

Supplemental Material

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1. Supplemental Tables

Supplemental Tables

Supplemental Table 1. Association of the 77 SNVs with BP in the pan-ancestry meta-analysis. Highlighted in green are SNVs with $P \leq 5 \times 10^{-8}$ (equivalent to $-\log_{10}P = 7.3$). In yellow are highlighted the 21 BP findings. (See Excel Table)

Note: **No**-order number, table is ordered by chromosome and HG38 position; **rsID**-SNV name, **Gene Name**-gene name from the Entrez Gene of NCBI; **Variation role**-SNVs' role as defined by the NCBI dbSNP database; **Chrom**- chromosome; position HG38 and position HG19- positions based on NCBI builds batch 138 (HG19) and batch 147 (HG38); **diffposneargene**- position distance of a SNV from the closest gene's SNV in the NCBI dbSNP, if within the gene we assigned a 0 value; **Closest gene**- a gene name the same as Gene Name, when the SNV is within gene boundaries, in parenthesis when within 500KB of the closest gene, and in parenthesis with (*)_beyond* when further intergenic; **Allele 1**-allele 1; **Allele 2**-allele 2; **Freq1**-allele frequency for Allele 1; **SBP beta** and its Standard Error as **SBP s.e.** followed by DBP and PP; **SBP direction**-direction of beta sign for contributing results in the following order: BP-EUROPEAN led Consortium, UK-BIOBANK and CHARGE-BP Consortium, similar for DBP and PP; followed by the same traits' order for **loghetp**-log₁₀p of heterogeneity; **N**-meta-sample; and **SBP-meta -Log₁₀p** for SBP, DBP and PP.

Supplemental Table 2. Association of the 77 SNVs for BP in the European ancestry meta-analysis. Highlighted in green are SNVs with $P \leq 5 \times 10^{-8}$ (equivalent to $-\log_{10}P = 7.3$). In yellow are highlighted the 21 BP findings. (See separate Excel Table).

See Note above for Supplemental Table 1.

Supplemental Table 3. Association findings for new BP SNVs, including any associations with other traits and top ranked eQTLs with $P < 5 \times 10^{-8}$. For the eQTL results we only report tissues and genes where the BP-associated SNV and the expression SNV are in high LD ($r^2 > 0.8$). Sources of information were GWAS Catalog access on 1.12.2017, PhenoScanner²⁷ and GTex⁴⁶ (See separate Excel Table for referenced PMIDs).

Supplemental Table 4. Cis- regulatory features of new BP SNVs based on HaploReg, which is using among others information from epigenome of ENCODE and RoadMap projects. (See separate Excel Table).

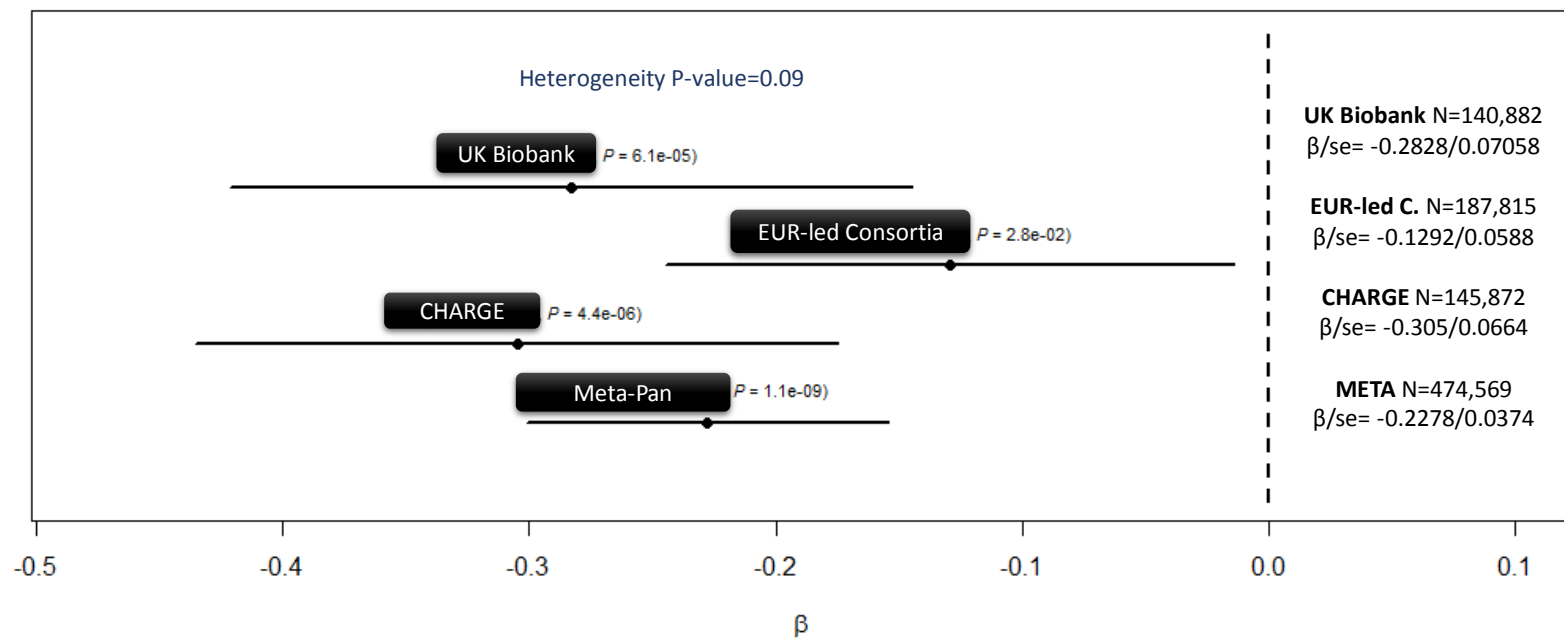
Supplemental Table 5. cis-eQTL identified in the Framingham heart study generation 3 whole blood expression data (See separate Excel Table).

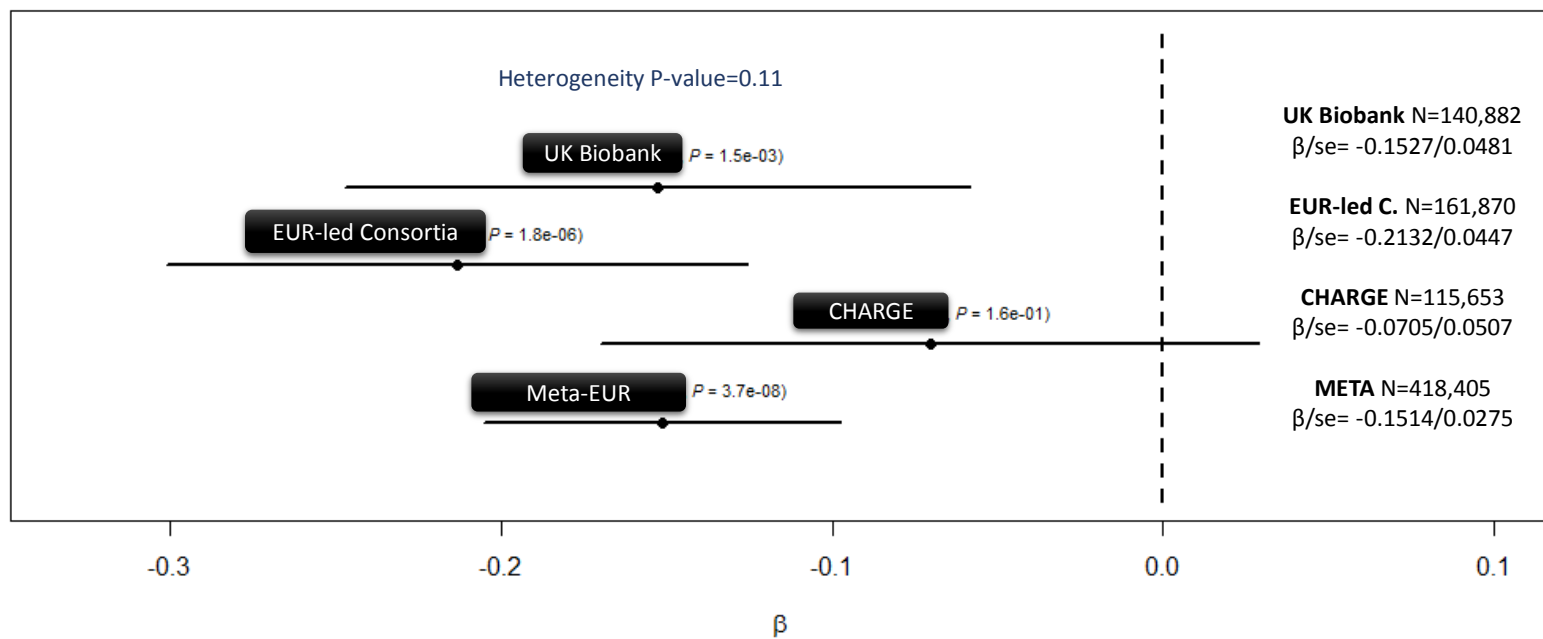
Supplemental Figures 1a-e. Forest plots of 5 novel selected SNVs in association with BP. Depicted are the beta, 95% confidence interval around the beta for the overall meta-analysis and for each contributing consortium. The heterogeneity p-value is estimated from the overall meta-analysis.

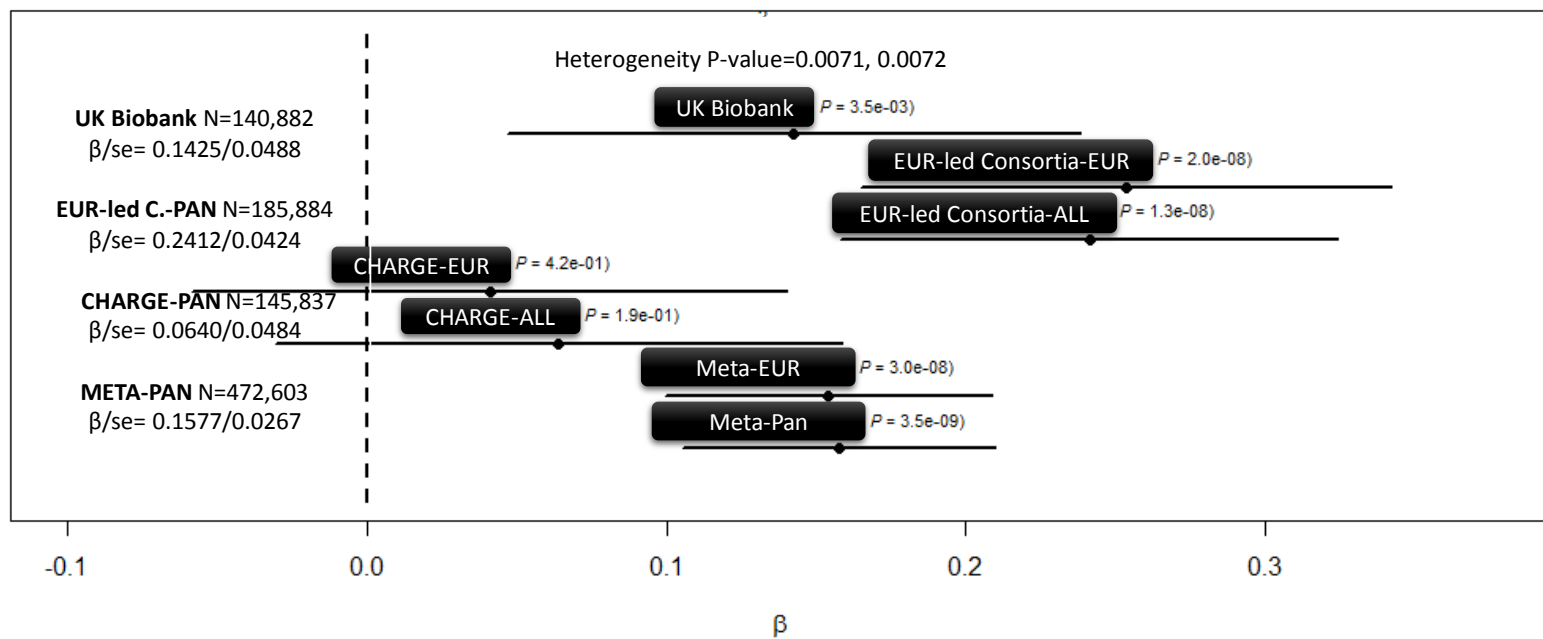
Supplemental Figures 2a-e. LocusZoom plots of 5 novel selected SNVs in association with BP. They represent regional association plots based on only UK Biobank results.

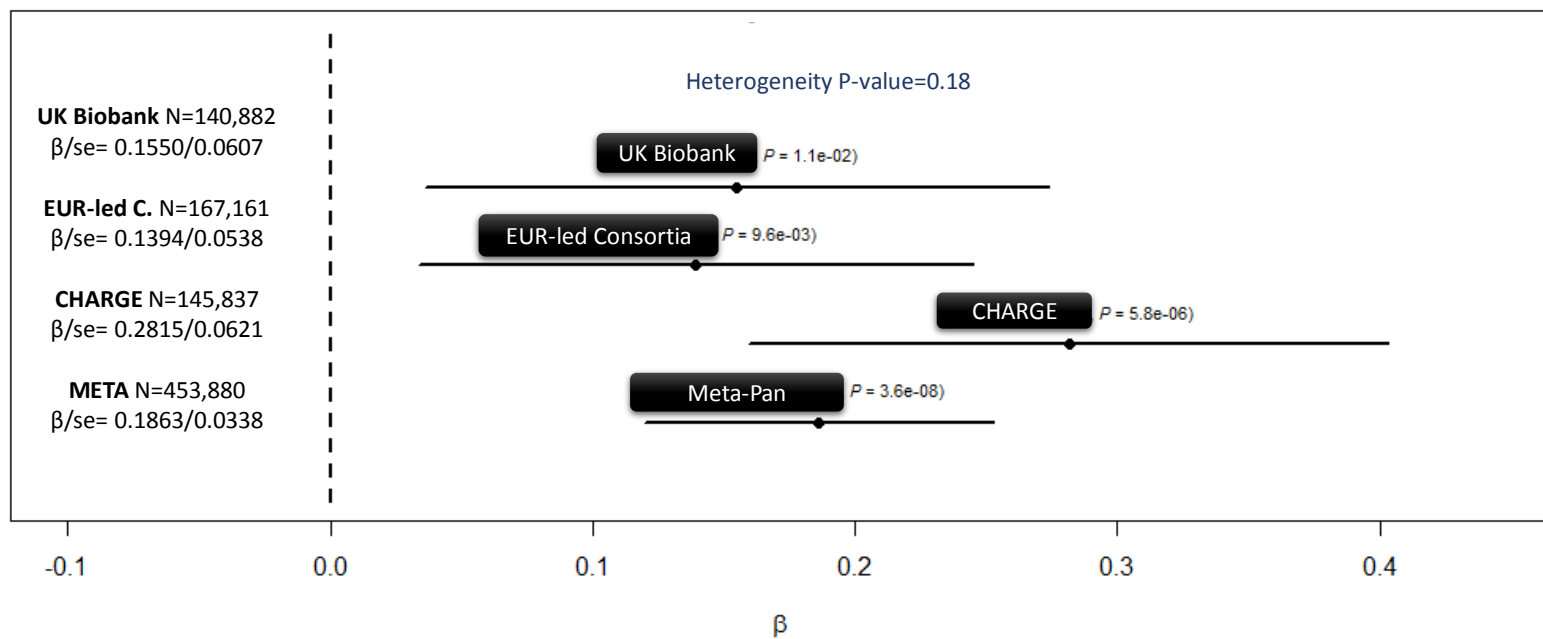
2. Supplemental Figures.

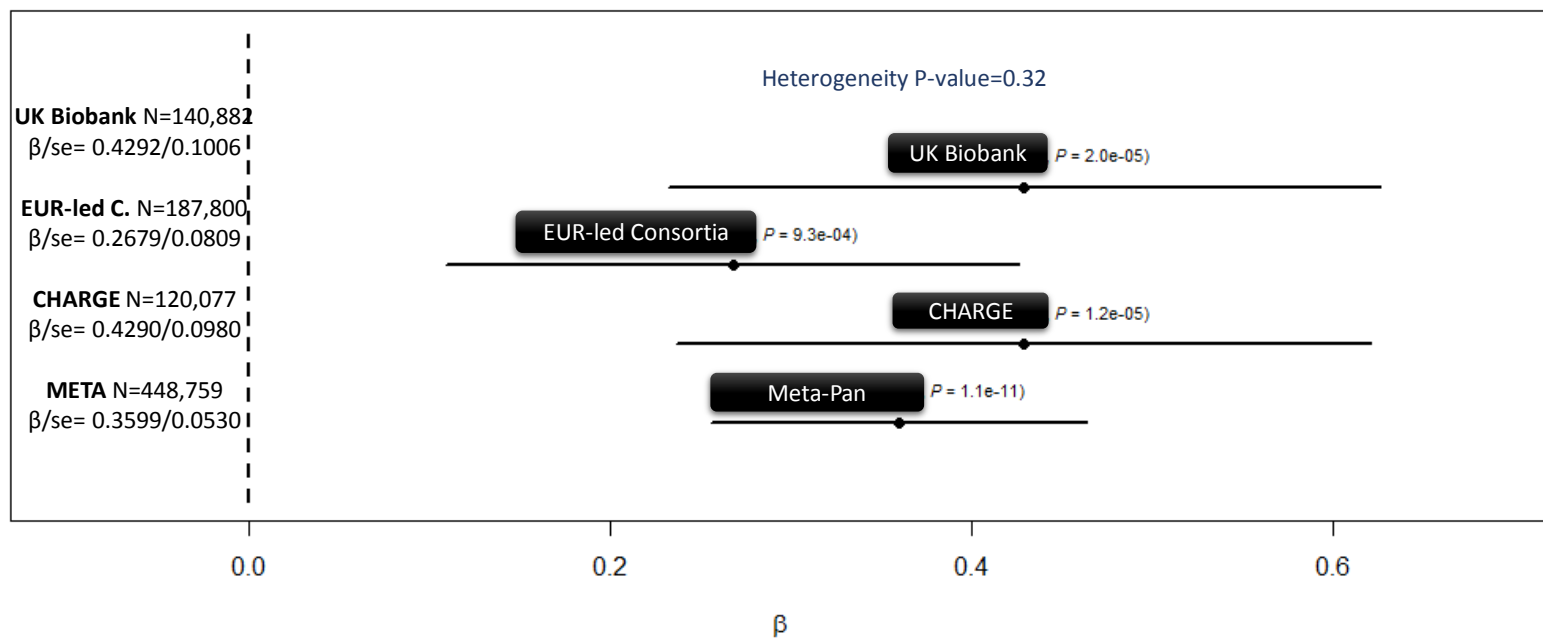
Supplemental Figure 1.a. The rs9678851 (missense) *SLC4A1AP* (SBP-Pan-ancestry, A=0.55)



Supplemental Figure 1.b. The rs13303 (missense) *STAB1* (PP-EUR-ancestry, T=0.44)

Supplemental Figure 1.c. The rs7437940 (intronic) *AFAP1* (PP-EUR & Pan-ancestry, T=0.47)

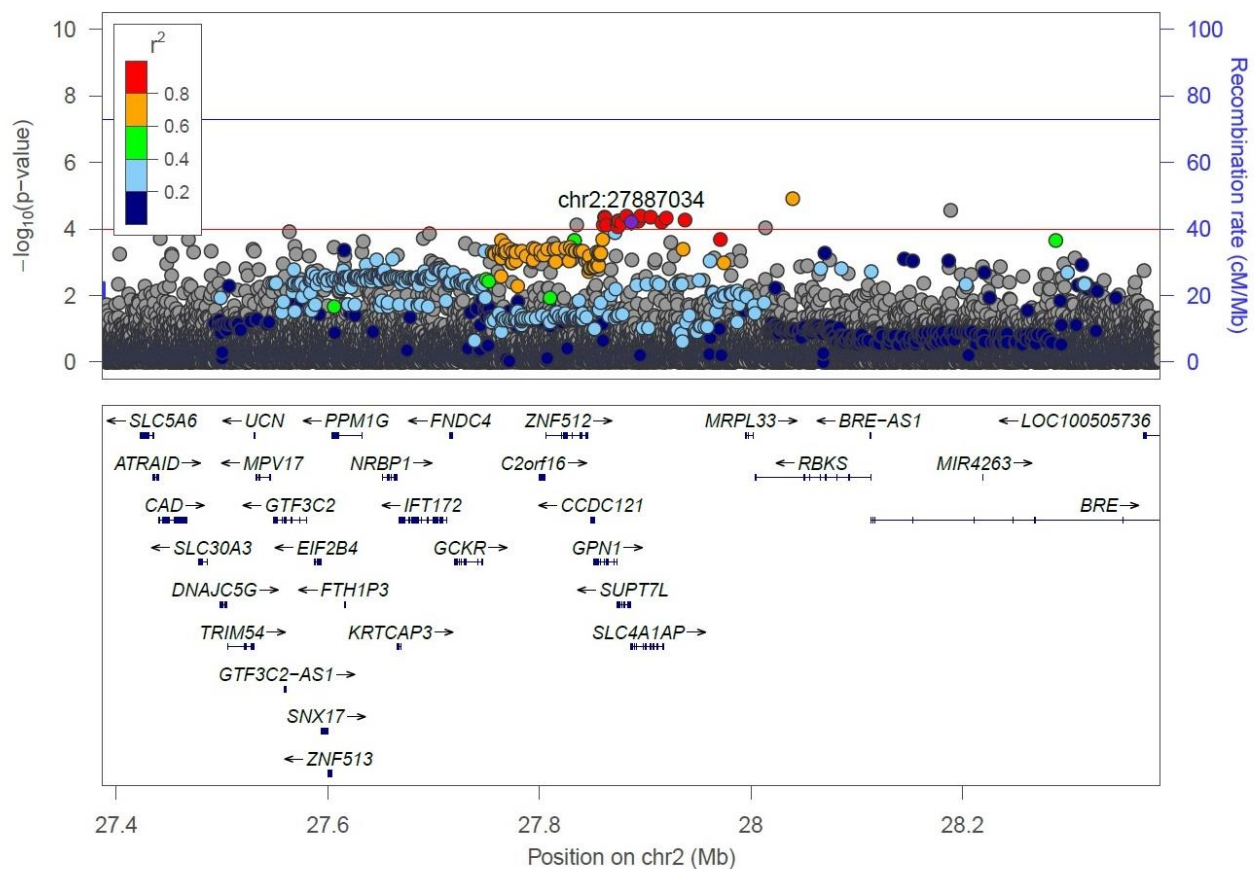
Supplemental Figure 1.d. The rs1055144 (nc-transcript) *7p15.2* (PP-Pan-ancestry, T=0.19)

Supplemental Figure 1.e. The rs34163229 (missense) *SYNPO2L* (SBP-Pan-ancestry, T=0.15)

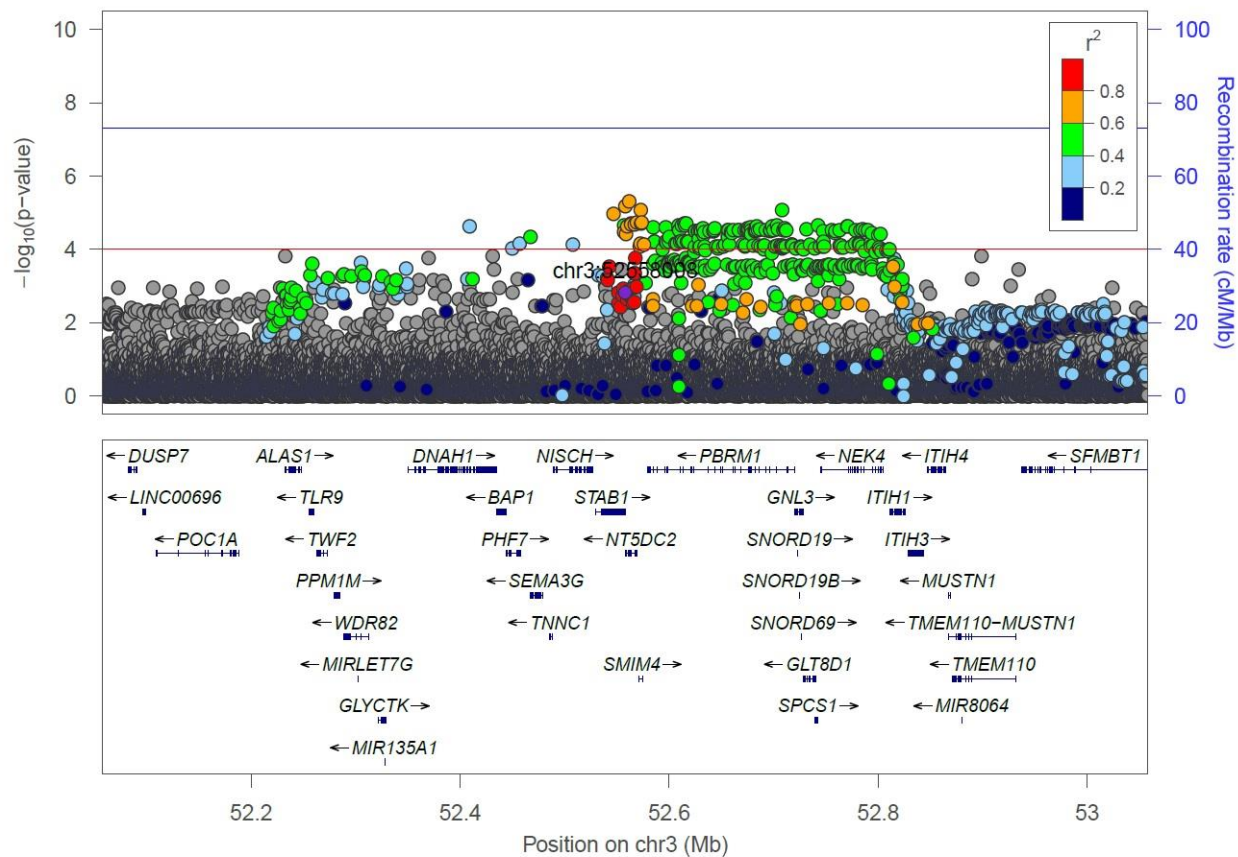
Notes for LocusZoom plots:

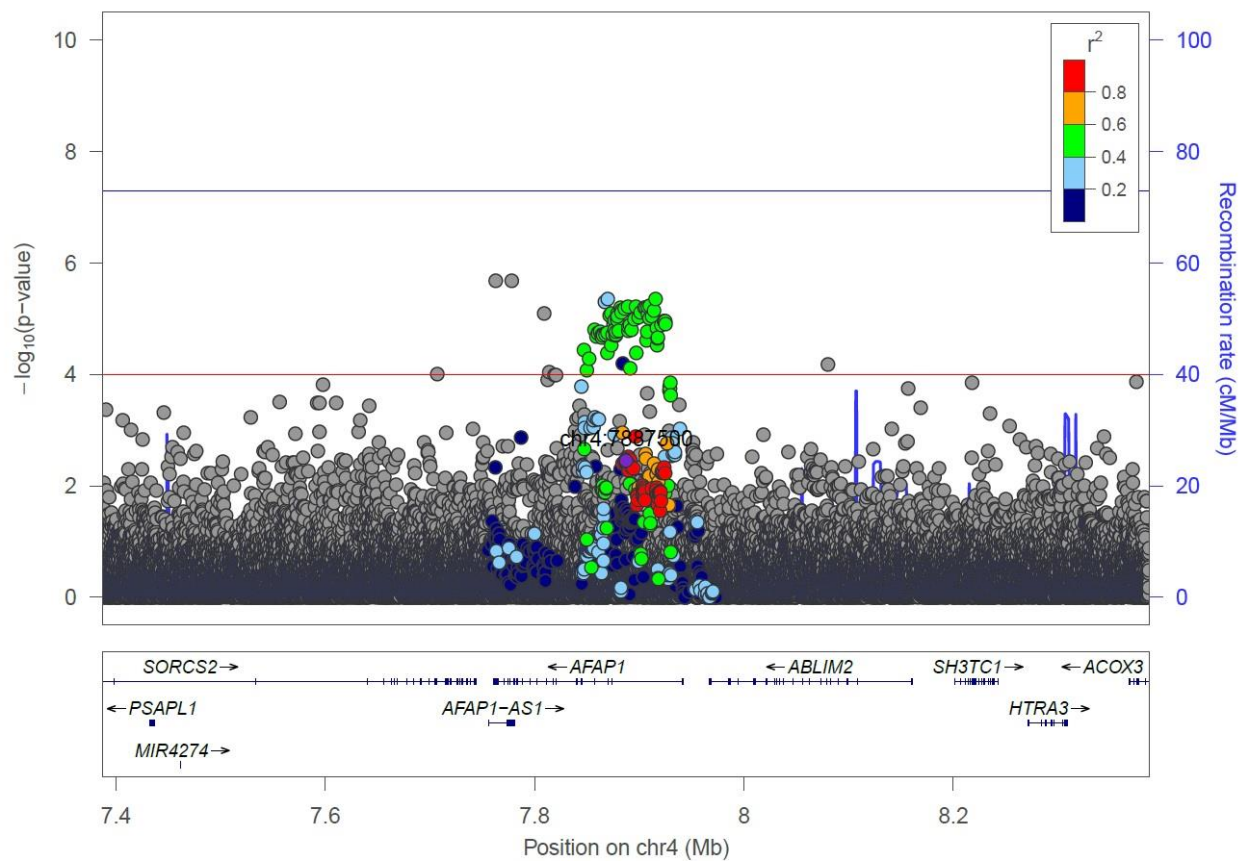
- Locus Zoom plots of region $\pm 500\text{kb}$ from the reference SNV
- Showing results for the primary trait from the Mega-Exome analysis
- Association p-value results according to full UKB-EUR BP GWAS data
- LD calculated from UKB-EUR data for all UKB variants
- Grey points if LD has $r^2 < 0.1$
- All plots on same y-axis scale limits for equivalent comparison
- Significance threshold reference lines at 1×10^{-4} and 5×10^{-8}

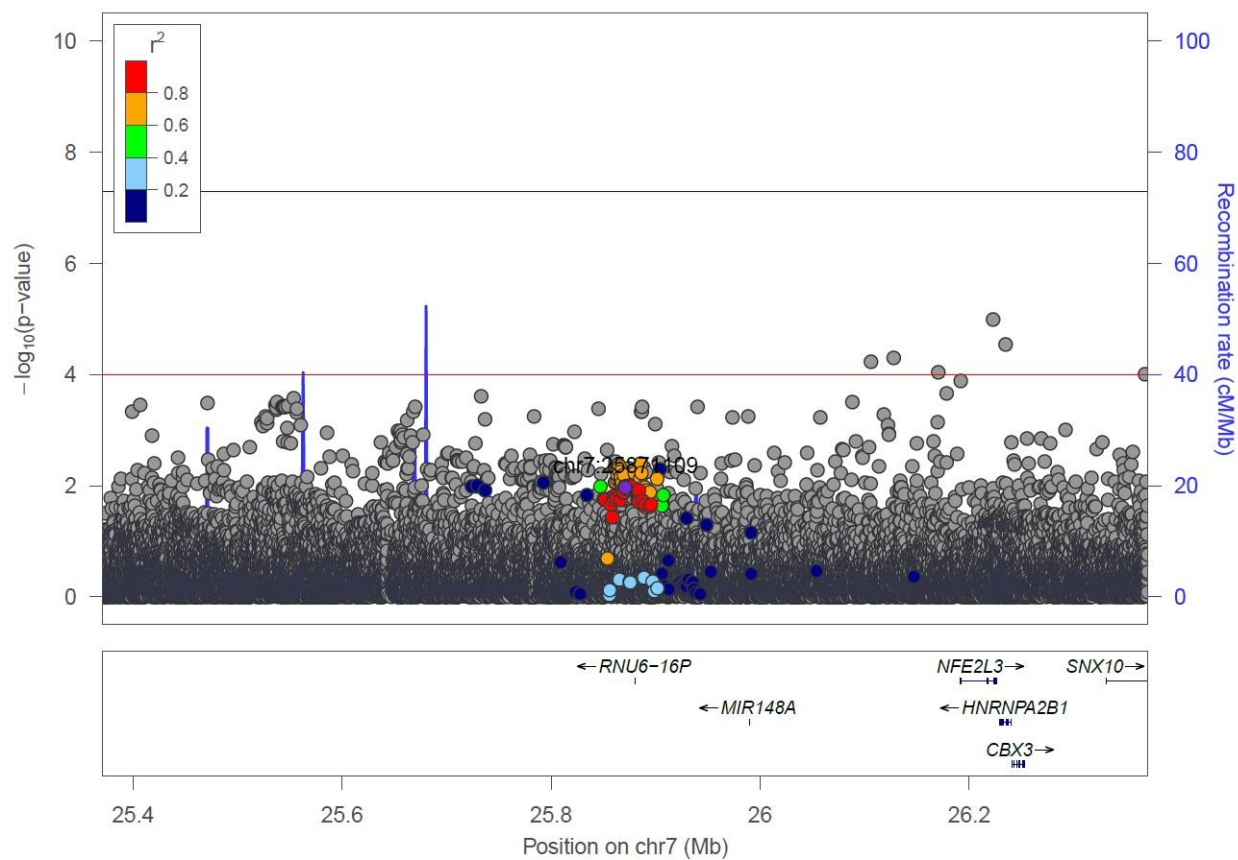
Supplemental Figure 2.a. The *SLC4A1AP* (rs9678851) for SBP (novel locus)

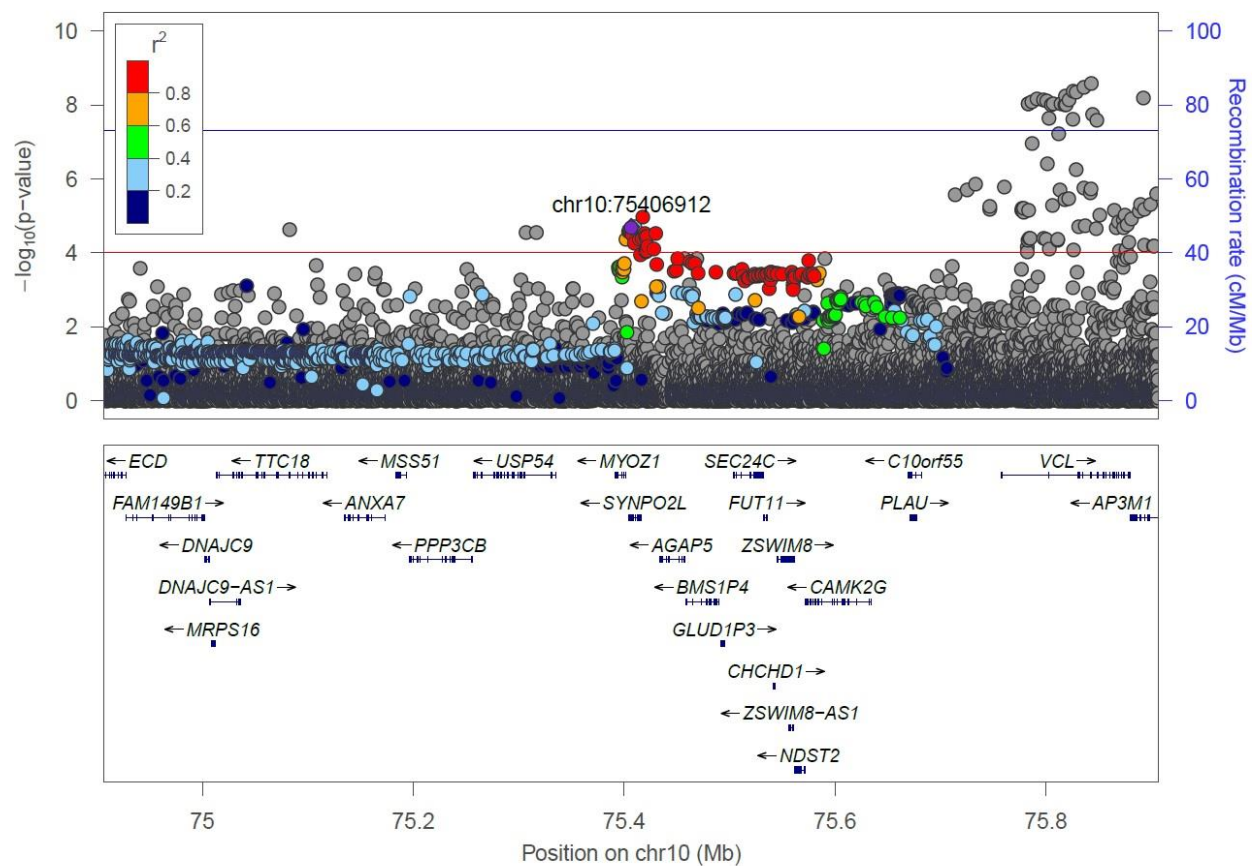


Supplemental Figure 2.b. The *STAB1* (rs13303) for PP (novel locus)



Supplemental Figure 2.c. The *AFAP1* (rs7437940) for PP (novel locus)

Supplemental Figure 2.d. The *7p15.2* (rs1055144) for PP (novel locus)

Supplemental Figure 2.e. The *SYNOPL2* (rs34163229) for SBP (secondary signal)

3. Acknowledgments

CHARGE EXOME BP

Cohort and Cohort Specific Acknowledgment

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CHS The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR000124, and the National Institute of Diabetes and Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center.

FamHS This study was supported in part by the NHLBI grant R01HL117078.

FHS This study is supported by NHLBI/NIH Contract #N01-HC-25195, NIH NIDDK R01 DK078616 and K24 DK080140, and by the Boston University School of Medicine.

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CHD Exome+ Consortium

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UK-Exome BP Consortium

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"ASCOT (ASCOT_SC / ASCOT_UK)" This work forms part of the research programme of the NIHR Cardiovascular Biomedical Research Unit at Barts and The London, Queen Mary University of London, UK.

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GoT2D Consortium

Cohort and Cohort Specific Acknowledgment

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UK-Biobank

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4. Consortia Members

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4.4. The Genetics of Type 2 Diabetes (GoT2D) and Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic

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4.5. UK Biobank CardioMetabolic Consortium BP working group

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