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; **Freq 1**-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).

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3. Acknowledgments

**CHARGE EXOME BP**

*Cohort and Cohort Specific Acknowledgment*

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CHD Exome+ Consortium

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UK-Exome BP Consortium

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GoT2D Consortium

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4. Consortia Members

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4.1. CHARGE+ Exome Chip Blood Pressure Consortium


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