Online supplement

Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney

Running title: Novel blood pressure locus and gene discovery

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Studies contributing to discovery (Stage 1) of signals of association with systolic (SBP) and diastolic blood pressure (DBP), and Pulse Pressure (PP)

All studies contributing genome-wide association results for SBP, DBP and PP to the discovery meta-analysis undertook genome-wide imputation to the 1000 Genomes Project reference panel. Study details are given in **Supplementary Table 1 (S1)** (including study design, ethnicity and key references), **Supplementary Table 2 (S2)** (overall descriptive statistics of SBP, DBP, PP, hypertension, age, sex and BMI, and blood pressure measurement details), **Supplementary Table 3 (S3)** (quality control, association testing method and adjustments for ancestry and relatedness) and **Supplementary Table 4 (S4)** (genotyping and imputation details).

Studies contributing association results for variants selected for replication/follow-up (Stage 2)

Details of all studies contributing data for the 61 variants followed-up to stage 2 are given in **Supplementary Table 5 (S5)**.

Studies contributing eQTL data

SABRe

The expression quantitative trait locus (eQTL) analysis was performed in 5,257 whole blood samples of Framingham Heart Study (FHS) Offspring and Generation 3 cohort participants having both genotypic and expression datasets. The genotypic data came from Affymetrix 500K and 50K MIPS platforms, imputed to the 1000-Genomes "Cosmopolitan" panel. Only 8,510,936 variants having minimum allele frequency (MAF) ≥ 0.01 and imputation R^2≥0.3 were chosen. The expression data came from Affymetrix Human Exon Array ST v1.0, processed using robust multi-chip average (RMA) algorithm under Affymetrix Power Tools (APT), yielding a total of 17,873 transcripts in log base 2 values. The association was performed on the expression values as the dependent variable, additive genetic dosage as an independent variable, adjusted for sex, age, imputed blood cell fractions, 20 factors of Bayesian confounding factors (PEER[1]), and familial correlations. The full details of eQTL analysis can be found in Joehanes, et al. Integrated Genome-wide Analysis of Expression Quantitative Trait Loci Identifies Putative Disease-Related Genes and Pathways.

The linkage disequilibrium (LD) database for the FHS was computed from 8,481 genotypic samples from individuals of FHS cohorts (Original, Offspring, and Generation 3), using the squared Pearson correlation of the imputed additive genotypic dosage, as defined by Hill and Robertson 1968[2]. All pairwise LDs of at least 0.1 were stored in the database and were used in this analysis.

NESDA/NTR

Subjects for eQTL analysis: The two parent projects that supplied data for the eQTL analysis are large-scale longitudinal studies: the Netherlands Study of Depression and Anxiety (NESDA)[3] and the Netherlands Twin Registry (NTR)[4]. NESDA and NTR studies were approved by the Central Ethics Committee on Research Involving Human Subjects of the VU University Medical Center, Amsterdam (institutional review board [IRB] number IRB-2991 under Federal wide Assurance 3703; IRB/institute codes: NESDA 03-183 and NTR 03-180). All participants provided written informed consent. The sample used for eQTL analysis consisted of 4,896 subjects with European ancestry (1,880 unrelated subjects from NESDA, 559 MZ twin pairs, 102 siblings of MZ twins (one per MZ twin pair), 594 DZ

twin pairs, 111 siblings of DZ twins (one per DZ twin pair), 51 parent-sibling trios and 344 unrelated subjects from NTR). The age of the participants ranged from 17 to 88 years (mean=38, *SD*=13); 65% of the sample was female.

Blood sampling, RNA extraction, and RNA expression measurement: Study protocols and biological sample collection methods were harmonized between NTR and NESDA. RNA processing and measurements have been described in detail previously[5, 6]. Venous blood samples were drawn in the morning after an overnight fast. Heparinized whole blood samples were transferred within 20 minutes of sampling into PAXgene Blood RNA tubes (Qiagen, Valencia, California, USA) and stored at −20°C. Gene expression assays were conducted at the Rutgers University Cell and DNA Repository. Samples were hybridized to Affymetrix U219 arrays (Affymetrix, Santa Clara, CA) containing 530,467 probes summarized in 49,293 probe sets. Array hybridization, washing, staining, and scanning were carried out in an Affymetrix GeneTitan System per the manufacturer's protocol. Gene expression data were required to pass standard Affymetrix QC metrics (Affymetrix expression console) before further analysis. We excluded from further analysis probes that did not map uniquely to the hg19 (Genome Reference Consortium Human Build 37) reference genome sequence, as well as probes targeting a messenger RNA (mRNA) molecule resulting from transcription of a DNA sequence containing a single nucleotide polymorphism (based on the dbSNP137 common database). After this filtering step, data for analysis remained for 423,201 probes, which could be summarized into 44,241 probe sets targeting 18,238 genes. Normalized probe set expression values were obtained using Robust Multi-array Average (RMA) normalization as implemented in the Affymetrix Power Tools software (APT, version 1.12.0, Affymetrix). Data for samples that displayed a low average Pearson correlation with the probe set expression values of other samples, and samples with incorrect sex-chromosome expression were removed, leaving 4,896 subjects for analysis.

Gene expression normalization: Inverse quantile normal transformation was applied for each expression probe set to obtain normal distributions. The transformed probeset data were then residualized by multiple linear regression with respect to the covariates sex, age, body mass index (kg/m^2), blood hemoglobin level, smoking status, several technical covariates (plate, well, hour of blood sampling, lab, days between blood sampling and RNA extraction and average correlation with other samples) and the scores on three principal components (PCs) as estimated from the imputed SNP genotype data[7] using the EIGENSOFT package. The residuals resulting from the linear regression analysis of the probe set intensity values onto the covariates listed above were subjected to a principal component analysis, with the aim to further filter out environmental variation from the data[8]. For each principal component a genome-wide association study was performed, and the first 50 principal components without genome-wide significant SNP associations were removed from the residualized probeset data before eQTL analysis.

DNA extraction and SNP genotyping and imputation: DNA was extracted from peripheral blood or buccal swabs as has described previously[9]. SNP genotype pre-imputation quality control, haplotype phasing and 1000 Genomes imputation were performed as described previously[10]. Imputed SNP genotypes were coded into reference allele dosage format, and filtered at MAF>0.01 and HW *P*>1E−04 resulting in 8,158,830 remaining SNPs for eQTL analysis.

eQTL analysis and FDR based on permutations accounting for relatedness: eQTL effects were detected with a linear model approach using MatrixeQTL[11] with expression level as dependent variable and SNP genotype values as independent variable. To account for relatedness of the NTR subjects, permutations were performed where in each permutation the relatedness was preserved (i.e, in each permutation the genotypes of the MZ twin pairs were assigned the expression of a random MZ twin pair, the genotypes of the DZ twin pairs were assigned the expression of a random DZ twin pair, the genotypes of the MZ twin pairs with sibling were assigned the expression of a random MZ twin pair with sibling, the genotypes of the parent-sibling trios were assigned the expression of a random parent-sibling trios and the genotypes of the unrelated subjects were

assigned the expression of a random subject from the group of unrelated subjects). For each permutation the complete *cis* or trans eQTL analysis was repeated, and after each permutation the *P*-value threshold for rejecting at FDR<0.05 was computed. This can be done in 2 ways: 1) divide the total number of significant eQTLs in the permuted data by the total number of significant eQTLs in the unpermuted data (=false positives/true positives) or 2) divide the total number of probesets with a significant eQTL in the permuted data by the total number of probesets with a significant eQTLs in the unpermuted data. We used the the second method which is more conservative and was proposed by[8] to account for large LD blocks with strong eQTL effects that inflate the FDR when using the first method. Similar as what was observed previously[8] only 10 permutations were needed to have the *P*-value threshold corresponding to FDR<5% converging. Of note, the eQTL P-values reported in this manuscript are based on the complete sample with related subject and thus are too liberal: however the FDR takes into account the family structure and should be used to draw conclusions. The reported betas from the linear models can be correctly estimated from samples containing related subjects.

eQTL effects were defined as *cis* when probe set–SNP pairs were at distance < 1M base pairs (Mb), and as *trans* when the SNP and the probe set were separated by more than 1 Mb on the genome according to hg19. For each probe set that displayed a statistically significant association with at least one SNP in the *cis* region, we identified the most significantly associated SNP (top eQTL). Conditional eQTL analysis was carried out by first residualizing probeset expression using the corresponding top eQTL and then repeating the eQTL analysis using the residualized data.

For this analysis, of the 164 SNPs requested, 12 were not available in the NESDA/NTR dataset leaving 152 for further analysis.

BIOS

eQTL analyses performed by the BIOS consortium have been described previously[12]. The method described in these papers are summarized below. Genotype data were harmonized towards the Genome of the Netherlands (GoNL)[13] using Genotype Hamonizer and subsequently imputed per cohort using Impute2 using the GoNL reference panel (v5). We removed SNPs with an imputation info-score below 0.5, a HWE *P*-value smaller than 10^{-4}, a call rate below 95% or a minor allele frequency smaller than 0.05. Total RNA from whole blood was deprived of globin using Ambions GLOBINclear kit and subsequently processed for sequencing using Illumina's Truseq version 2 library preparation kit. Paired-end sequencing of 2x50bp was performed using Illumina's Hiseq2000, pooling samples at 10 per lane, and aiming for >15M read pairs per sample. Finally, read sets per sample were generated using CASAVA, retaining only reads passing Illumina's Chastity Filter for further processing. The quality of the raw reads was checked using FastQC. The adaptors identified by FastQC (v0.10.1) were clipped using cutadapt (v1.1) applying default settings (min overlap 3, min length). Sickle (v1.200) (https://github.com/najoshi/sickle) used to trim low quality ends of the reads (min length 25, min quality 20). Read alignment was performed using STAR 2.3.0e. To avoid reference mapping bias all GoNL SNPs with MAF > 0.01 in the reference genome were masked. Read pairs with at most 8 mismatches, mapping to at most 5 positions were used. Mapping statistics from the BAM files were acquired through Samtools flagstat (v0.1.19-44428cd). The 5' and 3' coverage bias, duplication rate and insert sizes were assessed using Picard tools (v1.86). We estimated expression on the gene, exon, exon ratio and polyA ratio levels using Ensembl v.71 annotation (which corresponds to Gencode v.16). Overlapping exons (on either of the two strands) were merged into meta-exons and expression was quantified for the whole meta-exon. For that, custom scripts were developed which uses coverage per base from coverageBed and intersectBed from the Bedtools suite (v2.17.0) and R (v2.15.1). This resulted in base counts per exon or meta-exon. Expression data was first normalized using Trimmed Mean of M-values (TMM). Then expression values were log2 transformed, probe and sample means were centred to zero. To correct for batch effects, principal component analysis (PCA) was run on the sample correlation matrix and the first 25

PCs were removed. We saw that removing these PCs resulted in highest number of eQTLs detected. To ascertain that none of these 25 PCs are under genetic control, we ran separate QTL mapping on each principal component and ensured that there were no SNPs associated with them. After QC, data was available from 2,116 samples. Data was available for 123 of the 164 blood pressure associated SNPs. For each of the 123 SNPs, local (*cis*, genes < 1 MB from the SNP) effects were identified by computing Spearman rank correlations between SNPs and local gene expression. FDR was computed based on permutations[12]. For each of the significant associations, the genes were selected, the strongest eQTLs were identified for these genes sites, and LD between these strongest eQTLs and the corresponding SNP identified in the GWAS were computed. LD was computed using the European 1000G reference set.

TransplantLines eQTL data (kidney)

We performed an expression quantitative trait locus (eQTL) analysis in order to identify regulatory variants associated with the ICBP SNPs, using a gene-expression database from kidney biopsy specimens. The TransplantLines eQTL cohort used for the kidney analysis is part of a donor cohort for which gene expression results have been described previously[14]. The dataset includes kidneys from living donors, donated after brain death and donated after cardiac death (non-heart-beating). Time of biopsy (that is, before transplantation (T1), before reperfusion (T2) and after reperfusion (T3)) was recorded as well. For some donors multiple biopsies from different time points were taken. In addition, for some donors biopsies from both kidneys were available.

Samples were genotyped on the Illumina CytoSNP 12 v2 array and imputed using the 1000Genomes Phase 1 ALL reference panel[15] using Impute2[16]. Expression and genotype data were available for 236 kidney biopsies of 134 donors. Of the 164 SNPs identified by the ICBP consortium, two were not present in our dataset (chr 6: rs200999181; chr 9: rs9710247) and three were removed because of their proximity to the HLA region, leaving 159 SNPs available for eQTL analysis. In this study we only tested *cis* effects meaning that the probe was at a distance < 1Mb from the SNP on the genome according to GRCh37/hg19. Mixed model analyses were carried out in R[17] to account for multiple samples from a donor (package lme3 version 1.1.12[18]). SNP, sex, age, donor type, time of biopsy, and the first three principal components from the genotype data were included in the model as fixed effects; and sample ID was included as a random effect. Residuals of gene expression values after adjusting for the first 50 expression principal components to filter out environmental variation[8] were used as dependent variable. Probes with a false discovery rate <5% were considered statistically significant.

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Supplementary Table legends

Supplementary Table 1 (Table S1): Study design summary information for each of the studies contributing to Stage 1.
Details include study acronym, full study name, epidemiological study design, and total study sample size, information about ascertainment, ethnicity and origin and references (as PubMed ID [PMID]).

Supplementary Table 2 (Table S2): Summaries of blood pressure phenotypes and covariates for all studies contributing to Stage 1.
Mean, median, standard deviation (SD), minimum (min) and maximum (max) values for the blood pressure phenotypes being analysed (SBP, DBP and PP) and covariates (age, Body Mass Index [BMI]) in all stage 1 studies separately. Individuals were assigned as hypertension cases if they had SBP ≥140, or DBP ≥90, or used antihypertensive or blood pressure lowering medication. Method of blood pressure measurement is included.

Supplementary Table 3 (Table S3): Summaries of methods used to adjust for population stratification and kinship for all studies contributing to Stage 1.
PCA: Principal Components Analysis, PC: Principal Component. IBS: Identity By State.

Supplementary Table 4 (Table S4): Summary of genotyping and imputation strategy for all studies contributing to Stage 1.
HWE; Hardy-Weinberg Equilibrium P value threshold used for exclusion. MAF; Minor Allele Frequency.

Supplementary Table 5 (Table S5): Results for all 61 variants followed up in stage 2
Stage 2 results are shown separately for UK Biobank_CMC and all other replication studies separately and meta-analysed. The final column (Conclusion) includes an explanation as to why each signal was either classed as a novel signal or otherwise. Top_trait: trait for which the variant was found to be most strongly associated in Stage 1 and for which it was followed up in Stage 2. Se: standard error. gc: Genomic control correction applied. Neff: N effective (sum of the products of imputation quality and sample size for each contributing study). Results for rs1048238 and chr1:243458005:I were not available from UK Biobank_CMC and so proxy SNPs rs848309 and rs10926988 were selected as they had the next most significant P value, were in LD (r^2> 0.6) with the original sentinel variants and were measured in UK Biobank_CMC.

Supplementary Table 6 (Table S6): Stage 2 study details.
Details include study acronym, full study name, epidemiological study design, and total study sample size, information about ascertainment, ethnicity and origin and references (as PubMed ID [PMID]). Mean, median, standard deviation (SD), minimum (min) and maximum (max) values for the blood pressure phenotypes being analysed (SBP, DBP and PP) and covariates (age, Body Mass Index [BMI]) in all stage 1 studies separately. Individuals were assigned as hypertension cases if they had SBP ≥140, or DBP ≥90, or used antihypertensive or blood pressure lowering medication. Method of blood pressure measurement is included. PCA: Principal Components Analysis, PC: Principal Component. IBS: Identity By State. HWE; Hardy-Weinberg Equilibrium P value threshold used for exclusion. MAF; Minor Allele Frequency. *For UK Biobank_CMC, an additional 52 individuals were included in the HTN analysis as they used antihypertensive or blood pressure lowering medication (but did not have full data for SBP, DBP or PP and so were not included in the SBP, DBP and PP analyses).

Supplementary Table 7 (Table S7): a) Stage 1 and Stage 2 results separately and combined for all 22 novel signals of association with blood pressure b) Stage 1 and Stage 2 results separately and combined for a further 14 signals of association with blood pressure that were initially confirmed as putatively novel signals in this study but were subsequently reported in Hoffman et al 2016 and Warren et al 2017.

Results are shown separately for Stage 1, for the UK Biobank_CMC component of Stage 2 and for the other replication studies component of Stage 2 (see **Supplementary Figure 1** for list of other replication studies). Results are ordered by chromosome and position. Se: standard error. gc: Genomic control correction applied. Neff: N effective (sum of the products of imputation quality and sample size for each contributing study). Top_trait: trait for which the variant was found to be most strongly associated in Stage 1 and for which it was followed up in Stage 2.

Supplementary Table 8 (Table S8): Evidence for independence of secondary signals at previously reported loci
Summaries of conditional analyses establishing independence of novel secondary signals at previously reported loci. For each novel variant, association testing was repeated conditioning on the previously reported SNP. The conditional P value and the fold change in –log10 P value following conditioning are reported here. Linkage Disequilibrium (LD) r^2 and D' are from 1000 Genomes Project Phase 1. Se: standard error. gc: Genomic control correction applied. Neff: N effective (sum of the products of imputation quality and sample size for each contributing study).

Supplementary Table 9 (Table S9): Stage 1 association results for all 8 signals for all 3 blood pressure traits (SBP, DBP and PP)
Results from Stage 1 and from a meta-analysis of Stage 1 and Stage 2 are shown for all 3 blood pressure traits for all 8 signals. Genome-wide significant ($P < 5x10^{-8}$) signals are highlighted in green and results are ordered by chromosome and position. Se: standard error. gc: Genomic control correction applied. Neff: N effective (sum of the products of imputation quality and sample size for each contributing study).

Supplementary Table 10 (Table S10): Look-up of results in stage 1 for previously reported genome-wide significant signals of association with quantitative blood pressure traits.
Association results for SBP, DBP and PP from Stage 1 are shown for all previously reported signals of association. P values which are significant after Bonferroni adjustment for 141 tests are shown in green. Se: standard error. gc: Genomic control correction applied. Neff: N effective (sum of the products of imputation quality and sample size for each contributing study).[19-34]

Supplementary Table 11 (Table S11): Genes with levels of expression associated with novel or previously reported signals of association with blood pressure.
Each row represents a correlation of SNP genotype and gene expression. The 4 whole-blood data sets (BIOS, SABRe, NESDA/NTR, GTEx whole blood) are presented first in columns 6 to 9 followed by the all-tissue results from GTEx and from kidney. The number of blood data sets for which an eQTL signal was significant (FDR<5%) is indicated in column 5.

Supplementary Table 12 (Table S12): Kidney eQTL results
Variants in the TransplantLines eQTL analysis (see Supplementary Note) with a FDR < 0.05. FDR: False Discovery Rate.

Supplementary Table 13 (Table S13): Complete GTEx results.
The complete lookup results for each ICBP sentinel SNP are presented. If a proxy SNP was used for the GTEx lookup, it is indicated in this table.

Supplementary Table 14 (Table S14): LD lookup of sentinel SNPs in 1000G.
Variants with r^2>0.5 with novel and previously reported BP associated variants. LD: linkage disequilibrium, AF_EUR: Allele Frequency in 1000 Genomes Project EUR samples. Annotation also includes GWAScatalog results.

Supplementary Table 15 (Table S15): Gene-based pathway enrichment analysis of blood pressure genes

Summary of overrepresented known biological pathways for the 49 genes with evidence from 3 or 4 blood eQTL resources. FDR: False Discovery Rate.

Supplementary Table 16 (Table S16): Gene-based Gene Ontology enrichment analysis of blood pressure genes

Summary of overrepresented Gene Ontology (GO) for the 49 genes with evidence from 3 or 4 blood eQTL resources. FDR: False Discovery Rate. GO term categories (m= molecular function, b= biological process, c= cellular component) and levels (1 to 5, with highest level GO terms assigned to level 1) are indicated.

Supplementary Table 17 (Table S17): Network analysis

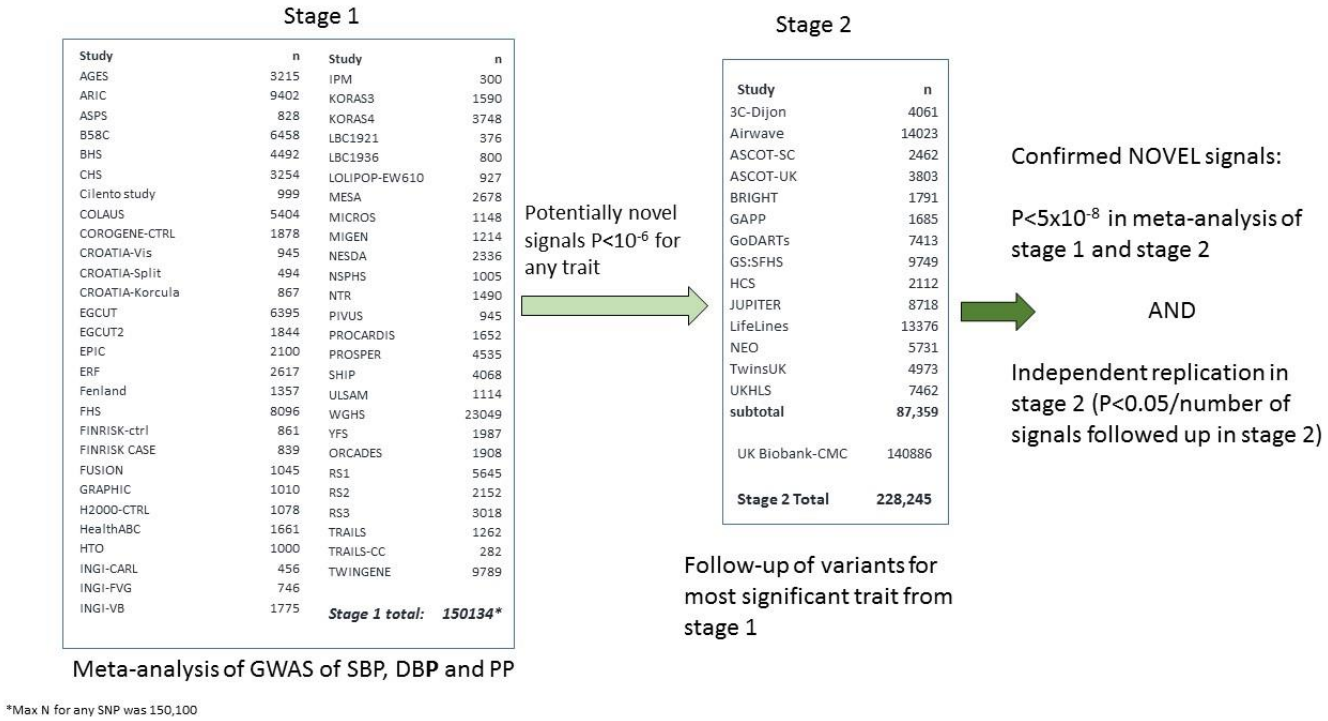
Results of GO term enrichment analysis following functional network construction. FDR: False Discovery Rate. An FDR cutoff of <0.01 was used.

Supplementary Table 18 (Table S18): Drug Target Analysis

Known drug-gene interactions and genes druggability prediction, investigating only expert curated data for the 48 genes with evidence from 3 or 4 blood eQTL resources and the non-synonymous SNPs in high LD (r2>0.50) with the sentinel BP associated SNPs (**Supplementary Table 13 (S13)**).

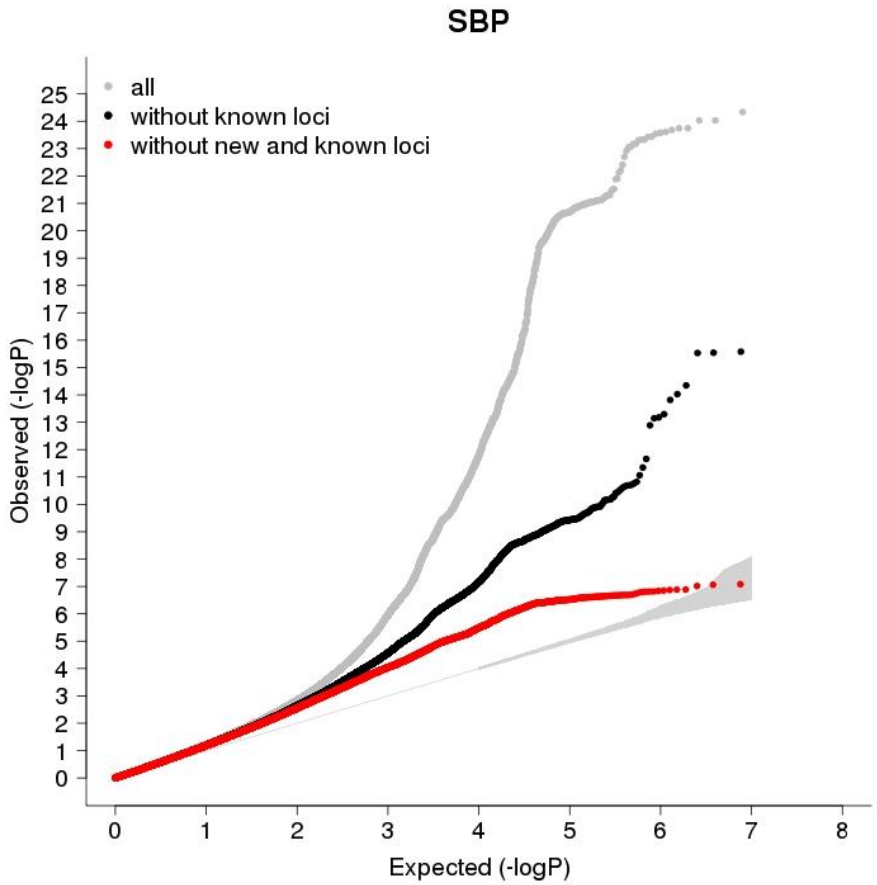
Supplementary Figures

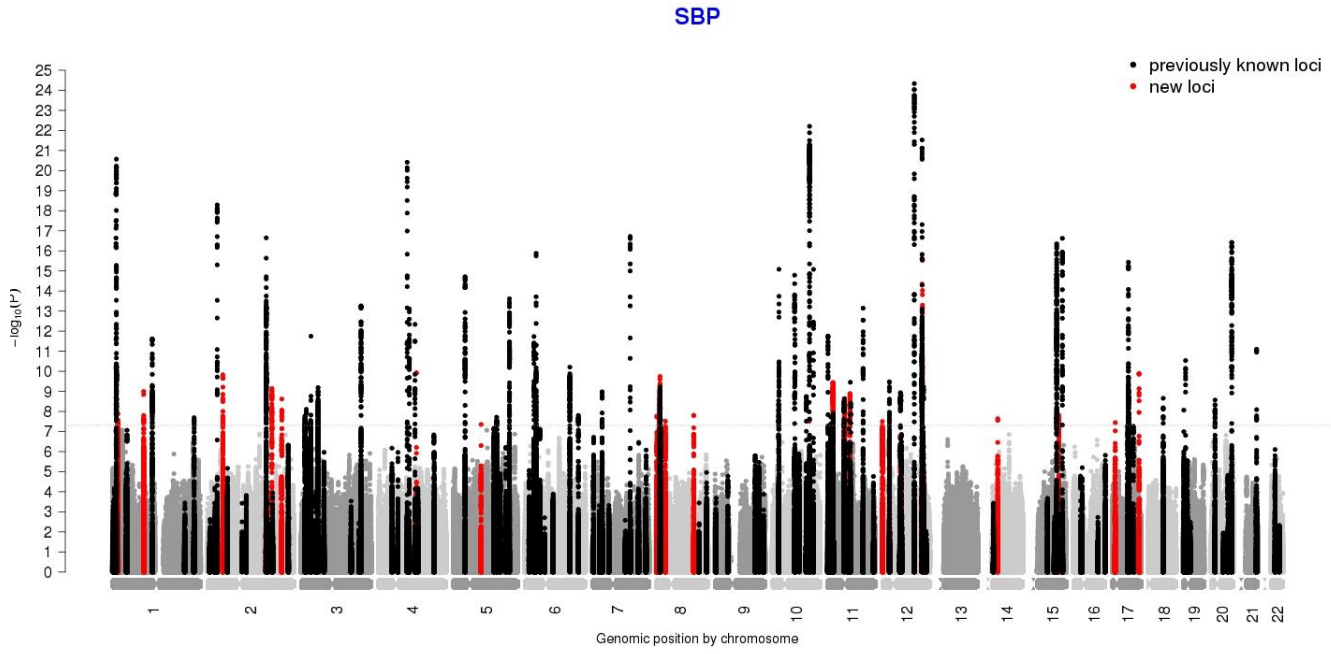
Supplementary Figure 1 (Figure S1): Study design.

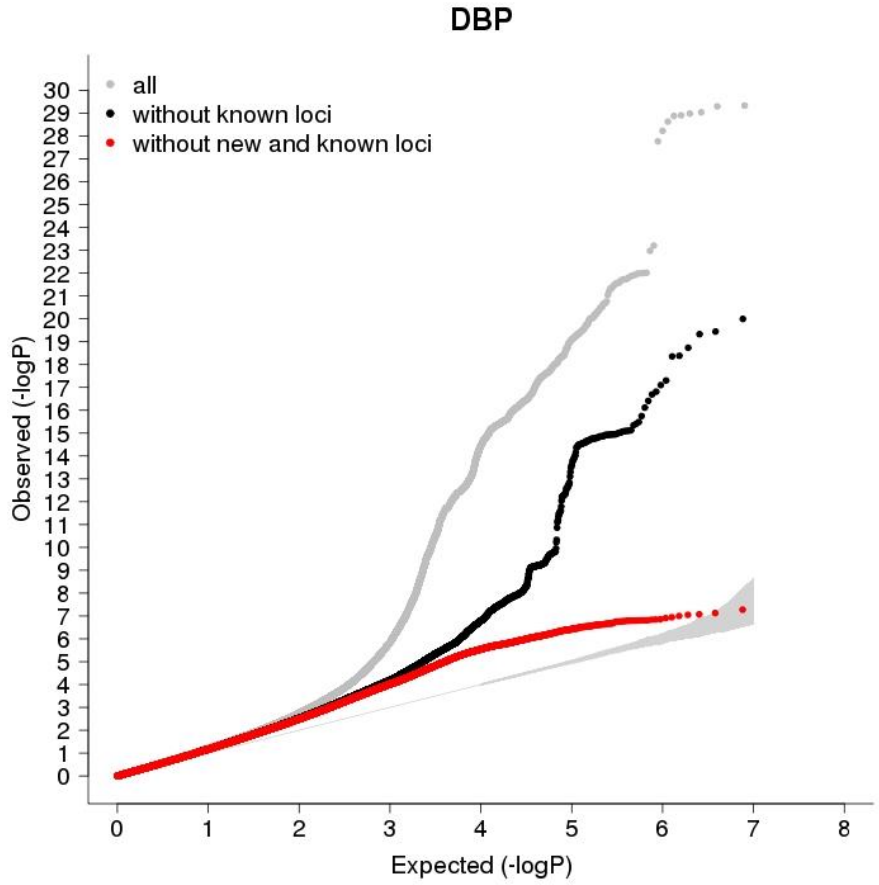


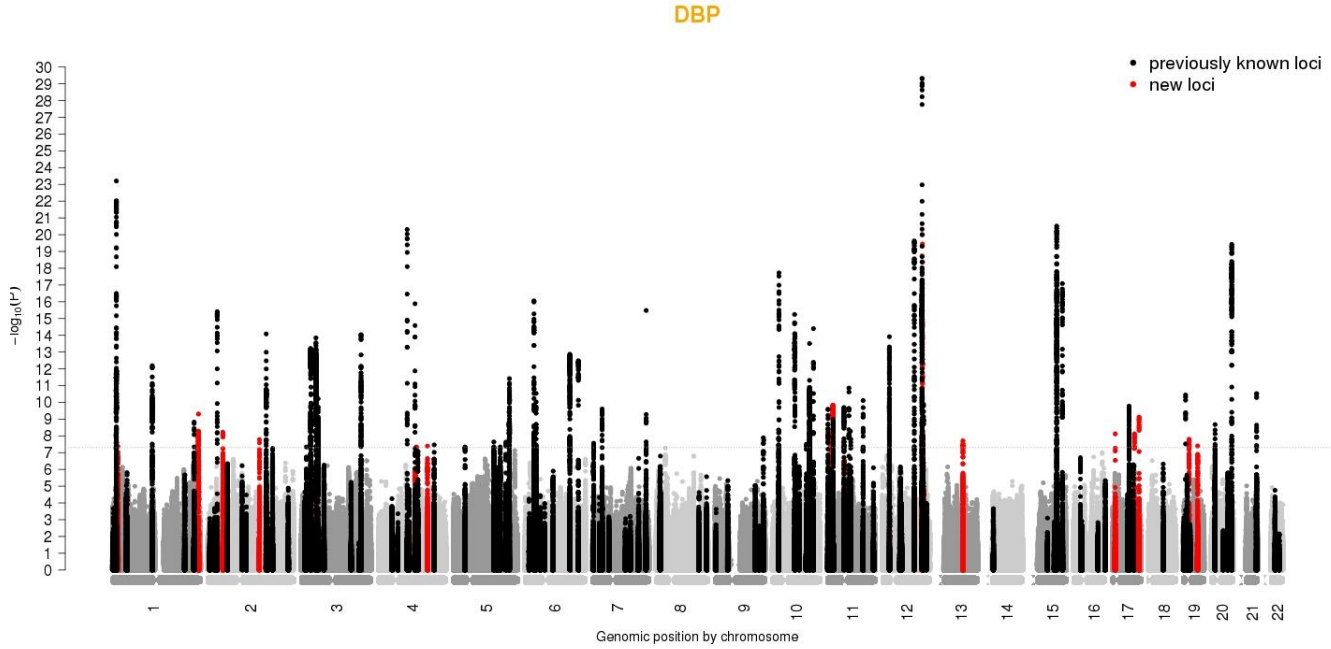
Overview of study design showing studies contributing to stage 1 (discovery) and studies contributing to stage 2 (replication/follow-up). Full study names are given in **Supplementary Table 1 (S1)** (Stage 1) and **Supplementary Table 6 (S6)** (Stage 2).

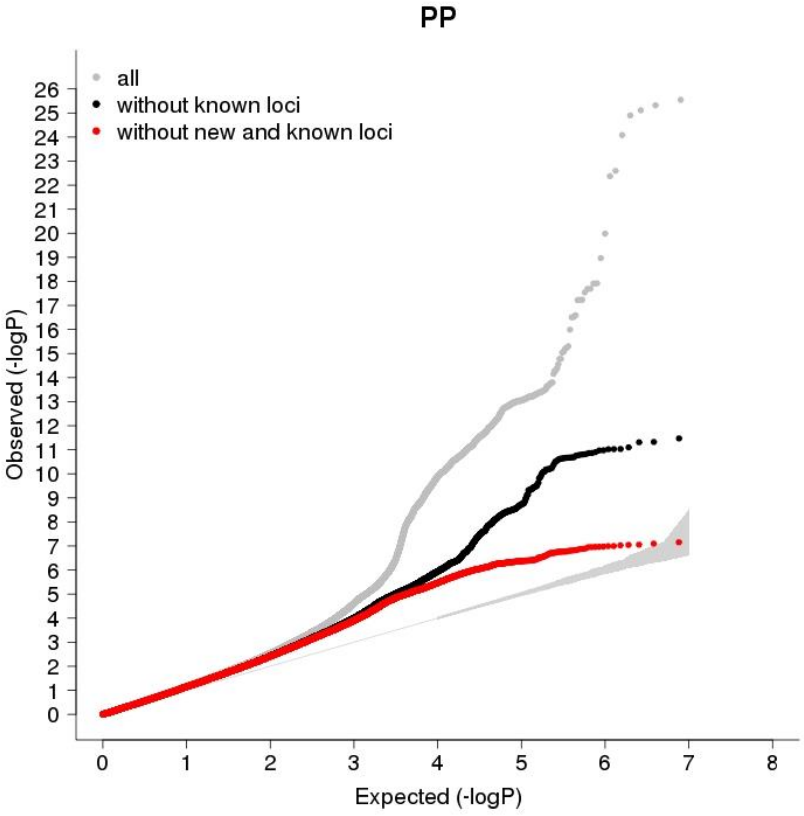
Supplementary Figure 2 (Figure S2): Manhattan and QQ plots

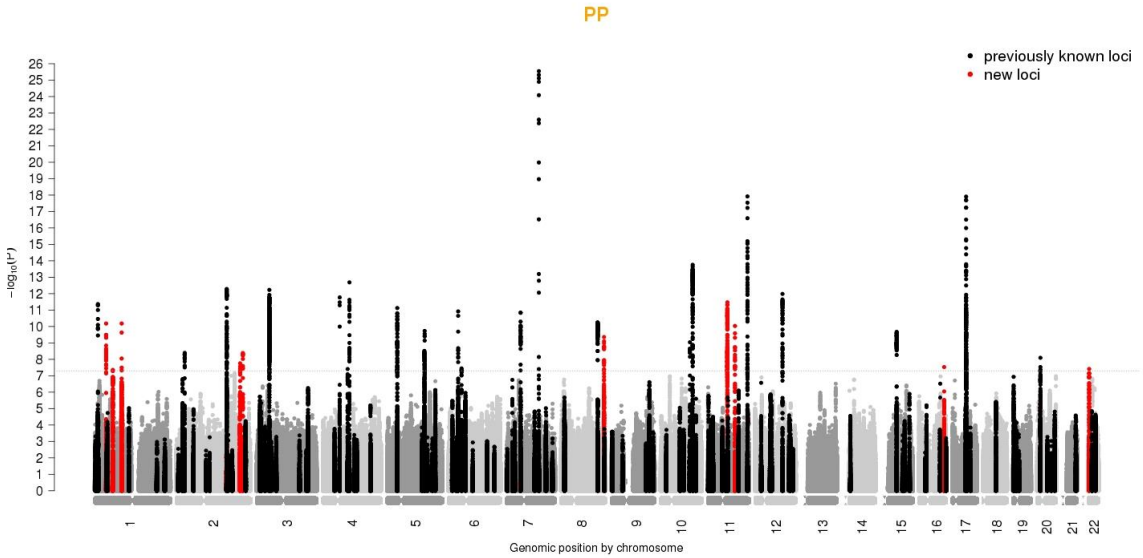





DBP
all
without known loci
without new and known loci
Observed (-logP)
Expected (-logP)


DBP
previously known loci
new loci
Genomic position by chromosome

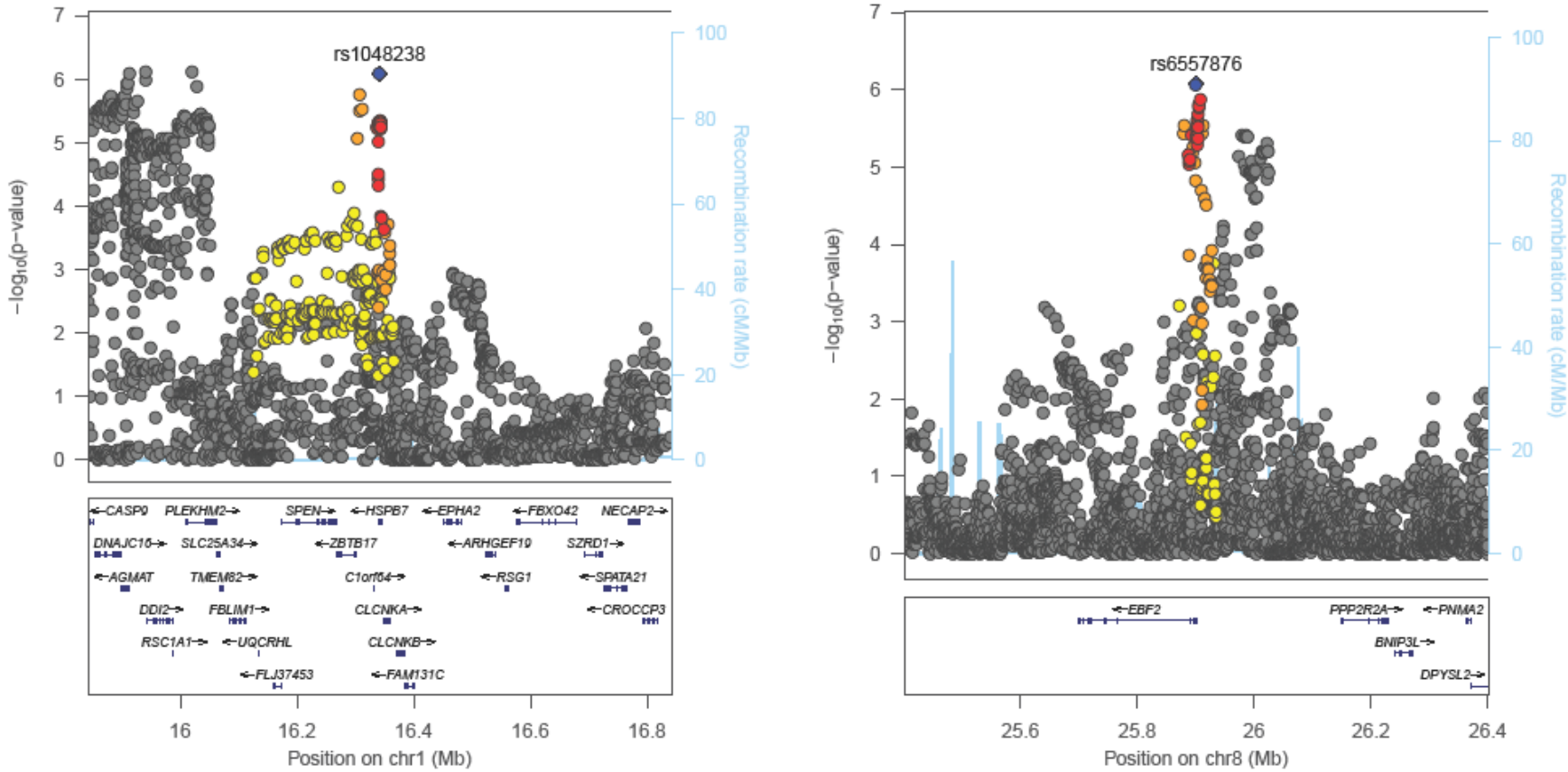


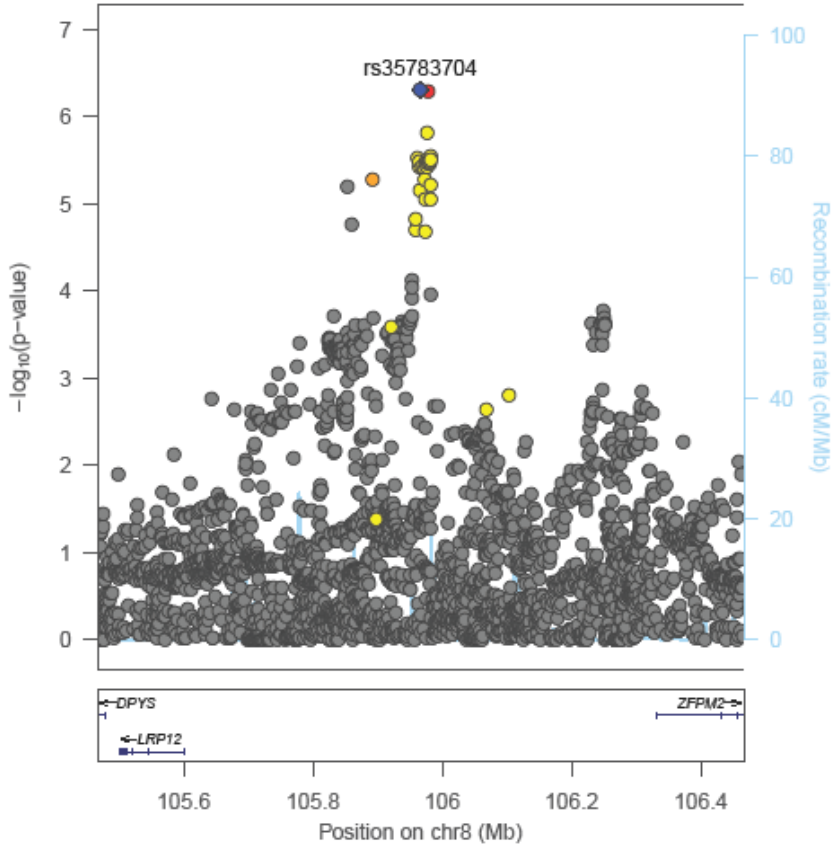


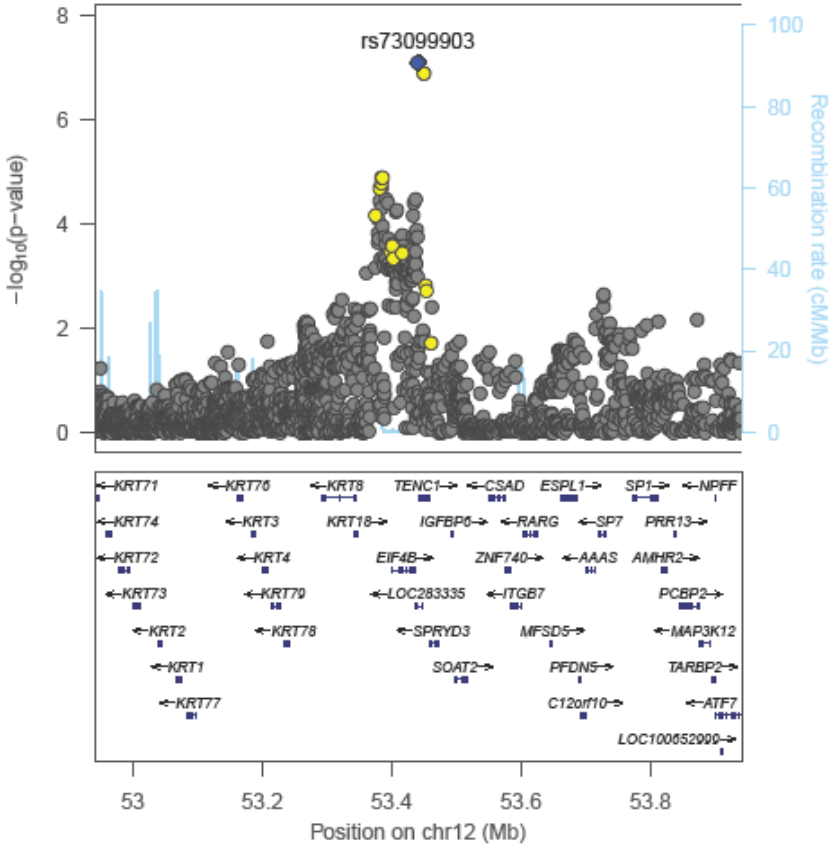
Known loci refers to signals published prior to this study. New includes signals that were initially identified as novel in this study but were subsequently reported in Warren et al 2017 and Hoffman et al 2016.

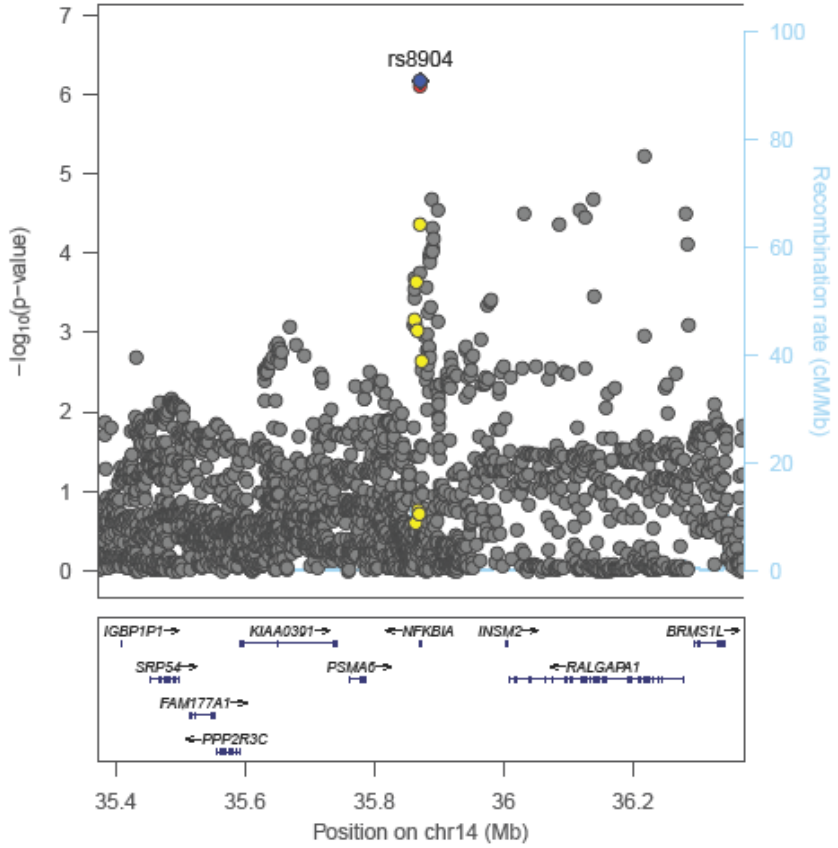
Supplementary Figure 3 (Figure S3): Region plots for 8 novel signals representing 7 novel regions of association for SBP (A), DBP (B) and PP (C).

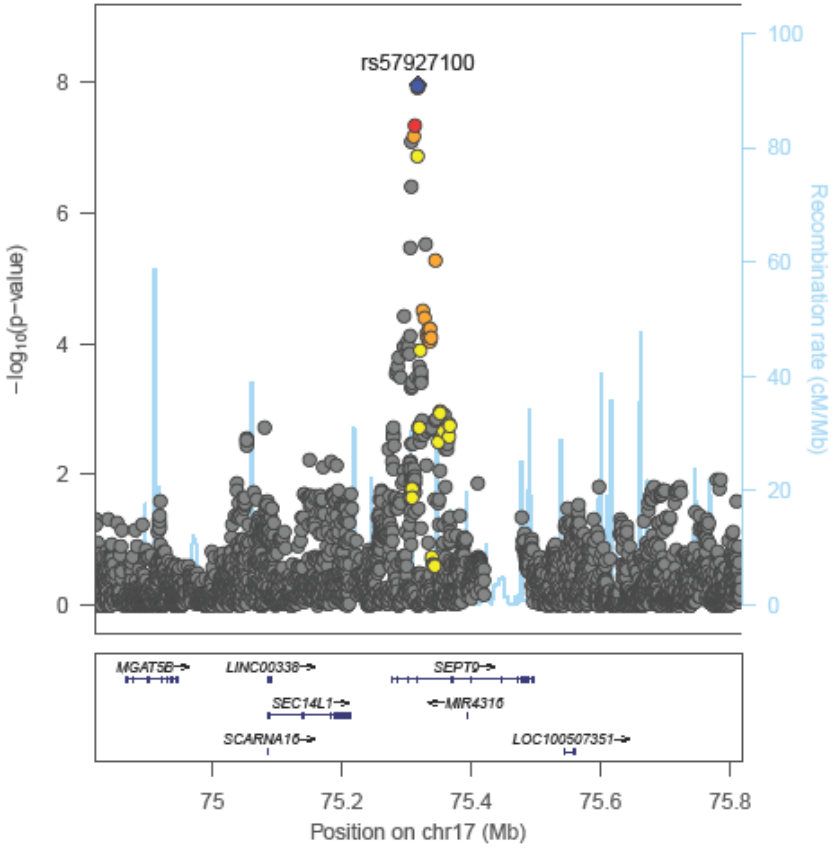
A) SBP



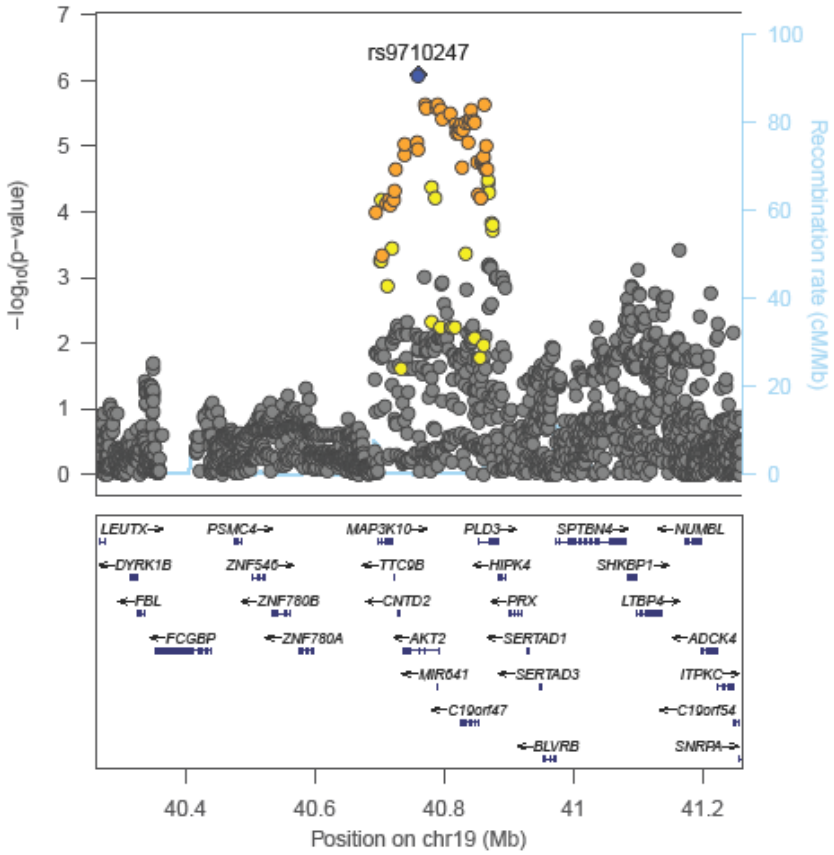

rs35783704
−log10(p−value)
Recombination rate (cM/Mb)
DPYS
ZFPM2
LRP12
105.6
105.8
106
106.2
106.4
Position on chr8 (Mb)


rs73099903
−log10(p−value)
Recombination rate (cM/Mb)
KRT71
KRT76
KRT8
TENC1
CSAD
ESPL1
SP1
NPFF
KRT74
KRT3
KRT18
IGFBP6
RARG
SP7
PRR13
KRT72
KRT4
EIF4B
ZNF740
AAAS
AMHR2
KRT73
KRT79
LOC283335
ITGB7
PCBP2
KRT2
KRT78
SPRYD3
MFSD5
MAP3K12
KRT1
SOAT2
PFDN5
TARBP2
KRT77
C12orf10
ATF7
LOC100652999
53
53.2
53.4
53.6
53.8
Position on chr12 (Mb)


rs8904
−log10(p−value)
Recombination rate (cM/Mb)
IGBP1P1
KIAA0391
NFKBIA
INSM2
BRMS1L
SRP54
PSMA6
RALGAPA1
FAM177A1
PPP2R3C
35.4
35.6
35.8
36
36.2
Position on chr14 (Mb)

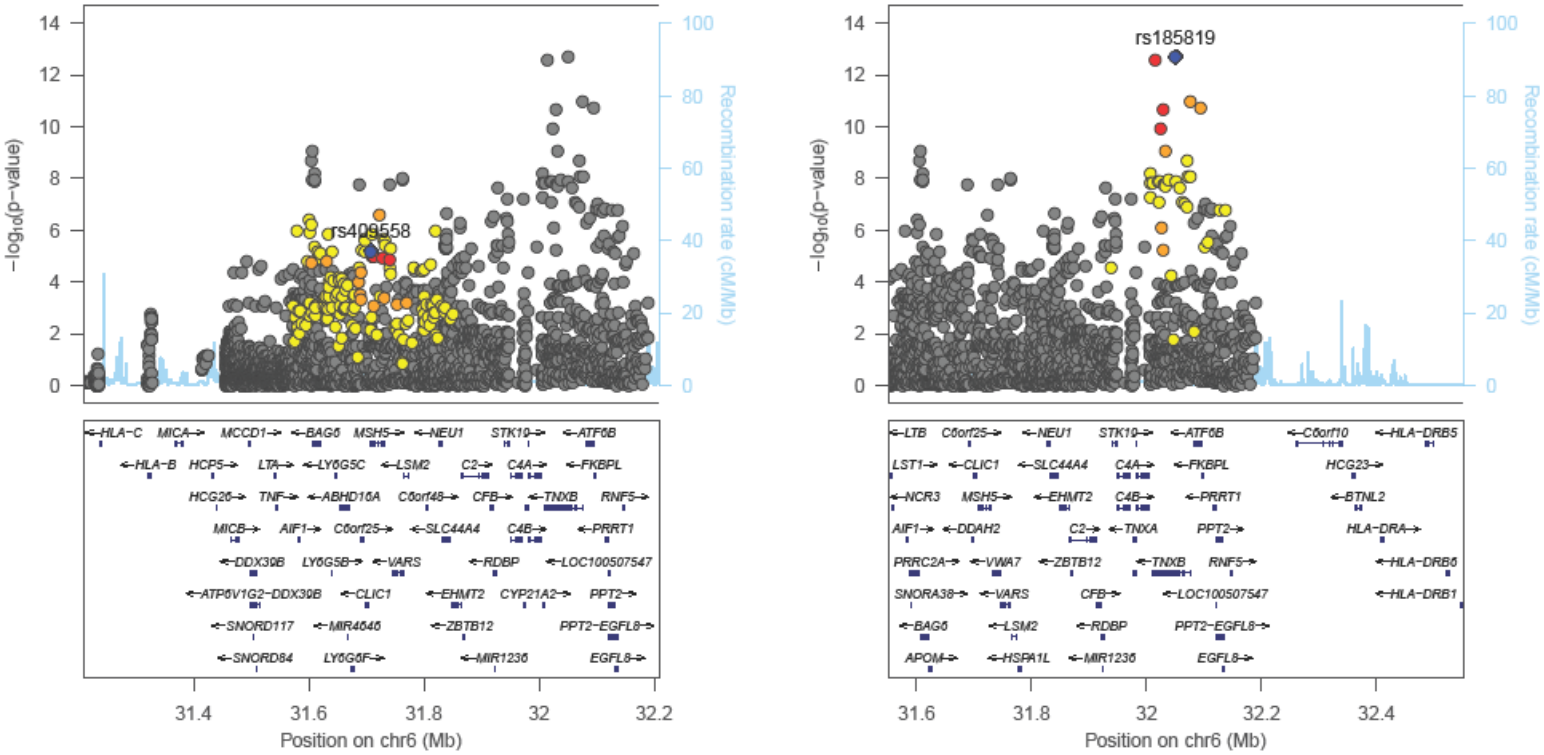

rs57927100
−log10(p−value)
Recombination rate (cM/Mb)
MGAT5B
LINC00338
SEPT9
SEC14L1
MIR4316
SCARNA16
LOC100507351
75
75.2
75.4
75.6
75.8
Position on chr17 (Mb)

B) DBP


rs9710247
−log10(p−value)
Recombination rate (cM/Mb)
LEUTX
PSMC4
MAP3K10
PLD3
SPTBN4
NUMBL
DYRK1B
ZNF546
TTC9B
HIPK4
SHKBP1
FBL
ZNF780B
CNTD2
PRX
LTBP4
FCGBP
ZNF780A
AKT2
SERTAD1
ADCK4
MIR641
SERTAD3
ITPKC
C19orf47
C19orf54
BLVRB
SNRPA
40.4
40.6
40.8
41
41.2
Position on chr19 (Mb)

Supplementary Figure 4 (Figure S4): Region plots for a novel signal at a previously reported region of association.

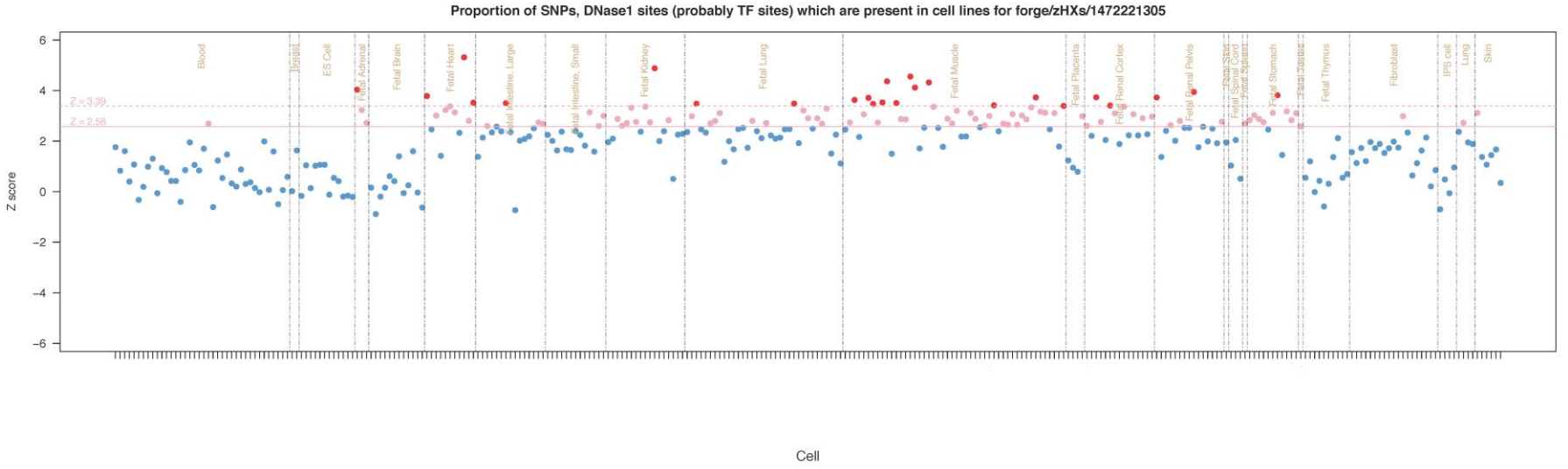
SBP: rs185819 (novel signal reported in this study)



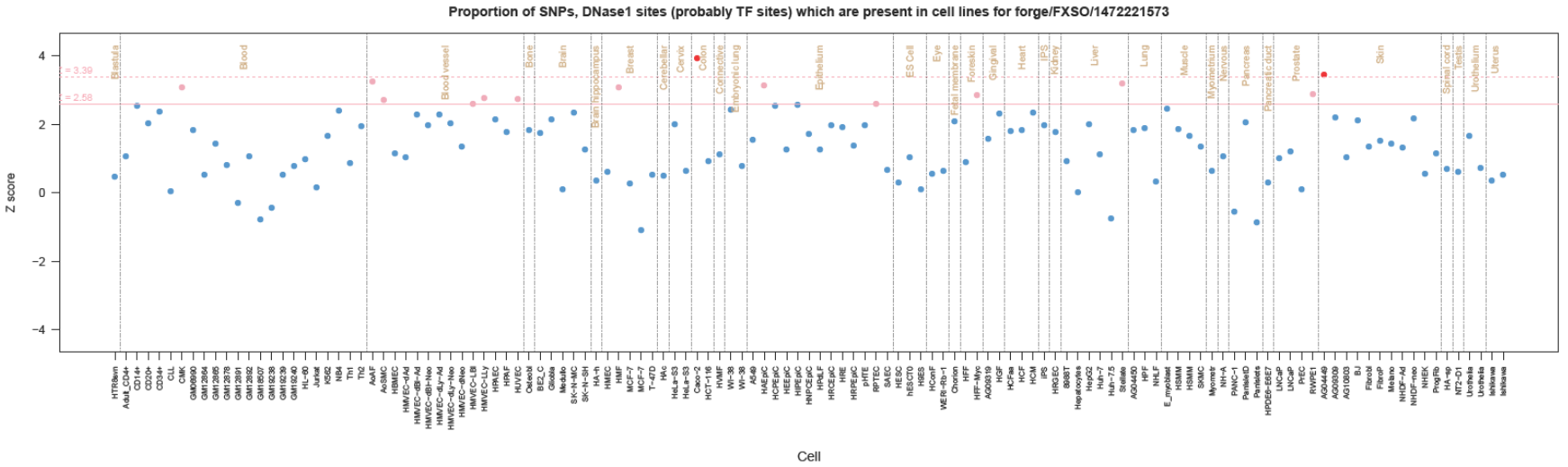
The region plot for the previously reported signal is shown (left) alongside the region plot for the novel signal. Results for association of the novel signal after conditioning on the previously reported signal are shown in **Supplementary Table 8 (S8)**.

Supplementary Figure 5 (Figure S5): Enrichment of overlap of DNase1 site in Roadmap (a) and ENCODE (b) tissues and cell lines.

a)



b)


Proportion of SNPs, DNase1 sites (probably TF sites) which are present in cell lines for forge/FXSO/1472221573
Z score
Cell
= 3.39
= 2.58
Blastula
Blood
Blood vessel
Bone
Brain
Brain hippocampus
Breast
Cerebellar
Cervix
Colon
Connective
Embryonic lung
Epithelium
ES Cell
Eye
Fetal membrane
Foreskin
Gingival
Heart
IPS
Kidney
Liver
Lung
Muscle
Myometrium
Nervous
Pancreas
Pancreatic duct
Prostate
Skin
Spinal cord
Testis
Urothelium
Uterus

Competing financial interests

Mike A. Nalls' participation is supported by a consulting contract between Data Tecnica International and the National Institute on Aging, NIH, Bethesda, MD, USA, as a possible conflict of interest Dr. Nalls also consults for Illumina Inc, the Michael J. Fox Foundation and University of California Healthcare among others.

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