.4739	0.0825	2.21E-08	+	ULK4	ULK4	ULK4	84954
LTA-PP	rs6802340 3	3p22	41869038 t	с	0.4709	0.0827	2.90E-08	+++++++	ULK4	ULK4	ULK4	109626
LTA-PP	rs1717027 3	3p22	41962924 t	С	-0.488	0.082	6.80E-09	+	ULK4	ULK4	ULK4	15740
LTA-PP	rs6796078 3	3p22	41992824 a	t	-0.5183	0.0861	4.62E-09	+	NA	ULK4	ULK4	14160
LTA-PP	rs6781326 3	3p22	41752032 t	С	0.4963	0.0817	3.28E-09	+++++++++	ULK4	ULK4	ULK4	226632
LTA-PP	rs7632387 3	3p22	41828165 t	С	-0.4687	0.0821	2.67E-08	+	ULK4	ULK4	ULK4	150499
LTA-PP	rs1624519 3	3p22	41959804 a	g	0.4838	0.0823	1.05E-08	+++++++	ULK4	ULK4	ULK4	18860
LTA-PP	rs809930 3	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.	Р	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-PP	rs6776724 3p22	41816274 a	g	0.4692	0.0823	2.79E-08	+++++++-	ULK4	ULK4	ULK4	162390
LIA-PP	rs6/91806 3p22	41864999 t	С	-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
LIA-PP	rs1/1/01/ 3p22	41890620 a	C	0.4/3/	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	С	-0.4915	0.0819	5.06E-09		ULK4	ULK4	ULK4	243035
LTA DD	rs9850310 3p22	41800102 t	C	0.4708	0.0827	2.92E-08	+++++++-	ULK4	ULK4	ULK4	112002
LTA-PP	rs12/05390 /q22	106198013 a	g	0.5865	0.0759	5.40E-14	+++++-+++	NA	NA	PIK3CG	95146
LTA DD	rs/646144 3p22	41828129 a	t	-0.4080	0.0821	2.69E-08	+	ULK4	ULIX4	ULK4	150535
	159850088 3p22	41830480 L	g	-0.4940	0.0847	1.29E-08	+	ULK4	ULIVA	ULK4	143178
	ro1717006 2p22	41009444 (	0	0.4717	0.0020	1 20E 00	++++++++	ULK4		ULK4	62212
	re0000345 4e28	41910402 d	L C	0.4791	0.002	1.29E-00	+++++++	CAC71	0.021	CAR74	03212
	ro1716075 2p22	41026010 +		0.421	0.0703	1.01E.09	(	ULKA		ULKA	42654
	rc17209575 7c22	106106699 0	с а	0.4037	0.0022	1.01E-00	+	NA	ULN4 NA	DIKACG	45054
	re1717020 3p22	/1056/0/ a	y c	0.0732	0.073	9.73E.09	++++++++++	LILKA		LILKA	22170
I TA-PP	re7620767 3p22	42018513 t	0	0.4049	0.002	2 75E-08	********	NA			39849
I TA-PP	rs284277 1n36	10713384 a	9	-0 4142	0.073	3 27E-08	2	CAS71	CAS71	CAS71	65910
I TA-PP	re17062109 3p22	41785368 t	c	-0.4773	0.082	1.46E-08				ULK4	193296
I TA-PP	rs1716984 3p22	41940536 a	0	0.4835	0.0823	1.46E-08		ULK4		ULK4	38128
I TA-PP	rs9866759 3p22	41733422 t	9	0.483	0.0821	9.91E-09	+++++++++	ULK4		ULK4	245242
I TA-PP	rs1716653 3p22	41950602 a	č	0.4838	0.0823	1.04E-08	++++++++	ULK4		ULK4	28062
I TA-PP	rs2128834 3p22	41837649 a	a	0.4694	0.0822	2.68E-08	++++++++	ULK4		ULK4	141015
I TA-PP	rs6599168 3p22	41725327 t	c C	0.5163	0.0865	6 11E-09	++++++++++	ULK4		ULK4	253337
LTA-PP	rs1716694 3p22	41961403 t	a	0.4864	0.0823	8.67E-09	++++++++-	ULK4		ULK4	17261
LTA-PP	rs1613233 3p22	41920148 a	a	-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 7g22	106192878 t	c	0.5759	0.0753	9.52E-14	+++++-+++	NA	NA	PIK3CG	100281
LTA-PP	rs11760498 7a22	106206208 a	a	0.4499	0.0803	4.89E-08	+++++-+++	NA	NA	PIK3CG	86951
LTA-PP	rs10212536 3p22	41802030 a	q	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	с	-0.4731	0.0826	2.43E-08	+	ULK4	ULK4	ULK4	107767
LTA-PP	rs1615243 3p22	41940238 t	С	0.4836	0.0823	1.05E-08	+++++++	ULK4	ULK4	ULK4	38426
LTA-PP	rs12536419 7q22	106206532 a	С	-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	С	-0.4772	0.0819	1.43E-08	+	ULK4	ULK4	ULK4	78359
LTA-PP	rs9847006 3p22	41730363 t	с	0.4844	0.0823	1.00E-08	+++++++++	ULK4	ULK4	ULK4	248301
LTA-PP	rs13087502 3p22	41990114 t	С	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	С	-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	С	0.3555	0.0625	3.04E-08	+++++++++	SLC22A7	CRIP3;SLC22A7;TTBK1;ZNF318	SLC22A7	3032
LTA-PP	rs939558 3p22	41951044 a	С	0.4839	0.0823	1.04E-08	+++++++-	ULK4	ULK4	ULK4	27620
LTA-PP	rs17477177 7q22	106199094 t	С	-0.589	0.0763	5.61E-14	+	NA	NA	PIK3CG	94065
LIA-PP	rs10948071 6p21	43388691 t	с	-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
LIA-PP	rs4973995 3p22	419064// t	C	-0.4796	0.0823	1.42E-08	+	ULK4	ULK4	ULK4	/218/
LTA-PP	rs9825741 3p22	41/36832 a	t	0.49	0.0817	5.25E-09	+++++++++	ULK4	ULK4	ULK4	241832
LTA DD	159866092 3p22	418/09/1 a	c	0.4734	0.0826	2.38E-08	+++++++	ULK4	ULN4	ULK4	10/093
LTA DD	150599176 3p22	41703490 t	g	0.4973	0.0818	3.23E-09	+++++++++++++++++++++++++++++++++++++++	ULK4		ULK4	210108
	150001021 3p22	+1//0845 a	c	0.4941	0.0821	4.03E-09	******	ULK4		ULK4	201018
	159630469 3p22	41/3/339 a	g	0.4917	0.0819	4.90E-09	+++++++++++++++++++++++++++++++++++++++	ULK4		ULK4	241120
	re6002560 2p22	41782452 L	c	-0.4769	0.082	1.39E-08	+				170100
	150603000 3p22	41/99484 a	g	0.4708	0.0822	1.04E-08	++++++++	ULK4		ULK4 SLC2247	2102
	re1716657 2622	41893460 +	с С	0.3030	0.0027	3.32E-00 2.24⊑ 00		ULKA	UNI GOLOZZAT, FEDRI, ZNEGIO	ULKA	85204
	re0846634 2e22	41960052	0	0.4/3/	0.0020	2.240-08	********			ULK4	100611
	re7650227 2622	41769941 +	9	0.5008	0.0829	2.220-00		ULK4			208723
	re100/157 3p22	41703341 1	g	0.000	0.0021	2.04E-03		ULK4			106178
	re9875107 3p22	41797317 a	9 t	0.4767	0.0020	1.64E-00	+	ULK4		ULK4	181347
	re11023562 3p22	41735335 t	0	0.4017	0.0022	5.06E.09	*******	ULK4			2/3320
LTA-PP	rs7626217 3n22	41817419 a	9	0.47	0.0821	2.52E-08	++++++++	ULK4	UI K4	ULK4	161245
I TA-PP	rs17060961 3p22	41738715 a	9	0 4946	0.0819	4 19E-09	+++++++++	ULK4	UI K4	ULK4	239949
LTA-PP	rs794902 3n22	42000943 t	с Э	-0.5158	0.0861	5.47E-09		NA	ULK4	ULK4	22279
I TA-PP	rs6599167 3p22	41725264 a	a	0.5164	0.0866	6.34E-09	+++++++++	UI K4	UI K4	ULK4	253400
LTA-PP	rs12635286 3p22	42026840 t	e C	0.4858	0.0867	4.95E-08	++++++++-	NA	ULK4	ULK4	48176
LTA-PP	rs1716642 3p22	41940869 a	ć	-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	a	0.4824	0.0823	1.17E-08	++++++++-	ULK4	ULK4	ULK4	51945
LTA-PP	rs1716693 3p22	41960604 t	č	0.4857	0.0823	9.18E-09	+++++++	ULK4	ULK4	ULK4	18060
LTA-PP	rs17063599 3p22	41836680 t	с	-0.4743	0.0825	2.16E-08	+	ULK4	ULK4	ULK4	141984
LTA-PP	rs2272006 3p22	41972063 t	с	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	с	-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	с	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	с	0.4966	0.0816	3.18E-09	+++++++++	ULK4	ULK4	ULK4	217651
LTA-PP	rs13325965	5 3p22	41889946 t	g	-0.4752	0.0825	2.04E-08	+	ULK4	ULK4	ULK4	88718
LTA-PP	rs9852303	3p22	41734529 t	с	-0.483	0.0819	9.49E-09		ULK4	ULK4	ULK4	244135
LTA-PP	rs794899	3p22	42003726 t	С	-0.5166	0.0861	5.22E-09	+	NA	ULK4	ULK4	25062
LTA-PP	rs13225723	3 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	с	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.

International         International        International        Internati								r^2 to	,		eSNP P					type of eQTL		Probe	Probe
numbernumbe	Ir	dexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	index	eSNPid	Tissue	value	Chr	B36pos	ArrayID	Transcript	(cis or trans)	Beta Allele	Chromosome	Position
numbernumbe	rs	13306561	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
Display         Display <t< td=""><td>rs</td><td>13306561</td><td>DBP/SBP/MAP</td><td>MTHFR</td><td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td><td>1</td><td>IndexSNP</td><td></td><td>rs13306561</td><td>LCL (MuTHER)</td><td>1.91E-16</td><td>1</td><td>11788391</td><td>ILMN_1734830</td><td>MTHFR</td><td>cis</td><td></td><td></td><td></td></t<>	rs	13306561	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			
INTEGEINTEG	rs	13306561	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	MTHER	cis	0.63		
Intractional problem beamImage of the problem be	rs	13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Skin (MuTHER)	2.36E-06	1	11788391	ILMN_1734830	MTHER	cis			
number behavior         number beh	rs	13306561	DBP/SBP/MAP	MTHFR	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	IndexSNP		rs13306561	Subc adipose (MuTHER)	5.98E-06	1	11788391	ILMN 1734830	MTHER	cis			
InstanceInstan	rs	13306561	DBP/SBP/MAP	MTHER	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
m1386000         m13860000         m13860000         m138600000         m1386000000000000000000000000000000000000	rs	13306561	DBP/SBP/MAP	MTHER	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
Inside         Image         Image <t< td=""><td>rs</td><td>13306561</td><td>DBP/SBP/MAP</td><td>MTHER</td><td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td><td>1</td><td>LDproxy(CEU-H3)</td><td>1</td><td>rs7537765</td><td>Whole blood (CHARGE)</td><td>3.23E-78</td><td>1</td><td>11809890</td><td>3990477</td><td>MTHFR,C1orf167</td><td>cis</td><td>18.72 G</td><td>1</td><td>11769609</td></t<>	rs	13306561	DBP/SBP/MAP	MTHER	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
n111       Display Autor       NPPE approx Autor Construment period and a set of	rs	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHFR:NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	LCL (MuTHER)	5.77E-19	1	11806318	ILMN 1734830	MTHER	cis			
number         number        number </td <td>rs</td> <td>13306561</td> <td>DBP/SBP/MAP</td> <td>MTHER</td> <td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td> <td>1</td> <td>LDproxy(CEU-H3)</td> <td>1</td> <td>rs2050265</td> <td>LCL (MuTHER)</td> <td>8.49E-19</td> <td>1</td> <td>11802286</td> <td>ILMN 1734830</td> <td>MTHER</td> <td>cis</td> <td></td> <td></td> <td></td>	rs	13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	LCL (MuTHER)	8.49E-19	1	11802286	ILMN 1734830	MTHER	cis			
number	rs	13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	LCL (MuTHER)	2.10E-18	1	11809890	ILMN 1734830	MTHER	cis			
n1313600       IDP/SPD AM       NPROPERA ALL/CONSTITUTORPARAGENA       1       1       0.000076       1.1111111       1.111111       MTRFR       6.1       0<	rs	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHFR:NPPA:AGTRAP	1	LDproxv(CEU-H3)	1	rs12567136	Monocytes	3.57E-14	1	11806318	_	MTHER	cis			
m1310600       m1000000000000000000000000000000000000	rs	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHFR:NPPA:AGTRAP	1	LDproxv(CEU-H3)	1	rs7537765	Monocytes	1.14E-13	1	11809890		MTHER	cis			
m1338883       pipeline       pipeline <th< td=""><td>rs</td><td>13306561</td><td>DBP/SBP/MAP</td><td>MTHER</td><td>NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP</td><td>1</td><td>LDproxy(CEU-H3)</td><td>1</td><td>rs17037429</td><td>Monocytes</td><td>2.33E-13</td><td>1</td><td>11796374</td><td></td><td>MTHER</td><td>cis</td><td></td><td></td><td></td></th<>	rs	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	1	rs17037429	Monocytes	2.33E-13	1	11796374		MTHER	cis			
m1313650       pipelysep Ass_CCONSMITERSPERATION       1       Dispress/Link       1       Instant       pipelysep Ass_CCONSMITERSPERATION       0       0       0         m1313660       pipelysep Ass_CCONSMITERSPERATION       1       Dispress/Link       1       m1313660       Dispress/Link       m1313660       m13136600       m13136600       m13136600<	r	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA:AGTRAP	1	IDproxy(CEU-H3)	1	rs7537765	PaxGeneWholeBlood(Mehta)	8.44E-10	1	11809890	ILMN 1731434	MTHER	cis			
n13130501       D0P3(RPMAP_HITEN       PMCR0(PMAP_ALT)(CMAP_HITEN,PPAA,ADTAP       1       D0P3(RUM_P)       D0P3(RUM_P)       D0P3(RUM_P)       D0P3(RUM_P)       D0P3(RUM_P)	r	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Whole blood (PaxGene) in Japanese	1.20E-09	1	11806318	A 23 P400081	MTHER	cis	-0.63		
m1338350 1097/89/Map       M109780294-A3L CLOWARTHENDERSACTUAD       1       1111 10727 A 22, P60001       M10FF       05       0.0       0         m1338550 1097/89/Map       M10PS Note-M10004       M10F       11110727 A 22, P60001       M10FF       05       0 <t< td=""><td>rs</td><td>13306561</td><td>DBP/SBP/MAP</td><td>MTHER</td><td>NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP</td><td>1</td><td>LDproxy(CEU-H3)</td><td>1</td><td>rs2050265</td><td>Whole blood (PaxGene) in Japanese</td><td>1 20E-09</td><td>1</td><td>11802286</td><td>A 23 P400081</td><td>MTHER</td><td>cis</td><td>0.63</td><td></td><td></td></t<>	rs	13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Whole blood (PaxGene) in Japanese	1 20E-09	1	11802286	A 23 P400081	MTHER	cis	0.63		
111100001 DBP/3BP/MAP MITHE       NUMER       NUMER <t< td=""><td>-</td><td>13306561</td><td></td><td>MTHER</td><td>NDDB:NDDA-AS1:CLCN6:MTHER:NDDA-AGTRAD</td><td>1</td><td>LDproxy(CEU-H3)</td><td>1</td><td>rs3753584</td><td>Whole blood (PayGene) in Japanese</td><td>1 205-09</td><td>1</td><td>11787173</td><td>A 23 P400081</td><td>MTHER</td><td>cis</td><td>0.63</td><td></td><td></td></t<>	-	13306561		MTHER	NDDB:NDDA-AS1:CLCN6:MTHER:NDDA-AGTRAD	1	LDproxy(CEU-H3)	1	rs3753584	Whole blood (PayGene) in Japanese	1 205-09	1	11787173	A 23 P400081	MTHER	cis	0.63		
13130501 Dely/Se/Map MIRE       NPRS NMA_ASCILLOX_MITER_EVPLAGTING       1       1.000000 (Levis)       1.1000000 (Levis)       1.1000000 (Levis)       0.02	1.	13306561		MTHER	NPPB;NPPA-AS1;CLCN6;MTHER;NPPA;AGTRAP	1	LDproxy(CEU_H3)	1	rs12567136	PayGeneWholeBlood(Mehta)	1.202-09	1	11806318	ILMN 1731/3/	MTHER	cis	0.05		
111100001       1000000       1000000       1000000       1000000       1000000       10000000       10000000       10000000       1000000000       10000000000000       1000000000000000000000000000000000000		12206561		MTHED	NDDB-NDDA AS1;CLCN6;MTHER:NDDA-AGTRAD	1	LDproxy(CEU H2)	1	rc7527765	Whole blood (PayGone) in Japanese	2 165 09	1	110000000	A 22 D400091	MTHEP	cis	0.62		
11313551         DepS/10/AP         Image Notes         Market         Markt         Market         Market         <	1.2	12206561	DBD/SBD/MAP	MTUED	NPPB,NPPA-AS1,CLCNG,MTHER,NPPA,AGTRAP	1	LDproxy(CEU H2)	1	137537765	Schodt iver	1.275.07	1	11000000	A_23_F400081	CLONE	cis	0.02		
11313651         DBPS/MPA MITHER         VPS/MPA ALSLC/LSKM/THR-FMPA/AGTAB         1         LDPPS/UELM1         1         2202025         Start (Mu/TER)         1.50         1.1023000         DEF/MAR         MTHR         Col         Col        Col        Col	12	12206561	DBD/SBD/MAD		NPPB,NPPA-ASI,CLCNO,WITHER,NPPA,AGTRAP	1	LDproxy(CEU-H3)	1	15/35/703	School (Muther)	1.372-07	1	11005050	U MANI 1724920	MTHER	cis			
1133555         DBPS/DPAIL         UPPS/DPAIL         UPPS/DPAIL        UPPS/DPAIL        UPPS/DPAIL </td <td>12</td> <td>12206561</td> <td>DBP/SBP/WAP</td> <td></td> <td>NPPB,NPPA-AS1,CLCN0,WITHER,NPPA,AGTRAP</td> <td>1</td> <td>LDproxy(CEU_H2)</td> <td>1</td> <td>1512307150</td> <td>Skin (MuTHER)</td> <td>1.442-07</td> <td>1</td> <td>11000510</td> <td>ILIVIN_1734830</td> <td></td> <td>cis</td> <td></td> <td></td> <td></td>	12	12206561	DBP/SBP/WAP		NPPB,NPPA-AS1,CLCN0,WITHER,NPPA,AGTRAP	1	LDproxy(CEU_H2)	1	1512307150	Skin (MuTHER)	1.442-07	1	11000510	ILIVIN_1734830		cis			
L3335631       Dery Syn / Jour Minite       Minite       Control Lines       Minite       Minit       Minite       Minite </td <td>12</td> <td>13300301</td> <td>DBP/SBP/WAP</td> <td>MILLER</td> <td>NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP</td> <td>1</td> <td>LDproxy(CEU-H3)</td> <td>1</td> <td>152030203</td> <td>Skin (MuTHER)</td> <td>1.50E-07</td> <td>1</td> <td>11802280</td> <td>ILIVIN_1734830</td> <td>MTUER</td> <td>cis</td> <td></td> <td></td> <td></td>	12	13300301	DBP/SBP/WAP	MILLER	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	152030203	Skin (MuTHER)	1.50E-07	1	11802280	ILIVIN_1734830	MTUER	cis			
11333550 DB/S/2/MAM       Imitery       Imps/NPA AS1_LCL/MM/HTMR/NPPA/AS1/LC/MM/HTMR/NPPA/AS1/LC/MM/HTMR/NPA/AS1/LC/MM/HTMR/HTMA/HTMR/LC/MM/HTMR/NPA/AS1/LC/MM/HTMR/NPA/AS1/LC/MM/HTM	12	12206561	DBP/SBP/IVIAP		NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	15/35/703	Skin (MuTHER)	5.30E-07	1	11005050	ILIVIN_1734650		cis			
B1330500       DBP/SP/AAD       MITHER       NPPB/SP/AAS_LLINEW_IMPROPERAGINATION       I       Lipprov(CEV-HB)       I       International (Control of Control of Contro of Control of Control of Control of Control of Control	rs	13300501	DBP/SBP/IVIAP	MITHER	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	1512507130	Subcadipose (MuTHER)	5.39E-07	1	11800318	ILIVIN_1734830	MIHER	CIS			
H130860       DBP       <	rs	13300501	DBP/SBP/IMAP	MINER	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	152050265	Subcadipose (MUTHER)	0.03E-07	1	11802280	ILIVIN_1734830	MIHER	cis			
F11308601 DBP/3BP/MAP MHTRR       NPPER/PMA-ASILLORM/INTER/PMPAAGTRAP       1       Diprov(CLU-H3)       1       r737785       UVEr(urersmalling)       1       Diprov(CLU-H3)       1       r737785       UVEr(urersmalling)       1       Diprov(CLU-H3)       1       r737785       UVEr(urersmalling)       1       Diprov(CLU-H3)	rs	13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs/53//65	Subc adipose (MUTHER)	8.64E-07	1	11809890	ILMIN_1/34830	MIHER	CIS			
Initiation       Image	rs	13306561	DBP/SBP/MAP	MIHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs/53//65	Liver(Greenawait)	1.02E-06	1	11809890	10023816366	CLUND	CIS			
In1303600, U0P/SBV/AAM       INTER       Interprotecture       Int	rs	13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs/53//65	Lymph	1.6/E-06	1	11809890	GI_12025672-A	CLCN6	CIS			
n13303603 DBP/SBP/MAM MTHER       NPPBR/PA-A31;CLCK6R/MTHER/NPPA,GATTAP       1       Diproxy(EU+H3)       0.37       n13737300       Minhe biood (CHARGE)       2,88-7       1       I1733430       3390477       MTHER,CLOTIO7       cis       1.5.8 G       1       11796909         n13306501 DBP/SBP/MAM MTHER       NPPBR/PA-A51;CLCK6R/MTHER/NPPA,GATTAP       1       Diproxy(EU+H3)       0.37       n13737300       LCL (MUTHER)       5.45E-18       1       11733430       MIHER       cis       0.4       0.4         n13306501 DBP/SBP/MAM MTHER       NPPBR/PA-A51;CLCK6R/MTHER/NPPA,GATTAP       1       Diproxy(EU+H3)       0.37       n13737300       Whole biood (PaxGene) in Japanese       1.0E       0.63 <td< td=""><td>rs</td><td>13306561</td><td>DBP/SBP/MAP</td><td>MTHFR</td><td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td><td>1</td><td>LDproxy(CEU-H3)</td><td>1</td><td>rs12567136</td><td>Dendritic cells after Mycobacetrium tube</td><td>2.41E-06</td><td>1</td><td>11806318</td><td></td><td>MTHER</td><td>cis</td><td></td><td></td><td></td></td<>	rs	13306561	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		MTHER	cis			
n13306501 DBP/SBP/MAP MTHR       NPER_NPAA.51;CLCNS,MTHR;NPPAA,GTRAP       1       1Dproxy(CEU-H8       0.97       rs13203551 DBP/SBP/MAP MTHR       NPER_NPAA.51;CLCNS,MTHR;NPPAA,GTRAP       1       Dproxy(CEU-H8       0.97       rs1327504       Subc adipose (MUTHER)       5.166-07       1       11783450 ILMN_173480       MTHR       cis	rs	13306561	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
rs1330650       DBP/SBP/MAP       MTHR       NPPS/NPPA       NPS/NPPA       NPS/NPAA	rs	13306561	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
rs1330551 DBP/SBP/MAP MTHFR       NPPBR/NPPA-AS1;CLCN6/MTHFR:NPPAAGTRAP       1       LDproxy(CEU+B)       0.97       rs1330551 DBP/SBP/MAP MTHFR       NPPBR/NPPA-AS1;CLCN6/MTHFR:NPPAAGTRAP       1       Dproxy(CEU+B)       0.97       rs1330551 DBP/SBP/MAP MTHFR       NPBR/NPPA-AS1;CLCN6/MTHFR:NPPAAGTRAP       1       Dproxy(CEU+B)       0.97       rs1330550 UP/SBP/MAP MTHFR       NPBR/NPPA-AS1;CLCN6/MTHFR:NPPAAGTRAP       1       Dproxy(CEU+B)       0.97       rs1330550 DBP/SBP/MAP MTHFR       NPBR/NPPA-AS1;CLCN6/MTHFR:NPPAAGTRAP       1       Dproxy(CEU+B)       0.97       rs1330550 DBP/SBP/MAP MTHFR       NPBR/NPPA-AS1;CLCN6/MTHFR:NPPAA	rs	13306561	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			
rs1330551 DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1330551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1335551       DDS3551       DBP/SBP/MAP MTHFR       NPPB;NPPA-AS1;LCLOS;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU+B)       0.57       rs1335551       DDS3551       D	rs	13306561	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			
r13303651 DBP/SBP/MAP MTHFR       NPPEN.PPA-A51;CLCN6;MTHFR;NPPA,A5TRAP       1       LDproxy(CEU+B)       0.57       r13737504       Whole blood (PaxGene) in Japanese       1.20E-09       1       11735365 A22_P400081       MTHFR       cis       0.63         r13300551 DBP/SBP/MAP MTHFR       NPPA-A51;CLCN6;MTHFR;NPPA-A5TRAP       1       LDproxy(CEU+B)       0.57       r1373730       Skin (MUTHER)       5.16E-07       1       11738340 ILMN_1734830       MTHFR       cis       0.63         r13300551 DBP/SBP/MAP MTHFR       NPPA-A51;CLCN6;MTHFR;NPPA-A51;CLCN6;MTHFR;NPPA,A5TRAP       1       Dproxy(CEU+B)       0.57       r13737504       Skin (MUTHER)       7.512-07       1       11783450       MTHFR       cis       0       0         r13300551 DBP/SBP/MAP MTHFR       NPPENPA-A51;CLCN6;MTHFR;NPPA,A5TRAP       1       Dproxy(CEU+B)       0.57       r13737504       View (SanDB)       5.54E-07       1       11785365       GP116       cis       0       0       0       0       r13306510       DBP/SBP/MAP MTHFR       NPPENPA-A51;CLCN6;MTHFR;NPPA,AGTRAP       1       Dproxy(CEU+B)       0.57       r13735704       Viemph       1.54E-05       1       11785365       G12025672-A       CLCN6       cis       0       0       113306510       DBP/SBP/MAP MTHFR       NPPENPA-A51;CLCN6;MTHFR;NPPA,AGT	rs	13306561	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		
n1330651 DB/SB/MAP MTHR       NPPB,NPPA-A51;CLONS,MTHR;NPPA,AGTRAP       1       LDprox/(CEU+B)       0.97       r1307390       Sub adjoose (MUTHER)       2.66E-07       1       11783430 (LMN,174830       MTHR       cis       Cis         r13306551 DB/SB/MAP MTHR       NPPB,NPPA-A51;CLONS,MTHR;NPPA,AGTRAP       1       Dprox/(CEU+B)       0.97       r13737500       Sub adjoose (MUTHER)       6.66E-07       1       11783430 (LMN,174830       MTHR       cis       C <td< td=""><td>rs</td><td>13306561</td><td>DBP/SBP/MAP</td><td>MTHFR</td><td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td><td>1</td><td>LDproxy(CEU-H3)</td><td>0.97</td><td>rs17367504</td><td>Whole blood (PaxGene) in Japanese</td><td>1.20E-09</td><td>1</td><td>11785365</td><td>A_23_P400081</td><td>MTHFR</td><td>cis</td><td>0.63</td><td></td><td></td></td<>	rs	13306561	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		
rs1330651 DBP/SBP/MAP       NTHFR       NPPEN/NPA-AS1;CLON6/MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3       0.97       rs13705704       Sub alloyes (MUTHER)       6.16E-07       1       11783430       IMTHFR       cis          rs1330651 DBP/SBP/MAP       MTHFR       NPPE,NPPA-AS1;CLON6/MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3       0.97       rs13767504       Sub allopses       NUTHER       7.50E-07       1       11785365       LLMN_1734830       MTHFR       cis           rs13306561 DBP/SBP/MAP       MTHFR       NPPE,NPPA-AS1;CLON6/MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3       0.97       rs13767504       Luver (scanDB)       9.54E-07       1       11785365       GBP/SBP/MAP       cis </td <td>rs</td> <td>13306561</td> <td>DBP/SBP/MAP</td> <td>MTHFR</td> <td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td> <td>1</td> <td>LDproxy(CEU-H3)</td> <td>0.97</td> <td>rs17037390</td> <td>Subc adipose (MuTHER)</td> <td>2.66E-07</td> <td>1</td> <td>11783430</td> <td>ILMN_1734830</td> <td>MTHFR</td> <td>cis</td> <td></td> <td></td> <td></td>	rs	13306561	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			
In13306561       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330561       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPA;AGTRAP       1       Diproxy(CEU-H3)       0.97       rs1330561       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPA;AGTRAP       1       Diproxy(CEU-H8)       0.97       rs1330561       DBP/SBP/MAP       MTHFR       NPB;NPA-AS1;CLN6;MTHFR;NPA;AGTRAP       1       Diproxy(CEU-H8)       0.97       rs1330561       DBP/SBP/MAP       MTHFR       NPB;NPA-AS1;CLN	rs	13306561	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       NPPE;NPPA-A51;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3       0.97       rs17367504       Skin (MUTHER)       7.50E-07       1       11785365       CPR116       cis       C         rs13306561 DBP/SBP/MAP MTHFR       NPPE;NPPA-A51;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3       0.97       rs17367504       Lvmph       1.54E-05       1       11785365       GPR116       cis       C	rs	13306561	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       rs13367504       Lymph       1.54E-05       1       117853656       GPR116       cis       Cis       Cis         rs13306561 DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3       0.97       rs13307504       Lymph       1.54E-05       1       11785365 G102594633       HS00048903       cis       Cis </td <td>rs</td> <td>13306561</td> <td>DBP/SBP/MAP</td> <td>MTHFR</td> <td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td> <td>1</td> <td>LDproxy(CEU-H3)</td> <td>0.97</td> <td>rs17367504</td> <td>Skin (MuTHER)</td> <td>7.50E-07</td> <td>1</td> <td>11785365</td> <td>ILMN_1734830</td> <td>MTHFR</td> <td>cis</td> <td></td> <td></td> <td></td>	rs	13306561	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       Upproxy(CEU-H3       0.97       rs13367504       omental       7.212-05       1       11785365 G1_202574.32       CLCN6       cis       cis       cis         rs13306561       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Upproxy(CEU-H3       0.97       rs17367504       omental       7.216-05       1       11785365 G1_202574:380       KOTK       cis           rs13306561       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Upproxy(CEU-H3       0.97       rs1737524       Blood(Fehrman et al)       1.062-77.19       1       11818262 LUM_174830       MTHFR       cis	rs	13306561	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       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3)       0.97       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3)       0.947       rs1330651       DBI/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3)       0.947       rs13307452       Subcadipose (MuTHER)       1.56E-07       1       11818262       LUMA 1744330       MTHFR       Cis       C	rs	13306561	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-1kg)       0.97       rs1330551       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-1kg)       0.947       rs1330551       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-1kg)       0.947       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-1kg)       0.853       rs1330651       DBP/SBP/MAP       MTHFR       NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-1kg)       0.853       rs1330551       DBP/SBP/MAP       MTHFR	rs	13306561	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-1kg)       0.947       rs1330521       CM (WTHER)       6.00E-24       1       11818262 LLMM_174830       MTHR       cis       distance         rs13306561       DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-1kg)       0.947       rs1330651       Sin (MTHER)       11818262 LLMM_174830       MTHFR       cis       0.66       1       11818262       LDproxy(CEU-1kg)       0.947       rs1330651       DBP/SBP/MAP       MTHFR       cis       0.66       1       1100000       1100000       11100000       111100000       11100000       11100000       11100000       11100000       11100000       11100000       11100000       11100000       11100000       11100000       111000000       111000000       111000000       111000000       111000000       111000000       111000000       111000000       111000000       1110000000       1110000000       1110000000       1110000000       1110000000       1110000000       1110000000       1110000000000       11100000000000       111000000000000000000       1110000000000000000000000000000000000	rs	13306561	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;1.90	1	11785365	3990477;385013	6 MTHFR;AL953897.6;0	cis			
rs13306561 DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Upproxy(CEU-1kg)       0.947       rs17037452       Whole blood (PaxGene) in Japanese       1.20E-09       1       11818262 (JA_23_P40008)       MTHFR       cis       0.63         rs13306561 DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       Upproxy(CEU-1kg)       0.947       rs17037452       Skin (MUTHER)       3.72E-09       1       11818262 (LUM_1734830       MTHR       Cis       - <td>rs</td> <td>13306561</td> <td>DBP/SBP/MAP</td> <td>MTHFR</td> <td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td> <td>1</td> <td>LDproxy(CEU-1kg)</td> <td>0.947</td> <td>rs17037452</td> <td>LCL (MuTHER)</td> <td>6.00E-24</td> <td>1</td> <td>11818262</td> <td>ILMN_1734830</td> <td>MTHFR</td> <td>cis</td> <td></td> <td></td> <td></td>	rs	13306561	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       Upproxy(CEU-1kg)       0.947       rs17037452       Skin (MuTHER)       3.72E-09       1       11818262 [LIML]1734830       MTHFR       cis       cis <td>rs</td> <td>13306561</td> <td>DBP/SBP/MAP</td> <td>MTHFR</td> <td>NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP</td> <td>1</td> <td>LDproxy(CEU-1kg)</td> <td>0.947</td> <td>rs17037452</td> <td>Whole blood (PaxGene) in Japanese</td> <td>1.20E-09</td> <td>1</td> <td>11818262</td> <td>A_23_P400081</td> <td>MTHER</td> <td>cis</td> <td>0.63</td> <td></td> <td></td>	rs	13306561	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	MTHER	cis	0.63		
rs13306551 DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;cLCN6;MTHFR;NPPA;AGTAPA       1       Upproxy(CEU-1kg       0.947       rs17037452       Sub calipose (MuTHER)       1.56E-07       1       11818262 ILMN_1741594       CLCN6       ctc	rs	13306561	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;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-Hg) 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;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-Hg) 0.853 rs17037452 Whole blood (CHARGE) 7.97E-95 1 1792970 1LMN_173430 MTHFR cis - 20.66 A 1 1179690 rs13306561 DBP/SBP/MAP MTHFR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-Hg) 0.853 rs17037425 LCL(MUTHER) 5.98E-20 1 11792970 1LMN_173430 MTHFR cis - 0.63 - 0.6	rs	13306561	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;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Whole blood (CHARGE) 7.97E-95 1 11792970 LDML_174830 MTHFR cis 20.66 A 1 11769609 rs13306561 DBP/SBP/MAP MTHFR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 LCL (MUTHER) 5.98E-20 1 11792970 LDML_174830 MTHFR cis -0.63 -0.64 -0.65 -0.	rs	13306561	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       CLC (MuTHER)       5.98E-20       1       11792970       ILMP1_274830       MTHFR       cis         rs13306561 DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3)       0.853       rs17037425       Whole blood (PacGene) in Japanese       1.20E-09       1       11792970       L2M_400281       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)       0.82-08       1       11792970       ILMP124M30       MTHFR       cis       -0.63         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       ILMP124300       MTHFR       cis       -0.63         rs13306561 DBP/SBP/MAP       MTHFR       NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP       1       LDproxy(CEU-H3)       0.853       rs17037425       LVUC(Licago)       0.0001275       1       11792970       ILMP124707A       2.22F04       cis       -0.65	rs	13306561	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 MTHR 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 MTHR cis -0.63 rs13306561 DBP/SBP/MAP MTHR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Site adjose (MuTHER) 2.2E-08 1 11792970 ILMN_1734830 MTHR cis -13306561 DBP/SBP/MAP MTHR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Liver(Uchicago) 0.0001727 1 11792970 A_24_P402374 CLCN6;MTHR cis -13306561 DBP/SBP/MAP MTHFR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Liver(Uchicago) 0.0001727 1 11792970 A_24_P302374 CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;AS1;CLCN6;MTHFR;NPA;NPA;AS1;CLCN6;MTHFR;NPA;AS1;NCN6;MTHFR;NPA;	rs	13306561	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	MTHER	cis			
rs13306561 DBP/SBP/MAP MTHFR NPP8;NPA-AS1;CLCN6;MTHFR;NPP4;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Skin (MuTHER) 1.03E-08 1 11792970 LLMN_1734830 MTHFR cis rs13306561 DBP/SBP/MAP MTHFR NPP8;NPA-AS1;CLCN6;MTHFR;NPP4;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Subc adjpose (MuTHER) 2.22E-08 1 11792970 LLMN_1734830 MTHFR cis rs13306561 DBP/SBP/MAP MTHFR NPP8;NPA-AS1;CLCN6;MTHFR;NPP4;AGTRAP 1 LDproxy(CEU-H3) 0.853 rs17037425 Liver(Uchicago) 0.0001275 1 11792970 LLMN_173430 MTHFR cis rs13306561 DBP/SBP/MAP MTHFR NPP8;NPA-AS1;CLCN6;MTHFR;NP4;AGTRAP 1 LDproxy(CEU-H3) 0.731 rs755314 LCL(M;MTHFR;NP4;AGTRAP 1 LDproxy(CEU-H3) 0.731 rs755314 LCL(M;MTHFR;N4) 2.97E-24 1 11785736 LMP317425 LCM	rs	13306561	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 MTHR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.83 rs17037425 Subc adipose (MuTHER) 2.22E-08 1 11792970 LUM_1734830 MTHR cis rs13306561 DBP/SBP/MAP MTHR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.83 rs17037425 Liver(UChicago) 0.00017275 1 11792970 A_24_P302374 CLCN6 cis rs13306561 DBP/SBP/MAP MTHR NPPB;NPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.713 rs753194 LCL (MuTHER) 2.97E-24 1 11786736 LUMN 1734830 MTHR cis	rs	13306561	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;APA-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;APA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.713 rs7553194 LCL (MuTHER) 2.975-24 1 11786736 ILUM 1734830 MTHFR cis	rs	13306561	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;APA-AS1;CLCN6;MTHFR;NPPA;AGTRAP 1 LDproxy(CEU-H3) 0.713 rs7553194 LCL (MuTHER) 2.97E-24 1 11786736 ILUMN 1734830 MTHFR cis	rs	13306561	DBP/SBP/MAP	MTHER	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			
	rs	13306561	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			

IndoxSND	Traite	InPofGon	PafCanas60kh	Locust	Index/ID status	r^2 to	Tissue	eSNP P	Chr	P26nos	ArroyID	Transcript	type of eQTL	Rota Allolo	Probe	Probe
rc12206561		MTUED	NDDB-NDDA-AS1-CI CN6-MTHED-NDDA-AGTDAD	1	Dorovy(CEILH2)	0 712 rc2226797		5 44E-24	1	11015227	ILMN 1724920	мтыср	(cis of trains)	beta Allele	cinomosonia	e rosition
rc12206561	DBD/SBD/MAP	MTHER	NPPB,NPPA-AS1,CLCN6,MTHEP,NPPA,AGTRAP	1	LDproxy(CEU_H2)	0.713 rs2075528		5 565-24	1	11010207	ILMN 1724820	MTHER	cis			
rs13206561	DBD/SBD/MAP	MTHER	NPPB,NPPA-AS1;CLCN6;MTHEP;NPPA;AGTRAP	1	LDproxy(CEU_H3)	0.713 rs2236797	PayGeneWholeBlood(Mehta)	1.64E-11	1	11815227	ILMN 1731434	MTHER	cis			
rs13306561	DBP/SBP/MAP	MTHER	NPPB,NPPA-AS1;CLCN6;MTHER;NPPA;AGTRAP	1	LDproxy(CEU_H3)	0.713 rs2075538	Whole blood (PayGene) in Jananese	7.495-10	1	11819189	A 23 P400081	MTHER	cis	0.64		
rs13306561	DBP/SBP/MAP	MTHER	NPPB/NPPA-AS1/CLCN6/MTHER/NPPA/AGTRAP	1	LDproxy(CEU_H3)	0.713 rs2236797	Whole blood (PaxGene) in Japanese	1 20E-09	1	11815237	A_23_P400081	MTHER	cis	-0.63		
rs13306561	DBD/SBD/MAD	MTHER	NPPB-NPPA-AS1-CLCN6-MTHER-NPPA-AGTRAP	1	LDproxy(CEU_H3)	0.713 rs7553194	Whole blood (PayGene) in Japanese	1.20E-09	1	11786736	A 23 P400081	MTHER	cis	-0.63		
rc12206561	DBD/SBD/MAD	MTHER	NPPB,NPPA-AS1,CLCN6,MTHEP,NPPA,AGTRAP	1	LDproxy(CEU_H2)	0.712 rc7552194	Skin (MuTHER)	2.045-09	1	11796726	H_23_F400081	MTHER	cis	-0.03		
rs12206561	DBD/SBD/MAD	MTHEP	NDDB-NDDA-AS1-CLCN6-MTHER-NDDA-AGTRAD	1	LDproxy(CEU_H2)	0.713 rs2075528	PNAseg(HapMapl CL)+DeepSage(blood)	2.042.09	1	11896602	ENST000027659	MTHER	cis			
rs13306561	DBD/SBD/MAD	MTHER	NDDB-NDDA-AS1-CLCN6-MTHER-NDDA-AGTRAD	1	LDproxy(CEU_H3)	0.713 rs2075538	Skin (MuTHER)	3 565-09	1	11819189	UMN 1734830	MTHER	cis			
rs13306561	DBP/SBP/MAP	MTHER	NPPB,NPPA-AS1;CLCN6;MTHER;NPPA;AGTRAP	1	LDproxy(CEU_H3)	0.713 rs2236797	Skin (MuTHER)	3.63E-09	1	11815237	ILMN 1734830	MTHER	cis			
rs13306561	DBP/SBP/MAP	MTHER	NPPB/NPPA-AS1/CLCN6/MTHER/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	DBD/SBD/MAD	MTHER	NPPB-NPPA-AS1-CLCN6-MTHER-NPPA-AGTRAP	1	LDproxy(CEU_H3)	0.713 rs7553194	Whole blood (CHARGE)	1.32E 07	1	11786736	60437	PLOD1	cis	-5.26 C	1	11958130
rs13306561	DBD/SBD/MAP	MTHER	NPPB:NPPA-AS1;CLCN6:MTHER:NPPA-AGTRAP	1	LDproxy(CEU_H3)	0.713 rs2236797	Subc adipose (MuTHER)	1.65E-07	1	11815237	UMN 1741594	CLCN6	cis	3.20 A	-	11550150
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1;CLCN6:MTHER:NPPA-AGTRAP	1	LDproxy(CEU-H3)	0.713 rs2075538	Subc adipose (MuTHER)	1.05E-07	1	11819189	ILMN 1741594	CLCN6	cis			
rs13306561	DBD/SBD/MAP	MTHER	NPPB,NPPA-AS1;CLCN6;MTHER;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	MTHER	NPPB/NPPA-AS1/CLCN6/MTHER/NPPA/AGTRAP	1	LDproxy(CEU_H3)	0.713 rs7553194	Subc adipose (MuTHER)	4 13E-07	1	11786736	UMN 17/159/	CLCN6	cis	-5.10	-	11550150
rs13306561	DBD/SBD/MAD	MTHER	NPDB:NPDA-AS1;CLCN6:MTHER:NPDA-AGTRAD	1	LDproxy(CEU_H3)	0.713 rs7553194	Lung	2 34E-06	1	11786736	1001/6210 TG	Unknown	cis			
rc12206561	DBD/SBD/MAD	MTHER	NDDB-NDDA-AS1-CLCN6-MTHEP-NDDA-AGTPAD	1	LDproxy(CEU_H2)	0.712 rc7552194	Monopytes (CD14+)	1.45E-05	1	11796726	TiKVCul2UloSz4	CLCN6	cis			
rc12206561	DBD/SBD/MAD	MTHER	NDDD:NDDA_AS1;CLCNG;MTHER;NDDA;ACTRAD	1	LDproxy(CEU H2)	0.713 137333194	Monocytes (CD14+)	5 105 05	1	11015337	TiKVCul2UloSz4	CLENE	cis			
rc12206561	DBP/SBP/WAP	MTHER	NPPB,NPPA-AS1,CLCN6,MTHER,NPPA,AGTRAP	1	LDproxy(CEU_H2)	0.713 152230737	Wohocytes (CD14+)	0.00104498	1	11013237	CL 12025672 A	CLENG	cis			
rc12206561	DBP/SBP/WAP	MTHER	NPPB,NPPA-AS1,CLCN6,MTHER,NPPA,AGTRAP	1	LDproxy(CEU_H2)	0.713 132230737	Monogator	1 425 24-1 20	1	11013237	GI_12025072-A	MTHEP-CLONE	cis			
rc12206561	DBP/SBP/MAP	MTHER	NDDB-NDDA AS1-CLCN6-MTHEP-NDDA-AGTPAD	1	LDproxy(CEU H2)	0.713 132073338	Blood(Echrmonn et al)	4 705 45-2 20	1	11015105	2000/77-Human	MTHER-AL952997 6-M	cis			
1515500301	DBP/SBP/IVIAP	ACT	COC3:ACT:CADNO	2	LDDIOXY(CEU-HS)	0.713 152230737	Coroballum (ScanDB)	4.70E-43,2.30	1	2200152257	5550477,Human	MITHER, AL555657.0,1	oic			
152004770	DBP/MAP	AGT	COG2,AGT,CAPN9	2	IDprovu(CEU H2)	0.754 rc1226999	Coroballum (ScanDB)	2.13E-03	1	220713523		AGT	cis			
152004770	DBP/IMAP	CED115		2	LDDIOXY(CEU-HS)	0.734 151520000	Cerebendin (Scanbb)	3.13E-10	2	06715567	100124941 TCL	CNNMA	cis			
157333333	DBP	CED115	LMAN2L, KIAA1210, FERILS	2	IndexSNP	157353550	Whole blood (CHARGE)	5 295 09	2	96715567	1100134341_101_		cis	5.44 A	2	96725621
rc7500500	DBP	CEP115	LMAN2L, KIAA1210, FERILS	2	IndexSNP	157555558	Rlood(Echrmann et al)	1 705 04	2	96715567	1190672		cis	-3.44 A	2	50755021
1573333350	DBP	FERILS		2	IndexSNP	157353336	Biolog(renimann et al)	1.702-04	2	90713307	fobyoruv/tich l		cis			
1573333350	DBP	FERILS		2	IndexSNP	157353356	BCEIIS (CD15T)	0.0008331	2	06715567			cis			
157333333	DBP	FERILS		2	IDprovu(CEU H2)	0.906 == 7593340	Whole blood (CHARGE)	2.205.00	2	06027256	01_15340355-3		cis	E 00 A	2	06725621
1573333338	DBP	FERILS		2	LDproxy(CEU-H3)	0.800 157382249	Skin (MuTUER)	2.202-03	2	06027230	1190075		cis	3.36 A	2	30733021
157599598	DBP	FERILS	LWANZL;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.300 157382249	Skin (Muthek)	3.04E-00	2	90827230	ILIVIN_1755221	CNINIAA	cis			
157333338	DBP	FERILS		3	LDproxy(CEU-H3)	0.791 150727304	Whole blood (Battle)	4.91E-40	2	97400324	1100672		cis	5.05 C	2	06725621
15/599598	DBP	FERILS	LWAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 15908470	Whole blood (CHARGE)	2.52E-09	2	90/8/353	1190673		CIS	5.96 C	2	90/35021
15/599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 157008001	Whole blood (CHARGE)	3.01E-09	2	90823047	1190673		cis	5.93 G	2	90/30021
157599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 150727384	Whole blood (CHARGE)	3.03E-09	2	90704051	1190073		cis	5.93 G	2	90735021
157599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 157608661	Blood(Fenrmann et al)	5.10E-06	2	90823047	1190073		cis			
157599598	DBP	FERILS	LIVIAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 157008001	Skin (MuTHER)	5.41E-00	2	90823047	LIVIN_1755221		cis			
157333338	DBP	FERILS		2	LDproxy(CEU-H3)	0.791 150727304	Skin (Muther)	5.03E-00	2	90704031	LIVIN_1755221		cis			
15/599598	DBP	FERILS	LWAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 15908470	Skin (MUTHER)	5.79E-06	2	90/8/303	10005000000		CIS			
15/599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 157008001	Cerebellum (all samples)	1.79E-05	2	90823047	10025902983		cis			
157599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 15908470	Lympn	0.00232082	2	90/8/303	GI_13540593-5		cis			
157599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-H3)	0.791 15908470	emental contex (all samples)	3.50E-02	2	90787333	10023902983		cis			
157399398	DBP	FERILS		3	LDproxy(CEU-H3)	0.791 157008001	Whele blood (CUARCE)	7.82E-09;2.23	2	90823047	10023820500;100	LNANDO	cis	5.04 T	2	06725621
157333338	DBP	FERILS		2	LDproxy(CEU-1kg)	0.771 15554450	Skip (MuTUER)	2.76E-05	2	06002720	1190075		cis	5.54 1	2	90753021
15/599598	DBP	FERILS	LWANZL;KIAA1310;FERILS	3	LDproxy(CEU-1kg)	0.7/1 15994430	Skin (MUTHER)	5.00E-00	2	90802728	100141076 TCI		CIS			
157599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-Reiz		Lung	1.74E-09	2	90805370	100141976_161_		cis	F 07 C	2	00705001
157599598	DBP	FERILS	LIVIAN2L;KIAA1310;FERILS	3	LDproxy(CEU-Reiz	0.757 151318597	whole blood (CHARGE)	2.40E-09	2	90820822	1190073	LIVIANZL	cis	5.97 C	2	96735621
rs7599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-Rel2	0.757 rs6730773	Whole blood (CHARGE)	3.04E-09	2	96805370	1190673		CIS	5.93 G	2	96735621
rs7599598	DBP	FERILS	LMAN2L;KIAA1310;FERILS	3	LDproxy(CEU-Rel2	0.757 157586317	whole blood (CHARGE)	3.21E-09	2	96811558	1190673		CIS	5.92 A	2	96735621
rs/599598	DBP	FERILS	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	0.757 rs1318597	Skin (MUTHER)	5.64E-06	2	96826822	ILMN_1755221	LMAN2L	CIS			
15/599598	DBD	FERILS	LWANZL;KIAA1310;FERIL5	3	LUPROXY(CEU-Rel2	0.757	SKIR (IVIUTHER)	5.00E-U0	2	96811558	ILIVIN_1/55221	LIVIANZL	CIS			
15/599598	DBD	FERILS	LIVIANZL;KIAA1310;FERIL5	3	LUPROXY(CEU-Rel2	0.735	SKIR (WUTHER)	3.0/E-Ub	2	96805370	1100672	LIVIANZL	CIS	5 CO 7	•	00700000
157599598	DBP	FERILS	LIVIANZL;KIAA1310;FEK1L5	3	LUproxy(CEU-1kg)	0.735 rs6576984	Whole blood (CHARGE)	1.39E-08	2	96818432	1130013	LIVIANZL	CIS	5.08 I	2	96/35621
rs/599598	DRb	FERILS	LMAN2L;KIAA1310;FER1L5	3	LUPROXY(CEU-1kg)	0.735 rs6576984	SKIN (MUTHER)	0.41E-06	2	96818432	ILIVIN_1/55221	LWAN2L	CIS			
rs/650227	20	ULK4	ULK4	4	IndexSNP	rs7650227	Intestine (normal lieum)	2.98E-05	3	41/94937		ULK4	cis			
rs7650227	22	ULK4	ULK4	4	LUproxy(CEU-1kg)	1 rs1615243	whole blood (Battle)	2.92E-190	3	41965234	10005010070	ULK4	cis			
rs7650227	22	ULK4	ULK4	4	LUproxy(CEU-1kg)	1 rs1052501	omentai	4.79E-21	3	41900402	10025919071	CINNBI	CIS			
rs/650227	PP	ULK4	ULK4	4	LUproxy(CEU-1kg)	1 rs3934103	Pretrontal 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			

IndexSND	Traite	InPofGono	PofGonorf0kh	locus#	Index/ID status	r^2 t	0 x oSNDid	Tissue	eSNP P	Chr	P26por	ArrayID	Transcript	type of eQTL (cis or trans)	Pota	Allolo	Probe	Probe
rs7650227	DD			4	Doroxy(CELL-1kg)	1	rs1716642	Parietal Johe (ScanDB)	6.48E-17	3	41940869	Anayio	Папаспре	cis	Deta	Allele	chromosome	POSICION
rs7650227	PP	ULK4	UIK4	4	I Dproxy(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				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9852303	Parietal lobe (ScanDB)	1.52E-15	3	41/34529		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9847006	Parietal lobe (ScanDB)	1.58E-15	3	41/30363		ULK4	CIS				
rs7650227	PP DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1052501	Cerebellum (ScanDB)	2.00E-15	3	41950394		ULK4	CIS				
rs/050227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	1513325905	Cerebellum (ScanDB)	2.00E-15	3	41889940		ULK4	CIS				
15/050227	PP DD	ULK4		4	LDproxy(CEU-1kg)	1	151/10085	Cerebellum (ScanDB)	2.00E-15	3	41900303		ULK4	cis				
rs/65022/	PP DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1/1/000	Cerebellum (ScanDB)	2.00E-15	3	41905223		ULK4	CIS				
15/050227	PP DD	ULK4		4	LDproxy(CEU-1kg)	1	151/1/000	Cerebellum (ScanDB)	2.00E-15	3	41915452		ULK4	cis				
157030227	PP	ULK4		4	LDproxy(CEU-1kg)	1	151/1/01/	Cerebellum (ScanDB)	2.00E-15	3	41890020		ULK4	cis				
rc7650227	PP DD			4	LDproxy(CEU-1kg)	1	152120034	Corobollum (ScanDB)	2.00E-15	2	41657045		ULK4	cis				
rc7650227	PP DD			4	LDproxy(CEU-1kg)	1	rc7649579	Corobollum (ScanDB)	2.00E-15	2	41020722		ULK4	cis				
rs7650227	DD	ULKA	ULK4	4	Dproxy(CEU-1kg)	1	rc9829200	Cerebellum (ScanDB)	2.00E-15	3	41903049		ULKA CEN4	cis				
rc7650227	DD			4	LDproxy(CEU-1kg)	1	rc1016669	Cerebellum (ScanDB)	2.00E-15	2	4196944			cis				
rs7650227	DD			4	LDproxy(CEU-1kg)	1	rc2774272	Cerebellum (ScanDB)	2.01E-15	2	41000444		ULK4	cis				
rs7650227	DD	ULK4	ULKA	4	LDproxy(CEU-1kg)	1	rs6791806	Cerebellum (ScanDB)	2.01E-15	3	41052410		ULKA	cis				
rs7650227	DD	ULKA	ULKA	4	LDproxy(CEU-1kg)	1	rs9873207	Cerebellum (ScanDB)	2.01E-15	3	4185975/		ULKA	cis				
rs7650227	DD	ULKA	ULKA	4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (ScanDB)	2.01E-15	3	41802030		ULKA	cis				
rs7650227	DD	ULKA	ULKA	4	LDproxy(CEU-1kg)	1	rs6803652	Cerebellum (ScanDB)	2.04E-15	3	41799560		ULKA	cis				
rs7650227	PP	ULK4	UIK4	4	I Dproxy(CEU-1kg)	1	rs17062109	Cerebellum (ScanDB)	2.05E-15	3	41785368		UI K4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CFU-1kg)	1	rs9874975	Cerebellum (ScanDB)	2,20E-15	3	41739304		ULK4	cis				
rs7650227	PP	ULK4	UI K4	4	IDproxy(CEU-1kg)	1	rs9847006	Cerebellum (ScanDB)	2.71E-15	3	41730363		ULK4	cis				
rs7650227	PP	ULK4	UI K4	4	IDproxy(CEU-1kg)	1	rs3890604	Cerebellum (ScanDB)	2.78E-15	3	41735629		ULK4	cis				
rs7650227	PP	ULK4	UI K4	4	I Dproxy(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	Locust	# Index/LD status	r^2 to inde	o x eSNPid	Tissue	eSNP <i>P</i> 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				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	1	rs1/169/5	Liver (ScanDB)	1.4/E-12	3	41935010		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1/1/01/	Liver (ScanDB)	3.08E-12	3	41890620		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6/96210	Liver (ScanDB)	3.08E-12	3	41826/22		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9825741	Peripheral artery plaque	3.91E-12	3	41/36832	100149945_IGI_	a ULK4	CIS				
15/050227	PP DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	150599179	Liver (ScanDB)	4.02E-12	3	41830288	10000000000	ULK4	CIS				
15/050227	PP DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	151052501	Liver(Greenawait)	7.81E-12	3	41900402	10023809218	ULK4	cis	0.00			
15/050227	PP DD	ULK4		4	LDproxy(CEU-1kg)	1	rs1/1/020	Hippocampus (CA1, h=61; Kim et al.)	1.00E-11	3	41981490	232206_at	ULK4	cis	0.00			
rc7650227	PP DD			4	LDproxy(CEU_1kg)	1	155674575	Liver (ScanDB)	1.240-11	2	41755504			cis				
rc7650227	PP DD			4	LDproxy(CEU_1kg)	1	150805032	EP+ broast tumor colls	1.230-11	2	41755500			cis				
rc7650227				4	LDproxy(CEU Pol2	1	rc1716975	Normal dondritic cells (before Myrchart	1.310-11	2	41986834		ULK4	cis				
rs7650227	DD	ULK4		4	LDproxy(CEU-1kg)	1	rs3774372	FR+ breast tumor cells	1 95E-11	3	41952418		ULK4	cis				
rs7650227	PP	LILK4		4	LDproxy(CEU-1kg)	1	rs1716685	ER+ breast tumor cells	2.66E-11	3	41900305		ULK4	cis				
rs7650227	PP	ULK4	UI K4	4	LDproxy(CEU-1kg)	1	rs1717006	ER+ breast tumor cells	2.66E-11	3	41915452		ULK4	cis				
rs7650227	PP	ULK4	UI K4	4	LDproxy(CEU-1kg)	1	rs1717020	EB+ 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	LDproxv(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	3 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	4 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				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9867627	Liver (ScanDB)	9.63E-10	3	417/0845		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs9873207	Liver (ScanDB)	6.65E-09	3	41859754	10000000000	ULK4	CIS				
rs/65022/	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Pretrontal cortex (Alzneimer's)	7.60E-09	3	41802030	10023809218	ULK4	CIS				
15/050227	PP DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	152272007		2.70E-08	3	419/1140	231149_5_at	ULK4	cis				
rc7650227	PP DD	ULK4		4	LDproxy(CEU-1kg)	1	rs1092301	LUL	3.90E-08	3	41900402	231149_5_at	ULK4	cis				
rc7650227	PP DD			4	LDproxy(CEU-Ikg)	1	rc1716975		7 005 09	2	41072400	221149 c at		cis				
rs7650227	PP DD			4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (Huntington's)	9.935-07	3	41933010	10025919071	CTNNB1	cis				
rs7650227	DD	LILKA	UI KA	4	LDproxy(CEU-1kg)	1	rs9852303	Cerebellum (normal samples)	1 1088F-05	3	41002030	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^21 inde	to ex eSNPid	Tissue	eSNP <i>P</i> 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;4.74	3	41802030	10023809218;10	0 ULK4;AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.95	53 rs6599167	Visual cortex (Alzheimer's)	3.11E-08	3	41725264	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs10510731	Lung	1.40E-14	3	41828314	100160459_TGI_	a ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs4299460	Lung	1.47E-14	3	41927449	100311290_TGI_	a ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs17214945	ER+ breast tumor cells	2.69E-11	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs17214987	ER+ breast tumor cells	2.69E-11	3	41785485		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	. 0.86	51 rs17218264	ER+ breast tumor cells	2.69E-11	3	41950851		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	. 0.86	51 rs1/283929	ER+ breast tumor cells	2.69E-11	3	41916902		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs1/218103	Liver (ScanDB)	5.14E-11	3	41918/28		ULK4	CIS				
rs/650227	pp	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs1/218264	Parietal lobe (ScanDB)	7.13E-11	3	41950851		ULK4	CIS				
rs/65022/	PP DD	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs1/215183	Parietal lobe (ScanDB)	1.21E-10	3	41/8/338		ULK4	CIS				
rs/65022/	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs1/214945	Parietal lobe (ScanDB)	1.24E-10	3	41/83664		ULK4	CIS				
rs/65022/	PP PD	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	51 rs1/215589	Parietal lobe (ScanDB)	1.2/E-10	3	41806207		ULK4	CIS				
15/050227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.80	51 1517218103	Careballum (ScanDB)	1.30E-10	3	41918/28		ULK4	cis				
157050227	PP DD	ULK4		4	LDproxy(CEU-Rel2	0.80	51 rc17292677	EP+ broast tumor colls	3.47E-10	3	41/83004		ULK4	cis				
rc7650227	PP DD		ULK4	4	LDproxy(CEU-Rel2	0.80	51 rc17015192	Corobollum (SconDR)	3.33E-10	2	41901132		ULK4	cis				
rc7650227	PD			4	LDproxy(CEU Rol2	0.80	51 rc17015590	Corobollum (ScanDB)	4.012-10	2	41/0/330		ULK4	cis				
rs7650227	DD	ULK4		4	LDproxy(CEU_Rel2	0.80	51 rs17215365	Cerebellum (ScanDB)	4.00E-10	3	41000207		ULK4	cis				
rs7650227	DD	ULK4	111 K4	4	LDproxy(CEU-Rel2	0.86	51 rs17218105	Cerebellum (ScanDB)	4.20E-10	3	41950851		ULK4	cis				
rs7650227	PP	LILK4		4	LDproxy(CEU-Rel2	0.86	51 rs10510731	Liver (ScanDB)	4.34E-10	3	41828314		ULK4	cis				
rs7650227	PP	ULK4	UI K4	4	Dproxy(CEU-1kg)	0.85	57 rs794894	Parietal lobe (ScanDB)	1.63E-16	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	57 rs7634985	Parietal lobe (ScanDB)	1.73E-16	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	57 rs13087502	Parietal lobe (ScanDB)	1.78E-16	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs794894	Cerebellum (ScanDB)	1.45E-13	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs7634985	Cerebellum (ScanDB)	1.56E-13	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	57 rs13087502	Cerebellum (ScanDB)	1.61E-13	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	57 rs13087502	ER+ breast tumor cells	1.55E-10	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs809930	Parietal lobe (ScanDB)	5.10E-15	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs7652506	Parietal lobe (ScanDB)	6.85E-15	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs939561	Parietal lobe (ScanDB)	7.69E-15	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs7629767	Parietal lobe (ScanDB)	7.83E-15	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs10510732	SubCutAdipose(Greenawalt)	1.06E-14	3	41982343	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs939561	Cerebellum (ScanDB)	5.72E-12	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs7629767	Cerebellum (ScanDB)	6.08E-12	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs809930	Cerebellum (ScanDB)	6.19E-12	3	42040009		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs7652506	Cerebellum (ScanDB)	7.19E-12	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs7652506	ER+ breast tumor cells	1.07E-11	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs10510732	ER+ breast tumor cells	2.69E-11	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	l2 rs17284313	ER+ breast tumor cells	2.69E-11	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs17284472	ER+ breast tumor cells	2.69E-11	3	41971308		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	12 rs17284313	Parietal lobe (ScanDB)	7.62E-11	3	41961791		ULK4	cis				
rs7650227	20	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	L2 rs10510732	Parietal lobe (ScanDB)	7.64E-11	3	41982343		ULK4	cis				
rs/650227	PP	ULK4	ULK4	4	LUPROXY(CEU-1kg)	0.81	L2 r51/284472	Parletal IODE (ScanDB)	7.64E-11	3	419/1308		ULK4	CIS				
15/000227	PP	ULK4		4	LDproxy(CEU-1kg)	0.81	L2 FS809930	ENT Dreast tumor cells	9.77E-11	3	42040009		ULK4	CIS				
15/03022/	PP DD	ULK4		4	LDproxy(CEU-1kg)	0.81	12 1510510/32	Coroballum (ScanDR)	1.11E-10 4.415 10	3	41982343			cis				
15/03022/	PP DD	ULK4		4	Dproxy(CEU-1kg)	0.81	12 rc10510722	Cerebellum (ScanDB)	4.410-10	3	41501/91			cis				
rs7650227	PP DD	ULK4		4	Dproxy(CEU-1kg)	0.81	12 rc17304473	Cerebellum (ScanDB)	4.420-10	3	41382343			cis				
137030227	P.P.	ULN4	ULIN4		cobioxy(cco-tkg)	0.01	12 131/2044/2	cerebendin (Scalibb)	4.420-10	3	+15/1308		ULIN4	UIS				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 te inde	o x eSNPid	Tissue	eSNP <i>P</i> value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	рр	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs10510732	Stomach	8.32E-10	3	41982343	100311290	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs10510732	Cerebellum (Alzheimer's)	5.26E-02	3	41982343	10023829862	AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	2 rs794899	LCL	1.30E-07	3	42003726	231149 s at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	L rs12635286	Parietal lobe (ScanDB)	7.75E-15	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	L rs12635286	Cerebellum (ScanDB)	6.72E-12	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	l rs12635286	Liver (ScanDB)	1.85E-08	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	l rs12635286	Liver(Greenawalt)	1.76E-07	3	42026840	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	l rs12635286	Cerebellum (Alzheimer's)	2.92E-05	3	42026840	10025919071	CTNNB1	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2	0.96	7 rs12656497	Lung	1.67E-07	5	32867696	100142475 TGI	e 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)	0.78	1 rs1173756	Lung	1.91E-08	5	32825609	100145622 TGI	eNPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-1kg)	0.78	l rs1173743	Primary PHA-stimulated T cells (GenCord	5.68E-07	5	32775047		ENSG0000056097.10	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	с	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:SI C22A7:7NE318	7	I Dproxy(CEU-1kg)	1	rs2242416	Whole blood (Battle)	4.88E-53	6	43273604		CRIP3	cis				
rs10948071	PP	NA	TTBK1:CRIP3:SI C22A7:7NE318	7	LDproxy(CEU-1kg)	1	rs1574430	Whole blood (CHARGE)	2.71E-16	6	43377007	50193	ZNE318	cis	-8.19	Α	6	43411954
rs10948071	pp	NΔ	TTBK1:CRIP3:SI C22A7:7NF318	7	LDproxy(CEU-1kg)	1	rs2242416	Whole blood (CHARGE)	2.83E-16	6	43381582	50193	ZNF318	cis	-8.18	Δ	6	43411954
rs10948071	DD	NA	TTBK1:CRIP3:SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2469	Whole blood (CHARGE)	4 13E-16	6	43407301	50193	ZNF318	cis	-8.13	ĉ	6	43411954
rc109/9071	DD	NA	TTBK1;CRID2;SIC22A7;ZNE219	7	Dproxy(CEU-1kg)	1	rc1574420	Intestine (normal ileum)	5 705-14	6	42269020	50155	CRID2	cis	0.10	·		43411334
rc109/8071	DD	NA	TTBK1;CRIP3;SEC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs28/16/8	Intestine (normal ileum)	5 705-14	6	43269179		CRIPS	cis				
rs10948071	DD	NA	TTBK1;CRIP3;SEC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Intestine (normal ileum)	1.375-13	6	43273604		CRIPS	cis				
rc10040071	DD	NA	TTBK1;CRIP3;SEC22A7;ZNE318	7	LDproxy(CEU_1kg)	1	rs2242410	Read(Eebrmann et al)	5 905 06	6	43273004	50102	7NE219	cis				
rc100/9071	DD	NA	TTPK1;CRIP3;5EC22A7;2NF516	7	LDproxy(CEU-1kg)	1	rs2469	Plood(Fehrmann et al)	5.905.06	6	43361362	50193	ZNE219	cis				
rc10040071	PD	NA	TTRK1,CRIP3,SEC22A7,ZNF318	7	LDproxy(CEU-1kg)	1	132403	Skin (MuTUER)	1 115 05	6	43407301	UNANI 1604711	MAD211RD	cis				
rc10040071	PP DD	NA	TTRK1,CRIP3,SLC22A7,ZNF516	7	LDproxy(CEU-1kg)	1	152403	Skin (Muther)	1.112-05	6	43407301	ILIVIN_1094711	MAD2LIBP	cis				
rc10949071	PP DD	NA	TTPK1;CRIP3;SLC22A7;ZNF516	7	LDproxy(CEU-1kg)	1	rc1574420	Skin (Muther)	1.402-05	6	43377137	ILIVIN_1094711	MAD2LIBP	cis				
1510948071	PP DD	NA	TTDK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	151374430	Skin (MuTHER)	1.402-05	0	43377007	ILIVIN_1094711	MAD2LIBP	cis				
1510946071	PP	NA NA	TTBK1;CRIP3;SEC22A7;ZNF516	-	LDproxy(CEU-1kg)	1	152242410	SKIT (MUTHER)	1.572-05	0	43301302	ILIVIN_1054711	INIAU2LIBP	cis				
1510948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	152841048	LCL (MUTHER)	2.12E-05	0	43377157	ILIVIN_1083279	PEXO	CIS				
1510948071	PP DD	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	151574430	LCL (MUTHER)	2.13E-05	0	43377007	ILIVIN_1083279	PEXO	cis				
1510948071	PP	NA NA	TTBK1;CRIP3;SLC22A7;ZNF318	-	LDproxy(CEU-1kg)	1	152242410		2.27E-05	0	43381582	ILIVIN_1083279	PEXO	cis				
1510948071	PP	NA NA	TTBK1;CRIP3;SEC22A7;ZNF318	-	LDproxy(CEU-1kg)	1	152409	LCC (MUTHER)	2.74E-05	0	43407301	ILIVIN_1083279	PEXO	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	/	LDproxy(CEU-1kg)	1	rs2469	Lympn	0.00015064	0	43407301	GI_37552195-5	CRIP3	CIS				
1510948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	/	LDproxy(CEU-1kg)	1	rs2242410	Liver(Uchicago)	0.000/1416	0	43381582	A_23_P150502	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	/	LDproxy(CEU-1kg)	1	rs2469	Liver(Greenawait)	1.75E-06;2.2	2 6	43407301	10025906643;10	USLC22A7;SLC22A7	CIS	0.77			
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	-	LDproxy(CEU-1kg)	0.96	5 rs2125738	Whole blood (CHARGE)	1.78E-18	6	43435728	50193	ZNF318	CIS	-8.77	A	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	-	LDproxy(CEU-1kg)	0.96	5 rs2125737	Whole blood (CHARGE)	1.53E-16	6	43435514	50193	ZNF318	CIS	-8.25	C -	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318		LDproxy(CEU-1kg)	0.96	5 rs4/146//	Whole blood (CHARGE)	1.53E-16	6	4343501/	50193	ZNF318	CIS	-8.25	G	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 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)	0.96	5 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)	0.96	5 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)	0.96	5 rs2254303	Intestine (normal ileum)	5.70E-14	6	43276390		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125738	Monocytes	4.97E-12	6	43435728		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9381237	Blood(Fehrmann et al)	2.50E-06	6	43428388	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2254303	Skin (MuTHER)	1.29E-05	6	43384368	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125737	LCL (MuTHER)	1.59E-05	6	43435514	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9369407	LCL (MuTHER)	1.59E-05	6	43435353	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs4714677	LCL (MuTHER)	1.59E-05	6	43435017	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2841642	LCL (MuTHER)	1.63E-05	6	43410263	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9381237	LCL (MuTHER)	1.63E-05	6	43428388	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125738	LCL (MuTHER)	1.97E-05	6	43435728	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2254303	LCL (MuTHER)	2.39E-05	6	43384368	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9369407	Skin (MuTHER)	2.98E-05	6	43435353	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125737	Skin (MuTHER)	2.98E-05	6	43435514	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs4714677	Skin (MuTHER)	2.98E-05	6	43435017	ILMN_1694711	MAD2L1BP	cis				

IndexSNP Traits	InRefGene	RefGenes60kb	Locus	# Index/LD status	r^2 to index eSN	Pid	Tissue	eSNP <i>P</i> 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 rs28	41642	Skin (MuTHER)	3.15E-05	6	43410263	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965 rs93	81237	Skin (MuTHER)	3.15E-05	6	43428388	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965 rs21	25738	Skin (MuTHER)	3.27E-05	6	43435728	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965 rs22	54303	Lymph	0.00025613	6	43384368	GI_37552195-S	CRIP3	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931 rs93	69408	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 rs93	69408	Skin (MuTHER)	6.63E-06	6	43440164	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931 rs93	69408	LCL (MuTHER)	1.72E-05	6	43440164	ILMN_1683279	PEX6	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892 rs23	96002	LCL (MuTHER)	5.60E-07	6	43367990	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892 rs23	96002	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 rs23	96002	Skin (MuTHER)	8.40E-06	6	43367990	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828 rs28	41647	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 rs28	41647	Skin (MuTHER)	1.15E-05	6	43377158	ILMN_1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828 rs28	41647	LCL (MuTHER)	2.68E-05	6	43377158	ILMN_1683279	PEX6	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	Liver(Greenawalt)	1.26E-28	6	43387699	10025905145	ZNF318	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs69	01866	Monocytes	1.18E-26	6	43368638		ZNF318	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	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 rs43	98731	omental	4.72E-23	6	43387699	10025905145	ZNF318	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	SubCutAdipose(Greenawalt)	6.30E-19	6	43387699	10025905145	ZNF318	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs69	01866	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 rs16	896398	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 rs43	98731	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 rs43	98731	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 rs43	98731	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 rs43	98731	Intestine (normal ileum)	5.10E-10	6	43279721		CRIP3	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	Cerebellum (Huntington's)	8.76E-10	6	43387699	10025905145	ZNF318	cis			
rs10948071 PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	Liver(Schroder)	1.82E-09	6	43387699		ZNF318	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2)	0.748 rs43	98731	Lymph	3.44E-08	6	43387699	GI 37552195-S	CRIP3	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2	0.748 rs69	01866	LCL (MuTHER)	1.72E-05	6	43368638	ILMN 1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	Tcells	1.83E-05	6	43387699	-	РТК7	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2	0.748 rs69	01866	Skin (MuTHER)	2.15E-05	6	43368638	ILMN 1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	LCL (MuTHER)	2.20E-05	6	43387699	ILMN 1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	Skin (MuTHER)	2.97E-05	6	43387699	ILMN 1694711	MAD2L1BP	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SI C22A7:7NF318	7	LDproxy(CEU-Rel2	0.748 rs43	98731	Blood(Fehrmann et al)	5.10F-20:1.00	6	43387699	50193:7210484	ZNF318:RP3-330M21	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SLC22A7:ZNF318	7	LDproxy(CEU-Rel2	0.715 rs22	79087	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 rs22	79087	Intestine (normal ileum)	4.60E-10	6	43299058		CRIP3	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SI C22A7:7NE318	7	I Dproxy(CEU-Rel2	0.715 rs22	79087	I CL (MUTHER)	1.75E-05	6	43407036	ILMN 1694711	MAD2I 1BP	cis			
rs10948071 PP	NA	TTBK1:CRIP3:SI C22A7:7NE318	7	I Dproxy(CEU-Rel2	0.715 rs22	79087	Skin (MuTHER)	2.70E-05	6	43407036	ILMN 1694711	MAD2I 1BP	cis			
rs12244842 DBP	C10orf107	C10orf107	9	Dproxy(CEU-1kg)	1 rs23	93833	Liver (ScanDB)	8.10F-07	10	63115322		SGTA	cis			
rs12244842 DBP	C10orf107	C10orf107	9	IDproxy(CEU-1kg)	1 rs12	246717	Liver (ScanDB)	9.54E-07	10	63129189		SERPIND1	cis			
rs12244842 DBP	C10orf107	C10orf107	9	IDproxy(CEU-1kg)	1 rs23	93833	Blood	0.0000286	10	63115322	HSG00268758	LOC219790	cis			
rs7070797 SBP	NA	C10orf107	9	LDproxy(CEU-Rel2	0.786 rs10	509158	Adipose	0.0000037	10	63177675	HSG00269025	NM 173554	cis			
rs2166122 MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.778 rs25	88918	EndometrialTumor	0.00379818	10	63195030		C10orf107	cis			
rs2166122 MAP	C10orf107	C10orf107	9	I Dproxy(CEU-Rel2	0.734 rs97	3237	Liver (ScanDB)	5.92E-07	10	63195307		EUCA1	cis			
rs2166122 MAP	C10orf107	C10orf107	9	I Dproxy(CEU-Rel2	0 734 rs97	3237	Prefrontal cortex (Alzheimer's)	9 15E-05	10	63195307	10025902662	C10orf107	cis			
rs2681472 DBP/SBP/MAP	ΔTP2B1	ΔTP2R1	10	IndexSNP	rs26	81472	Whole blood (CHARGE)	1.83E-15	12	88533090	7320717	WDR51B	cis	7.95 G	12	88439646
rs2681472 DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP	rs26	81472	Liver (ScanDB)	3.74E-07	12	88533090	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	LOC100131662	cis	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		00105010
rs2681472 DBP/SBP/MAP	ATP2B1	ATP281	10	IndexSNP	rs26	81472	Blood(Febrmann et al)	2 20E-08-2 20	12	88533090	6650035-732071	7 ·WDR51B·ATP2B1	cis			
rs2681472 DBP/SBP/MAP	ATP281	ATP281	10	I Dproxy(CEU-1kg)	1 rs11	105368	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 rs11	105364	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 rs11	105354	Whole blood (CHARGE)	3.82E-15	12	88550654	7320717	WDR51B	cis	7.86 G	12	88439646
rs2681472 DBP/SBD/MAD	ΔTP2B1	ATP2B1	10	I Dproxy(CEU-1kg)	1 rc17	249754	Whole blood (CHARGE)	4.81E-15	12	88584717	7320717	WDR51B	cis	7.83 Δ	12	88439646
rs2681472 DBD/SBD/MAD	ATD2B1	ATD281	10	Doroxy(CEU-1kg)	1 rc12	579302	Whole blood (CHARGE)	5.09E-15	12	88574624	7320717	WDR51B	cis	7.82 G	12	88439646
rs2681472 DBD/SBD/MAD	ΔTP2B1	ATP2B1	10	Doroxy(CEU_Pel2	1 rc12	230074	Whole blood (CHARGE)	5 11E-15	12	88614999	7320717	WDR51B	cis	7.82 G	12	88439646
rc2681472 DBD/SBD/MAP	ATD281	ATD281	10	Doroxy(CEIL Pol2	1 rc11	105379	Whole blood (CHARGE)	7 125-15	12	8861/1970	7320717	WDR51B	cis	7.02 G	12	88439646
rs2681472 DBD/SBD/MAD	ATD2B1	ATD281	10	Doroxy(CEIL Pol2	0.92 rc26	81/192	Whole blood (CHARGE)	7 765-13	12	88537220	7320717	WDR51B	cis	717 C	12	88/396/6
rs2681472 DDP/3DP/WAP	ATD201	ATD281	10	Doroxy(CEU Polo	0.92 1520	81/107	Liver (ScanDB)	3 155.07	12	88527220	/320/1/	100100131662	cic	7.17 C	14	00435040
rc2691472 DDP/3DP/MAP	ATD201	ATD201	10	Dorowy(CELL Polo	0.02 1520	01402	Plood(Eebrmann et al)	2 105 09-5 00	12	00537220	6650025-722071	7-W/DD51D-ATD201	cis			
rc2691472 DBP/30P/MAP	ATD201	ATD201	10	Doroxy(CEU, 1kg)	0.915 rc49	01472 42666	Whole blood (CHARGE)	2.100-00,0.90	12	99465690	7160609	WDP51P	cis	-5.08 C	12	99227054
rc2691472 DBP/36P/WAP	ATD201	ATD201	10	Dorowy(CEU 14-	0.915 rc40	42000	Monorator (CD14+)	4 255 05	12	00403080	0N100005	CALNTA	cis	-5.06 C	12	0000/904
152001472 UBP/58P/MAP	ATP2B1	AIF201	10	robioxA(ceo-tkg)	0.913 1548	42000	Monocytes (CD14+)	4.30E-U0	12	88403680	этатакцокорт??	GALIN14	CIS			

						r^2 to	5		eSNP P					type of eQTL			Probe	Probe
IndexSNP	Traits	InRefGene	RefGenes60kb	Locus	Index/LD status	index	eSNPid	Tissue	value	Chr	B36pos	ArrayID	Transcript	(cis or trans)	Beta	Allele	Chromosome	Position
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-H3)	0.805	rs11105328	Monocytes (CD14+)	5.41E-05	12	88466521	9N1yRYI6R8pJ.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	Т	12	110373489
rs3184504	DBP/MAP	SH2B3	ATXN2;SH2B3	11	IndexSNP		rs3184504	Whole blood (CHARGE)	5.02E-19	12	110368991	6560301	SH2B3	cis	8.91	Т	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	Т	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	Α	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	С	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	Α	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	Т	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	Т	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	Т	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	FU21127	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	Т	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_FC	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_a	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_FC	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	Α	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	Α	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	С	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 <i>P</i> value	Chr	B36pos	ArravID	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 rs64951	7 LCL (MuTHER)	1.36E-07	15	72981543	ILMN 1761262	MPI	cis	Deta	, and the	cinomosonic	. I controll
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs80319	7 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 rs64951	6 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 rs649512	6 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 rs649513	7 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 rs80319	7 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 rs64951	6 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 rs74972	1 Bcells (CD19+)	3.92E-06	15	72977743	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs64951	7 Bcells (CD19+)	4.00E-06	15	72981543	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs649512	6 Blood	0.0000646	15	72962079	HSG00291325	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs80319	7 Bcells (CD19+)	6.61E-06	15	72968174	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs649512	6 SchadtLiver	8.60E-06	15	72962079		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs649512	6 Bcells (CD19+)	8.77E-06	15	72962079	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs649512	6 Monocytes (CD14+)	7.18E-05	15	72962079	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs649512	7 Monocytes (CD14+)	7.50E-05	15	72981543	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs80319	7 Monocytes (CD14+)	0.000101	15	72968174	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs74972	1 Monocytes (CD14+)	0.000152	15	72977743	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs64951	6 Adipose	0.0001963	15	72962079	HSG00291325	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.754 rs649512	6 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 rs64951	6 Blood(Fehrmann et al)	2.00E-28;3.00	15	72962079	3170239;448013	2 CSK;ULK3;C15orf17;0	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.751 rs11636	52 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 rs11636	52 Bcells (CD19+)	1.06E-08	15	72901375	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-1kg	0.75 rs11333	3 Monocytes	8.25E-26	15	72999278		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-1kg	0.75 rs11333	3 Whole blood (CHARGE)	5.97E-21	15	72999278	4480132	ULK3	cis	-9.39	т	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-1kg	0.75 rs11333	3 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 rs11333	3 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 rs11333	3 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 rs11333	3 Bcells (CD19+)	3.86E-05	15	72999278	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.735 rs48866	3 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-Rel	0.735 rs48866	3 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 rs13789	2 Monocytes	3.21E-35	15	72864420		ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs137894	0 Whole blood (CHARGE)	6.15E-35	15	72870547	4480132	ULK3	cis	12.33	С	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs37847	9 Whole blood (CHARGE)	3.65E-34	15	72869605	4480132	ULK3	cis	12.19	С	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs137894	1 Whole blood (CHARGE)	4.77E-34	15	72867203	4480132	ULK3	cis	12.17	С	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs48864	0 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 rs13789	2 Whole blood (CHARGE)	5.71E-33	15	72864420	4480132	ULK3	cis	11.96	С	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs13789	0 Whole blood (Battle)	1.79E-27	15	75083494		CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs137894	0 Bcells (CD19+)	1.33E-08	15	72870547	ubt12tlW7_Z_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs137894	0 Skin (MuTHER)	1.37E-08	15	72870547	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs37847	9 Skin (MuTHER)	1.75E-08	15	72869605	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs13789	1 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 rs13789	2 Skin (MuTHER)	3.12E-08	15	72864420	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs48864	0 Skin (MuTHER)	3.16E-08	15	72852697	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs37847	9 Subc adipose (MuTHER)	4.43E-08	15	72869605	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs137894	1 Subc adipose (MuTHER)	4.62E-08	15	72867203	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs13789	0 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 rs13789	2 Subc adipose (MuTHER)	6.30E-08	15	72864420	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs48864	0 Subc adipose (MuTHER)	7.48E-08	15	72852697	ILMN_1679495	ULK3	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs37847	9 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-Rel	: 0.733 rs48864	0 LCL (MuTHER)	3.79E-06	15	72852697	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs13789	0 LCL (MuTHER)	4.06E-06	15	72870547	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	: 0.733 rs13789	1 LCL (MuTHER)	4.16E-06	15	72867203	ILMN_1761262	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.733 rs37847	9 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 rs137894	2 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 rs137894	2 Lung	3.02E-05	15	72864420	100132373_TGI_	e CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-H3)	0.733 rs13789	2 Blood(Fehrmann et al)	2.00E-45;3.20	( 15	72864420	3170239;448013	2 CSK;ULK3;COX5A	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-1kg	0.719 rs12591	13 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-Rel	: 0.701 rs488660	6 Whole blood (CHARGE)	6.50E-29	15	72844800	4480132	ULK3	cis	11.16	Α	15	72915933
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12 LDproxy(CEU-Rel	0.701 rs48866	6 Skin (MuTHER)	7.34E-08	15	72844800	ILMN_1679495	ULK3	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 inde	to ex eSNPid	Tissue	eSNP P value	Chr	B36pos	ArravID	Transcript	type of eQTL (cis or trans)	Beta	Allel	Probe Chromosome	Probe
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.70	01 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	0.70	01 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	3	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Whole blood (CHARGE)	5.97E-21	15	72999278	3 4480132	ULK3	cis	-9.39	т	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	LCL (MuTHER)	3.18E-08	15	72999278	3 ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Skin (MuTHER)	1.30E-05	15	72999278	3 ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Subc adipose (MuTHER)	2.40E-05	15	72999278	3 ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	IndexSNP		rs1133323	Bcells (CD19+)	3.86E-05	15	72999278	ubt12tlW7_Z_F	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11638130	Whole blood (Battle)	7.31E-79	15	75183935	5	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	4 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	3 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	8 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	7 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	L 4480132	ULK3	cis	-9.38	Т	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11072514	Whole blood (CHARGE)	7.20E-21	15	73008918	3 4480132	ULK3	cis	-9.37	Α	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	2 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	l 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	3 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	3 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	3 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	5 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	7 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	L 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	3 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	3 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	L 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	L 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	8 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_F	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs11633472	Bcells (CD19+)	3.86E-05	15	7297113	7 ubt12tlW7_Z_F0	D 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_F0	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Monocytes (CD14+)	0.0001945	15	72999410	r_tdN3VF1vV3q	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	LCL in asthmatics (Liang 1kg)	1.02E-20	15	72986945	5 218143_s_at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Whole blood (CHARGE)	3.32E-20	15	72986945	5 4480132	ULK3	cis	-9.21	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Liver(Greenawalt)	1.34E-18	15	72986945	5 10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	LCL (MuTHER)	3.91E-08	15	72986945	5 ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Lymph	4.27E-06	15	72986945	GI_4505234-S	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Skin (MuTHER)	1.33E-05	15	72986945	5 ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Prefrontal cortex (all samples)	1.3997E-05	15	72986945	5 10026392220	SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Subc adipose (MuTHER)	3.12E-05	15	72986945	5 ILMN_2364535	SNUPN	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Bcells (CD19+)	3.86E-05	15	72986945	6 ubt12tlW7_Z_F0	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Induced sputum (COPD cases)	0.00015722	15	72986945	5 224805_s_at	C15orf17	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.98	32 rs11856413	Blood(Fehrmann et al)	2.20E-21;2.2	15	72986945	5 3170239;50341;4	CSK;SCAMP2;ULK3;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs1130741	Whole blood (Battle)	4.09E-124	15	75189930	)	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs7495739	Monocytes	3.25E-29	15	72972723	3	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs7495739	LCL in asthmatics (Liang 1kg)	5.96E-29	15	72972723	3 202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs1130741	LCL in asthmatics (Liang 1kg)	1.45E-28	15	72976983	3 202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs11072512	LCL in asthmatics (Liang 1kg)	3.40E-28	15	72991079	9 202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs4886636	LCL in asthmatics (Liang 1kg)	3.40E-28	15	72983229	9 202472_at	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs1127796	Monocytes	6.08E-27	15	72980057	7	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs4886636	Whole blood (CHARGE)	1.49E-22	15	72983229	9 4480132	ULK3	cis	-9.77	Α	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs1130741	Whole blood (CHARGE)	5.14E-22	15	72976983	3 4480132	ULK3	cis	-9.65	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs7495739	Whole blood (CHARGE)	5.40E-22	15	72972723	3 4480132	ULK3	cis	-9.64	G	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.96	57 rs7497393	Whole blood (CHARGE)	5.71E-22	15	72962510	4480132	ULK3	cis	-9.63	С	15	72915933

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index es	SNPid	Tissue	eSNP <i>P</i> 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 rs	1127796	Whole blood (CHARGE)	1.00E-21	15	72980057	4480132	ULK3	cis	-9.58	с	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs	11072511	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 rs	7497393	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 rs	11072512	Whole blood (CHARGE)	7.79E-21	15	72991079	4480132	ULK3	cis	-9.36	т	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs	11072511	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 rs	4886636	SubCutAdipose(Greenawalt)	7.68E-11	15	72983229	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs	4886636	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 rs	11072512	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 rs	1127796	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 rs	1130741	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 rs	7495739	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 rs	11072511	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 rs	7497393	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 rs	7495739	RNAseq(HapMapLCL)+DeepSage(blood)	2.76E-07	15	75185670	ENST00003796	9 MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs	7497393	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 rs	11072511	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 rs	4886636	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 rs	7495739	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 rs	1130741	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 rs	7497393	Skin (MuTHER)	2.44E-05	15	72962510	ILMN 1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxv(CEU-Rel2	0.967 rs	1127796	Subc adipose (MuTHER)	2.49E-05	15	72980057	ILMN 1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxv(CEU-Rel2	0.967 rs	4886636	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 rs	11072512	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 rs	11072512	Skin (MuTHER)	3.01E-05	15	72991079	ILMN 1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:BPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	11072512	Bcells (CD19+)	3.21E-05	15	72991079	ubt12tIW7 7 FC	CSK	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:BPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	1127796	Bcells (CD19+)	3.21E-05	15	72980057	ubt12tIW7 7 FC	CSK	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:BPP25:C15orf17:MPI	13	I Dproxy(CEU-Rel2	0.967 rs	4886636	Bcells (CD19+)	3.35E-05	15	72983229	ubt12tIW7 7 FC	CSK	cis				
rs1133323	DBP	NΔ	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	1130741	Bcells (CD19+)	4.67E-05	15	72976983	ubt12tlW7_7_E	D CSK	cis				
rs1133323	DBP	NΔ	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	4886636	Monocytes (CD14+)	0.000135	15	72983229	r tdN3VE1vV3g	VULK3	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CELL-Rel2	0.967 rs	11072511	Bcells (CD19+)	0.0001942	15	72946486	ubt12tlW7 7 FC	n CSK	cis				
rs1133323	DBP	NΔ	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	11072512	Monocytes (CD14+)	0.0001945	15	72991079	r tdN3VE1vV3g	VIIIK3	cis				
rs1133323	DBP	NΔ	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	1127796	Monocytes (CD14+)	0.0001945	15	72980057	r_tdN3VF1vV3g	VUIK3	cis				
rs1133323	DBP	NΔ	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	4886636	Visual cortex (all samples)	2 80F-04	15	72983229	10023814330	MPI	cis				
rc1133323	DBP	NA	COX5A:SCAMP2:RDP25:C15orf17:MPI	13	LDproxy(CEU_Rel2	0.967 rs	1130741	Monocytes (CD14+)	0.0003045	15	72976983	r tdN3VE1vV3o	1111143	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU_Rel2	0.967 rs	4886636	Liver(IIChicago)	0.000119825	15	72983229	A 23 P60579-A	MDI-SCAMD2	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-Rel2	0.967 rs	4886636	Blood/Febrmann et al)	1 60E-19-1 10	15	72983229	3170239-50341-4	CSK-SCAMP2-ULK3-C	cis				
rc1122222	DBP	NA	COY5A:SCAMP2:RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs	12902515	ICL in asthmatics (Liang 1kg)	4.405-20	15	72948051	2181/13 c at	SCAMP2	cis				
rc1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs	2415251	Whole blood (CHARGE)	1.495-19	15	72079208	4480132	ULK3	cis	-9.05	C	15	72915933
rc1122222	DPD	NA	COX5A;SCAMP2;RPP25;C15orf17;MP1	12	Dproxy(CEU 1kg)	0.966 rc	1996611	ICL in asthmatics (Liang 1kg)	2 225 10	15	72015709	219142 c at	SCAMD2	cis	-5.05			72515555
rc1122222	DPD	NA	COX5A;SCAMP2;RDP25;C15orf17;MP1	12	LDproxy(CEU_1kg)	0.966 rc	11620/12	ICL in asthmatics (Liang 1kg)	2.555.10	15	72020247	210145_5_dt	SCAMD2	cis				
rc1122222	DRD	NA	COY5A:SCAMP2:RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.966 rc	2415251	ICL in asthmatics (Liang 1kg)	2.595-19	15	72029209	210143_3_at	SCAMP2	cis				
rc1122222	DBP	NA	COY5A:SCAMP2:RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.966 rs	2415251	omental	2.085-19	15	73029208	10025911267	PDD25	cis				
rc1133323	DBP	NA	COY5A:SCAMP2:RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs	2415231	ICL in asthmatics (Liang 1kg)	4 75E-19	15	73029208	218143 s at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs	2415245	LCL (MuTHER)	4.195-08	15	73029208	UMN 1761262	MPI	cis				
rc1122222	DPD	NA	COX5A;SCAMP2;RDP25;C15orf17;MP1	12	LDproxy(CEU_1kg)	0.966 rc	2415251	Subs adipose (MuTHER)	2.095.05	15	72020200	ILMNL 2264525	SNUDN	cis				
rc1122222	DRD	NA	COV5A:SCAMP2:RPP25;C15orf17;MPI	12	LDproxy(CEU-1kg)	0.966 rc	2415251	Skip (MuTHER)	2.050-05	15	72020200	ILMN 1679495		cis				
151155525	DBP	NA	COX5A,SCAMP2,RPP25,C15orf17,MPI	13	LDproxy(CEU_1kg)	0.900 15	2413231	Beolic (CD19+)	2.402-05	15	73029200	ub+12+10/3433		cis				
151155525	DBP	NA NA		13	LDproxy(CEU-1kg)	0.900 15	11054704	I CL in asthmatics (Linna 1kg)	3.172-03	15	73029200	0011211VV7_2_FC	MDI	cis				
151133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.905 15	11630010	Whole blood (CLARCE)	4.902-28	15	73008008	202472_at		cis	0.70	-	15	72015022
151133323	DBP	NA NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.905 15	11620010	(Charde)	1.20E-22	15	72942949	4460152 218142 c at	SCAMP2	cis	-9.79		13	/2913935
151133323	DBP	NA NA	COX5A,SCAMP2,RPP25,C15orf17,MPI	10	LDproxy(CEU-H3)	0.903 15	11620010	LCL (MUTUER)	1.54E-20	15	72542545	210145_5_dt	SCAWP2	cis				
151133323	DBP	INA NA	CONSA, SCAMP2;RPP25;C150(117;MPI	13	LDproxy(CEU-H3)	0.905 15	11620010	LUDG	0.40E-U8	15	72942949	100161996 701	IVIPI	cis				
151133323	DBP	NA NA	CONJA;SCAMP2;RPP25;C150ff17;MPI	13	LOPIOXY(CEU-H3)	0.905 FS	11630012	Lung	2.801-00	15	72942949	100101886_IGI_	CAMP2	cis				
151133323	DBP	INA NA	COX5A;SCAMP2;RPP25;C150ff17;MPI	13	LOproxy(CEU-H3)	0.965 FS	11630918	Skin (WUTHER)	4.23E-00	15	72942949	LIVIN_10/9495	ULK3	CIS				
rs1133323	DRP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965 rs	11630918	Subc adipose (MUTHER)	3.//E-05	15	72942949	ILIVIN_16/9495	ULK3	CIS				
rs1133323	DBD	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LUProxy(CEU-H3)	0.965 FS	11030918	BCEIIS (CD19+)	5.10E-05	15	72942949	upt12tiW/_Z_F0	JUSK	CIS				
rs1133323	DBD	NA NA	COX5A;SCAMP2;RPP25;C150fT1/;MPI	13	LUPROXY(CEU-1kg)	0.932 rs	12913293	LCL in asthmatics (Liang 1kg)	5.44E-29	15	/29/1511	2024/2_at	MPI	CIS				
151133323	DBP	NA	CUX5A;SCAMP2;RPP25;C150rf17;MPI	13	LUPROXY(CEU-1kg)	0.932 rs	8025447	LCL III asthmatics (Liang 1kg)	1.59E-28	15	72979275	202472_at	MPI	CIS				
rs1133323	DRb	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LUPROXY(CEU-1kg)	0.932 rs	1730/838	LCL In asthmatics (Liang 1kg)	3.26E-28	15	/2994925	2024/2_at	MPI	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LUproxy(CEU-1kg)	0.932 rs	12904897	LCL in asthmatics (Liang 1kg)	3.85E-28	15	73004739	202472_at	MPI	cis				

				_	r^2 t	D		eSNP P					type of eQTL			Probe	Probe
IndexSNP	Traits	InRefGene	RefGenes60kb	Locus# Index/LD status	inde	k eSNPid	Tissue	value	Chr	B36pos	ArrayID	Transcript	(cis or trans)	Beta	Allele	Chromosome	Position
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-1kg	) 0.93	2 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)	0.93	l rs12487	Monocytes	5.36E-26	15	72923747		ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-H3)	0.93	L rs12487	Whole blood (CHARGE)	3.69E-24	15	/2923/4/	4480132	ULK3	CIS	-10.14	С	15	/2915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-H3)	0.93	L rs12487	LCL in astrimatics (Liang 1kg)	9.19E-21	15	/2923/4/	218143_s_at	SCAMP2	CIS				
r51133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-H3)	0.93	L rs12487	LCL (MUTHER)	2.3/E-0/	15	72923747	ILMIN_1/61262	MPI	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-H3)	0.93	L rs12487	Skin (MuTHER)	3.95E-06	15	72923747	ILMN_1679495	ULK3	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;CI50rT17;MPI	13 LDproxy(CEU-H3)	0.93	L rs12487	Subc adipose (MUTHER)	4.58E-05	15	72923747	ILMIN_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	/29264/9	218143_s_at	SCAMP2	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Whole blood (CHARGE)	3.44E-23	15	/2912698	4480132	ULK3	CIS	-9.92	С	15	/2915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel.	2: 0.87	3 rs6495122	LCL in astrimatics (Liang 1kg)	4.34E-20	15	72912698	218143_5_at	SCAMP2	CIS				
r51133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel.	2. 0.87	3 rs6495122	Cerebellum (Alzheimer's)	7.49E-10	15	72912698	10025927424	ULK3	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Bcells (CD19+)	3.92E-07	15	72912698	ubt12tlW7_Z_FC	DCSK	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Lymph	4.4/E-0/	15	/2912698	GI_39930360-S	ULK3	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	LCL (MuTHER)	6.72E-07	15	72912698	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Skin (MuTHER)	5.50E-06	15	72912698	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Subc adipose (MuTHER)	3.13E-05	15	72912698	ILMN_1695271	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Monocytes (CD14+)	9.64E-05	15	72912698	r_tdN3VF1vV3q	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel:	2: 0.87	3 rs6495122	Blood	0.0002728	15	72912698	HSG00290189	ARID3B	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.87	3 rs6495122	Lung	<2E-16	15	72912698	100312245_TGI_	a RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel)	2: 0.87	3 rs6495122	Blood(Fehrmann et al)	1.00E-25;1.5	( 15	72912698	3170239;448013	2 CSK;ULK3;SCAMP2;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-1kg	0.83	2 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	0.83	2 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	0.80	3 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	0.80	L 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	0.80	L 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	0.80	L rs35556055	Bcells (CD19+)	0.0001316	15	73040467	ubt12tlW7 Z FC	CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-H3)	0.79	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)	0.79	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 LDproxv(CEU-H3)	0.79	rs2290573	LCL (MuTHER)	3.57E-07	15	72916647	ILMN 1761262	MPI	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13 LDproxv(CEU-H3)	0.79	rs2290573	Skin (MuTHER)	8.85E-06	15	72916647	ILMN 1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13 LDproxy(CEU-1kg	0.79	3 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 IDproxy(CEU-1kg	0.79	3 rs62029217	ICL in asthmatics (Liang 1kg)	3.24E-18	15	73048952	218143 s at	SCAMP2	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13 IDproxy(CEU-1kg	0.77	rs12912343	I CL in asthmatics (Liang 1kg)	1.30E-18	15	73038094	218143 s at	SCAMP2	cis				
rs1133323	DBP	NΔ	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 IDproxy(CEU-1kg	0.76	7 rs4886413	I CL in asthmatics (Liang 1kg)	3 29E-18	15	73049363	218143 s at	SCAMP2	cis				
rc1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13  Dproxy(CEII-1kg	0.75	rs11072518	Whole blood (CHARGE)	1 575-34	15	73021663	4480132	LILK3	cis	12.26	т	15	72915933
rc1122222	DPD	NA	COV5A;SCAMD2;RDD25;C15orf17;MD1	13 LDproxy(CEU 1kg	0.75	rc11072518	omental	1.115.12	15	72021662	10022914220	MDI	cis	12.20		15	72515555
rc1122222	DRD	NA	COV5A;SCAMP2;RPP25;C15orf17;MP1	13 LDproxy(CEU-1kg	0.75	rc11072518	Subcadinose (MuTHER)	9.695.09	15	72021662	ILMN 1679495		cis				
re1122222	DRD	NA	COVEA:SCAMP2;RPP25;C15orf17;MP1	13 LDproxy(CEU 1kg	0.75	rc11072518	Jumph	8 135 09	15	73021003	CL 4505224 S	MDI	cis				
151155525	DBP	N/A	COX5A,SCAMP2,RPP25,C150117,MP1	13 EDproxy(CEU-1kg	0.75	1511072518	LCL (MUTUER)	6.12E-00	15	73021003	GI_4000254-5	MPI	cis				
151133323	DBP	NA	COX5A;SCAMP2;RPP25;C150H17;MPI	13 LDproxy(CEU-1kg	0.75	1511072518	ECE (MUTHER)	3.2/E-07	15	73021003	ILIVIN_1701202		cis				
151133323	DBP	NA NA	COX5A;SCAMP2;RPP25;C150(117;MP1	13 EDproxy(CEU-1kg	0.75	1511072518	Skin (Muther)	7.092-07	15	73021003	ILIVIN_1079495	ULK5	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C150f117;MPI	13 LDproxy(CEU-1kg	0.75	11072518	Bcells (CD19+)	3.32E-00	15	73021003	UDT12t1VV7_2_FC	J LSK	CIS				
151133323	DBP	NA	COXSA;SCAMP2;RPP25;CISOTI7;MPI	13 LDproxy(CEU-1kg	0.75	1511072518	Prefrontal cortex (Alzheimer's)	3.32E-04	15	73021003	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;CI50rT17;MPI	13 LDproxy(CEU-1kg	0.75	rs11072518	Monocytes (CD14+)	0.000374	15	/3021663	r_taN3VF1VV3q	VULK3	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-1kg	) 0.75	rs110/2518	Blood(Fehrmann et al)	1.90E-27;7.9	15	/3021663	31/0239;448013	2 CSK;ULK3;COX5A;SC	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.70	3 rs2290572	Whole blood (CHARGE)	2.42E-29	15	/291/626	4480132	ULK3	CIS	11.25	A	15	/2915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15ort17;MPI	13 LDproxy(CEU-Rel	2: 0.70	3 rs2290572	LCL (MuTHER)	1.67E-07	15	72917626	ILMN_1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.70	3 rs2290572	Subc adipose (MuTHER)	1.58E-06	15	72917626	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel	2: 0.70	3 rs2290572	Bcells (CD19+)	5.64E-06	15	72917626	ubt12tIW7_Z_FC	DCSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13 LDproxy(CEU-Rel:	2: 0.70	3 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	С	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	Α	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	С	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	Т	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	Т	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	Α	20	57003893
rs6092743	DBP/SBP/MAP	NA	NA	14 LDproxy(CEU-1kg	0.91	5 rs1465537	Whole blood (CHARGE)	2.37E-08	20	57131415	4220259	CTSZ	cis	5.58	Т	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.

						SBP, mmHg,	DBP, mmHg,
					Anti-	adjusted for	adjusted for
	Age,	BMI,	SBP, mmHg	DBP,	hypertensive	antihypertensive	antihypertensive
Ν	years (sd)	kg/m2 (sd)	(sd)	mmHg (sd)	therapy (%)	therapy (sd)	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 Asso	ciation Res	ults		
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGenes	ClosestRe	Direction	Beta	s.e.	Р	Trait		SNPID	Beta	s.e.	Р
CHARGE_LTA - DBP	rs1204627	1	10722164	t	С	CASZ1	CASZ1	CASZ1	?	-0.3223	0.0597	2.29E-07	GBPG	/1-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	с		KCNK3;CII	KCNK3	+	-0.2814	0.0534	4.25E-07	GBPG	/1-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	а	t	MDS1	MDS1	MDS1	+++++++++	0.2738	0.0522	4.96E-07	GBPG	1-DBP	rs1528293	0.2427	0.0769	0.00161
CHARGE_LTA - DBP	rs1952650	5	157746045	а	t			EBF1	++++-++++	0.2862	0.0523	1.58E-07	GBPG	/1-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	с	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	а	t			PDE3A	+++++++++	0.3604	0.0651	1.09E-07	GBPG	/1-DBP	rs1084142	0.3446	0.0941	0.0002492
CHARGE LTA - DBP	rs2681472	12	88533090	a	q	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	с		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	a	RGL3	EPOR:EL/	RGL3	??	-0.3913	0.0729	2.67E-07	GBPG	1-DBP	rs167479	-0.942	0.597	0.1146
CHARGE LTA - DBP	rs6092743	20	57133765	a	q			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	a	MTHER	MTHFR:N	MTHER	+++++++++	0.8795	0.1235	6.38E-12	GBPG	V1-SBP	rs1330656	0.7349	0.1646	0.000007978
CHARGE I TA - SBP	rs2004776	1	228915325	t	c	AGT	AGT.COG	AGT	+-+++++++	0 5488	0 1049	4 45E-07	GBPG	/1-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	2	a	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	/1-SBP	rs9823197	-0 2888	0 1168	0.01344
CHARGE I TA - 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 I TA - SBP	rs1253434	7	27242452	a	0	NA	HOXA13 H	EVX1	?	-1 5903	0 292	1 48E-07	GBPG	/1-SBP	rs1253434	-0.6512	0.3214	0.04273
CHARGE LTA - SBP	rs1270539	7	106198013	a	g	NA	NA	PIK3CG	++++++-	0 6307	0.202	3 17E-08	GBPG	V1-SBP	rs1270539	0 4007	0 1371	0.003466
CHARGE ITA - SBP	rs1267714	8	11488146	с	9	ΝΔ	BLK	RIK		-0 5272	0.0988	2.60E-07	GBPG	/1_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	0.1210	0 002244
CHARGE I TA - SBP	re7070797	10	63221779	-	9	NA	C10orf107	C10orf107		-0 7415	0 1306	4.30E-08	GBPG	V1-SBP	re7070797	-0.6611	0 174	0 0001443
CHARGE LTA - SBP	rs1926032	10	104819459	t	9	CNNM2	NT5C2·CN	CNNM2		_0.9087	0.1715	3 15E-07	GBPG	/1_SBP	re1026032	-1.0971	0.2137	2 826E-07
	re2681472	12	88533090		с п	ATP2B1	ATP2B1	ATP2R1		0 9457	0.118	1 04E-14	GBPG		re2681472	0 6305	0.1646	0.0001282
CHARGE I TA - SBP	rs4766578	12	110388754	3	+	ATTXN2	SH2B3-AT			-0 5599	0.000	2.82E-09	GBPG	V1-SBD	re/766578	-0.4787	0.1040	0.00006713
CHARGE I TA - SBP	re35444	12	114036820	2		NA NA	+++++-+-4	TRX3	+++++.+.+	0.5452	0.0000	1.02E-03	GBPG	V1-SBD	re35444	0.1568	0.1201	0.00000710
	rc1107251	15	72021662	a •	y o		COVENSE	COVEN		0.5402	0.0923	6.54E.00	GBPG	VI-SDF	re1107251	0.1500	0.1220	0.2003
CHARGE_LITA SBP	rc6002742	20	57422765	-	с а		NA	C20arf174	+++++	0.0032	0.0347	2.255 09	GBPG	VI-SDF	re6002742	0.0040	0.12	0.000102
CHARGE LTA MAD	150092743		07103760	a •	g		NA CAS74	C2001114	+++++++++	0.0390	0.1443	2.200-00	CBBC		150092743	0.0099	0.2202	0.00009393
CHARGE_LTA - MAP	15000310	1	10719403	<b>L</b>	C	CASZI	MTUEDIN	MTUED	?	-0.4097	0.007	0.49E-11	GBPG		15000315	-0.244967	0.108505	0.023966954
CHARGE_LIA - MAP	rs1330656	1	11/88391	a	g	MINER	MITHER;N		++++-++++	0.6133	0.0832	1.83E-12	GBPG		rs1330606	0.0469	0.11/48	3.23009E-06
CHARGE_LIA - MAP	rs2004//6	1	228915325	t	C	AGI	AG I;COG	AGI	+++++++++	0.4226	0.0708	1.18E-08	GBPG	V1-MAP	rs2004//6	0.1149	0.099071	0.246143016
CHARGE_LIA - MAP	rs12/5988	2	26/6/868	t	C	NA	KCNK3;C	KCNK3	+	-0.3894	0.0616	1.51E-09	GBPG	V1-MAP	rs12/5988	-0.16	0.083983	0.056759651
CHARGE_LTA - MAP	rs6/12094	2	164/51/06	а	g	NA	NA	GRB14	++++-++++	0.385	0.0677	5.42E-08	GBPG	1-MAP	rs6/12094	0.2/13	0.092326	0.003297944
CHARGE_LTA - MAP	rs1528293	3	170637205	а	t	MDS1	MDS1	MDS1	+++++++++	0.3361	0.0602	9.29E-08	GBPG	V1-MAP	rs1528293	0.279367	0.083395	0.000808377
CHARGE_LTA - MAP	rs//28845	_5	122933582	а	g	CSNK1G3	CSNK1G3	CSNK1G3	+++++++++	0.3766	0.0712	4.34E-07	GBPG	1-MAP	rs//28845	0.3521	0.099069	0.000379275
CHARGE_LTA - MAP	rs198846	6	26215442	а	g	NA	HIST1H2B	HISTIHIT	++++++++	0.4829	0.085	5.69E-08	GBPG	V1-MAP	rs198846	0.5286	0.120456	1.1423E-05
CHARGE_LTA - MAP	rs//94193		27261226	а	g	NA	HOXA13;E	EVX1	+-+-	-0.914	0.1724	4.03E-07	GBPG	V1-MAP	rs//94193	-0.296533	0.205208	0.148447395
CHARGE_L TA - MAP	rs1225896	10	18/6/965	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	CHARGE DISCOVERYGBPG 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	а	t	NA	NA	PDE3A	+++++++-	0.4081	0.0749	1.91E-07	GBPG \	/1-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	с	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	3 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	5 t	g	RGL3	EPOR;EL	RGL3	+-??	-0.4521	0.0839	2.60E-07	GBPG \	/1-MAP	rs167479	-0.848267	0.716338	0.236345161
CHARGE_LTA - MAP	rs6092743	20	57133765	i a	g	NA	NA	C20orf17	+++++++++++++++++++++++++++++++++++++++	0.6372	0.0971	3.60E-10	GBPG	V1-MAP	rs6092743	0.512833	0.156357	0.001038468
CHARGE_LTA - PP	rs880315	1	10719453	3 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	3 t	с	NA	C5orf23;N	C5orf23		-0.3328	0.0629	2.57E-07	GBPG \	/1-PP	rs7733331	-0.2292	0.083972	0.006343693
CHARGE_LTA - PP	rs1094807	6	43388691	t	с	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	3 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	2 t	g	TCF7L2	TCF7L2	TCF7L2	+++++++++	0.3527	0.0676	3.71E-07	GBPG \	/1-PP	rs1225537	0.0856	0.093633	0.360610278
CHARGE_LTA - PP	rs2681485	12	88549753	3 a	g	ATP2B1	ATP2B1	ATP2B1	++++-++++	0.3373	0.0627	1.61E-07	GBPG \	/1-PP	rs2681485	0.1402	0.08435	0.096489798
CHARGE_LTA - PP	rs1077479	12	114036981	t	С	NA	NA	TBX3	+	-0.3362	0.0649	4.61E-07	GBPG \	/1-PP	rs1077479	0.0242	0.085378	0.776834436
CHARGE_LTA - PP	rs672154	20	10421266	a a	g	C20orf94	MKKS;C20	C20orf94	+	-0.3288	0.0629	3.54E-07	GBPG \	/1-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	/1-PP	rs6077869	0.11	0.098691	0.265026095

Rows in **bold** show LTA analysis P values <  $5 \times 10^{-8}$ .

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

Number of significant SNPs										
	<i>P</i> value < 5x10 <sup>-8</sup>									
	#LTA SNPs	#V1 SNPs								
SBP	117	122								
DBP	96	126								
MAP	155	153								
PP	120	1								
Total	488	402								

Numbe	Number of significant Loci										
	<i>P</i> value < 5x10 <sup>-1</sup>	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 <i>P</i> 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 <i>P</i> 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 <i>P</i> 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 <i>P</i> 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	SBP	SBP	SBP
	V I	٧Z	٧J	V - T
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 Star	Position End	# SNPs	DPvalue	D+.Pvalue	DPvalue	D+.Pvalue
LTA	SBP	rs13306561	а	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	а	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	а	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	а	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	а	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	а	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	а	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	а	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	а	7p13	45960903	NA	IGFBP3	IGFBP3	2.94E-08	6.88E-06	45929639	45960903	49	1	<0.0001	1	<0.0001
LTA	PP	rs12705390	а	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	а	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	а	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	С	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	а	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	С	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	а	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	С	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	а	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	а	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	а	2q11	96715567	NA	FLJ10081;FER1L5;L	FER1L5	2.91E-08	6.54E-08	96715567	rs7599598	1	1	0.4993	1	0.5046
No difference	DBP	rs1801253	С	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	а	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	С	10q25	115795046	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 0.0071	1BX3	3.20E-08	8.38E-07	114036820	114039913	14	0.7605	0.3228	0.7945	0.2617
No difference	PP DC	rs880315	t	1p36	10/19453	CASZ1	CASZ1	UASZ1	5.45E-09	3.31E-06	10/13384	10/22164	6	0.8323	0.1492	0.8929	0.1943
No difference	۲۲	1812031867	а	J3p24	30437485	INA	INA	I GFBRZ	0.023903474	9.25E-10	30437485	IS12031807	1	0.0002	1	0.0043	1

### SUPPLEMENTAL COHORT DESCRIPTIONS

### **Cohort Descriptions**

#### **Discovery cohorts**

The CHARGE Consortium<sup>1</sup> 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<sup>2-4</sup> and HapMap reference panels<sup>5</sup> 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<sup>4,6</sup>. 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<sup>4,6</sup>.

### AGES Reykjavik

The Age Gene/Environment Susceptibility-Revkjavik (AGES- Revkjavik) 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.<sup>7</sup> 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.

### <u>ARIC</u>

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<sup>8</sup> 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.

# <u>CARDIA</u>

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.<sup>17</sup> 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 selfreport and principal component analysis using genome-wide genotypes.

# <u>CHS</u>

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<sup>9</sup>. 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.

# <u>FHS</u>

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.<sup>10-12</sup> 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.

# <u>MESA</u>

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.<sup>15</sup> 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.<sup>16</sup> 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.<sup>13</sup> 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.

# <u>WGHS</u>

The Women's Genome Health Study (WGHS)<sup>14</sup> 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,  $\geq$ 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  $\geq$  140 or DBP  $\geq$  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 metaanalysis have been previously reported.<sup>18</sup> Adjustment was performed for the use of antihypertensive 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.

### <u>Peking University – University of Michigan Study of Atherosclerosis (PUUMA) Beijing</u> <u>Shijensheng Cohort</u>

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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### 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<sup>-8</sup> are shown in red, and regions reaching *P* value < 5x10<sup>-7</sup> 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)







(C)





### 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.



SBP; locus MTHFR, rs13306561, chr1:11775103-11851301,1p36









NPR3



SUB1



PIK3CG

C7orf74



CTort74

PIK3CG

SBP; locus PIK3CG, rs12705390, chr7:106192878-106203703,7q22

17



(a7)













CLCN6

PLOD1

MFN2

MIIP

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



(a11)



DBP; locus HIST1H2BC, rs198823, chr6:26065371-26233321,6p22




DBP; locus SH2B3, rs3184504, chr12:110368991-111390798,12q24



MTHFR CLCN6

AGTRAP

C10/1187

FBX02 FBX044 FBX06 MAD2L2

NPPB

KIAA2013

PLOD1

MFN2

MIIP

MAP; locus MTHFR, rs13306561, chr1:11772952-11847887,1p36



MAP; locus KCNK3, rs1275988, chr2:26765249-26786300,2p23





(a17)







PP; locus CRIP3, rs10948071, chr6:43367990-43472472,6p21



(a20)



(a21)







SBP; locus COX5A, rs11072518, chr15:72820453-73029208,15q24



(b4)







(b6)









PP; locus ULK4, rs7650227, chr3:41725264-42040009,3p22

41



(d1)



SBP; locus CACNB2, rs12258967, chr10:18726458-18796887,10p12



SBP; locus ATP2B1, rs2681472, chr12:88465680-88637201,12q21



SBP; locus TBX3, rs35444, chr12:114036820-114039913,12q24





DBP; locus FER1L5, rs7599598, chr2:96715567-96715567,2q11



DBP; locus CACNB2, rs12258967, chr10:18745126-18780638,10p12



DBP; locus ADRB1, rs1801253, chr10:115779365-115795046,10q25







MAP; locus AGT, rs2004776, chr1:228882807-228929783,1q42



MAP; locus CACNB2, rs12258967, chr10:18726458-18796887,10p12









CASZI

PEX14



C1ort127

**Figure S8**. K-S test comparison cumulative fraction plot, where x-axis is the  $-\log 10(P)$  values and y-axis is the cumulative fraction.



K-S Test Comparison Cumulative Fraction plot, D(lta-v1)+= 0.12,P=0.0067; D(lta-v1)-= 0.13,P=0.0032

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  $-\log 10(P \text{ values})$  within each region meeting criteria for genome-wide significance ( $P \text{ value} < 5x10^{-8}$ ). Regions with at least one marker with  $P \text{ value} < 5x10^{-8}$  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  $-\log 10(P \text{ value})$ .

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

				Age,	BMI,	SBP,	DBP,	Anti-hypertensive
		Year	N	years (sd)	kg/m2 (sd)	mmHg (sd)	mmHg (sd)	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 S2: Cohort summaries across all visit included in the analyses

## Table S3: Genomic control inflation factors ( $\lambda_{GC}$ ).

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

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

#### LTA - MAP

									Meta-
ARIC	CHS	FHS	RS1	RS2	AGES	WGHS	MESA	CARDIA	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

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

#### Visit 1 - DBP

									Meta-
AGES	ARIC	CHS	FHS	RS1	RS2	WGHS	MESA	CARDIA	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	CLCNB	972
LTA-SBP	rs1275979	2p23	26777072 t	с	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	9	1.1766	0.1994	1.23E-08	********	NPPA	MTHER;NPPA;CLCN6;NPPB	NPPA	199
LTA-SBP	rs11105354	12q21	88550654 a	9	0.9429	0.1186	1.69E-14	****	ATP2B1	ATP2B1	ATP2B1	23321
LTA-SBP	rs13031603	2q24	164803435 t	С	-0.582	0.0996	1.71E-08	+	NA	NA	GRB14	254143
LTA-SBP	rs10774625	12q24	110394602 a	9	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	с	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	9	0.8355	0.1225	4.60E-11	********	MTHER	MTHFR;NPPA;CLCN6;NPPB;AGTRAP	MTHER	3337
LTA-SBP	rs13035163	2q24	164781173 a	9	0.5775	0.0996	2.22E-08	++++-++++	NA	NA	GRB14	276405
LTA-SBP	rs13035934	2q24	164781318 a	9	-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	с	-0.577	0.0995	2.23E-08		NA	NA	GRB14	254311
LTA-SBP	rs1173743	5p13	32810804 t	9	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	9	-0.5763	0.0995	2.28E-08		NA	NA	GRB14	268654
LTA-SBP	rs6100343	20q13	57133607 a	9	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	12g21	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	15g24	72856335 t	c	-0.5733	0.1004	3.58E-08		NA	CYP1A2 CYP1A1 CSK LMAN1L CPLX3 ULK3	CSK	5432
LTA-SBP	rs6707357	2024	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	7	CASZ1	CASZ1	CASZ1	59841
LTA-SBP	rs2166122	10021	63193080 t	c	-0.6435	0.1137	4.75E-08		C10orf107	C10of107	C10orf107	3015
LTA-SBP	rs653178	12024	110492139 t	c	-0.5508	0.0902	3 76E-09		ATXN2	ATXN2	ATXN2	29724
LTA-SBP	rs13034053	2024	164784645 a		-0 5762	0.0996	2 34E-08		NA	NA	GRB14	272933
LTA-SBP	rs4842667	12021	88490785 a	a	0.5579	0 0894	1.69E-09	****	NA	ATP2B1 WDR51B GALNT4	ATP2B1	15173
LTA-SBP	rs284277	1036	10713384 a	c	-0.7091	0.1044	5.54E-11	7	CASZ1	CASZ1	CASZ1	65910
LTA-SBP	rs1275982	2023	26772593 t	c .	-0.5881	0.0919	6 56E-10		KCNK3	KCNK3 CIB4	KCNK3	3471
LTA-SBP	rs6100342	20013	57132658 a	c	-0.7232	0.127	3.89E-08		NA	NA	C20orf174	66813
LTA-SBP	rs11072518	15024	73021663 t	c	0.5692	0.0947	6 54E-09	*****	NA	COX5A SCAMP5 RPP25 C15orf17 MPI	COX5A	4238
ITA-SBP	rs1401982	12021	88513730 a	a	0.6828	0.0906	3.59E-13	*****	ATP2B1	ATP2B1	ATP2B1	7772
LTA-SBP	rs998981	20013	57133036 t	c	0.7246	0.1271	3.78E-08	*****	NA	NA	C20orf174	66433
ITA SBP	rs2070759	12021	88541867 t	0	0.5881	0.0902	3 19E-10		ATP2B1	ATP281	ATP2B1	32108
LTA-SBP	rs12442901	15024	72870965 a	a	0.5675	0.1	4.34E-08	********	CSK	CPLX3 CYP1A2 SCAMP2 CSK ULK3 MAN1L	CSK	9198
LTA-SBP	rs11014049	10p12	18726458 a	a	-0.5453	0.0964	4 77E-08		CACNB2	CACNB2	CACNB2	3060
LTA-SBP	rs13306561	1p36	11788391 a	a	0.8795	0.1235	6 38E-12	********	MTHER	MTHER:NPPA-CLCN6:NPPB-AGTRAP	MTHER	311
LTA-SBP	rs1439214	2g24	164778248 t	c	-0.5791	0.0997	2.07E-08		NA	NA	GRB14	279330
LTA-SBP	rs2681492	12021	88537220 t	c	0.8967	0 1158	7 18E-14		ATP2B1	ATP281	ATP2B1	31262
LTA-SBP	rs2168519	15g24	72867925 t	c	0.5879	0.0999	4.18E-08	++++++++++	CSK	CYP1A2 CSK LMAN1L CPLX3 SCAMP2 ULK3	CSK	6158
ITA-SRP	rs1275977	2n23	26776359 a		-0.5862	0.099	1.11E-08		KCNK3	KCNK3 CIB4	KCNK3	7237
I TA-SBP	rs492945	1036	10723185 a	9	-0.5838	0 1005	2 10E-08	?	CAS71	CAST	CAS71	56109
ITA-SBP	rs13027527	2024	164786950 a	0	-0.5768	0.0995	2 19E-08		NA	NA	GRB14	270628
ITA SBP	re11105364	12021	88593407 t	9	0.9392	0 1197	3.81E-14		NA	ATP281	ATP2B1	19432
ITA-SBP	rs13021222	2024	164756151 c	0	-0.5902	0 1008	1.60E-08		NA	NA	GRB14	301427
ITA SBP	re12579302	12021	88574634 a	9	0.9342	0 1194	4 31E-14		NA	ATP281	ATP2B1	659
ITA.SBP	rs35441	12024	114037498 1	9	-0 5471	0.0933	1.54E-08		NA	NA	TBX3	431146
ITA SBP	re17376328	1036	11700240 9		1 1341	0 1958	2 265-09		CLONE	MTHED-NPPA-CLCNS-NPPR	CLCNS	10458
I TA-SBP	re9292488	5013	32854830		-0.5451	0.0911	7 78E-00		NA	C5-d23 NPD3	C5orf23	27254
ITA COD	re13006494	2024	164789612		0.5759	0.0005	2 355 00		NA	NA	GRB14	287966
ITA SPD	re4788679	12024	110388754 a		0.5500	0.0000	2.80E-00		ATYN2	SH2R3 ATVN2	ATXN2	14363
ITA COP	154700578	7022	106199094		-0.8333	0.1108	3 48E 00		NA	NA	PIK3CG	94065
I TA COD	13114/11/1	12021	0000100004 1		0.7644	0.1100	3.40E-08		NA	ATC2D1	ATDOD	67460
LTA CDD	1511100383	10012	10750072 a	-	0.7044	0.1329	1.075.00	********	CACNES	CACNER	CACHIDO	27255
LTA COD	154548524	2022	16/308/3 a	9	0.044	0.0935	2.615 40	*******	CACINEZ NA	KONK2-CIE4	CAGNE2	1360
LTA COD	1512/0988	2023	20/0/000 T	C .	-0.0004	0.0000	2.01E-10	++	CEV	CDI V2-CVD142-CCAUD2-CEV-III V2-I MANU	CEK	2420
LTA COD	152301249	2-24	120/943/ t	c	0.000	0.0990	9.13E-08	********	NA	UPLAS, OTPINE, SUMMPE, USK, ULKS, LMANTL	CODIA	200204
LTA-SBP	150/20/40	2024	104/303/4 1	g	0.5849	0.0000	2.10E-08	*****	NIA.	310	CDD14	202074
LTA ODD	151108/999	2024	104//4004 [	C	0.5809	0.0998	1.92E-08	*****	TRA		ATDOD4	202314
LTA-SBP	15/299436	12021	60037201 L	9	0.7672	0.1334	2.84E-08	*******	PS4		AIP2B1	03220
LIA-SBP	190100340	20013	or110007 a	9	-0.7158	0.1201	4.31E-08		1924	195	JLMU2	00111

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Trait SNPID Chr	Position.Bui Allele1	Allele2	Beta	s.e.	P	Direction	InRefGene	RefGenes.60kbfromSNP	ClosestRefGene	DistanceFromClosestRefGene
LTA-SBP rs8033381 15q24	72867738 a	9	-0.5689	0,1	3.97E-08		CSK	CPLX3,CYP1AZ,SCAMPZ,CSR,ULK3,LMAN1L	CSK	59/1
LTA-SBP 1512995799 2024	164/98636 1	C	0.5788	0.0996	2.03E-08	*****	CART	NA CARZI	GRB14 CAR71	258942
LTA SPP 1512040276 1030	164704002 0		-0.707	0.1039	1.585.09		NA		CRD11	262695
TA-SBP rs7070797 10o21	63221779 a		-0.3044	0.1306	4 30E-08		NA	C10od107	C10od107	26884
1TA-SBP rs4886629 15g24	72859611 c	9	-0.5728	0 1004	3.63E-08		NA	CPLX3 CVP1a2 CVP1a1 CSK1II K31 MAN1	CSK	2158
LTA-SBP rs7733331 5013	32864603 t	C	-0.5505	0.0911	5 38E-09		NA	C5orf23 NPR3	C5orf23	37027
LTA-SBP rs4845953 1p36	10724576 a	a	-0.5626	0 0995	4.84E-08	?	CASZ1	CAS71	CASZ1	54718
LTA-SBP rs12656497 5p13	32867696 t	c	-0.5432	0.0911	8.73E-09		NA	C5orf23:NPR3	C5orf23	40120
LTA-SBP rs17249754 12g21	88584717 a	q	-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	с	-0.596	0.092	4.01E-10	+	NA	KCNK3;CIB4	KCNK3	3873
LTA-SBP rs1173771 5p13	32850785 a	9	-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	9	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	9	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	********	CACNBZ	CACNE2	CACNBZ	19286
LTA-SBP 1810//4/92 12024	114036981 t	c	-0.550Z	0.094	1.63E-08		NA CEndos	NA OE-102 NDD2	TBX3	430629
LTA CDD m1225000 2022	32825009 1	C	-0.51/5	0.0890	2.52E-08		CSON23	CODI23,NPR3	C50HZ3	908
LTA SPP (51275960 2023	10747454 1	C	-0.5947	0.0919	4.10E-10		CACNES	CACNICS, GID4	CACNES	17026
LTA-SBP (\$6676300 1036	11847887 a	0	0.5541	0.0900	1.40E-08	******	NA	MTHER KIAA2013 NPPA CLONG NPPB	NPPR	6308
LTA-SBP rs12567136 1p36	11806318 t	9	0.8529	0 1222	1.63E-11		CLONG	MTHER NPPA CLONG NPPB	CLONG	4544
LTA SBP rs2681472 12021	88533090 a	0	0.9457	0.118	1.04E 14		ATP2B1	ATP2B1	ATP2B1	27132
LTA-SBP rs17037425 1p36	11792970 a	a	-0.8574	0.1292	1.51E-10		CLCN6	MTHER NPPA CLCN6 NPPB AGTRAP	CLCN6	4177
LTA-SBP rs1371181 2g24	164784974 t	c	0.5764	0.0995	2 28E-08	++++++++++	NA	NA	GRB14	272604
LTA-SBP rs10432461 2g24	164772752 a	1	-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	9	-0.9371	0.1197	4.21E-14	+	NA	ATP2B1	ATP2B1	24597
LTA-SBP rs13007966 2q24	164784819 t	с	-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	9	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	9	-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		MTHER	MTHER:NPPA;CLCN5;NPPB;AGTRAP	MTHER	5272
LTA-SBP r\$11/3/66 5013	32840285 t	c	-0.5294	0.0917	2.52E-08		CACUER	C50HZ3/NPK3	C50ff23	12/09
LTA DPD	72001070	c	-0.3019	0.0937	4.97E-09		CACNE2		CAGND2	21003
LTA-DBP 1511072512 15q24	72991079 1	0	0.3159	0.0525	7 79E-00		MPI	COY6A SCAMP2, REP25, C150F17, MPI	MPI	3261
TA DBP rs7537765 1036	11809890 a	9	0.4718	0.0714	2 36E-10		CLONG	MTHER NPBACI CNR NPBB	CLONG	972
LTA-DBP rs7085 15024	72882536 t	9	0.3468	0.0582	1 10E-08		CSK	CYPTA2 CSKI MAN1I CPI X3 SCAMP2 II K3	CSK	21
LTA-DBP r5198833 6022	26222487 a	0	-0.4345	0.0741	191E-08		NA	HIST1H1T HIST1H2BD HIST1H2BC HIST1H1E HEE HIST1H1C HIST1H4C HIST1H2AC	HIST1H1T	6144
LTA-DBP rs6495127 15g24	72981543 t	c	-0.3262	0.0571	4.40E-08		C15orf17	COX5A:MPI:SCAMP2:RPP25:C15orf17:ULK3	C15orf17	2163
LTA-DBP rs11105354 12g21	88550654 a	g	0.5235	0.0696	5.40E-13	+++++	ATP2B1	ATP2B1	ATP2B1	23321
LTA-DBP rs12246717 10g21	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	9	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	9	0.3166	0.0553	3.98E-08	********	CSK	CYP1A2;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	7838
LTA-DBP r54842666 12q21	88465680 t	c	0.5108	0.0745	4.88E-11	*******	NA	ATM281,WURD18(GALN14	WDR51B	21/12
LTA DBD re11070514 45-04	11/85305 a	9	0.4098	0.0/1/	7.01E-10	+++++++++++	SCAND3	COVER MENT AND COLVER CAMPERIA CAMPERIA CAMPACITIE V2	SCAMD?	3331 6227
TA DBP re17606736 43-34	110071201 a	9	0 3105	0.0526	2 16E-00		C120d30	EDD30/THEN416/C12xd30	C120d20	22225
1TA-DRP rs7136260 12/24	88605319 +	9	-0.3131	0.0536	1.55E-00		NA	ATP2R1	ATP2R1	31344
LTA-DBP rs2681485 12021	88549753 a	a	0 3385	0.053	9 22E-10	****	ATP2B1	ATP281	ATP2B1	24222
LTA-DBP rs1799945 8o22	26199158 c	g	-0.4226	0.074	4.33E-08		HFE	HIST1H2BC HIST1H1C HIST1H3B HIST1H4C HIST1H2BB HIST1H2AC HIST1H1T HIST1H2AB HEE HIST1H3C	HFE	3671
LTA-DBP rs2120702 10021	63192664 a	t	-0.3402	0.0592	3.56E-08		C10orf107	C10orf107	C10orf107	3431
LTA-DBP rs12258967 10p12	18767965 c	q	0.3548	0.0571	2.48E-09	+++-+-+++	CACNB2	CACNB2	CACNB2	38447
LTA-DBP rs16916504 10g21	63122962 a	9	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	9	-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	9	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	9	-0.3534	0.0543	4.52E-10		NA	BRAP,ATXN2,ACAD10	BRAP	9471
LTA-DBP rs936226 15q24	72856335 t	с	-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	G100r1107	C10orf107	3015
LIA-UBP rs653178 12q24	110492139 t	c	-0.3911	0.0524	7.85E-13		ATXN2	ATXNZ	ATXN2	29/24
LTA-DBP rs1378942 15q24	72864420 a	c	-0.3128	0.055	5.00E-08	********	CSK	CYPTA2;CYPTA1;CSK;LMAN1L;CPLX3;SCAMP2;ULK3	CSK	2053
LTA-DBP 1511066320 12024	111390/98 a	9	0.303	0.053	4.11E-08	********	CIONTIOT	C10-1107	C10ed107	1301
LTA DBD rs276606 45-24	03183272 t	C	0.3502	0.0593	1.4/E-08		CTUOH107	CRUX2-SCAMP2-C1Eed17-MPI-CSV-11-V2-1 MAN(1)	C1000107	2023
LTA-DBP re260014 20-12	57102854 +	9	-0.3308	0.0703	1 925-09		MA	C20vrf174	C20ort174	6615
LTA-DBP rs11072518 15c24	73021683	c	0.3405	0.0552	3 29E-00	*****	NA	COX5A SCAMP5 RPP25 C15orf17 MPI	COX5A	4238
LTA-DRP rc8031937 15024	72968174 a	a	0.3264	0.057	4 01E-09	*****	NA	COX5A MPLCPLX3 SCAMP2 C15orf17 ULK3	MPI	1288
			2/28/27	2.991						

Label = 14198         Label = 14198 <thlabel 14198<="" =="" th="">         Label = 1</thlabel>	Trait SNPID Ch	ClosestRefGene DistanceFromClosest		InceFromClosestRefGene
Laber         Construction	LTA-DBP rs1401982 12r	ATP2B1 7772		1
LADDE         Distance         Distance <thdistance< th="">         Distance         <th< td=""><td>LTA-DBP rs11630918 150</td><td>SCAMP2 9774</td><td></td><td>52 <b>-</b></td></th<></thdistance<>	LTA-DBP rs11630918 150	SCAMP2 9774		52 <b>-</b>
Label Prior         Label Prior         Loss Prior         COCA         POSA         P	LTA-DBP rs12442901 150	CSK 9198		
Linkop         resultion         ATP3B	LTA-DBP (\$13300001 1p)	COVEA 9250		
Link Die         Carbon         Construction	LTA-DBP rs2681492 120	ATP2B1 31262		2
Lin Lobp         model         State         model         Clocked of Mark         Clocked of Mar	LTA-DBP rs2168519 15	CSK 6158		1
Lindpin         Constraint         Sector         ACT         ACT Constraint         ACT         ACT         ACT Constraint         ACT         ACT <td>LTA-DBP rs2393833 10</td> <td>C10orf107 22598</td> <td></td> <td>8</td>	LTA-DBP rs2393833 10	C10orf107 22598		8
Lin Lubp         Interface         State of the state o	LTA-DBP rs2004776 1q	AGT 1239		6 <u>-</u>
LA CLP mitHosh1 1544         720005 a         g         0.310         0.82         5.94 50         mitHosh1 1544         ChenTY         470           LA CLP mitHosh1 1544         720005 a         0.0000         0.000         0.000 <td>LTA-DBP rs4886633 150</td> <td>MPI 4202</td> <td></td> <td>19</td>	LTA-DBP rs4886633 150	MPI 4202		19
LADBP         113522         164         720416         a         g         0.206         495.0         MA         COMMAPSCAMP2PPEC16sH7         COMA         231           LADBP         157202         128.0         0.001         128.0         0.001         128.0         0.001         128.0         0.001	LTA-DBP rs11856413 15r	C15orf17 430		
Like Dep         Constraint         Alf 2001         Constraint         Alf 2001	LTA-DBP rs1133322 15r	COX5A 261		
Lick Leg Pictorsex Pick Pick Pick Pick Pick Pick Pick Pick	LTA-DBP rs11105364 120	ATP2B1 19432		.2
Link Leep         Classifier         Classifi	LTA-DBP rs12579302 120	ATP2B1 659		0
Link Logs         Control         Contro         Control <thcontrol< th=""> <t< td=""><td>LTA DBD #4786579 10</td><td>C1000107 16468</td><td></td><td>8</td></t<></thcontrol<>	LTA DBD #4786579 10	C1000107 16468		8
Link Jobp         endstand         Construct         Closefier         Closefier <thclosefier< th="">         Closefier         <thclosefier< th=""> <thclosefier< th=""> <thclo< td=""><td>LTA DEP (54/005/8 120</td><td>ATR201 67462</td><td></td><td>3 12</td></thclo<></thclosefier<></thclosefier<></thclosefier<>	LTA DEP (54/005/8 120	ATR201 67462		3 12
Lik ADBP         mithod         c         -0.322         0650         2.086.00         MA         COXAMP 200PS C150.017         COXAM         030           Lik ADBP         mithod         5544         7.007.04         0.0319         0.654         2.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.654         7.007.04         0.0319         0.641         0.779         2.0564         0.0319         <	LTA.DBP re1002625 10	C10od107 5301		*
Link Obs         Pristore 1929         Desc         2 and	LTA-DBP rs1133323 15	COX5A 393		
Link Dep         registry	LTA-DBP rs1378940 15	CSK 8780		1
Lin Longer         mining         field         200000         mining         Clisonit         Clisonit <thclisonit< th=""> <thclis< td=""><td>LTA-DBP rs2301249 15/</td><td>CSK 3120</td><td></td><td>)</td></thclis<></thclisonit<>	LTA-DBP rs2301249 15/	CSK 3120		)
LTADE         Prof/Prof 303         Fódd         Prof 2020         MA         CONSUMPLICADIPS         MA	LTA-DBP rs1127796 15/	C15orf17 677		
LTADEP         nr22453         f222         8832201         1         9         0.451         0.779         2.986.8         ************************************	LTA-DBP rs7497393 150	MPI 6952		£1.
LTA DB       refress22       1524       72802949       a       g       0.388       0.989       4.35E.06       LMANIL       CPX       <	LTA-DBP rs7299436 120	ATP2B1 63226		6
LTA DBP         endlesse         6pc.2         2021-6142         a         0         0.437         0.0737         1726 00	LTA-DBP rs7162232 150	LMAN1L 2203		£3
LTA DBP #803381         Hsp4         7287738         a         g         -0.3403         0.0883         217E-08         CSK         CPNA_CYP1A2_SCAMP2_CSK.UKSLUMANIL         CSK         6971           LTA DBP #803381         Hsp4         739727         1021         0.311411         a         0.3782         0.0883         217E-08	LTA DBP rs198816 6p2	HIST1H1T 177	C;HIST1H2AC;HIST1H1T;HFE	
LALBUM         PR20013         2014411         a         g         0.4985         0.0183         2.316.30	LTA-DBP rs8033381 15r	CSK 5971		
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	LTA-DBP rs260013 200	C20ort174 5351		
Lin ADD       rix 0/11/91       1022       1/2 <td>LTA-DBP rs3/50/2/ 100</td> <td>C100ff107 21687</td> <td></td> <td></td>	LTA-DBP rs3/50/2/ 100	C100ff107 21687		
$ \begin{array}{c} \mbox{Lin} Lin Dep \mbox{rel} 1 \mbox{rel} 1 \mbox{rel} 2 \mbox{rel} 1 \mbo$	LTA DBP (\$100097 100	C1001107 20084		2
LTA DBP       98931403       1       0       0.450       0.774       2.21E.08       **********************************       A       ATP281       ATP281       ATP281       ATP281       57428         LTA DBP       959205       1524       923251       1       c       0.353       0.058       4186.08       PTP111       RF0.67EM11       1483         LTA DBP       75388       0.066       4186.08       PTP111       RF0.67EM11       Clorit07	LTA DBP 154660029 150	ATP2P1 10742		2
TA DBP         respansion         SCAMP2         IMPCSR(LMANIL_CPU3)SCAMP2, C15orf17,ULV3         SCAMP2         PTPH11           LTA DBP         respansion         Q         0.3355         0.0568         4.98E.08         PTPH11	LTA-DBP rs11105382 120	ATP2B1 57428		8
LTA_DBP         rs1068301         12224         11135755         a         g         -0.304         0.0322         4.182.08	LTA-DBP rs936230 15	SCAMP2 7902		
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	LTA-DBP rs11066301 12/	PTPN11 14837		17
LTA.DBP       rstord       fsq24       7297683       a       g       0.315       0.0525       s.20E-00	LTA-DBP rs2588992 104	C10orf107 11418		8
LTA-DBP       rs2050265       fp36       1102226       a       g       0.479       0.0715       2.68E-10       ++++++++++++++++++++++++++++++++++++	LTA-DBP rs1130741 150	MPI 635		
LTA-DBP       rs042894       15924       73012468       a       g       -0.311       0.0573       2.97E-06	LTA-DBP rs2050265 1p.	CLCN6 8576		F
LTA-DBP       rs113353       10p12       10f747454       t       c       0.342       0.0568       6.84E-09       ++++++++++++++++++++++++++++++++++++	LTA-DBP rs8042694 15r	COX5A 4957		
LTA-DBP       r529128       6p22       2823321       t       c       -0.4462       0.0749       1.10E-08	LTA-DBP rs1813353 10r	CACNB2 17936		8
LTA-DBF r52415251 15024 7302208 t c 0.3255 0.0548 1.22E-08 ******** NA COX5A, SCAMPS,MPI,MP25,C150117 PP2 (C150117) PP2 (C100) PP3 (	LTA-DBP rs129128 6p2	HIST1H2AC 425	4C,HIST1H2AC,HIST1H1T,HFE	
LIA-DBP r5128/738 1p36 108318 t c - 0.4716 0.0716 2.448-10	LTA-DBP rs2415251 150	RPP25 5287		
LIA DBP       r508142       1242       8853000       a       g       0.3231       0.0091       4.01E-13       AIP281       CXX6A       8507         LTA.DBP       r51107514       f5024       0.0524       6.0524       0	LTA-DBP rs1256/136 1p3	CLCN6 4544		
LTADBP rs103/rs21 lp33       1192/10       a       g       -0.980/       0.0524       2.49E-10	LTA DBP (\$20814/2 120	ATP2B1 2/132		2
LTA-DBP       r5107201       r5107401	LTA DBP 1517037425 103	CLONG 91177		,
LTADBP rs11105388 12Q2       B859857 c       g       -0.5267       0.0704       7.32±13	LTA-DBP (\$3184504 12)	SH2B3 4818		( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( )
LTA-DBP         rs198051         6p22         28212811         t         g         0.4493         0.0777         2.97E-08         ++++++         NA         HISTIN2BD_HISTIN4C_HIS	LTA-DBP rs11105368 120	ATP2B1 24597		7
LTA-DBP         rs11105378         12221         B8814872         t         c         -0.5253         0.0718         2.0346         0.0653         6.57E-09	LTA-DBP rs198851 6p	HIST1H4C 68	C:HIST1H2AC:HIST1H1T:HFE:HIST1H3C	
LTA-DBP         rs198823         6p2         2820912         t         g         -0.3348         0.658         6.57E-09	LTA-DBP rs11105378 12/	ATP2B1 40897		17
LTA-DBP         rst11105329         1224         88640621         a         g         0.4968         0.072         5.59E-11         NA         ATP2B1         WDR51B_GALNT4         WDR51B         22613           LTA-DBP         rst11105329         1229         88640621         a         0.4968         0.077         5.59E-11         NA         ATP2B1	LTA-DBP rs198823 6p2	HIST1H2BC 761	AC,HIST1H1T,HFE	
LTA-DBP rs11105379 12021       88919004 t       c       0.4551       0.0774       1.71E-08       ATP2B1       ATP2B1       45329         LTA-DBP rs11105379 12021       88566073 c       g       0.04551       0.052       582E-10        ATP2B1       ATP2B1       ATP2B1       7702         LTA-DBP rs17037390 1p36       11783430 a       g       0.0487       0.0717       3.70E-10        ATP2B1       ATP2B1       7702         LTA-DBP rs17307390 1p36       11783430 a       g       0.0487       0.0717       3.70E-10        MTHFR       MTP2B1       MTHFR       5272         LTA-DBP rs17307390 1p36       11783430 a       g       0.0487       0.0518       2.82E-10        MTHFR       MTHFR, MPPA,CLCN0,NPPB,AGTRAP       TRAFD1       274         LTA-DBP rs17307391 1p36       11783938       152,47       208174       1.0588       3090-00        NA       CPLX3,CYP142,SCAUP2,CSK,ULK3,LMAN1L       CSK       939         LTA-MAP rs1075851 1202       2855553 a       c       0.0387       0.0618       8.40E-10       +++       NA       C20x174       C20x174       20450       C20x174       20450       C20x174       20450       C20x174       20450 <td>LTA-DBP rs11105328 120</td> <td>WDR51B 22613</td> <td></td> <td>3</td>	LTA-DBP rs11105328 120	WDR51B 22613		3
LTA_DBP rs11105589 12q21 88566273 c g -0.3434 0.053 5.82E-10 — — ATP281 ATP281 ATP281 ATP281 T02 LTA_DBP rs1703739 1bg 16 11783430 a g -0.6487 0.0717 3.70E-10 — — ATP281	LTA-DBP rs11105379 120	ATP2B1 45329		.9
LTA-DBP rs103/390 1p36 11/83430 a g -0.4687 0.0717 370E-10 MTHFR MTH-RNPPA.CLCM8/NPB.AGTRAP MTH-RN 5272 LTA-DBP rs1378938 15q24 111076069 a g 0.3354 0.0539 2.43E-09 NA TTAFD1;C124730 TARD1;C124730 TARD1;C124730 CSK 939 LTA-MAP rs1275986 2p23 26765593 a c -0.3875 0.0616 1.80E-09 NA CCPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L CSK 939 LTA-MAP rs10755914 1221 88555526 t c 0.3913 0.061 8.48E-10 NA CCPLX3;CYP1A2;SCAMP2;CSK;ULK3;LMAN1L CSK 939 LTA-MAP rs1075512 15q24 72991079 t c -0.3902 0.0605 7.19E-10 NA C2047174 C20450 C204174 20450 LTA-MAP rs1075512 15q24 72991079 t c -0.3902 0.0605 7.19E-10 NA C2047174 C2054,SCAMP2;C1504717,MP1 LTA-MAP rs1072512 15q24 72991079 t c -0.3902 0.0605 7.19E-10 NA C2047174 C21504717,MP1 LTA-MAP rs7537765 1p36 11809980 a g 0.0828 0.0605 0.06E-09 NA C2047174 C21504717,MP1 LTA-MAP rs7537756 1p36 11809980 a g 0.0805 0.06E-09 NA C2047174 C21504717,MP1 LTA-MAP rs7537756 1p36 11809980 a g 0.0802 0.982 2.49E-12 CLCN8 MTH-RNPA,CLCN8,NPPB LTA-MAP rs7537756 1p36 11809980 a g 0.0805 0.0824 2.49E-12 CLCN8 MTH-RNPA,CLCN8,NPPB	LTA-DBP rs11105358 120	ATP2B1 7702		6 ·
LTA-UBP rs1753023 15242       111070098 a       g       0.3394       0.0539       2.442-09       11070-017,0120130       1100001       2/4         LTA-UBP rs173023 15242       72803406 t       c       0.3391       0.0588       3090-00       ++++++++       NA       CPUX3CY142SCAMP2.CSK/ULK3LMAN1L       CSK       939         LTA-MAP rs1275980 t223       2676593 a       c       -0.3875       0.0616       1.80E-09       +++++++       NA       KCNK3.GIB4       KCNK3.3539         LTA-MAP rs1075951 t322       88555526 t       c       0.3910       0.618       8.48E-10       +++++++       ATP2B1       ATP2B1       ATP2B1       18449         LTA-MAP rs1075512 t5c24       72991079 t       c       -0.3902       0.0605       7.19E-10       +++++++       NA       C20ort174       C20ort174       20450         LTA-MAP rs1072512 t5c24       72991079 t       c       -0.3902       0.0605       7.19E-10       +++++++       NA       C20ort174       C20ort174       20450         LTA-MAP rs1072512 t5c24       72991079 t       c       -0.3902       0.0605       1.06E-09       ++++++++       NA       C0X6A,SCAMP2,C150rt17,MPI       C150rt17       4664         LTA-MAP rs7527756 1p36       11809690 a       g	LTA-DBP r517037390 1p3	MTHER 5272		
LTA-MAP         rst025986         223         26765533         a         c         0.0371         0.0586         3.902-00          NA         CFCA3_CFT_M2_SCAD_CFT_M2_S	LTA DBD m1270020 15	CEK 020		
LTA.MAP         rs10058914         1224         8855526         t         c         0.3913         0.061         8.48E-10         ++++++         ATP2B1         ATP2B1         18449           LTA.MAP         rs10058914         12241         56770019         a         g         0.5438         0.094         3.20E-08         ++++++         ATP2B1         ATP2B1         18449           LTA.MAP         rs5028747         20013         57770019         a         g         0.5438         0.094         3.20E-08         ++++++         ATP2B1         ATP2B1         2000174         20450           LTA.MAP         rs749739         1524         72991079         c         -0.3902         0.0605         7.19E-10         -++++         NA         C20ort174         20450           LTA.MAP         rs7537765         1924         124479739         1524         72971273         a         9         0.882         9.49819         ++++++         CCX6A, SCAMP2, C150r17, MP1ULK3         MP1         3261           LTA.MAP         rs7537765         1926         11800990         a         g         0.892         2.49E-12         +++++++         CLCN6         MTHER, MPA, CLCN6, MP2B         CLCN6         972           LTA.MA	LTA-MAP rs1275986 20	KCNK3 3539		13 A A A A A A A A A A A A A A A A A A A
LTA-MAP         rs8028747         20q13         57179019         a         g         0.5438         0.094         3.20E-08         +-+++++         NA         C20orf174         C20orf174         20450           LTA-MAP         rs1072512         fcg         72991079         t         c         -0.3902         0.0605         7.19E-10         NA         COX6A, SCAMP2, RPP25, C15orf17, MPI         C15orf17         4564           LTA-MAP         rs7537765         1p36         11800980         a         g         0.882         2.49E-12         ++++++         CLCN8         MTHER MPA, CLCN8, NPPB         CLCN8         972           LTA-MAP         rs7537765         1p36         11800980         a         g         0.982         2.49E-12         ++++++         CLCN8         MTHER MPA, CLCN8, NPPB         CLCN8         972	LTA-MAP rs10858914 12	ATP2B1 18449		19
LTA-MAP         rs11072512         15q24         72991079         t         c         -0.3902         0.0605         7.19E-10	LTA-MAP rs6026747 20/	C20orf174 20450		0
LTA-MAP rs7495739 15q24 72972723 a g 0.3859 0.0605 1.05E-09 +++++++ MPI COX5A;SCAMP2;C15orf17;MPI;ULK3 MPI 3261 LTA-MAP rs7537766 1p36 11809890 a g 0.6026 0.0822 2.49E-12 ++++++ CLCN8 MTHFR,NPA,CLCN6,NPPB CLCN6 972	LTA-MAP rs11072512 15	C15orf17 4564		Ê.
LTA.MAP (s7537765 1p36 1180980 a g 0.0026 0.0822 2.49E-12 +++++++ CLCN8 MTH/FR.MPPA.CLCN8,NPPB CLCN8, NPPB CLCN8 972	LTA-MAP rs7495739 150	MPI 3261		
TA MAD #1275070 2622 26777072 + A 0.295 0.0617 2.525.00 KCNV2 KCNV2 CIDA	LTA-MAP rs7537765 1p.	CLCN6 972		
LIMMAR ISTETOTI 2020 2011112 U 0.365 0.0011 2.52E-08 +++++ KUNKA KUNKA,0184 KUNKA 1850	LTA-MAP rs1275979 2p2	KCNK3 7950		1
LTA-MAP rs10858911 12q21 88487272 a g -0.3729 0.0603 3.32E-09++- NA ATP2B1;WDR51B;GALNT4 ATP2B1 18686	LTA-MAP rs10858911 120	ATP2B1 18686		8
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 rs7085 15r	CSK 21		
LTA-MAP rs11905512 20g13 57187391 c g -0.5575 0.0944 1.68E-08 NA C200r1174 12078	LTA-MAP rs11905512 200	C20orf174 12078		8
LIA-MAP ISS088 1p35 11525501 a g 0.8103 0.1348 9.00E-09 ++++++++ MPA MIHPK/MPA_CLCM0/MPB NPA 199	LTA MAP 155068 103	NPPA 199 C15orf17 2162		e -
LIN-MAP 159499127 15024 72001945 1 C - 4.589 0.0556 7.552-09 C150111 COX94/87,504/872,0150111/0LN3 C150111 2105	LTA MAP 190495127 150	ATD2D1 22103		
Lindman (3110000) 1842 (30000) 8 y 0.000 0.0001 2.300-10 4117201 AIT201 AIT201 AIT201 AIT201 C10a/107 C10a/107 24465	TA-MAP rs12246717 10	C10orf107 38485		15
LTAMAP (s1077462512024 110394602 a 0 0.443 0.0609 3.66E-12 ATXN2 SH283ATXN2 ATXN2 37004	LTA-MAP rs10774625 12	ATXN2 20201		11
LTA MAP rs882384 20d13 57132808 t c 0.5221 0.0854 5.03E.09 ++++++ NA NA NA	LTA-MAP rs882384 20	C20orf174 66661		1
LTA-MAP rs6092743 20g13 57133765 a g 0.6372 0.0971 3.60E-10 ++++++ NA NA NA	LTA-MAP r56092743 20	C20orf174 65704		14
LTA-MAP rs11634474 15q24 72903237 c g 0.4099 0.0685 1.05E-08 +++++++ LMAN1L CSK;LMAN1L;CPLX3;SCAMP2;ULK3 LMAN1L 1914	LTA-MAP rs11634474 15	LMAN1L 1914		6
LTA-MAP rs11105381 12q21 88630968 a g -0.506 0.0827 5.00E-09 NA ATP2B1 ATP2B1 56991	LTA-MAP rs11105381 120	ATP2B1 56991		1
LTA-MAP rs4886636 15q24 72983229 a g -0.387 0.0604 9.37E-10 C15orf17 COX5A(MPE;CAMP2;C15orf17 C15orf17 3286	LTA-MAP rs4886636 15r	C15orf17 3286		F
LTA-MAP rs3784789 15q24 72869805 c g 0.3899 0.0638 5.18E-09 +++++++ CSK CYP1A2,CSK,LMAN1L,CPLX3,SCAMP2,ULK3 CSK 7838	LTA-MAP rs3784789 15r	CSK 7838		1
LIA-MAP rssb444 12q24 114038620 a g 0.3621 0.0626 3.20E-08 +++++++ NA NA TBX3 430468	LIA-MAP rs35444 120	1BX3 430468		68

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	rs1/36/504	1036	11/85365 a	9	0.5888	0.0825	9.08E-12	*****	MIHER SCAMP?	MTHER, NPPA, CLONE, NPPB, AGTRAP	MIHER SCAMP2	3337
I TA MAP	rc17696736	12024	110971201 a	9	0.3667	0.0605	1.32E-09	*****	C12orf30	ERP29 TMEM118 C120//30	C120d30	22325
I TA-MAP	rs7136259	12021	88605319 t	9	-0.4383	0.0607	4 98E-12		NA	ATP281	ATP2B1	31344
LTA-MAP	rs236713	20013	57128972 a	q	-0.4742	0.0791	9.92E-09		NA	NA	C20orf174	70497
LTA-MAP	rs2681485	12021	88549753 a	q	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	с	-0.3935	0.0633	2.84E-09	+	KCNK3	KCNK3;C2orf18	KCNK3	17178
LTA-MAP	rs12487	15q24	72923747 t	с	0.3523	0.0609	3.24E-08	*******	NA	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	502
LTA-MAP	rs2120702	10q21	63192664 a	1	-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	1516916504	10021	63122962 a	g	0.43/1	0.0721	6.92E-09	*-******	G100m107	C100m107	G100m107	30238
LTA MAP	r56495126	15Q24 20o12	72902079 a	9	0.3953	0.0055	4 02E 00	*****	NA	COX5A(MPI;LMAN1L;CPLX3;SCAMP2;C150T17;ULK3	MP1 C20od174	7383
I TA MAP	rc2586886	20013	26785535 t	g	0.0220	0.0628	4.82E-09	*****	KCNK3	C20418-KCNK3	KCNK3	16413
I TA-MAP	15236706	20013	57124811 t	c	-0 4863	0.0793	4 66E-09		NA	NA	SLMO2	73515
LTA-MAP	rs12230074	12g21	88614998 a	a	0.6822	0.0825	2.82E-15	****	NA	ATP2B1	ATP2B1	41023
LTA-MAP	rs11066188	12g24	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	CAS21	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		C20orf174	69834
LTA MAP	rs1869959	15921	72934385 a	c	0.3941	0.0677	2.66E 08		SCAMP2	MPI(GSK;LMAN1L;GPLX3;SGAMP2;G16off17;ULK3 C20+4474	SCAMP2	10136
LTA-MAP	re652179	120213	5/182115 a	9	-0.5043	0.0604	2 36E-12		ATYNIS	G200H174	G2000174	20724
I TA-MAP	rs6015450	20013	57184512 a	0	-0.4433	0.0943	1.84E-08		NA	C20orf174	C20orf174	14957
LTA-MAP	rs1378942	15024	72864420 a	c	-0.3853	0.0635	6.63E-09		CSK	CYP1A2 CYP1A1 CSK I MAN1L CPLX3 SCAMP2 ULK3	CSK	2853
LTA-MAP	rs11066320	12g24	111390798 a	a	0.3536	0.061	3.06E-08	********	PTPN11	RPL6/PTPN11	PTPN11	41301
LTA-MAP	rs2675612	10g21	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	9	-0.4075	0.0649	1.99E-09		SCAMP2	CPLX3;SCAMP2;C15orf17;MPI;CSK;ULK3;LMAN1L	SCAMP2	3658
LTA-MAP	rs1275982	2p23	26772593 t	С	-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	C200f174	C200rf174	6615
LTA MAP	r\$110/2518	15024	73021063 t	c	0.4315	0.0636	8.95E-11	*****	NA	COX5A(SCAMP5)(RP25)C150F17(MP1	COX5A	4238
LTA MAP	150031937	12021	72900174 a	g	0.397	0.0600	R 00E 12	*****	ATP2R1	ATP2R1	ATP2R1	7772
I TA-MAP	rs11630918	15024	72942949 1	9	-0.3901	0.062	1 77E-09		SCAMP2	COX54 MPU MAN1L CPLX3 SCAMP2 C15or(1711) K3	SCAMP2	9774
LTA-MAP	rs998981	20013	57133036 t	c	0.5224	0.0854	5.00E-09	*****	NA	NA	C20orf174	66433
LTA-MAP	rs2070759	12021	88541867 t	a	0.3891	0.0608	9.54E-10	****	ATP2B1	ATP2B1	ATP2B1	32108
LTA-MAP	rs12442901	15924	72870965 a	a	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	****	MTHER	MTHFR,NPPA,CLCN6,NPPB,AGTRAP	MTHER	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	с	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	9	-0.3812	0.0664	4.04E-08	+	KCNK3	KCNK3,CIB4	KCNK3	7237
LTA MAP	rs2393833	10021	63115322 t	C	-0.4359	0.072	1.35E-09	-+	G10orf107	CTUDITIO/	G100rf107	22598
LTA-MAP	rs4886833	15024	72985280 a	0	0.4220	0.0708	6.81E-09	*******	NO	COX54/CPLX3/SCAMP2/C154/17/MPLILK3	MPI	4202
LTA-MAP	rs236715	20013	57130490 t	c	-0 4819	0.0794	6 55E-09		NA	NA	C20orf174	68979
LTA-MAP	rs1543927	15g24	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	CASZI	CASZ1	56109
LTA-MAP	rs11856413	15q24	72986945 a	9	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	9	0.6848	0.0809	6.17E-16	****	NA	ATP2B1	ATP2B1	19432
LTA-MAP	rs6495122	15q24	72912698 a	c	0.3842	0.0611	1.23E-08	*******	NA	CPLX3,SCAMP2,MPI,CSK;ULK3,LMAN1L	CPLX3	1509
LTA MAP	rs125/9302	12021	885/4634 a	g	0.6809	0.0808	7.72E-16	+++++++++++	NA	AIP281	ATP2B1	009
LTA MAD	1530441	12024	114037498 1	C	0.3031	0.0029	1 70E 00		CLONE	MTHED NIDDA CLONE NIDDD	CLONE	431146
I TA MAP	rc12244842	10021	63109192 t	9	-0.4425	0.0723	4 97E-09		C10orf107	C10of107	C10off107	16468
I TA-MAP	1512244042	12024	110388754 a	t	-0.4436	0.0609	3.45E-12		ATXN2	SH2B3:ATXN2	ATXN2	14353
LTA-MAP	rs11105383	12021	88631437 t	c	0.5824	0.0895	4.96E-10	********	NA	ATP2B1	ATP2B1	57462
LTA-MAP	rs1992625	10g21	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	с	-0.3986	0.0606	3.22E-10		NA	COX5A,MPI,SCAMP2,RPP25,C15orf17	COX5A	393
LTA-MAP	rs1378940	15q24	72870547 a	с	-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	15024	72980057 t	c	0.3864	0.0605	1.02E-09	+++++++++	C150f17	COX5A(SCAMP2)RPP25(C156f117/MPI/ULK3	C150f17	677
LTA MAD	154880406	10q24 20a12	12044200 T	9	-0.3941	0.00/0	2.00E-08		NA	NA NA	SI MO2	6202
I TA-MAP	re7407302	15024	72962510 c	9	.0 3872	0.0604	9 16E-10		NA	COX54 MPH MAN1L CPL X3 SCAMP2 C15orf1711LK3	MPI	6952
LTA-MAP	rs7299436	12021	88637201 t	a	0.5845	0.0898	5.02E-10	********	NA	NA	ATP2B1	63226
LTA-MAP	rs7162232	15q24	72902948 a	9	-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	9	-0.4293	0.0673	1.07E-09		CSK	CPLX3,CYP1A2,SCAMP2,CSK,ULK3,LMAN1L	CSK	5971
LTA-MAP	rs260013	20q13	57194118 a	9	-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	5	CASZ1	CASZ1	CASZ1	57130
LIA-MAP	153/50/2/	10q21	63114411 a	g	0.4423	0.0723	5.01E-09	+-++++++++	G100rf107	Closeflor	C100/110/	21687
LTA MAP	15/30259/	20013	5/112829 a	9	0.5054	0.0848	1.22E-08	+++++-++-	PEA NA	NA (10-1107)	SLMU2 CADed107	01033
LTA MAP	15/0/0/9/	20012	63221119 a	g	-0.0400	0.0878	2.89E-09		NA		CIU0ITIU/	20004
LTA.MAP	15230703	10:21	63105307 a		0.487	0.0718	2 26E-09		C10od107	C10xf107	C10od107	799
I TA.MAP	re4886629	15024	72859611 c	9	-0.4308	0.0675	1.09E-00		NA	CPL X3 CVP142 CVP141 CSK-ULK31 MAN4L	CSK	2156
LTA-MAP	rs11854147	15024	72839824 t	c	0.401	0.0671	1.09E-08		NA	CYP1A2 CYP1A1 CSK-LMAN1L	CYP1A2	3830
LTA-MAP	rs4845953	1036	10724578 a	a	-0.3955	0.0667	1.43E-08	?	CASZ1	CASZ1	CASZ1	54718
LTA-MAP	rs17249754	12021	88584717 a	g	-0.6855	0.0808	5.07E-16		NA	ATP2B1	ATP2B1	10742
LTA-MAP	rs2408046	12g21	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	с	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	9	-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;C15or17;ULK3	SCAMP2	7902
LTA-MAP	rs11066301	12q24	111355/55 a	g	-0.3558	0.0612	2.79E-08		PIPN11	RPL6,PTPN1	PIPN11	14837
LTA MAP	rs2588992	10021	631846// t	c	-0.4589	0.0762	8.55E-09	-++	G100m107	C100r107	G100rf10/	11418
LTA MAP	1530432	12024	114039913 t		-0.35/6	0.0037	3.43E-00		NA	NA AT2204	ATDODA	40552
LTA MAD	152110004	15024	72045554	l.	0.0072	0.0027	4.04E-00	********	LIL MO	ATE2DT MANULODI VS-SCANDS-TILKS	AIF2DI	40000
I TA MAP	158210	15024	72976983 a	0	0.3858	0.0605	1.07E-00		MPI	COX5A:SCAMP2:RPP25:C15adf17:MPI/ULK3	MPI	635
LTA-MAP	rs10858915	12021	88575678 a	9	0.3548	0.0609	2 58E-08	****	NA	ATP2B1	ATP2B1	1703
LTA-MAP	rs2050265	1p36	11802286 a	a	0.602	0.0823	2.77E-12	****	CLCN6	MTHER 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	9	-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	9	0.3641	0.0634	4.03E-08	***-*-***	NA	MTHFR;KIAA2013;NPPA;CLCN6;NPPB	NPPB	6308
LTA-MAP	rs2415251	15q24	73029208 t	с	0.3962	0.0631	1.99E-09	*****	NA	COX5A;SCAMP5;MPI;RPP25;C15or17	RPP25	5287
LTA-MAP	rs12567136	1036	11806318 t	c	-0.6025	0.0823	2.64E-12		CLCN6	MTHER, NPPA, CLCN6, NPPB	CLCN6	4544
LTA-MAP	rs20814/2	12021	88533090 a	9	0.6861	0.0796	1.77E-10	*****	AIP2B1	ATTER NEED ACTOR ACTOR	AIP2B1	2/132
LTA MAP	1517037425	15024	11/929/0 a	9	-0.0215	0.0808	1.70E-12		COVER	MITHY, NETRA, GLUND, NETBAGI IKAP	COVER	91/7
LTA MAD	15110/2014	12024	110269001 1	L.	-0.390	0.0006	4.04E-10		CUASA SU2D2		SU2B2	4919
I TA MAP	rs11105368	12021	88598572	0	0.4409	0.081	6.61E-16	******	NA	ATP2R1	ATP2B1	24597
I TA MAP	rc4845843	1036	10724172 a	9	0.6025	0 1056	4 97E-09		CAS71	CAS71	CAS71	55122
LTA-MAP	rs11105378	12021	88614872 t	c c	-0.6822	0.0824	2.46E-15		NA	ATP2B1	ATP2B1	40897
LTA-MAP	rs11105328	12021	88466521 a	a	0.6393	0.0837	2.84E-13	********	NA	ATP2B1 WDR51B GALNT4	WDR51B	22613
LTA-MAP	rs11105379	12g21	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	9	-0.6015	0.0826	3.37E-12	+	MTHER	MTHFR,NPPA,CLCN6,NPPB,AGTRAP	MTHER	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	rs110141/1	10p12	18751201 t	c	-0.3892	0.0632	3.88E-09		CACNEZ	CACNB2	CACNEZ	21683
LTA DD	r51/1/014	3p22	41892399 1	c	-0.4739	0.0825	2.22E-08		ULKA	ULK4	ULKA	220002
LTA PP	re1717003	3022	41750581 t	c	0.4900	0.082	1 36E-09		ULKA		ULKA	66660
I TA PP	151717034	3022	41930917 9		0.4803	0.0823	1.10E-08		LILKA		ULKA	47747
LTA-PP	rs2469	6p21	43407301 t	C C	-0.3519	0.0623	3.88E-08		NA	TTBK1 2NF318 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	с	-0.4879	0.082	6.77E-09	+	ULK4	ULK4	ULK4	7524
LTA-PP	rs9874975	3p22	41739304 a	9	-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	9	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	/3619
LTA DD	15/631057	3p22	41/92955 1	c	-0.4//2	0.0822	1.58E-08	+	ULK4	ULK4	ULK4	185/09
LTA DD	159865780	3p22	418/0806 a	g	0.4729	0.0826	2.49E-08	+++++++++	ULK4		ULK4	04054
TA DD	151/10000	3p22	41093710 a	9	-0.4739	0.0825	2.212-08	+	ULKA		ULK4	100626
I TA.PP	rs1717027	3022	41962924 +	c	.0 499	0.082	6 80E-08	*******	ULKA		ULKA	15740
I TA-PP	156796079	3022	41992824 8		0.100	0.0861	4 62E.00		NA	UI K4	UI K4	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	9	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	9	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	с	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	3022	41866102 t	c	0.4708	0.0827	2 92E-08	*******	ULK4	ULK4	ULK4	112562
LTA-PP	rs12705390	7022	106198013 a		0.5865	0.0759	5.40E-14	*****	NA	NA	PIK3CG	95146
ITA.PP	rs7646144	3022	41828129 a		-0.4686	0.0821	2 69E-08		LILK4	11 K4	ULKA	150535
I TA.PP	199856088	3022	41835486 1		-0.4946	0.0847	1 295-08		LILKA		LILKA	143178
LTA DD	153030000	2022	41000444	9	0.4717	0.0047	2 725 00		ULIVA		ULIVA	100220
LTA DD	131010009	3p22	410034444 (		0.4701	0.0020	1 20E 00	********	ULIVA		ULINA	R00220
LTA DD	151/1/000	3p22	41910402 8	c	0.4791	0.082	1.29E-00	*******	CAR71	04821	CAR74	60212
LTA-PP	15880315	1030	10/19453 1	c	-0.421	0.0703	5.45E-09	/	GASZT	64521	GASZI	59641
LIA-PP	rs1/169/5	3p22	41935010 t	c	-0.4837	0.0822	1.01E-08	+	ULK4	ULK4	ULK4	43654
LIA-PP	rs1/3985/5	/q22	106196688 a	9	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	3022	41837649 a	a	0.4694	0.0822	2 68E-08	++++++++	ULK4	ULK4	ULK4	141015
LTA-PP	rs6599168	3022	41725327 t	c	0.5163	0.0865	6.11E-09	********	ULK4	ULK4	ULK4	253337
I TA PP	rs1716694	3022	41961403 t	0	0.4964	0.0823	8 67E-09	*******	ULKA	ULK4	ULK4	17261
I TA PP	rs1613233	3022	41920148 a	9	0 4819	0.0824	1 22E 08		ULKA	ULK4	ULKA	58516
ITA.PP	re0882320	3022	41742159 +	9	0.4949	0.092	4 10E-00		LIL KA		ULKA	236506
I TA DD	m1270E200	7022	106103070 +		0 5750	0.0752	0 525 14		NA		DIVICC	100201
LTA DD	1512705389	7922	100192878 1	C .	0.5759	0.0753	9.52E-14	******	NA	104	PIKGGG	00201
LIAPP	100498	7922	100200208 a	9	0.4499	0.0803	4.89E-08	******	TRA L		PIKSUG	00951
LIA-PP	1510212530	Spzz	41802030 a	9	0.4749	0.0823	1.90E-08	+++++++++	ULK4	ULK4	ULN4	170034
LIA-PP	126789260	3p22	41/51354 c	9	-0,4961	0.0817	3.36E-09		ULK4	ULK4	ULK4	22/310
LIA-PP	rs10865914	3p22	41894503 t	C	0.4741	0.0825	2.17E-08	++++++++	ULK4	OLK4	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
I TA-PP	rs2125738	Bn21	43435728 a	a	0.3589	0.0628	3 20E-08		7NE318	CRIP3 SI C22A7 7NE318	ZNE318	9431
I TA-PP	192825887	3022	41875955 a	c	-0.4736	0.0826	2 39E-08		ULK4	11 K4	UII KA	102709
ITA.PP	rc1716983	3022	41939132 a	0	0.4935	0.0823	1.055-08		ULKA		ULKA	39532
I TA PP	re1716692	3022	41959790 3	9	0.494	0.0923	1.045.09		LILKA		LILKA	19974
LTA DD	151710082	2622	41900054	9	0.4020	0.0023	0.04E-00	********	NA		ULKA	10100
LTA DD	158800033	Sp22	41800004 a	9	-0.4830	0.0819	3.04E-09		CL CODAT	ULN4	CLC22A7	10190
LIAPP	151574430	0021	43377007 a	L	0.3300	0.0025	3.04E-08	********	SLGZZAI	GRIPS, SLG22A, TIBRT, 2NP318	SLG22AI	3032
LIA-PP	18939558	3p22	41951044 a	c	0.4839	0.0823	1.04E-08	++++++++	ULK4	ULK4	ULK4	27620
LIA-PP	rs1/4//1//	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	9	-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	9	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	a	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
I TA PP	100046824	2022	41960052 9		0 4764	0.0929	2 225 09		ULKA		ULKA	109611
I TA DD	133040034	2022	41700041 +	9	0.5008	0.0025	2 845 00		ULKA		ULKA	200722
LTA DD	r510001157	2022	41070400	9	0.4724	0.0021	2 425 00		LILICA		LILICA	100120
LIAPP	151994107	3p22	410/2400 a	g	0.4707	0.0820	2.422-08		ULKA	ULV4	ULKA	100178
LIAPP	1598/510/	opzz	41/8/31/ a		0.4767	0.0822	1.04E-08	+++++++++	ULK	ULK4	ULN4	181347
LIA-PP	rs11923562	3pzz	41735335 t	9	-0.4917	0.0819	5.06E-09		ULK4	ULK4	ULK4	243329
LIAPP	rs/626217	Sp22	41817419 8	g	0.47	0.0821	2.52E-08	*******	ULK4	ULK4	ULK4	101245
LTA-PP	rs17060961	3p22	41738715 a	9	0.4946	0.0819	4.19E-09	+++++++++++++++++++++++++++++++++++++++	ULK4	ULK4	ULK4	239949
LTA-PP	rs794902	3p22	42000943 t	c	-0.515B	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	с	-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	3022	41926719 a	a	0.4824	0.0823	1.17E-08	*****	ULK4	ULK4	ULK4	51945
I TA-PP	rs1716693	3022	41960604 t	0	0.4857	0.0823	9 18E-00	*******	ULK4	11 K4	ULK4	18060
ITA PD	re17063500	3022	41836680 +	6	-0 4743	0.0825	2 165 00		111 K4	11 64	LIL KA	141984
ITA PP	re2272006	3022	41972063	~	0.4981	0.082	6 77E.00		111 164		LIL KA	6601
ITA DD	132212000	3022	41940094		0.4001	0.002	2 105 00		LILKA		LILKA	139590
LTA DD	130/08128	2022	41040004 8	9	-0.4000	0.0025	2.192-08	+	ULIV4		ULIV4	140270
LIA-PP	130399179	opzz	+1000200 L	C	-0.4085	0.0021	2.10E-08	+	VLN4	ULINY	ULN4	1403/0

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	с	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	9	-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	с	-0.5166	0.0861	5.22E-09	+	NA	ULK4	ULK4	25062
LTA-PP	rs13225723	7q22	106203703 a	9	0.6031	0.0827	1.26E-12	+++++-+++	NA	NA	PIK3CG	89456
LTA-PP	rs9815354	3p22	41887655 a	9	-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.

						r^2 to			eSNP P					type of eQTL			Probe	Probe
IndexSNP	Traits	InRefGene	RefGenes60kb	Locus	# Index/LD status	index	eSNPid	Tissue	value	Chr	B36pos	ArrayID	Transcript	(cis or trans)	Beta	Allel	e Chromosome	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	MTHER	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	MTHER	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	т	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	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	LCL (MuTHER)	2.10E-18	1	11809890	ILMN 1734830	MTHER	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Monocytes	3.57E-14	1	11806318	_	MTHER	cis				
rs13306561	DBP/SBP/MAP	MTHER	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	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs17037429	Monocytes	2.33E-13	1	11796374		MTHER	cis				
rs13306561	DBP/SBP/MAP	MTHER	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	MTHER	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	MTHER	cis	-0.63			
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Whole blood (PaxGene) in Japanese	1.20E-09	1	11802286	∧ 23 P400081	MTHER	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHER	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	MTHER	cis	0.63			
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	PaxGeneWholeBlood(Mehta)	1.44E-09	1	11806318	ILMN 1731434	MTHER	cis				
rs13306561	DBP/SBP/MAP	MTHER	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	MTHER	cis	0.62			
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA:AGTRAP	1	Dproxy(CEU-H3)	1	rs7537765	Schadtliver	1.37E-07	1	11809890		CI CN6	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Skin (MuTHER)	1 44E-07	1	11806318	ILMN 1734830	MTHER	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA-AGTRAP	1	LDproxy(CEU-H3)	1	rs2050265	Skin (MuTHER)	1 50E-07	1	11802286	ILMN 1734830	MTHER	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Skin (MuTHER)	3.50E-07	1	11809890	ILMN 1734830	MTHER	cis				
rs13306561	DBD/SBD/MAD	MTHER	NPPB:NPPA-AS1;CLCN6:MTHER:NPPA-AGTRAP	1	LDproxy(CEU-H3)	1	rs12567136	Subc adipose (MuTHER)	5.39E-07	1	11806318	ILMN 1734830	MTHER	cis				
rs12206561	DBD/SBD/MAD	MTHER	NPPB,NPPA-AS1,CLCN6,MTHER,NPPA,AGTRAP	1	LDproxy(CEU-H2)	1	rs2050265	Subc adipose (MuTHER)	5.55E-07	1	11000310	ILMN 1724830	MTHER	cis				
rs13306561	DBD/SBD/MAD	MTHER	NPPB,NPPA-AS1;CLCN6;MTHER;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Subcadipose (MuTHER)	8.64E-07	1	11809890	ILMN 1734830	MTHER	cis				
rs13306561	DBD/SBD/MAD	MTHER	NPPB,NPPA-AS1;CLCN6;MTHER;NPPA;AGTRAP	1	LDproxy(CEU-H3)	1	rs7537765	Liver(Greenawalt)	1.02E-06	1	11809890	10023816366	CLCN6	cis				
rc12206561	DBP/SBP/MAP	MTHER	NDDB-NDDA AS1-CLCN6-MTHER-NDDA-AGTRAD	1	LDproxy(CEU H2)	1	157527765	Liver(Greenawart)	1.022-00	1	11000000	GL 12025672 A	CLCN6	cis				
rc12206561	DBD/SBD/MAD	MTHED	NDDB-NDDA_AS1;CLCN6;MTHEP:NDDA-AGTPAD	1	LDproxy(CEU_H2)	1	rc12567126	Dondritic colls after Mysobasotrium tubs	2.415.06	1	11005050	01_12025072-A	MTHEP	cis				
rc12206561	DBD/SBD/MAD	MTHER	NPPB,NPPA-AS1,CLCNG,MTHER,NPPA,AGTRAP	1	LDprovy(CEU H2)	0.07	rc17027290	Whole blood (CHARGE)	7.045.92	1	11702420	2000477	MTHER Clorf167	cis	10.00	•	1	11760600
rc12206561	DBD/SBD/MAD		NPPB,NPPA-AS1,CLCN0,WITHFR,NPPA,AGTRAP	1	LDproxy(CEU-H3)	0.97	rc17267504	Whole blood (CHARGE)	2 995 70	1	11705365	2000477	MTHER Clorf167	cis	10.05	A C	1	11769609
rc12206561	DBP/SBP/WAP		NPPB,NPPA-AS1,CLCN0,MTHFR,NPPA,AGTRAP	1	LDproxy(CEU-H3)	0.97	rc17027290		5 455 19	1	11702420	1724920	MTHER, CIOILO	cis	10.05	G	1	11/05005
1515500501	DBP/SBP/IVIAP	MTUCD	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	1517037390	LCL (MUTHER)	3.43E-18	1	11705365	LIVIN_1734830	MILLER	cis				
rs13306561	DBP/SBP/WAP		NPPB;NPPA-AS1;CLCN0;WITHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rc17027200	Whole blood (PayCane) in Japanese	7.40E-18	1	11702420	1LIVIN_1754650		cis	0.62			
rs13306561	DBP/SBP/WAP			1	LDproxy(CEU-H3)	0.57	151/05/550	Whole blood (PaxGene) in Japanese	1.202-09	1	11705365	A_23_P400081		cis	-0.05			
1513300501	DBP/SBP/MAP	MINER	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LUproxy(CEU-H3)	0.97	151/30/304	Whole blood (PaxGene) in Japanese	1.20E-09	1	11/85305	A_23_P400081	MIHER	cis	0.03			
1313300501	DBP/SBP/WAP		NPPB,NPPA-ASI,CLCNO,WITHFR,NPPA,AGTRAP	1	LDproxy(CEU-H3)	0.97	1517037390	Subcaupose (Muther)	2.002-07	1	11703430	LIVIN_1734630		cis				
1313300501	DBP/SBP/WAP		NPPB,NPPA-AS1,CLCNO,WITHER,NPPA,AGTRAP	1	LDproxy(CEU-H3)	0.97	1517057590	Skin (Muthek)	5.102-07	1	11705365	LIVIN_1734830		cis				
1313300501	DBP/SBP/WAP		NPPB,NPPA-AS1,CLCNO,WITHER,NPPA,AGTRAP	1	LDproxy(CEU-H3)	0.97	1517307304	Shine (MUTHER)	7.505.07	1	11705303	LIVIN_1734830		cis				
1313300501	DBP/SBP/MAP	MITHER	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	151/30/304	Skin (Muther)	7.50E-07	1	11785365	LIVIN_1734830	CDD116	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs1/36/504	Liver (ScanDB)	9.54E-07	1	11/85365	01 40005 670 4	GPRIID	CIS				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs1/36/504	Lympn	1.54E-05	1	11/85365	GI_12025672-A	CLCN6	CIS				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCNb;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs1/36/504	omental	7.21E-05	1	11/85365	10025934633	HSS00048903	CIS				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCNb;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.97	rs1/36/504	Blood(Fenrmann et al)	1.50E-27;1.90	1	11/85365	3990477;385013	MTHFR;AL953897.6;0	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	Α	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	MTHER	cis				

						r^2	to		eSNP P					type of eQTL			Probe	Probe
IndexSNP	Traits	InRefGene	RefGenes60kb	Locus	# Index/LD status	ind	ex eSNPid	Tissue	value	Chr	B36pos	ArrayID	Transcript	(cis or trans)	Beta	Allel	Chromosome	Position
rs13306561	DBP/SBP/MAP	MIHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 rs2236/9/	LCL (MUTHER)	5.44E-24	1	11815237	ILMIN_1734830	MTHER	CIS				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 rs2075538	LCL (MUTHER)	5.56E-24	1	11819189	ILIVIN_1734830	MTHER	CIS				
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 152236797	PaxGenewholeBlood(Menta)	1.04E-11	1	11815237	ILIVIN_1731434	MIHER	CIS	0.64			
1513300501	DBP/SBP/MAP	MIHER	NPPB;NPPA-AS1;CLCN0;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 152075538	Whole blood (PaxGene) in Japanese	7.49E-10	1	11015007	A_23_P400081	MIHER	CIS	0.04			
rs13306561	DBP/SBP/MAP	MTHER	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 rs2236/9/	Whole blood (PaxGene) in Japanese	1.20E-09	1	11815237	A_23_P400081	MTHER	CIS	-0.63			
1513300501	DBP/SBP/MAP	MTUED	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 157553194	Skie (Muturn)	1.20E-09	1	11/80/30	A_23_P400081	MTUER	cis	-0.03			
1513300301	DBP/SBP/WAP	MTUED	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 157553194	SKITI (MUTHER)	2.04E-09	1	11/80/30	LIVIN_1734830		cis				
1513300301	DBP/SBP/WAP	MTUED	NPPB;NPPA-AS1;CLCN6;MTHFR;NPPA;AGTRAP	1	LDproxy(CEU-H3)	0.7	13 152075558	skip (MuTUER)	3.462-09	1	11030002	EINST000003765		cis				
1515500501	DBP/SBP/WAP		NPPB,NPPA-AS1,CLCN6,MTHER,NPPA,AGTRAP	1	LDproxy(CEU-H3)	0.7	13 152075556	Skin (MUTHER)	3.502-09	1	11015105	ILIVIN_1734650		cis				
rc12206561	DBD/SBD/MAD	MTHED	NDDB:NDDA-AS1;CLCN6:MTHEP:NDDA:AGTRAD	1	Dproxy(CEU-H2)	0.7	12 rc2075529	Whole blood (CHARGE)	1 225-07	1	11010207	60427	RIOD1	cis	-5.29	c	1	11059120
rc12206561	DBD/SBD/MAP	MTHER	NDDB:NDDA-AS1;CLCN6:MTHEP:NDDA:AGTRAD	1	Dproxy(CEU-H2)	0.7	12 rc7552194	Whole blood (CHARGE)	1.322-07	1	11796726	60427	PLOD1	cis	-5.26	^	1	11959120
rs13306561	DBD/SBD/MAP	MTHER	NDDB:NDDA-AS1;CLCN6:MTHEP:NDDA:AGTRAD	1	LDproxy(CEU-H3)	0.7	13 rs2226797	Subc adipose (MuTHER)	1.402-07	1	11815227	ILMN 1741594	CLONE	cis	-5.20	^	-	11556150
rs13306561	DBD/SBD/MAP	MTHER	NDDB:NDDA-AS1;CLCN6:MTHER:NDDA:AGTRAD	1	LDproxy(CEU_H3)	0.7	13 rs2075538	Subc adipose (MuTHER)	1.05E-07	1	11819189	ILMN 1741594	CLCN6	cis				
rs13306561	DBD/SBD/MAP	MTHER	NDDB:NDDA-AS1;CLCN6:MTHER:NDDA:AGTRAD	1	LDproxy(CEU_H3)	0.7	13 rs2236797	Whole blood (CHARGE)	3.425-07	1	11815237	60437	PLOD1	cis	-5.10	т	1	11958130
rs13306561	DBD/SBD/MAD	MTHER	NDDB:NDDA-AS1;CLCN6:MTHER:NDDA:AGTRAD	1	LDproxy(CEU_H3)	0.7	13 rs7553194	Subc adipose (MuTHER)	4 135-07	1	11786736	ILMN 1741594	CLODE	cis	5.10		-	11550150
rs13306561	DBD/SBD/MAD	MTHER	NDDB:NDDA-AS1;CLCN6:MTHER:NDDA:AGTRAD	1	LDproxy(CEU-H3)	0.7	13 rs7553194	Lung	2 345-06	1	11786736	100146210 TGL	Linknown	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	0.7	13 rs7553194	Monorytes (CD14+)	1.45E-05	1	11786736	TiKVCul2UleSz4	CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	Dproxy(CEU-H3)	0.7	13 rs2236797	Monocytes (CD14+)	5.10E-05	1	11815237	TiKVCul2UleSz4	7 CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA:AGTRAP	1	Dproxy(CEU-H3)	0.7	13 rs2236797	lymph	0.00104498	1	11815237	GL 12025672-A	CI CN6	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CLCN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	0.7	13 rs2075538	Monocytes	1.43E-34:1.20	1	11819189		MTHER:CLCN6	cis				
rs13306561	DBP/SBP/MAP	MTHER	NPPB:NPPA-AS1:CI CN6:MTHER:NPPA:AGTRAP	1	LDproxy(CEU-H3)	0.7	13 rs2236797	Blood(Eehrmann et al)	4.70E-45:2.30	1	11815237	3990477:Human	MTHER: 41 953897.6:	v cis				
rs2004776	DBP/MAP	AGT	COG2:AGT:CAPN9	2	IndexSNP		rs2004776	Cerebellum (ScanDB)	2.19E-09	1	228915325	000000000000000000000000000000000000000	AGT	cis				
rs2004776	DBP/MAP	AGT	COG2:AGT:CAPN9	2	LDproxy(CEU-H3)	0.7	54 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	¢CNNM4	cis				
rs7599598	DBP	FER1L5	LMAN2L:KIAA1310:FER1L5	3	IndexSNP		rs7599598	Whole blood (CHARGE)	5.38E-08	2	96715567	1190673	LMAN2L	cis	-5.44	Α	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.l	a 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)	0.8	06 rs7582249	Whole blood (CHARGE)	2.20E-09	2	96827256	1190673	LMAN2L	cis	5.98	Α	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.8	06 rs7582249	Skin (MuTHER)	5.64E-06	2	96827256	ILMN 1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs6727384	Whole blood (Battle)	4.91E-46	2	97400324	_	CNNM4	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs968470	Whole blood (CHARGE)	2.52E-09	2	96787353	1190673	LMAN2L	cis	5.96	С	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 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)	0.7	91 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)	0.7	91 rs7608661	Blood(Fehrmann et al)	5.10E-06	2	96823647	1190673	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs7608661	Skin (MuTHER)	5.41E-06	2	96823647	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs6727384	Skin (MuTHER)	5.63E-06	2	96764051	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs968470	Skin (MuTHER)	5.79E-06	2	96787353	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs7608661	Cerebellum (all samples)	1.79E-05	2	96823647	10025902983	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs968470	Lymph	0.00232082	2	96787353	GI_13540593-S	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs968470	Prefrontal cortex (all samples)	3.50E-02	2	96787353	10025902983	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-H3)	0.7	91 rs7608661	omental	7.82E-09;2.2	12	96823647	10023820566;10	0 CNNM4;LMAN2L;AN	l cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.7	71 rs994430	Whole blood (CHARGE)	2.78E-09	2	96802728	1190673	LMAN2L	cis	5.94	Т	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.7	71 rs994430	Skin (MuTHER)	5.66E-06	2	96802728	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	2 0.7	57 rs6730773	Lung	1.74E-09	2	96805370	100141976_TGI_	aLMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	2: 0.7	57 rs1318597	Whole blood (CHARGE)	2.40E-09	2	96826822	1190673	LMAN2L	cis	5.97	С	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	. 0.7	57 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	2: 0.7	57 rs7586317	Whole blood (CHARGE)	3.21E-09	2	96811558	1190673	LMAN2L	cis	5.92	Α	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	2. 0.7	57 rs1318597	Skin (MuTHER)	5.64E-06	2	96826822	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	2 0.7	57 rs7586317	Skin (MuTHER)	5.66E-06	2	96811558	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-Rel2	2 0.7	57 rs6730773	Skin (MuTHER)	5.67E-06	2	96805370	ILMN_1755221	LMAN2L	cis				
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.7	35 rs6576984	Whole blood (CHARGE)	1.39E-08	2	96818432	1190673	LMAN2L	cis	5.68	Т	2	96735621
rs7599598	DBP	FER1L5	LMAN2L;KIAA1310;FER1L5	3	LDproxy(CEU-1kg)	0.7	35 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	Pretrontal 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/ID status	r^2 t inde	o x eSNPid	Tissue	eSNP <i>P</i> value	Chr	836005	ArravID	Transcript	type of eQTL (cis or trans)	Beta Allele	Probe	Probe Position
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1716642	Parietal lobe (ScanDB)	6.48E-17	3	41940869	, and the	ULK4	cis	beta fuicie	chronicosonic	- oontoon
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			
rs/65022/	PP DD	ULK/I		1	LDproxy(CEU-1kg)	1	r\$1016669	Parietal lobe (ScanDB)	2.55E-16	3	11869111		ULKA	CIS			
15/050227	PP DD	ULK4		4	LDproxy(CEU-1kg)	1	152128834	Parietal lobe (ScanDB)	2.55E-10	3	41837049		ULK4	cis			
157030227	PP DD			4	LDproxy(CEU-1kg)	1	155774572	Parietal lobe (ScanDB)	2.555-10	2	41032410		ULK4	cis			
157050227	PP DD			4	LDproxy(CEU-1kg)	1	rc9972207	Parietal lobe (ScanDB)	2.555 16	2	41004555			cis			
rc7650227	PP DD			4	LDproxy(CEU_1kg)	1	153873207	Parietal lobe (ScanDB)	2.532-10	2	41033734			cis			
rs7650227	DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6599175	Parietal Jobe (ScanDB)	2.75E-16	3	41761013		ULKA	cis			
rs7650227	DD	ULK4	ULKA OEK4	4	LDproxy(CEU-1kg)	1	rs985/1833	Parietal Jobe (ScanDB)	4 38E-16	3	41750581		ULKA	cis			
rs7650227	PP	ULK4		4	LDproxy(CEU-1kg)	1	rs9854833	Cerebellum (ScanDB)	8.69E-16	3	41750581		ULK4	cis			
rs7650227	PP	ULK4	UIK4	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			
rs/650227	44	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs1/1/006	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			
rs/65022/	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs3774372	Cerebellum (ScanDB)	2.01E-15	3	41852418		ULK4	CIS			
rs/65022/	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6/91806	Cerebellum (ScanDB)	2.01E-15	3	41864999		ULK4	CIS			
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs98/320/	Cerebellum (ScanDB)	2.01E-15	3	41859754		ULK4	CIS			
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs10212536	Cerebellum (ScanDB)	2.04E-15	3	41802030		ULK4	CIS			
rs7650227	PP DD	ULK4	ULK4	4	LDproxy(CEU-1kg)	1	rs6803652	Cerebellum (ScanDB)	2.04E-15	3	41795360		ULK4	CIS			
rs7650227	PP DD			4	LDproxy(CEU-1kg)	1	rc987407F	Cerebellum (ScanDB)	2.03E-15	2	41/00308			cis			
rs7650227	DD			4	LDproxy(CEU-1kg)	1	rs98/7006	Cerebellum (ScanDB)	2.20E-13	3	41730262			cis			
rs7650227	pp	UI K4	111 K4		Dproxy(CEU-1kg)	1	rs3890604	Cerebellum (ScanDB)	2.710-13	2	41735620			ric			
rs7650227	pp	UI K4			Dproxy(CEU_1kg)	1	rs9852202	Cerebellum (ScanDB)	2.78E-15	2	4173/570			ric			
rs7650227	PP	UI K4	UI K4	4	Dproxy(CEU-1kg)	1	rs9825741	Cerebellum (ScanDB)	2.79E-15	3	41736832		UI K4	cis			
rs7650227	PP	ULK4	UIK4	4	I Dproxy(CEU-1kg)	1	rs1716642	Cerebellum (ScanDB)	2.97E-15	3	41940869		UI K4	cis			
rs7650227	PP	ULK4	ULK4	4	LDproxy(CFU-1kg)	1	rs3934103	Cerebellum (ScanDB)	3,44E-15	3	41952218		ULK4	cis			
rs7650227	PP	ULK4	UIK4	4	IDproxy(CEU-1kg)	1	rs1717020	Cerebellum (ScanDB)	5.61E-15	3	41956494		ULK4	cis			
	17.7					-				_							

IndexSNP	Traits	InRefGene	e RefGenes60kb	Locus#	f Index/LD status	r^2 ti inde	o x eSNPid	Tissue	eSNP <i>P</i> value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe e 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	- 1	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	e 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	ENST000030183	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				
rs/650227	99	ULK4	ULK4	4	LUproxy(CEU-1kg)	1	rs9842261	ER+ breast tumor cells	3.95E-10	3	41/9//12		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 t inde	o ex eSNPid	Tissue	eSNP <i>P</i> 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;4.74	3	41802030	10023809218;10	0 ULK4;AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.95	3 rs6599167	Visual cortex (Alzheimer's)	3.11E-08	3	41725264	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs10510731	Lung	1.40E-14	3	41828314	100160459_TGI_	a ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs4299460	Lung	1.47E-14	3	41927449	100311290_TGI_	e ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs17214945	ER+ breast tumor cells	2.69E-11	3	41783664		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs17214987	ER+ breast tumor cells	2.69E-11	3	41785485		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs17218264	ER+ breast tumor cells	2.69E-11	3	41950851		ULK4	cis				
rs7650227	pp	ULK4	ULKA	1	LDproxy(CEU-Rel2	0.86	1 rs17283929	ER+ breast tumor cells	2.69E-11	3	41916902		ULKA	cis				
15/050227	PP DD	ULK4	ULK4	4	LDproxy(CEU-Rei2	0.80	1 1517218103	Liver (ScanDB)	5.14E-11	3	41918/28		ULK4	cis				
15/050227	PP DD	ULK4	ULK4	4	LDproxy(CEU-Rei2	0.80	117215102	Parietal lobe (ScanDB)	7.13E-11	3	41950851		ULK4	cis				
15/050227	PP	ULK4		4	LDproxy(CEU-Rei2	0.80	1 1517215185	Parietal lobe (ScanDB)	1.21E-10	3	41787338		ULK4	cis				
157050227	PP DD	ULK4		4	LDproxy(CEU-Rel2	0.80	1 rc17214943	Parietal lobe (ScanDB)	1.24E-10	2	41/83004		ULK4	cis				
rs7650227	PP DD	ULK4		4	LDproxy(CEU-Rel2	0.80	1 rs17213383	Parietal lobe (ScanDB)	1.365-10	3	41000207		ULK4	cis				
rs7650227	DD	ULKA		4	LDproxy(CEU_Rel2	0.86	1 rs17210105	Cerebellum (ScanDB)	3.47E-10	3	41783664		ULKA	cis				
rs7650227	DD	LILKA		4	LDproxy(CEU_Rel2)	0.86	1 rs17283677	FB+ breast tumor cells	3 555-10	3	41901152		ULK4	cis				
rs7650227	PP	ULK4	UIK4	4	LDproxy(CEU-Rel2	0.86	1 rs17215183	Cerebellum (ScanDB)	4.01E-10	3	41787338		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs17215589	Cerebellum (ScanDB)	4.05E-10	3	41806207		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs17218103	Cerebellum (ScanDB)	4.20E-10	3	41918728		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	1 rs17218264	Cerebellum (ScanDB)	4.54E-10	3	41950851		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-Rel2	0.86	i1 rs10510731	Liver (ScanDB)	4.74E-10	3	41828314		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs794894	Parietal lobe (ScanDB)	1.63E-16	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs7634985	Parietal lobe (ScanDB)	1.73E-16	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs13087502	Parietal lobe (ScanDB)	1.78E-16	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs794894	Cerebellum (ScanDB)	1.45E-13	3	42007487		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs7634985	Cerebellum (ScanDB)	1.56E-13	3	41994569		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs13087502	Cerebellum (ScanDB)	1.61E-13	3	41990114		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.85	7 rs13087502	ER+ breast tumor cells	1.55E-10	3	41990114		ULK4	cis				
rs/650227	чч	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs809930	Parietal lobe (ScanDB)	5.10E-15	3	42040009		ULK4	CIS				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs7652506	Parietal lobe (ScanDB)	6.85E-15	3	42035239		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs939561	Parietal lobe (ScanDB)	7.69E-15	3	42032105		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs7629767	Parietal lobe (ScanDB)	7.83E-15	3	42018513		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs10510732	SubCutAdipose(Greenawalt)	1.06E-14	3	41982343	10023809218	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs939561	Cerebellum (ScanDB)	5.72E-12	3	42032105		ULK4	CIS				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs7629767	Cerebellum (ScanDB)	6.08E-12	3	42018513		ULK4	CIS				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs809930	Cerebellum (ScanDB)	6.19E-12	3	42040009		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs7652506	Cerebellum (ScanDB)	7.19E-12	3	42035239		ULK4	CIS				
rs/650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs/652506	ER+ breast tumor cells	1.0/E-11	3	42035239		ULK4	CIS				
15/050227	PP	ULK4		4	LUPROXY(CEU-1kg)	0.81	2 1510510/32	ER+ preast tumor cells	2.09E-11	3	41982343		ULK4	CIS				
rs7650227	PP DD	ULK4		4	Dproxy(CEU-1kg)	0.81	2 rs17204313	ER+ breast tumor cells	2.09E-11	2	41901/91			cis				
rs7650227	DD			4	Dproxy(CEU-1kg)	0.01	2 rs17284312	Parietal Johe (ScanDB)	7.625-11	3	419/1308			cis				
rs7650227	pp	UI KA	111 K4	4	Dproxy(CEU-1kg)	0.01	2 rs10510732	Parietal Jobe (ScanDB)	7.64E-11	2	419222/2			cis				
rs7650227	pp	UI KA	111 K4	4	Dproxy(CEU-1kg)	0.01	2 rs1728//72	Parietal Jobe (ScanDB)	7.64E-11	2	41971209		UI K4	ric				
rs7650227	pp	UI K4	111 K4	4	Dproxy(CEU-1kg)	0.81	2 rs809930	FB+ breast tumor cells	9.77E-11	3	42040009		UI KA	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CFU-1kg)	0.81	2 rs10510732	Liver (ScanDB)	1.11F-10	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs17284313	Cerebellum (ScanDB)	4.41E-10	3	41961791		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs10510732	Cerebellum (ScanDB)	4.42E-10	3	41982343		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs17284472	Cerebellum (ScanDB)	4.42E-10	3	41971308		ULK4	cis				
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IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 t inde	o x eSNPid	Tissue	eSNP <i>P</i> value	Chr	B36pos	ArravID	Transcript	type of eQTL (cis or trans)	Beta	Allele	Probe Chromosome	Probe Position
rs7650227	рр	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs10510732	Stomach	8.32E-10	3	41982343	100311290	ULK4	cis				
rs7650227	pp	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.81	2 rs10510732	Cerebellum (Alzheimer's)	5.26E-02	3	41982343	10023829862	AK022066	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	2 rs794899	LCL	1.30E-07	3	42003726	231149 s at	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	1 rs12635286	Parietal lobe (ScanDB)	7.75E-15	3	42026840		ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	1 rs12635286	Cerebellum (ScanDB)	6.72E-12	3	42026840	)	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	1 rs12635286	Liver (ScanDB)	1.85E-08	3	42026840	)	ULK4	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	1 rs12635286	Liver(Greenawalt)	1.76E-07	3	42026840	10025919071	CTNNB1	cis				
rs7650227	PP	ULK4	ULK4	4	LDproxy(CEU-1kg)	0.76	1 rs12635286	Cerebellum (Alzheimer's)	2.92E-05	3	42026840	10025919071	CTNNB1	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2	0.96	7 rs12656497	Lung	1.67E-07	5	32867696	100142475 TGI	e NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-Rel2	0.84	rs1173766	Lung	7.02E-08	5	32840285	100303568 TGI	e NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-H3)	0.78	4 rs1173756	Lung	1.91E-08	5	32825609	100145622 TGI	a NPR3	cis				
rs7733331	SBP	NA	NPR3	5	LDproxy(CEU-1kg)	0.78	1 rs1173743	Primary PHA-stimulated T cells (GenCord	5.68E-07	5	32775047		ENSG0000056097.10	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	с	6	43412137
rs10948071	PP	NΛ	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	Α	6	43411954
rs10948071	PP	NA	TTBK1:CRIP3:SI C22A7:7NE318	7	LDproxy(CEU-1kg)	1	rs2242416	Whole blood (CHARGE)	2.83E-16	6	43381582	50193	ZNE318	cis	-8.18	A	6	43411954
rs10948071	PP	NΔ	TTBK1:CRIP3:SI C22A7:ZNE318	7	LDproxy(CEU-1kg)	1	rs2469	Whole blood (CHARGE)	4 13E-16	6	43407301	50193	ZNF318	cis	-8.13	c	6	43411954
rs10948071	pp	NΔ	TTBK1:CRIP3:SI C22A7:7NF318	7	LDproxy(CEU-1kg)	1	rs1574430	Intestine (normal ileum)	5 70E-14	6	43269029	00155	CRIP3	cis	0.110	-		10111001
rs10948071	pp	NΔ	TTBK1:CRIP3:SI C22A7:7NF318	7	LDproxy(CEU-1kg)	1	rs2841648	Intestine (normal ileum)	5.70E-14	6	43269179		CRIP3	cis				
rs10948071	DD	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	rs2242416	Intestine (normal ileum)	1 375-13	6	4327360/		CRIP3	cis				
rc109/9071	DD	NA	TTBK1;CRID2;SIC22A7;ZNE218	7	Dproxy(CEU-1kg)	1	rs2242416	Plood(Febrmann et al)	5 905-06	6	43291593	50192	7NE219	cis				
rc109/8071	DD	NA	TTBK1;CRIP3;SEC22A7;ZNI 518	7	LDproxy(CEU-1kg)	1	rs2469	Blood(Febrmann et al)	5.905-06	6	43301302	50193	ZNF310	cis				
rc10949071	DD	NA	TTBK1;CRIP3;SEC22A7;ZNIF318	7	LDproxy(CEU_1kg)	1	132405	Skip (MuTHER)	1 115 05	6	42407201	UMNL 1694711	MAD2LIPD	cis				
rc10949071	PP DD	NA	TTEK1;CRIP3;SEC22A7;ZNF516	7	LDproxy(CEU-1kg)	1	152403	Skin (MuTHER)	1.112-05	6	43407303	UMN 1694711	MAD2LIBP	cis				
rc10040071	DD.	NA	TTEK1;CRIP3;SEC22A7;ZIVF318	7	LDproxy(CEU-1kg)	1	rc1574420	Skin (MuTHER)	1.465.05	6	43377137	UMN 1694711	MAD2LIBP	cis				
rc10040071	PP DD	INA NA	TTRK1,CRIP3,SLC22A7,ZNF316	7	LDproxy(CEU-1kg)	1	151374450	Skin (MuTHER)	1.402-05	6	43377007	1LIVIN_1054711	MAD2LIBP	cis				
rc10040071	PP DD	NA	TTRK1,CRIP3,SLC22A7,ZNF316	7	LDproxy(CEU-1kg)	1	152242410	Skill (MuTHER)	2.125.05	6	43301302	LIVIN_1094711	DEXE	cis				
rc10949071	PP DD	NA	TTRK1,CRIP3,SLC22A7,ZNF516	7	LDproxy(CEU-1kg)	1	152041040		2.122-05	6	43377137	ILIVIN_1003279	PEXO	cis				
1510948071	PP	NA NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	151374430	LCL (MUTHER)	2.13E-05	0	43377007	LIVIN_1083279	PEXO	cis				
1510946071	PP DD	NA NA	TTRK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	152242410	LCL (MUTHER)	2.272-05	0	43361362	LIVIN_1003279	PEXO	cis				
rc10048071	PP DD	INA NA	TTDK1;CRIP3;SLC22A7;ZNF316	7	LDproxy(CEU-1kg)	1	152409	Lumph	2.74E-03	6	43407301	CL 27552105 S	CRIPS	cis				
1510948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	1	152409	Lympn	0.00015064	0	43407303	GI_37552195-5	CRIPS	CIS				
1510948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318		LDproxy(CEU-1kg)	1	152242410	Liver(Ochicago)	0.000/1416	0	43381582	A_23_P150502	CRIP3	CIS				
1510546071	PP DD	INA NA	TTBK1,CRIP5,SLC22A7,ZNF518	-	LDproxy(CEU-1kg)	1	152403	Liver (Greenawart)	1.735-00,2.2	. 0	43407503	50102	ZNE210	cis	0 77		6	42411054
1510948071	PP DD	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 152125738	Whole blood (CHARGE)	1.785-18	0	43435728	50193	ZINF318	cis	-8.77	A	0	43411954
1510948071	PP	NA NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 152125737	Whole blood (CHARGE)	1.53E-10	0	43435514	50193	ZINF318	cis	-8.25	C C	6	43411954
1510948071	PP DD	NA NA	TTRK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.90	5 154714077	Whole blood (CHARGE)	1.535-10	0	43435017	50193	ZNF310	cis	-8.25	•	6	43411934
1510946071	PP	INA NA	TTBK1;CRIP3;SLC22A7;ZNF318	-	LDproxy(CEU-1kg)	0.90	5 155505407	Whole blood (CHARGE)	1.552-10	0	43433333	50195	2015310	cis	-6.25	A T	0	43411934
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 159381237	Whole blood (CHARGE)	1.53E-10	0	43428388	50193	ZNF318	CIS	-8.25	1	0	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	/	LDproxy(CEU-1kg)	0.96	5 rs2841642	Whole blood (CHARGE)	1.66E-16	6	43410263	50193	ZNF318	CIS	-8.24	G	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	-	LDproxy(CEU-1kg)	0.96	5 rs2254303	Intestine (normal lieum)	5.70E-14	6	43276390		CRIP3	CIS				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	/	LDproxy(CEU-1kg)	0.96	5 rs2125738	Monocytes	4.97E-12	6	43435728		ZNF318	CIS				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9381237	Blood(Fehrmann et al)	2.50E-06	6	43428388	50193	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2254303	Skin (MuTHER)	1.29E-05	6	43384368	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	IIBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125737	LCL (MUTHER)	1.59E-05	6	43435514	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9369407	LCL (MuTHER)	1.59E-05	6	43435353	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs4714677	LCL (MUTHER)	1.59E-05	6	43435017	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2841642	LCL (MuTHER)	1.63E-05	6	43410263	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9381237	LCL (MuTHER)	1.63E-05	6	43428388	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125738	LCL (MuTHER)	1.97E-05	6	43435728	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2254303	LCL (MuTHER)	2.39E-05	6	43384368	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs9369407	Skin (MuTHER)	2.98E-05	6	43435353	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs2125737	Skin (MuTHER)	2.98E-05	6	43435514	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.96	5 rs4714677	Skin (MuTHER)	2.98E-05	6	43435017	ILMN_1694711	MAD2L1BP	cis				

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus	# Index/LD status	r^2 to index eSNF	Pid	Tissue	eSNP <i>P</i> 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 rs284	41642	Skin (MuTHER)	3.15E-05	6	43410263	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965 rs938	81237	Skin (MuTHER)	3.15E-05	6	43428388	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965 rs212	25738	Skin (MuTHER)	3.27E-05	6	43435728	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.965 rs225	54303	Lymph	0.00025613	6	43384368	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931 rs936	59408	Whole blood (CHARGE)	1.72E-16	6	43440164	50193	ZNF318	cis	-8.24	С	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931 rs936	59408	Skin (MuTHER)	6.63E-06	6	43440164	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-1kg)	0.931 rs936	59408	LCL (MuTHER)	1.72E-05	6	43440164	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892 rs239	96002	LCL (MuTHER)	5.60E-07	6	43367990	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892 rs239	96002	Whole blood (CHARGE)	5.68E-07	6	43367990	7050040	ZNF318	cis	-5.00	С	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.892 rs239	96002	Skin (MuTHER)	8.40E-06	6	43367990	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828 rs284	41647	Whole blood (CHARGE)	3.05E-16	6	43377157	50193	ZNF318	cis	-8.17	С	6	43411954
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828 rs284	41647	Skin (MuTHER)	1.15E-05	6	43377158	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.828 rs284	41647	LCL (MuTHER)	2.68E-05	6	43377158	ILMN_1683279	PEX6	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Liver(Greenawalt)	1.26E-28	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs690	01866	Monocytes	1.18E-26	6	43368638		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	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 rs439	98731	omental	4.72E-23	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NΛ	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	SubCut∧dipose(Greenawalt)	6.30E-19	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs690	01866	Whole blood (CHARGE)	5.81E-18	6	43368638	7050040	ZNF318	cis	-8.64	С	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs168	896398	Whole blood (CHARGE)	8.93E-18	6	43370682	7050040	ZNF318	cis	-8.59	т	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Whole blood (CHARGE)	1.55E-17	6	43387699	7050040	ZNF318	cis	-8.52	Α	6	43412137
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	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 rs439	98731	Whole blood (PAX) in breast cancer survi	i 6.97E-11	6	43387699	6200307	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Intestine (normal ileum)	5.10E-10	6	43279721		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Cerebellum (Huntington's)	8.76E-10	6	43387699	10025905145	ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Liver(Schroder)	1.82E-09	6	43387699		ZNF318	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Lymph	3.44E-08	6	43387699	GI_37552195-S	CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs690	01866	LCL (MuTHER)	1.72E-05	6	43368638	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Tcells	1.83E-05	6	43387699		PTK7	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs690	01866	Skin (MuTHER)	2.15E-05	6	43368638	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	LCL (MuTHER)	2.20E-05	6	43387699	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	Skin (MuTHER)	2.97E-05	6	43387699	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.748 rs439	98731	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 rs227	79087	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 rs227	79087	Intestine (normal ileum)	4.60E-10	6	43299058		CRIP3	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715 rs227	79087	LCL (MuTHER)	1.75E-05	6	43407036	ILMN_1694711	MAD2L1BP	cis				
rs10948071	PP	NA	TTBK1;CRIP3;SLC22A7;ZNF318	7	LDproxy(CEU-Rel2	0.715 rs227	79087	Skin (MuTHER)	2.70E-05	6	43407036	ILMN_1694711	MAD2L1BP	cis				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1 rs239	93833	Liver (ScanDB)	8.10E-07	10	63115322		SGTA	cis				
rs12244842	DBP	C10orf10/	C100rf10/	9	LDproxy(CEU-1kg)	1 rs122	246/1/	Liver (ScanDB)	9.54E-07	10	63129189		SERPIND1	CIS				
rs12244842	DBP	C10orf107	C10orf107	9	LDproxy(CEU-1kg)	1 rs239	93833	Blood	0.0000286	10	63115322	HSG00268758	LOC219790	cis				
rs7070797	SBP	NA	C10orf107	9	LDproxy(CEU-Rel2	0.786 rs105	509158	Adipose	0.000037	10	63177675	HSG00269025	NM_173554	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.778 rs258	88918	EndometrialTumor	0.00379818	10	63195030		C10orf107	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.734 rs973	3237	Liver (ScanDB)	5.92E-07	10	63195307		FUCA1	cis				
rs2166122	MAP	C10orf107	C10orf107	9	LDproxy(CEU-Rel2	0.734 rs973	3237	Prefrontal cortex (Alzheimer's)	9.15E-05	10	63195307	10025902662	C10orf107	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP	rs268	81472	Whole blood (CHARGE)	1.83E-15	12	88533090	7320717	WDR51B	cis	7.95	G	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP	rs268	81472	Liver (ScanDB)	3.74E-07	12	88533090		LOC100131662	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	IndexSNP	rs268	31472	Blood(Fehrmann et al)	2.20E-08;2.2	12	88533090	6650035;732071	7;WDR51B;ATP2B1	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1 rs111	105368	Whole blood (CHARGE)	3.56E-15	12	88598572	7320717	WDR51B	cis	7.87	С	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1 rs111	105364	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 rs111	105354	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 rs172	249754	Whole blood (CHARGE)	4.81E-15	12	88584717	7320717	WDR51B	cis	7.83	Α	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	1 rs125	579302	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 rs122	230074	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 rs111	105378	Whole blood (CHARGE)	7.12E-15	12	88614872	7320717	WDR51B	cis	7.78	т	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92 rs268	81492	Whole blood (CHARGE)	7.76E-13	12	88537220	7320717	WDR51B	cis	7.17	С	12	88439646
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92 rs268	81492	Liver (ScanDB)	3.15E-07	12	88537220		LOC100131662	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-Rel2	0.92 rs268	81492	Blood (Fehrmann et al)	2.10E-08;5.9	12	88537220	6650035;732071	7;WDR51B;ATP2B1	cis				
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	0.915 rs484	42666	Whole blood (CHARGE)	3.74E-07	12	88465680	7160609	WDR51B	cis	-5.08	С	12	88337954
rs2681472	DBP/SBP/MAP	ATP2B1	ATP2B1	10	LDproxy(CEU-1kg)	0.915 rs484	42666	Monocytes (CD14+)	4.35E-05	12	88465680	9N1yRYl6R8pJ.S	W GALNT4	cis				

la deuchin	Tusita	la Daf Cana	D-fC(0)			r^2 to		Tions	eSNP P	Cha	<b>D</b> 2(	America	Terreriet	type of eQTL	Dete		Probe	Probe
maexSNP	Traits	InkerGene	ATDOR1	LOCUSE	Index/LD status	index	esnPia	hissue	value	Unr 10	B30pos	ArrayiD	Transcript	(cis or trans)	вета	Allele	Chromosome	Position
152081472	DBP/SBP/MAP	ATP2B1	ATP2BI	10	LDproxy(CEU-H3)	0.805	2104504	Monocytes (CD14+)	5.41E-05	12	88400521	10022848120	GALN14	cis				
155104304	SPD SPD	50205	ATXN2,30203	11	IndexSNP		155104304	Whole blood (CHARGE)	4.03E-20	12	110200754	6560201	AL043313	cis	0.15	т	12	110272499
rc2194504		50205	ATXN2,3H2B3	11	IndexSNP		rc2184504	Whole blood (CHARGE)	5.025-20	12	110269001	6560201	511205	cis	9.13	т	12	110373403
153104304	DBP/WAP	50205	ATXN2;5H2B3	11	IndexSNP		155164504	Wide blood (CHARGE)	1 755 10	12	110306331	1000301	50205	cis	0.91	1	12	110575465
155104304	DBP/WAP	50205	ATXN2;30283	11	IndexSNP		155164504	Profrontal cortex (normal camples)	7.005.11	12	110300331	10023040135	AL049919	cis				
155104304	DBP/WAP	50205		11	IndexSNP		155104304	Whole blood (CUARCE)	2.005.07	12	110300331	7570572	AL045515	tranc	5 20	т	7	40114477
155104304	DBP/IMAP	50205		11	IndexSNP		155104304	Plood (Charde)	2.002-07	12	110300331	6560201	SHORD ATVND	uans	5.20		,	40114477
155104304	DBP/WAP	50205	ATXN2,30203	11	IndexSNP		155104304	Blood	0.0002027	12	110269001	USC00276944	5H2B5,ATAIN2	cis				
153184304	DBP/IVIAP	5H2B3	ATXN2;5H2B3	11	IndexSNP	1	153184504	Blood	0.0002037	12	110308991	6560201	FUZIIZ/	cis	0.11		12	110272490
rc2194504		50205	ATXN2,3H2B3	11	LDproxy(CEU Rol2	1	1510774025	Whole blood (CHARGE)	1 695 19	12	110/02120	6560201	51205	cis	9.02	с С	12	110373403
rc4766579	SPD	5H2B3	ATAN2,3H2B3	11	LDproxy(CEU Rol2	1	rc10774625	Whole blood (CHARGE)	2 565 09	12	110294603	2070170	100016	trans	5.51	^	11	57075756
154700376		50205		11	LDproxy(CEU_Rel2	1	1510774023	Coroballum (all camples)	0.565.08	12	110354002	10022848120	062210	uans	5.51	A	11	37073730
155104304	DBP/IMAP	50205		11	LDproxy(CEU_Rel2	1	15035176	Whole blood (CHARCE)	4.275.07	12	110492135	7570572	AL045515	tranc	5.05	c	7	40114477
155104304	DBP/WAP	50205	ATXN2,30203	11	LDproxy(CEU_Rol2	1	15055178	Read(Entrann et al)	2 205 07:0 90	12	110492135	6560201/940252	SHOPPI	uans	5.05	C	,	40114477
153184504	DBP/IVIAP	5H2B3	ATXN2;5H2B3	11	LDproxy(CEU-Reiz.	1	15053178	biood(Fenrmann et al)	2.20E-07;9.80	12	110492139	10022848120	SH2B3;ATXIN2;ALDH2	cis				
154700378	DDD /MAD	50205	ATXN2;5H2B3	11	LDproxy(CEU-1kg)	0.907	7 153164304	Whole blood (CUARCE)	4.03E-20	12	110306391	6560201	AL049919	cis	0.15	<b>T</b>	12	110272490
155104304	CDD CDD	50205	ATXN2;30283	11	LDproxy(CEU-1kg)	0.907	7 154700376	Whole blood (CHARGE)	5.022-20	12	110366734	6560301	50205	cis	9.13	T T	12	110373403
15/1/005/8	SBP	SH283	ATXN2;5H2B3	11	LDproxy(CEU-1kg)	0.96	7 15318/150/1	Visual cortex (Huntington's)	1.7EC 10	12	110368991	10022848120	SH2B3	cis	8.91		12	110373/189
154700378	50P	01200	ATXN2,3H2B3	11	LDproxy(CEU-1kg)	0.907	7 155104504	Visual cortex (Huntington's)	7.005.11	12	110300331	10023040133	AL049919	us eie				
154700578	SBP	SH2B3	ATXN2;5H2B3	11	LDproxy(CEU-1kg)	0.967	7 153184504	Whele bleed (CLARCE)	7.00E-11	12	110308991	7570672	AL049919	cis	5 20	-	7	40114477
154700578	SBP	5H2B3	ATXN2;5H2B3	11	LDproxy(CEU-1kg)	0.967	153184504	whole blood (CHARGE)	2.00E-07	12	110308991	7570073		trans	5.20	1	/	48114477
154700378	SBP	5H2B3	ATXN2;5H2B3	11	LDproxy(CEU-1kg)	0.967	153184504	Blood(Ferrmann et al)	3.30E-07	12	110308991	0300301	SH2B3;ATAN2	cis				
rs4/005/8	SBP CDD (MAD	SH2B3	A1XN2;SH2B3	11	LDproxy(CEU-1kg)	0.90	rs3184504	Blood	0.0002037	12	110368991	HSG00276844	FU21127	CIS	10.00	-	45	70015000
rs11072518	SBP/IVIAP	NA	SCAMPS;CUXSA;RPP25;CI50ff17;MPI	12	IndexSNP		1511072518	Whole blood (CHARGE)	1.57E-34	15	73021003	4480132	ULK3	cis	12.20	1	15	72915933
1511072518	SBP/IVIAP	NA	SCAMPS;COX5A;RPP25;CI50f17;MPI	12	IndexSNP		1511072518	omental	1.11E-13	15	73021003	10023814330	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMPS;COXSA;RPP25;CISOTT17;MPI	12	IndexSNP		rs11072518	Subcadipose (MUTHER)	8.68E-09	15	73021663	ILMIN_1679495	ULK3	CIS				
rs11072518	SBP/MAP	NA	SCAMPS;COXSA;RPP25;CISOFT17;MPI	12	IndexSNP		rs11072518	Lympn	8.12E-08	15	73021663	GI_4505234-S	MPI	CIS				
rs11072518	SBP/MAP	NA	SCAMPS;CUXSA;RPP25;CISoff17;MPI	12	IndexSNP		rs11072518	LCL (MUTHER)	5.2/E-07	15	73021663	ILMIN_1761262	MPI	CIS				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs110/2518	Skin (MUTHER)	7.69E-07	15	/3021663	ILMN_1679495	ULK3	CIS				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs11072518	Bcells (CD19+)	3.32E-06	15	73021663	ubt12tiW/_2_FC	CSK	CIS				
rs11072518	SBP/MAP	NA	SCAMPS;COXSA;RPP25;CISorT17;MPI	12	IndexSNP		rs11072518	Pretrontal cortex (Alzheimer's)	3.32E-04	15	73021663	10023814330	MPI	CIS				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;CI50rT17;MPI	12	IndexSNP		rs11072518	Monocytes (CD14+)	0.000374	15	/3021663	r_taN3VF1VV3q	ULK3	CIS				
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	IndexSNP		rs110/2518	Blood(Fehrmann et al)	1.90E-27;7.90	15	/3021663	31/0239;4480132	CSK;ULK3;COX5A;SC	CIS		-		
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3765066	Whole blood (CHARGE)	5.55E-45	15	/292/90/	4480132	ULK3	CIS	14.07	G	15	72915933
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3/65066	LCL in asthmatics (Liang 1kg)	1.06E-23	15	/292/90/	202472_at	MPI	CIS				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15ort17;MPI	12	LDproxy(CEU-Rel2	0.861	rs3/65066	Subc adipose (MUTHER)	1.16E-09	15	/292/90/	ILMN_1679495	ULK3	CIS				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C150rf17;MPI	12	LDproxy(CEU-Rel2.	0.861	rs3/65066	SKIN (MUTHER)	1.15E-08	15	/292/90/	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	SCAMPS;COXSA;RPP25;CISOTT17;MPI	12	LDproxy(CEU-Rel2.	0.861	rs3765066	Bcells (CD19+)	4.65E-07	15	72927907	ubt12tiw/_2_FC	CSK	CIS				
rs11072518	SBP/MAP	NA	SCAMPS;CUXSA;RPP25;CI50fT17;MPI	12	LDproxy(CEU-Rel2.	0.861	rs3765066	LCL (MUTHER)	4.26E-06	15	72927907	ILIVIN_1761262	MPI	CIS		-		
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Whole blood (CHARGE)	2.10E-47	15	/3012468	4480132	ULK3	CIS	14.46	G	15	72915933
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	Subc adipose (MuTHER)	3.46E-12	15	/3012468	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	/3012468	ILMN_1/61262	MPI	CIS				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C150rf17;MPI	12	LDproxy(CEU-H3)	0.77	rs8042694	SKIN (MUTHER)	6.16E-07	15	/3012468	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				
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495126	Monocytes	4.69E-54	15	/29620/9		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	Α	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	SCAMPS;COX5A;RPP25;C15ort17;MPI	12	LDproxy(CEU-H3)	0.754	rs6495127	Whole blood (CHARGE)	5.76E-48	15	72981543	4480132	ULK3	cis	14.55	С	15	72915933
rs11072518	SBP/MAP	NA	SCAMPS;COX5A;RPP25;C15ort17;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	LUproxy(CEU-H3)	0.754	rs6495126	LCL in asthmatics (Liang 1kg)	5.33E-23	15	72962079	202472_at	MPI	cis				
rs11072518	SBP/MAP	NA	SCAMP5;C0X5A;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;C0X5A;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;C0X5A;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 <i>P</i> value	Chr	B36pos	ArravID	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 F	D 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_F	D CSK	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754 rs6495126	Blood	0.0000646	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_F	D 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_F	D 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	Wu17hRSKTiKh	B 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	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754 rs8031937	Monocytes (CD14+)	0.000101	15	72968174	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-H3)	0.754 rs7497201	Monocytes (CD14+)	0.000152	15	72977743	Wu17hRSKTiKh	B C15ORF17	cis				
rs11072518	SBP/MAP	NΛ	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;3.00	15	72962079	3170239;448013	2 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_F	D 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	т	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_F	D 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	С	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	С	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	С	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	С	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_F	D CSK	cis				
rs110/2518	SBP/MAP	NA	SCAMP5;COX5A;RPP25;C15orf17;MPI	12	LDproxy(CEU-Rel2	0.733 rs1378940	Skin (MuTHER)	1.37E-08	15	/28/054/	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_	e 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;3.20	15	72864420	3170239;448013	2 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	Α	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 <i>P</i> 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	т	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_F0	O 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;C15ort17;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;C15ort17;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	730018/12	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	/3008298	218143_s_at	SCAMP2	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs110/2514	LCL in asthmatics (Liang 1kg)	1.10E-19	15	/3008918	218143_s_at	SCAMP2	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15ort17;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;C15ort17;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;C15ort17;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	/3008021	ILMN_1761262	MPI	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs110/2514	LCL (MUTHER)	3.03E-08	15	/3008918	ILMN_1/61262	MPI	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	1	rs110/2514	Skin (MuTHER)	1.37E-05	15	/3008918	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-Rei2	1	rs11072513	Subcadipose (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	COXSA;SCAMP2;RPP25;C150ff17;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Subc adipose (MUTHER)	2.19E-05	15	72999410	ILMIN_1679495	ULK3	CIS				
rs1133323	DBP	NA	COXSA;SCAMP2;RPP25;CISOFI7;MPI	13	LDproxy(CEU-Rel2	1	rs1133322	Skin (MUTHER)	3.02E-05	15	72999410	ILMIN_1679495	ULK3	CIS				
rs1133323	DBP	NA	COXSA;SCAMP2;RPP25;CISOFI7;MPI	13	LDproxy(CEU-Rei2	1	rs1133322	Bcells (CD19+)	3.21E-05	15	72999410	ubtiztiw7_2_FC	JCSK	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;CI5off17;MPI	13	LDproxy(CEU-1kg)	1	rs11633472	Bcells (CD19+)	3.80E-05	15	72971137	ubt12tiw7_2_F0	JUSK	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;CI50FI7;MPI	13	LDproxy(CEU-1kg)	1	rs11038130	Bcells (CD19+)	3.80E-U5	15	72970988	ubtiztiw/_2_FC	JUSK	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;CI50H17;MPI	13	LDproxy(CEU-Reiz	1	151133322	Monocytes (CD14+)	0.0001945	15	72999410	210142	CCAMP2	CIS				
151133323	DBP	NA	COX5A;SCAMP2;RPP25;CI50f17;MPI	13	LUproxy(CEU-H3)	0.982	1511850413	Whole blood (CHARGE)	1.02E-20	15	/2980943	218143_5_at	SCAIVIPZ	cis	0.00	<i>c:</i>	15	0015022
rc1122222	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.962	1511050415	liver(Groopawalt)	5.52E-20	15	72500543	10022814220	MDI	cis	-9.21	9	15	72913955
rc1122222	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU_H2)	0.962	1511050415	Liver (Greenawart)	2.015.09	15	72500545	UMNL 1761262	MDI	cis				
rc1122222	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MP1	13	LDproxy(CEU-H3)	0.982	rc11856413	Lymph	4 27E-06	15	72986945	GL 4505234-S	MDI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.982	rc11856413	Skin (MuTHER)	4.272-00	15	72986945	UMN 1679495	IIIK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RP25;C15orf17;MP1	13	LDproxy(CEU-H3)	0.982	rs11856413	Prefrontal cortex (all samples)	1.33E-05	15	72986945	10026392220	SCAMD2	cis				
rc1122222	DBP	NA	COX5A;SCAMP2;RP25;C15orf17;MP1	10	LDproxy(CEU H2)	0.982	rc11956412	Subcadiposo (MuTHER)	2 125 05	15	72500545	UMNL 2264525	SNUDN	cis				
rc1122222	DBP	NA	COX5A;SCAMP2;RP25;C15orf17;MP1	12	LDproxy(CEU H2)	0.002	rc11956412	Beolic (CD19+)	2 965 05	15	72006045	ubt12tlw/7 7 E		cis				
rc1122222	DBD	NA	COX5A;SCAMP2;RP25;C15orf17;MP1	12	LDproxy(CEU_H2)	0.002	rc11956412	Induced sputum (CORD cases)	0.00015722	15	72006045	224905 c at	C15orf17	cis				
rc1122222	DBD	NA	COX5A;SCAMP2;RP25;C15orf17;MP1	12	Dproxy(CEU_H2)	0.982	rc11956412	Riood(Eehrmann et al)	2 205-21-2 20	15	72006045	2170229-50241-4	CISCIND 2-ULK2-C	cis				
rc1122222	DBD	NA	COX5A;SCAMP2;RP25;C15orf17;MP1	12	LDproxy(CELLRel2)	0.967	re1120741	Whole blood (Battle)	4 095-124	15	75199920	3170233,30341,4	MDI	cis				
rc1122222	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU Rol2	0.907	151150741	Monoratos	2.255.20	15	73103330			cis				
rc1122222	DBP	NA	COV5A-SCAMP2-RPP25-C15orf17-MPI	13	Doroxy(CELL Pol2	0.967	rc7/95729	ICL in asthmatics (Liang 1kg)	5.965-29	15	72972723	202472 at	MDI	cis				
rc1133323	DBP	NA	COY5A:SCAMP2:RDD25:C15orf17:MDI	13	Doroxy(CEIL Pol2	0.967	rs11207/1	ICL in asthmatics (Liang 1kg)	1.455-28	15	72976993	2024/2_at	MDI	cis				
rc1133323	DBP	NA	COY5A:SCAMD2:RDD25:C15orf17:MDI	10	Doroxy(CELL Pol2	0.967	rs11072512	ICL in asthmatics (Liang 1kg)	3.40E-28	15	72991070	2024/2_at	MDI	cis				
rs112222	DBP	NA	COY54-SCAMD2-RDD25-C15-rf17-MDI	10	Doroxy(CEU Polo	0.907	rc/886626	ICL in asthmatics (Liang 1kg)	3.40E-20	15	729910/5	2024/2_at	MDI	cic				
rc1122222	DBP	NA	COY54-SCAMD2-RDD25-C15-rf17-MDI	10	Doroxy(CEU Polo	0.907	rs1127706	Monorytes	6.08F.27	15	72900057	2024/2_at	111.K3	cic				
rs1122222	DRD	NA	COY54-SCAMD2-RDD25-C15-cf17-MDI	10	Dproxy(CEU_Polo	0.507	rc/886626	Whole blood (CHAPGE)	1 495-22	15	7200007	4480132	UIK3	cic	-9 77	۵	15	72915022
rs1122222	DRP	NA	COX5A-SCAMD2-RDD25-C15orf17-MDI	10	Dproxy(CEU_Polo	0.507	rs1120741	Whole blood (CHARGE)	5.14F-22	15	72976003	4480132	UIK3	cic	-9.65	G	15	72915022
rs1122222	DRP	NA	COX54-SCAMD2-RDD25-C15orf17-MDI	13	Dproxy(CEU_Polo	0.907	rs7495720	Whole blood (CHARGE)	5.40E-22	15	72970703	4480132	LILK3	cic	-9.64	6	15	72915022
rs1122222	DBP	NA	COV5A-SCAMD2-PDD25-C15-cf17-MDI	13	Doroxy(CEU B-12	0.507	rc7/197202	Whole blood (CHARGE)	5.71E 22	15	72062510	4480132	ULK2	cic	-9.62	6	15	72915933
131133323	DOP	IN/A	CONDRIGCAIMPZ,RPPZJ,CIJUITT,IMPI	13	coproxy(cco-keiz	0.507	13/47/373	Whole blood (CHARGE)	3.710-22	10	72502510	4400132	OLK3	UIS	-5.05	~	10	12913933

IndexSNP	Traits	InRefGene	RefGenes60kb	Locus#	Index/LD status	r^2 to index eSN	Pid	Tissue	eSNP <i>P</i> value	Chr	B36pos	ArrayID	Transcript	type of eQTL (cis or trans)	Beta	Allel	Probe e Chromosome	Probe Position
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	27796	Whole blood (CHARGE)	1.00E-21	15	72980057	4480132	ULK3	cis	-9.58	с	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	072511	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 rs74	97393	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 rs11	072512	Whole blood (CHARGE)	7.79E-21	15	72991079	4480132	ULK3	cis	-9.36	т	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	072511	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 rs48	86636	SubCutAdipose(Greenawalt)	7.68E-11	15	72983229	10023814330	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs48	86636	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 rs11	072512	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 rs11	27796	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 rs11	30741	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 rs74	95739	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 rs11	072511	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 rs74	97393	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 rs74	95739	RNAseq(HapMapLCL)+DeepSage(blood)	2.76E-07	15	75185670	ENST00003796	9 MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs74	97393	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 rs11	072511	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 rs48	86636	Subc adipose (MuTHER)	1.94E-05	15	72983229	ILMN_1679495	ULK3	cis				
rs1133323	DBP	NΛ	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs74	95739	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 rs11	30741	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 rs74	97393	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 rs11	27796	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 rs48	86636	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 rs11	072512	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 rs11	072512	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 rs11	072512	Bcells (CD19+)	3.21E-05	15	72991079	ubt12tlW7_Z_F	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	27796	Bcells (CD19+)	3.21E-05	15	72980057	ubt12tlW7_Z_F	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs48	86636	Bcells (CD19+)	3.35E-05	15	72983229	ubt12tlW7_Z_F0	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	30741	Bcells (CD19+)	4.67E-05	15	72976983	ubt12tlW7_Z_F0	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs48	86636	Monocytes (CD14+)	0.000135	15	72983229	r_tdN3VF1vV3q	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	072511	Bcells (CD19+)	0.0001942	15	72946486	ubt12tlW7_Z_F0	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	072512	Monocytes (CD14+)	0.0001945	15	72991079	r_tdN3VF1vV3q	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs11	27796	Monocytes (CD14+)	0.0001945	15	72980057	r_tdN3VF1vV3q	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs48	86636	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 rs11	30741	Monocytes (CD14+)	0.0003045	15	72976983	r_tdN3VF1vV3q	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.967 rs48	86636	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 rs48	86636	Blood(Fehrmann et al)	1.60E-19;1.10	15	72983229	3170239;50341;4	4 CSK;SCAMP2;ULK3;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs12	902515	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 rs24	15251	Whole blood (CHARGE)	1.49E-19	15	73029208	4480132	ULK3	cis	-9.05	С	15	72915933
rs1133323	DBb	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs48	86641	LCL in asthmatics (Liang 1kg)	2.23E-19	15	/3015/08	218143_s_at	SCAMP2	CIS				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs11	639413	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 rs24	15251	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 rs24	15251	omental	3.08E-19	15	73029208	10025911367	RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.966 rs24	15249	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 rs24	15251	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 rs24	15251	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 rs24	15251	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 rs24	15251	Bcells (CD19+)	3.17E-05	15	73029208	ubt12tlW7_Z_F	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965 rs11	854704	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 rs11	630918	Whole blood (CHARGE)	1.26E-22	15	72942949	4480132	ULK3	cis	-9.79	Т	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965 rs11	630918	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 rs11	630918	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 rs11	630918	Lung	2.86E-06	15	72942949	100161886_TGI_	a SCAMP2	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.965 rs11	630918	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 rs11	630918	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 rs11	630918	Bcells (CD19+)	5.10E-05	15	72942949	ubt12tlW7_Z_F	D CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.932 rs12	913293	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 rs80	25447	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 rs12	907898	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 rs12	904897	LCL in asthmatics (Liang 1kg)	3.85E-28	15	73004739	202472_at	MPI	cis				

IndexSNP	Traits	InRefGene	RefGenes60kh	Locust	t Index/ID status	r^2 to	) c eSNPid	Tissue	eSNP P value	Chr	B36nos	ArravID	Transcript	type of eQTL (cis or trans)	Beta	Allel	Probe	Probe
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	I Dproxy(CEU-1kg)	0.93	rs59945415	I CL in asthmatics (Liang 1kg)	8.04E-28	15	73015480	202472 at	MPI	cis	betu	Anci	. emonosome	rosition
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxy(CEU-H3)	0.93	rs12487	Monocytes	5.36E-26	15	72923747		ULK3	cis				
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxv(CEU-H3)	0.93	rs12487	Whole blood (CHARGE)	3.69E-24	15	72923747	4480132	ULK3	cis	-10.14	с	15	72915933
rs1133323	DBP	NA	COX5A:SCAMP2:RPP25:C15orf17:MPI	13	LDproxv(CEU-H3)	0.93	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)	0.93	rs12487	LCL (MuTHER)	2.37E-07	15	72923747	ILMN 1761262	MPI	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.93	rs12487	Skin (MuTHER)	3.95E-06	15	72923747	ILMN 1679495	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-H3)	0.93	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	С	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	0.87	rs6495122	Cerebellum (Alzheimer's)	7.49E-10	15	72912698	10025927424	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.87	rs6495122	Bcells (CD19+)	3.92E-07	15	72912698	ubt12tlW7 Z FC	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	0.87	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	0.87	rs6495122	Monocytes (CD14+)	9.64E-05	15	72912698	r tdN3VF1vV3q	ULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.87	rs6495122	Blood	0.0002728	15	72912698	HSG00290189	ARID3B	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.87	rs6495122	Lung	<2E-16	15	72912698	100312245 TGI	a RPP25	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.873	rs6495122	Blood(Fehrmann et al)	1.00E-25;1.50	15	72912698	3170239;448013	2 CSK;ULK3;SCAMP2;C	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.832	2 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	s 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)	0.80	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)	0.80	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)	0.80	rs35556055	Bcells (CD19+)	0.0001316	15	73040467	ubt12tlW7 Z FC	сѕк	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	Α	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	s 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	s 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)	0.77	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)	0.76	7 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	т	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_F0	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	VULK3	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-1kg)	0.75	rs11072518	Blood(Fehrmann et al)	1.90E-27;7.90	15	73021663	3170239;448013	2 CSK;ULK3;COX5A;SC	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	s rs2290572	Whole blood (CHARGE)	2.42E-29	15	72917626	4480132	ULK3	cis	11.25	Α	15	72915933
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	s 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	s 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	s rs2290572	Bcells (CD19+)	5.64E-06	15	72917626	ubt12tlW7_Z_FC	O CSK	cis				
rs1133323	DBP	NA	COX5A;SCAMP2;RPP25;C15orf17;MPI	13	LDproxy(CEU-Rel2	0.708	s 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	С	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	Α	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	С	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	т	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	т	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	Α	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	т	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.

						SBP, mmHg,	DBP, mmHg,
					Anti-	adjusted for	adjusted for
	Age,	BMI,	SBP, mmHg	DBP,	hypertensive	antihypertensive	antihypertensive
Ν	years (sd)	kg/m2 (sd)	(sd)	mmHg (sd)	therapy (%)	therapy (sd)	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 \	/1 Asso	ciation Res	ults		
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGenes	ClosestRe	Direction	Beta	s.e.	Р	Trait		SNPID	Beta	s.e.	Р
CHARGE_LTA - DBP	rs1204627	1	10722164	t	С	CASZ1	CASZ1	CASZ1	?	-0.3223	0.0597	2.29E-07	GBPG V	'1-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 \	/1-DBP	rs1330656	0.4529	0.1083	0.00002905
CHARGE_LTA - DBP	rs2004776	1	228915325	t	с	AGT	AGT;COG	AGT	+++++++++	0.3545	0.0615	3.20E-08	GBPG \	/1-DBP	rs2004776	0.1014	0.091	0.2656
CHARGE_LTA - DBP	rs1275988	2	26767868	t	с		KCNK3;CI	KCNK3	+	-0.2814	0.0534	4.25E-07	GBPG V	1-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 \	/1-DBP	rs7599598	-0.0403	0.0799	0.6139
CHARGE_LTA - DBP	rs1528293	3	170637205	а	t	MDS1	MDS1	MDS1	++++++++	0.2738	0.0522	4.96E-07	GBPG V	1-DBP	rs1528293	0.2427	0.0769	0.00161
CHARGE_LTA - DBP	rs1952650	5	157746045	а	t			EBF1	++++-++++	0.2862	0.0523	1.58E-07	GBPG V	1-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 \	/1-DBP	rs198823	-0.1705	0.0801	0.03331
CHARGE_LTA - DBP	rs1225896	10	18767965	с	g	CACNB2	CACNB2	CACNB2	+++-++++	0.3548	0.0571	2.48E-09	GBPG \	/1-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 \	/1-DBP	rs1224484	-0.432	0.0901	0.000001618
CHARGE_LTA - DBP	rs1084142	12	20046661	а	t			PDE3A	+++++++++	0.3604	0.0651	1.09E-07	GBPG V	1-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 \	/1-DBP	rs2681472	0.336	0.1065	0.001608
CHARGE_LTA - DBP	rs3184504	12	110368991	t	с	SH2B3	SH2B3;AT	SH2B3	+++++++++++++++++++++++++++++++++++++++	0.3936	0.0524	6.08E-13	GBPG \	/1-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 \	/1-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 V	1-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 \	/1-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 \	/1-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 \	/1-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 V	1-SBP	rs2004776	0.1419	0.1395	0.3091
CHARGE_LTA - SBP	rs1275988	2	26767868	t	с	NA	KCNK3;C	KCNK3	+	-0.6004	0.0917	2.61E-10	GBPG \	/1-SBP	rs1275988	-0.2554	0.1175	0.02977
CHARGE_LTA - SBP	rs6712094	2	164751706	a	q	NA	NA	GRB14	++++-++++	0.598	0.1007	9.89E-09	GBPG \	/1-SBP	rs6712094	0.4239	0.1298	0.001095
CHARGE LTA - SBP	rs9823197	3	11478133	а	t	ATG7	ATG7	ATG7	+-+-	-0.4884	0.0915	2.58E-07	GBPG V	1-SBP	rs9823197	-0.2888	0.1168	0.01344
CHARGE_LTA - SBP	rs7733331	5	32864603	t	с	NA	C5orf23;N	C5orf23	+	-0.5505	0.0911	5.38E-09	GBPG \	/1-SBP	rs7733331	-0.4965	0.118	0.00002564
CHARGE LTA - SBP	rs1253434	7	27242452	а	q	NA	HOXA13;H	EVX1	?	-1.5903	0.292	1.48E-07	GBPG V	1-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 \	/1-SBP	rs1270539	0.4007	0.1371	0.003466
CHARGE LTA - SBP	rs1267714	8	11488146	С	q	NA	BLK	BLK		-0.5272	0.0988	2.60E-07	GBPG V	1-SBP	rs1267714	-0.1581	0.1218	0.194
CHARGE_LTA - SBP	rs1225896	10	18767965	с	g	CACNB2	CACNB2	CACNB2	++++++++++	0.6307	0.0976	4.53E-10	GBPG \	/1-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 \	/1-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 V	1-SBP	rs1926032	-1.0971	0.2137	2.826E-07
CHARGE_LTA - SBP	rs2681472	12	88533090	a	q	ATP2B1	ATP2B1	ATP2B1	++++-++++	0.9457	0.118	1.04E-14	GBPG \	/1-SBP	rs2681472	0.6305	0.1646	0.0001282
CHARGE_LTA - SBP	rs4766578	12	110388754	a	ť	ATXN2	SH2B3;AT	ATXN2		-0.5599	0.0909	2.82E-09	GBPG \	/1-SBP	rs4766578	-0.4787	0.1201	0.00006713
CHARGE LTA - SBP	rs35444	12	114036820	a	q	NA	+++++-+-1	твх3	+++++-+-+	0.5452	0.0929	1.47E-08	GBPG \	/1-SBP	rs35444	0.1568	0.1226	0.2009
CHARGE LTA - SBP	rs1107251	15	73021663	t	c	NA	COX5A:SC	COX5A	+++++-+++	0.5692	0.0947	6.54E-09	GBPG \	/1-SBP	rs1107251	0.3548	0.12	0.003102
CHARGE LTA - SBP	rs6092743	20	57133765	a	a	NA	NA	C20orf174		0.8396	0.1449	2.25E-08	GBPG \	/1-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 \	/1-MAP	rs880315	-0.244967	0.108505	0.023966954
CHARGE LTA - MAP	rs1330656	1	11788391	a	a	MTHER	MTHFR:N	MTHFR	++++-++++	0.6133	0.0832	1.83E-12	GBPG \	/1-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 \	/1-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 \	/1-MAP	rs1275988	-0.16	0.083983	0.056759651
CHARGE I TA - MAP	rs6712094	2	164751706	а	a	NA	NA	GRB14	++++-++++	0 385	0.0677	5 42E-08	GBPG V	1-MAP	rs6712094	0 2713	0 092326	0 003297944
CHARGE I TA - MAP	rs1528293	3	170637205	a	t	MDS1	MDS1	MDS1	+++++++++	0.3361	0.0602	9 29F-08	GBPG V	1-MAP	rs1528293	0 279367	0.083395	0 000808377
CHARGE LTA - MAP	rs7728845	5	122933582	a	a	CSNK1G3	CSNK1G3	CSNK1G3	+++++++++	0.3766	0.0712	4.34E-07	GBPG V	1-MAP	rs7728845	0.3521	0.099069	0.000379275
CHARGE LTA - MAP	rs198846	6	26215442	a	a	NA	HIST1H2B	HIST1H1T	+++++++++	0.4829	0.085	5.69E-08	GBPG V	1-MAP	rs198846	0.5286	0.120456	1.1423E-05
CHARGE LTA - MAP	rs7794193	7	27261226	а	a	NA	HOXA13:E	EVX1	+-+-	-0.914	0.1724	4.03E-07	GBPG V	1-MAP	rs7794193	-0.296533	0.205208	0.148447395
CHARGE LTA - MAP	rs1225896	10	18767965	c	a	CACNB2	CACNB2	CACNB2	+++++-+++	0.452	0.0657	4.98E-11	GBPG \	/1-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 \	/1-MAP	rs2166122	-0.439133	0.101765	1.5948E-05

CHARGE DISCOVERY	CHARGE DISCOVERYGBPG V1 Association Results																	
Trait	SNPID	Chr	Pos2	Allele1	Allele2	InRefGen	RefGene	ClosestR	Direction	Beta	s.e.	P	Trait		SNPID	Beta	s.e.	P
CHARGE_LTA - MAP	rs1084142	12	20046661	а	t	NA	NA	PDE3A	+++++++-	0.4081	0.0749	1.91E-07	GBPG \	/1-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	I 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	i t	g	RGL3	EPOR;EL	RGL3	+-??	-0.4521	0.0839	2.60E-07	GBPG \	/1-MAP	rs167479	-0.848267	0.716338	0.236345161
CHARGE_LTA - MAP	rs6092743	20	57133765	i a	g	NA	NA	C20orf17	+++++++++++++++++++++++++++++++++++++++	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	l t	С	NA	C5orf23;N	IC5orf23		-0.3328	0.0629	2.57E-07	GBPG \	/1-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 t	g	TCF7L2	TCF7L2	TCF7L2	+++++++++	0.3527	0.0676	3.71E-07	GBPG \	/1-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 \	/1-PP	rs2681485	0.1402	0.08435	0.096489798
CHARGE_LTA - PP	rs1077479	12	114036981	t	С	NA	NA	TBX3	+	-0.3362	0.0649	4.61E-07	GBPG \	/1-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	/1-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	/1-PP	rs6077869	0.11	0.098691	0.265026095

Rows in **bold** show LTA analysis P values <  $5 \times 10^{-8}$ .

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

Number of significant SNPs										
	<i>P</i> value < 5x10 <sup>-8</sup>									
	#LTA SNPs	#V1 SNPs								
SBP	117	122								
DBP	96	126								
MAP	155	153								
PP	120	1								
Total	488	402								

Numbe	Number of significant Loci											
	<i>P</i> value < 5x10 <sup>-</sup>	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	SBP	SBP	SBP
	V1	V2	V3	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 Star	Position End	# SNPs	DPvalue	D+.Pvalue	DPvalue	D+.Pvalue
LTA	SBP	rs13306561	а	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	а	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	а	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	а	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	а	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	а	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	а	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	а	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	а	7p13	45960903	NA	IGFBP3	IGFBP3	2.94E-08	6.88E-06	45929639	45960903	49	1	<0.0001	1	<0.0001
LTA	PP	rs12705390	а	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	а	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	а	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	С	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	а	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	С	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	а	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	С	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	а	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	а	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;L	FER1L5	2.91E-08	6.54E-08	96715567	rs7599598	1	1	0.4993	1	0.5046
No difference	DBP	rs1801253	С	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	а	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	С	10q25	115795046	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 04074	NA QAOZA	1BX3	3.20E-08	8.38E-07	114036820	114039913	14	0.7605	0.3228	0.7945	0.2617
No difference		15880315	1	1036	20427405	UASZ1	UASZ1	CASZI TGERRO	5.45E-09	3.31E-06	20427405	10/22164	0	0.8323	0.1492	0.8929	0.1943
No difference	rr	1512031607	a	J3pz4	130437465	INA	INA	TOPBRZ	0.023903474	9.20E-10	30437483	151203100/	11	0.0002	1	0.0043	1

#### SUPPLEMENTAL COHORT DESCRIPTIONS

#### **Cohort Descriptions**

#### **Discovery cohorts**

The CHARGE Consortium<sup>1</sup> 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<sup>2-4</sup> and HapMap reference panels<sup>5</sup> 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<sup>4,6</sup>. 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<sup>4,6</sup>.

#### AGES Reykjavik

The Age Gene/Environment Susceptibility-Revkjavik (AGES- Revkjavik) 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.<sup>7</sup> 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.

#### <u>ARIC</u>

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<sup>8</sup> 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.<sup>17</sup> 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 selfreport and principal component analysis using genome-wide genotypes.

#### <u>CHS</u>

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<sup>9</sup>. 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.

### <u>FHS</u>

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.<sup>10-12</sup> 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.

#### <u>MESA</u>

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.<sup>15</sup> 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.<sup>16</sup> 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.<sup>13</sup> 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.

#### <u>WGHS</u>

The Women's Genome Health Study (WGHS)<sup>14</sup> 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,  $\geq$ 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  $\geq$  140 or DBP  $\geq$  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 metaanalysis have been previously reported.<sup>18</sup> Adjustment was performed for the use of antihypertensive 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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