# Supplemental Material

**Content:**

## 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 $P \leq 5x10^{-8}$ (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; **Variant 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 - $\mathbf{Log_{10}p}$** 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 $P \leq 5x10^{-8}$ (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, PhenoScanner [27] and GTex [46] (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).

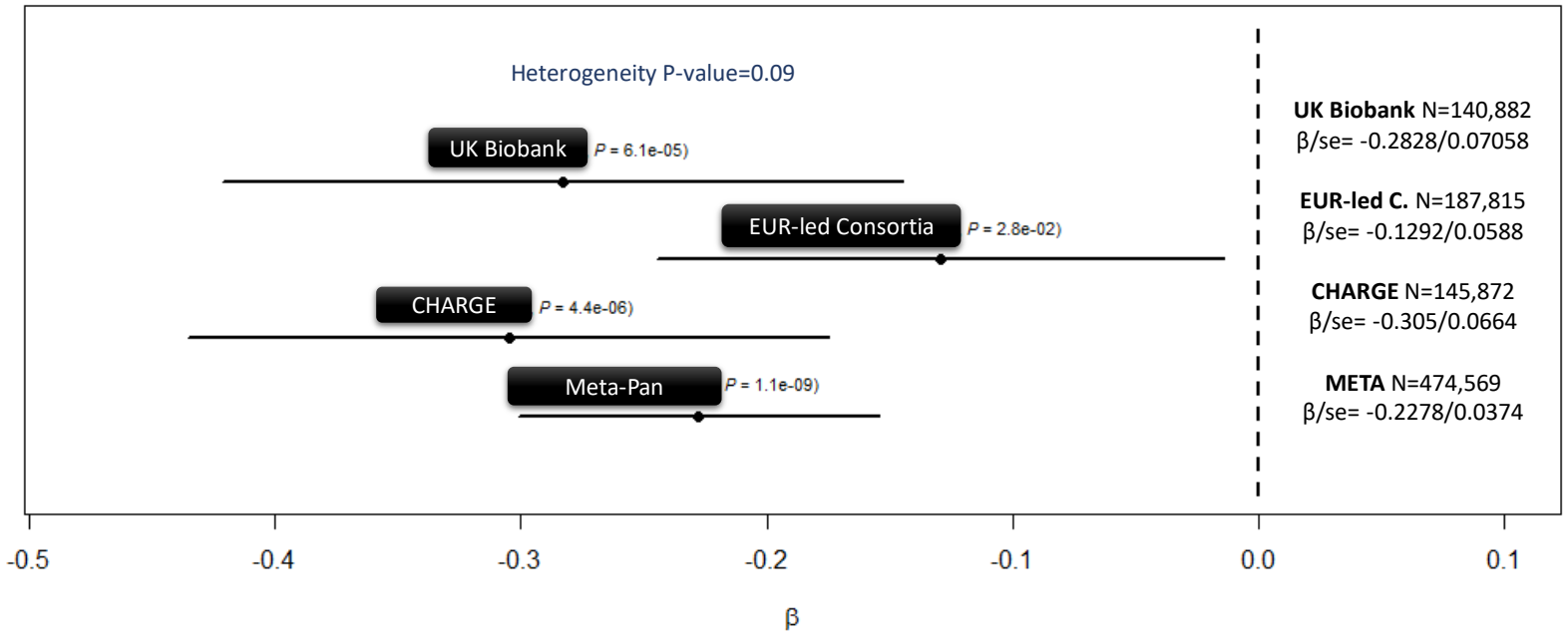
**Supplemental Table 5**. cis-eQTL identified in the Framingham heart study generation 3 whole blood expression data (See separate Excel Table).

**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.

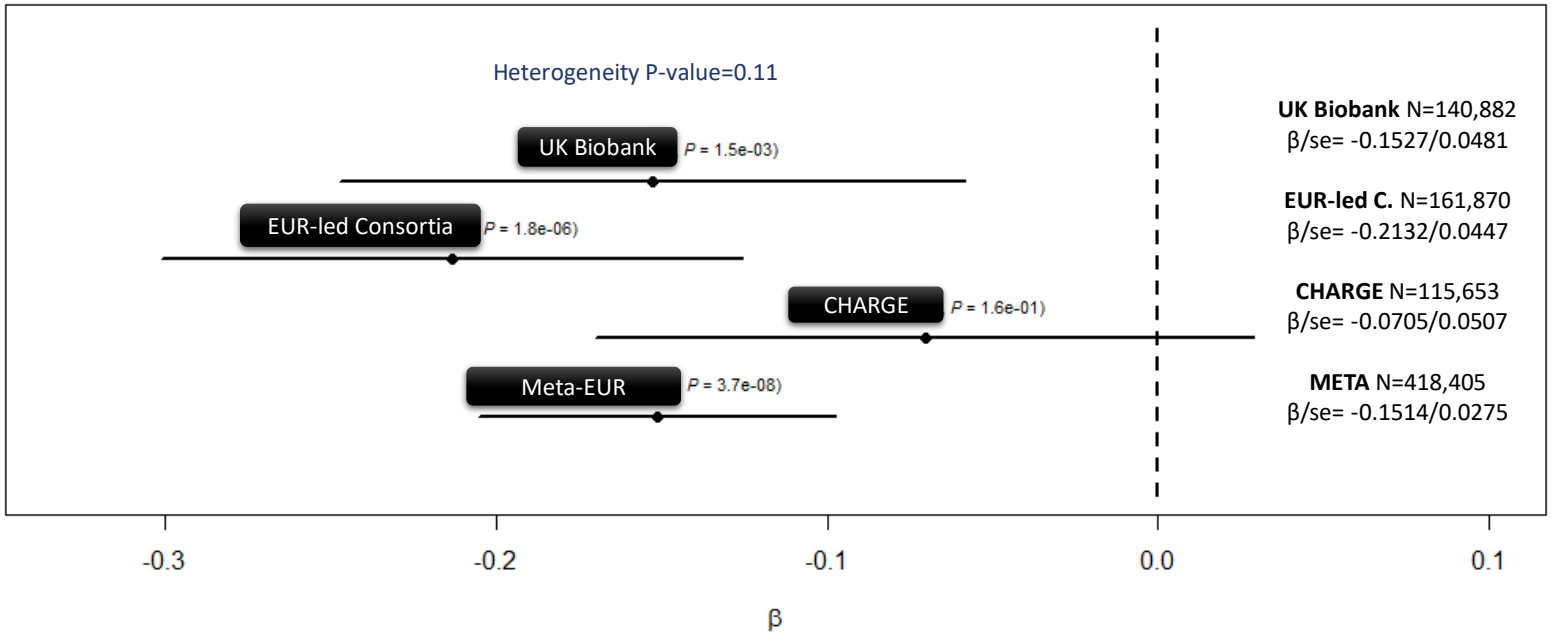
**Supplemental Figures 2a-e**. LocusZoom plots of 5 novel selected SNVs in association with BP. They represent regional association plots based on only UK Biobank results.

## 2. Supplemental Figures.

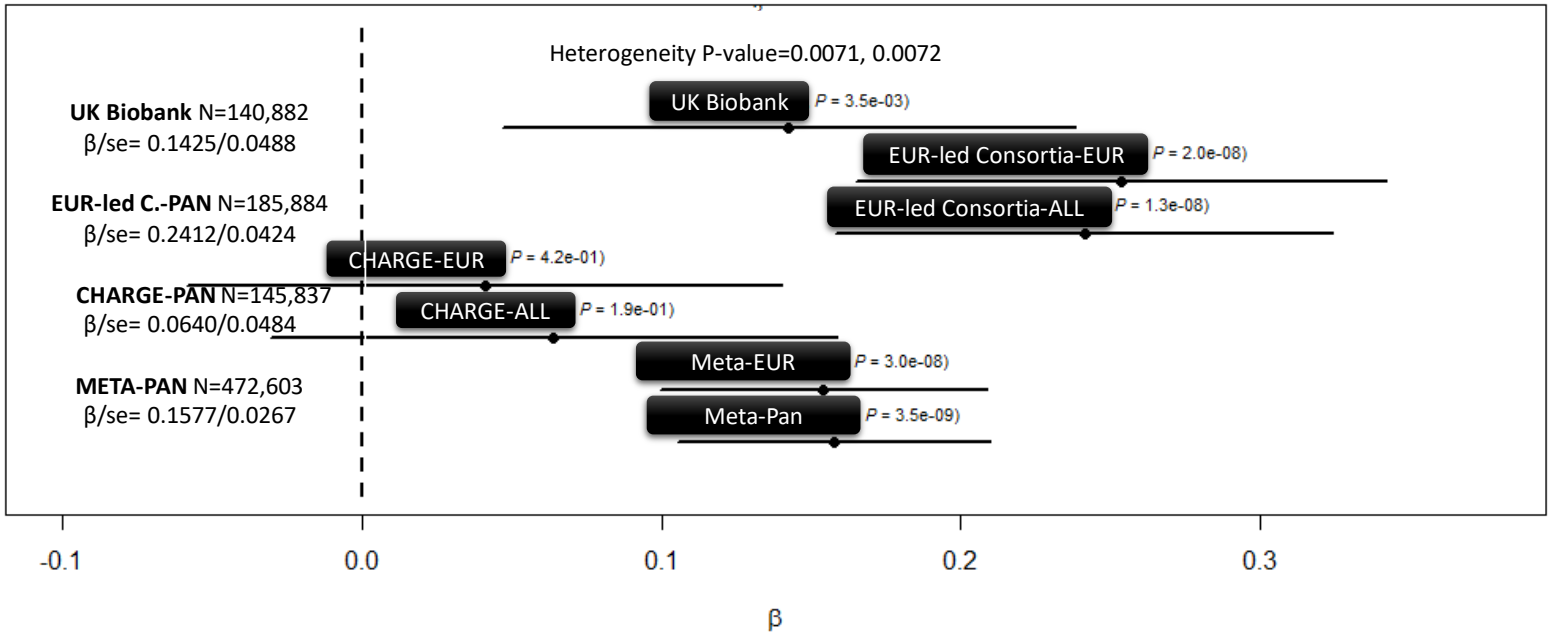
**Supplemental Figure 1.a.** The rs9678851 (missense) *SLC4A1AP* (SBP-Pan-ancestry, A=0.55)



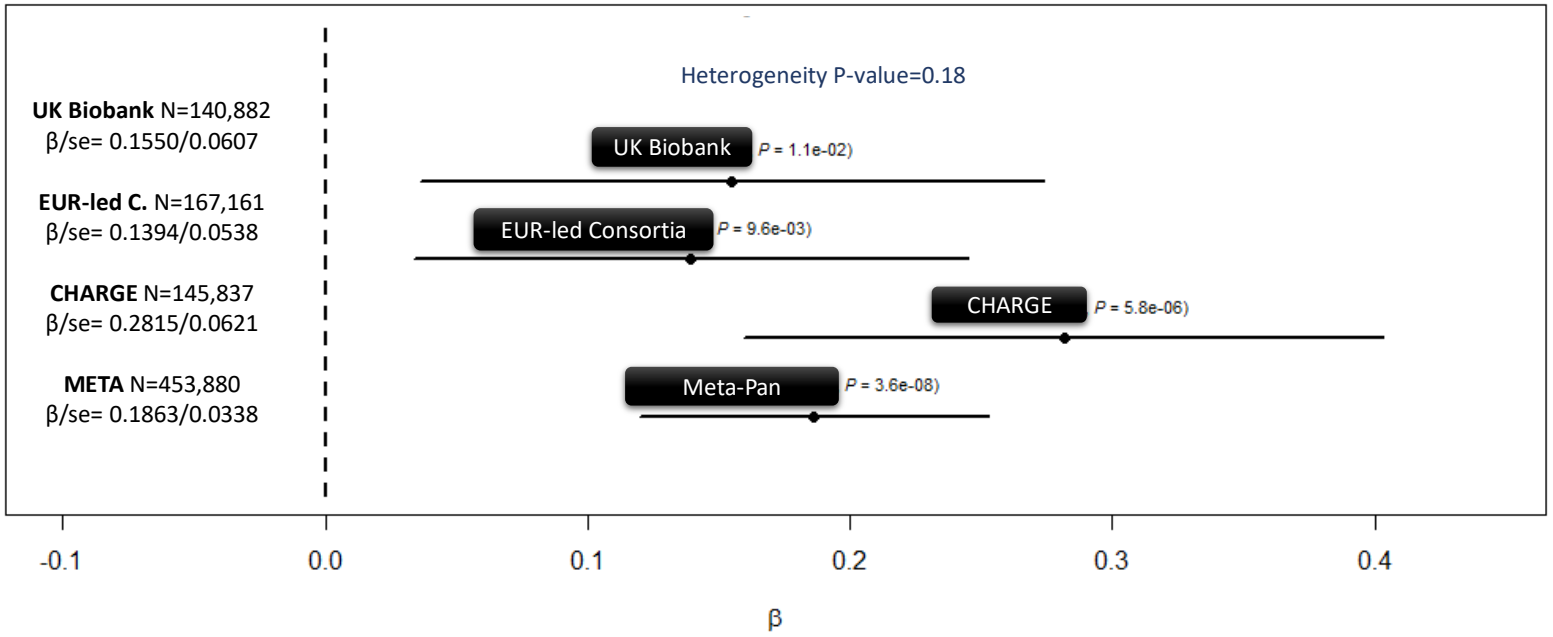
**Supplemental Figure 1.b.** The rs13303 (missense) *STAB1* (PP-EUR-ancestry, T=0.44)



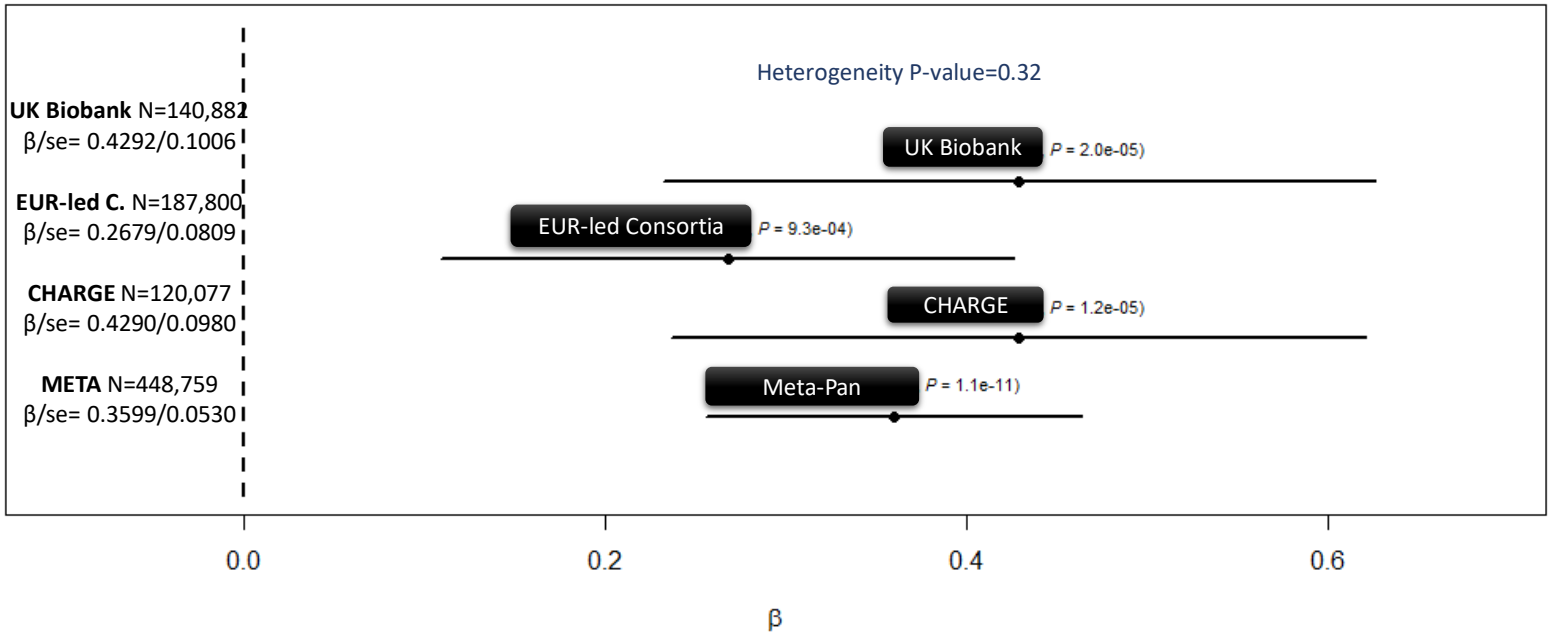
**Supplemental Figure 1.c.** The rs7437940 (intronic) *AFAP1* (PP-EUR & Pan-ancestry, T=0.47)



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



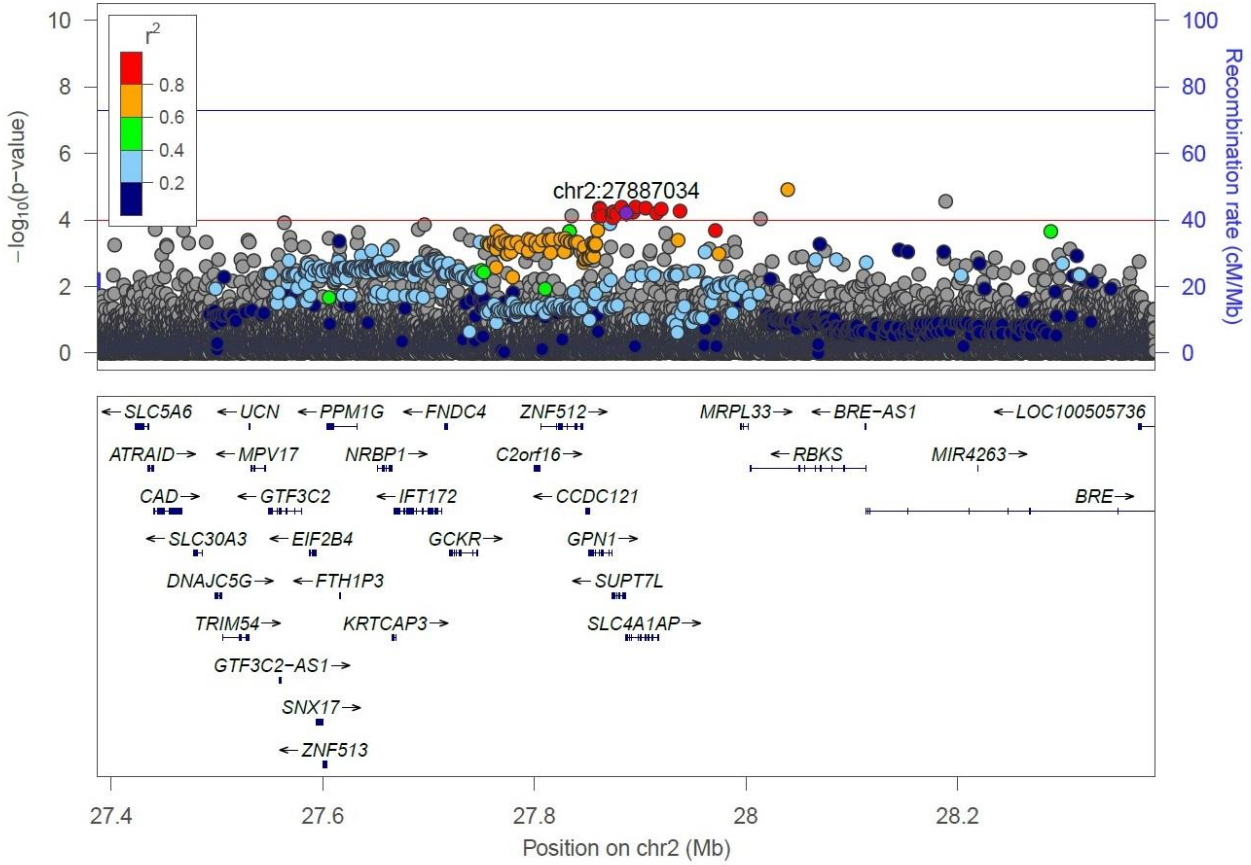
**Supplemental Figure 1.e.** The rs34163229 (missense) *SYNPO2L* (SBP-Pan-ancestry, T=0.15)



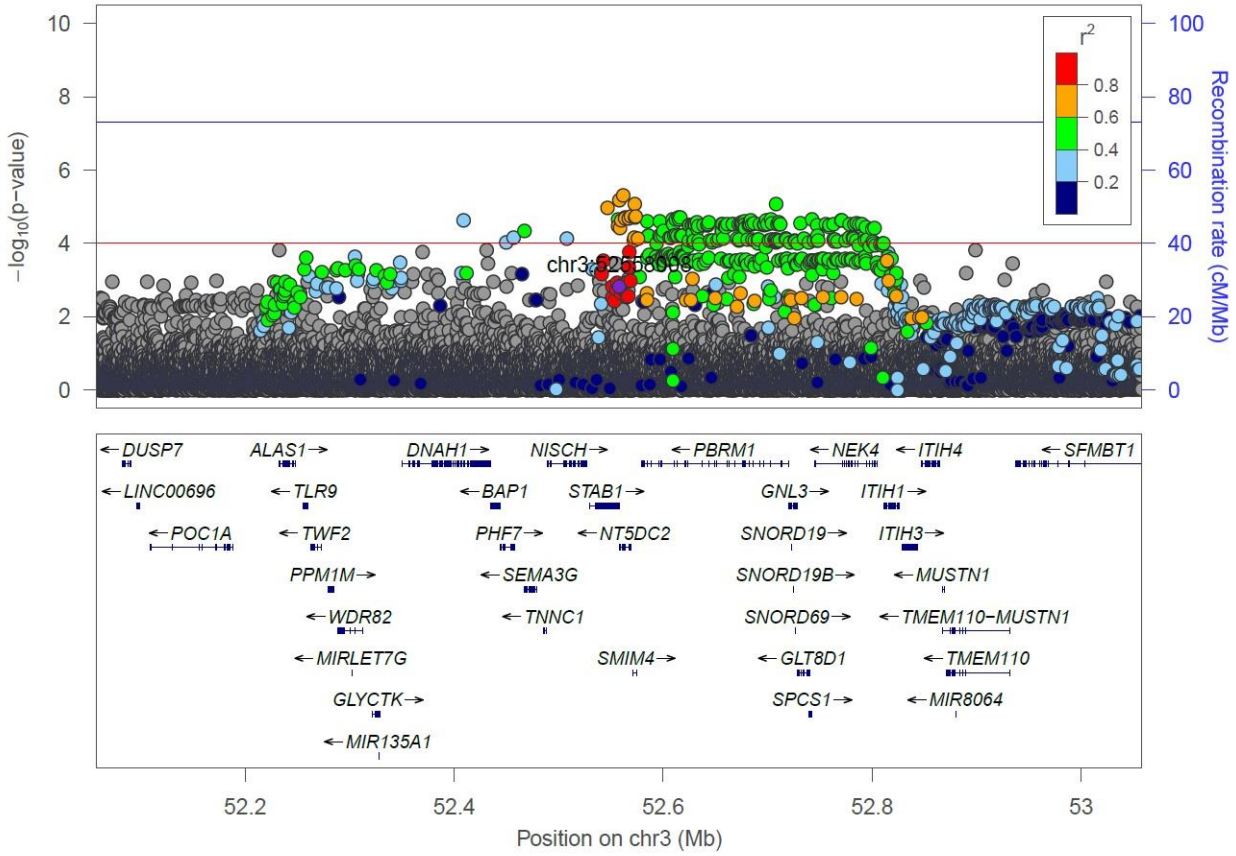
**Notes for LocusZoom plots:**

- Locus Zoom plots of region ±500kb 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 $1\times10^{-4}$ and $5\times10^{-8}$

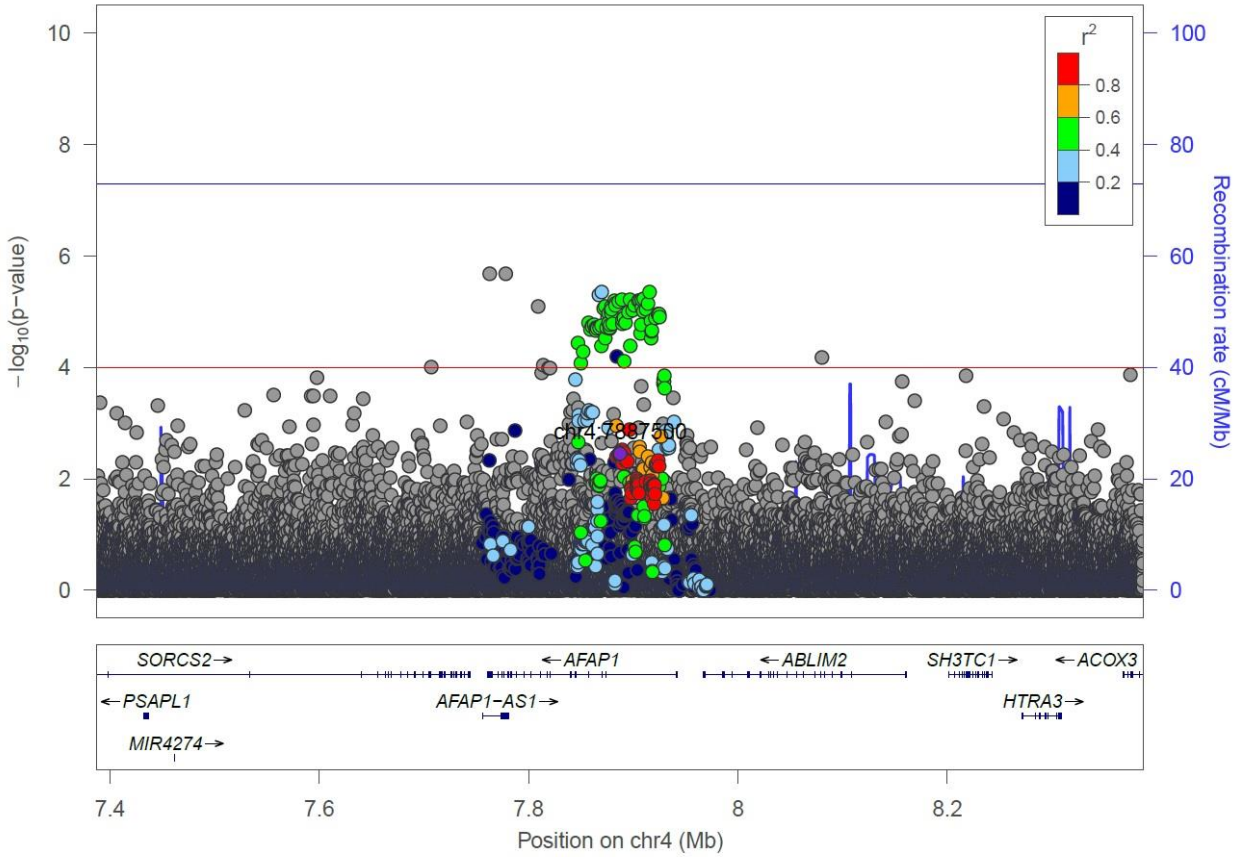
**Supplemental Figure 2.a.** The *SLC4A1AP* (rs9678851) for SBP (novel locus)



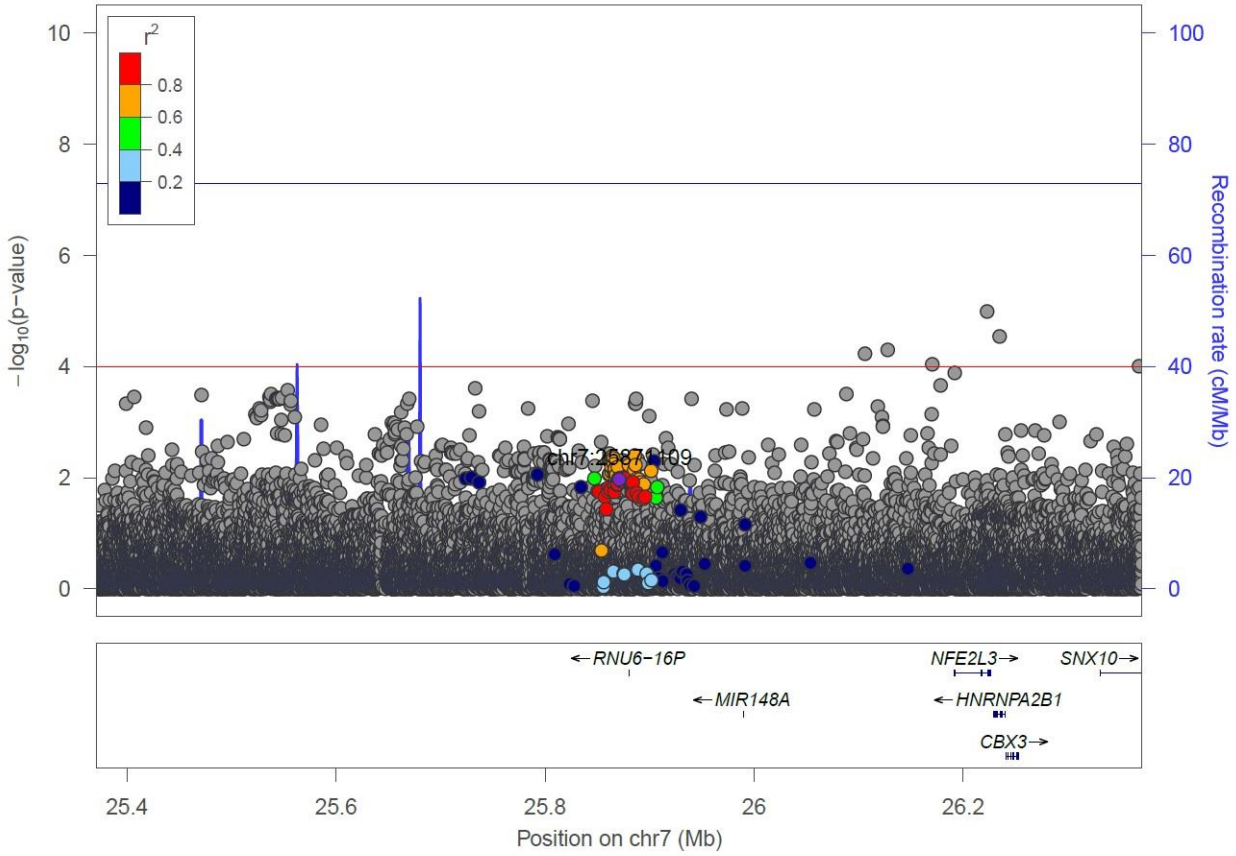
**Supplemental Figure 2.b.** The *STAB1* (rs13303) for PP (novel locus)



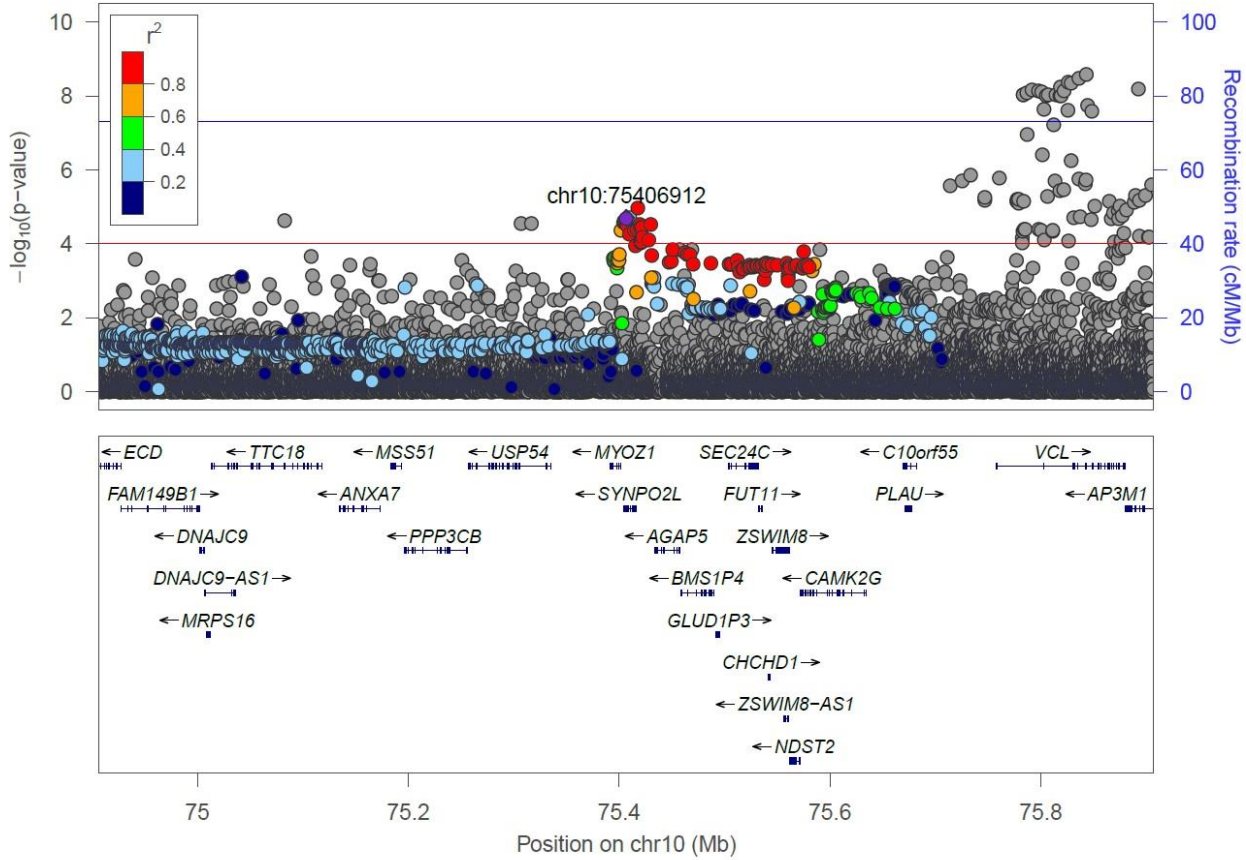
**Supplemental Figure 2.c.** The *AFAP1* (rs7437940) for PP (novel locus)



**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

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## UK-Exome BP Consortium

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## GoT2D Consortium

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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 Samples**

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