Supplemental Material

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1. 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; **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 - 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, 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)

UK Biobank N=140,882
β/se= 0.4292/0.1006

EUR-led C. N=187,800
β/se= 0.2679/0.0809

CHARGE N=120,077
β/se= 0.4290/0.0980

META N=448,759
β/se= 0.3599/0.0530

Heterogeneity P-value=0.32
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 $1 \times 10^{-4}$ and $5 \times 10^{-8}$
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 SYNPL2 (rs34163229) for SBP (secondary signal)
3. Acknowledgments

**CHARGE EXOME BP**

Cohort and Cohort Specific Acknowledgment

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UK-Exome BP Consortium
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GoT2D Consortium

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4. Consortia Members

Content:

4.1. CHARGE+ Exome Chip Blood Pressure Consortium  
4.2. CHD Exome+ Consortium  
4.3. Exome BP Consortium  
4.4. GoT2D and T2D-GENES Consortia  
4.5. UK-Biobank CardioMetabolic Consortium BP working group
4.1. CHARGE+ Exome Chip Blood Pressure Consortium


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