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Genetic Variants in Novel Pathways Influence Blood Pressure and Cardiovascular Disease Risk

The International Consortium for Blood Pressure Genome-Wide Association Studies

Abstract

Blood pressure (BP) is a heritable trait¹ influenced by multiple biological pathways and is responsive to environmental stimuli. Over one billion people worldwide have hypertension (BP 140 mm Hg systolic [SBP] or 90 mm Hg diastolic [DBP])². Even small increments in BP are associated with increased risk of cardiovascular events³. This genome-wide association study of SBP and DBP, which used a multi-stage design in 200,000 individuals of European descent, identified 16 novel loci: six of these loci contain genes previously known or suspected to regulate BP (*GUCY1A3-GUCY1B3*; *NPR3-C5orf23*; *ADM*; *FURIN-FES*; *GOSR2*; *GNAS-EDN3*); the other 10 provide new clues to BP physiology. A genetic risk score based on 29 genome-wide significant variants was associated with hypertension, left ventricular wall thickness, stroke, and coronary artery disease, but not kidney disease or kidney function. We also observed associations with BP in East Asian, South Asian, and African ancestry individuals. Our findings provide new insights into the genetics and biology of BP, and suggest novel potential therapeutic pathways for cardiovascular disease prevention.

Genetic approaches have advanced the understanding of biological pathways underlying inter-individual variation in BP. For example, studies of rare Mendelian BP disorders have identified multiple defects in renal sodium handling pathways⁴. More recently two genome-wide association studies (GWAS), each of >25,000 individuals of European-ancestry, identified 13 loci associated with SBP, DBP, and hypertension^{5,6}. We now report results of a new meta-analysis of GWAS data that includes staged follow-up genotyping to identify additional BP loci.

Primary analyses evaluated associations between 2.5 million genotyped or imputed single nucleotide polymorphisms (SNPs) and SBP and DBP in 69,395 individuals of European ancestry from 29 studies (Supplementary Materials Sections 1–3, Supplementary Tables 1–2). Following GWAS meta-analysis, we conducted a three-stage validation experiment that made efficient use of available genotyping resources, to follow up top signals in up to 133,661 additional individuals of European descent (Supplementary Fig. 1 and Supplementary Materials Section 4). Twenty-nine independent SNPs at 28 loci were

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Note added in proof: Since this manuscript was submitted, Kato et al published a BP GWAS in East Asians that identified a SNP highly correlated to the SNP we report at the *NPR3-c5orf23* locus²⁸.

Author contributions

Full author contributions and roles are listed in the Supplementary Materials Section 19.

significantly associated with SBP, DBP, or both in the meta-analysis combining discovery and follow up data (Fig. 1, Table 1, Supplementary Figs 2–3, Supplementary Tables 3–5). All 29 SNPs attained association $P < 5 \times 10^{-9}$, an order of magnitude beyond the standard genome-wide significance level for a single stage experiment (Table 1).

Sixteen of these 29 associations were novel (Table 1). Two associations were near the *FURIN* and *GOSR2* genes; prior targeted analyses of variants in these genes suggested they may be BP loci^{7,8}. At the *CACNB2* locus we validated association for a previously reported⁶ SNP rs4373814 and detected a novel independent association for rs1813353 (pairwise $r^2 = 0.015$ in HapMap CEU). Of our 13 previously reported associations^{5,6}, only the association at *PLCD3* was not supported by the current results (Supplementary Table 4). Some of the associations are in or near genes involved in pathways known to influence BP (*NPR3*, *GUCY1A3-GUCY1B3*, *ADM*, *GNAS-EDN3*, *NPPA-NPPB*, and *CYP17A1*; Supplementary Fig. 4). Twenty-two of the 28 loci did not contain genes that were *a priori* strong biological candidates.

As expected from prior BP GWAS results, the effects of the novel variants on SBP and DBP were small (Fig. 1 and Table 1). For all variants, the observed directions of effects were concordant for SBP, DBP, and hypertension (Fig. 1, Table 1, Supplementary Fig. 3). Among the genes at the genome-wide significant loci, only *CYP17A1*, previously implicated in Mendelian congenital adrenal hyperplasia and hypertension, is known to harbour rare variants that have large effects on BP⁹.

We performed several analyses to identify potential causal alleles and mechanisms. First, we looked up the 29 genome-wide significant index SNPs and their close proxies ($r^2 > 0.8$) among *cis*-acting expression SNP (eSNP) results from multiple tissues (Supplementary Materials Section 5). For 13/29 index SNPs, we found association between nearby eSNP variants and expression level of at least one gene transcript ($10^{-4} > p > 10^{-51}$, Supplementary Table 6). In 5 cases, the index BP SNP and the best eSNP from a genome-wide survey were identical, highlighting potential mediators of the SNP-BP associations.

Second, because changes in protein sequence are strong *a priori* candidates to be functional, we sought non-synonymous coding SNPs that were in high LD ($r^2 > 0.8$) with the 29 index SNPs. We identified such SNPs at 8 loci (Table 1, Supplementary Materials Section 6, Supplementary Table 7). In addition we performed analyses testing for differences in genetic effect according to body mass index (BMI) or sex, and analyses of copy number variants, pathway enrichment, and metabolomic data, but we did not find any statistically significant results (Supplementary Materials Sections 7–9, Supplementary Tables 8–10).

We evaluated whether the BP variants we identified in Europeans were associated with BP in individuals of East Asian (N=29,719), South Asian (N=23,977), and African (N=19,775) ancestries (Table 1, Supplementary Tables 11–13). We found significant associations in individuals of East Asian ancestry for SNPs at 9 loci and in individuals of South Asian ancestry for SNPs at 6 loci; some have been reported previously (Supplementary Tables 12 and 15). The lack of significant association for individual SNPs may reflect small sample sizes, differences in allele frequencies or LD patterns, imprecise imputation for some

ancestries using existing reference samples, or a genuinely different underlying genetic architecture. Because of limited power to detect effects of individual variants in the smaller non-European samples, we created genetic risk scores for SBP and DBP incorporating all 29 BP variants weighted according to effect sizes observed in the European samples. In each non-European ancestry group, risk scores were strongly associated with SBP ($P=1.1\times 10^{-40}$ in East Asian, $P=2.9\times 10^{-13}$ in South Asian, $P=9.8\times 10^{-4}$ in African ancestry individuals) and DBP ($P=2.9\times 10^{-48}$, $P=9.5\times 10^{-15}$, and $P=5.3\times 10^{-5}$, respectively; Supplementary Table 13).

We also created a genetic risk score to assess association of the variants in aggregate with hypertension and with clinical measures of hypertensive complications including left ventricular mass, left ventricular wall thickness, incident heart failure, incident and prevalent stroke, prevalent coronary artery disease (CAD), kidney disease, and measures of kidney function, using results from other GWAS consortia (Table 2, Supplementary Materials Sections 10–11, Supplementary Table 14). The risk score was weighted using the average of SBP and DBP effects for the 29 SNPs. In an independent sample of 23,294 women¹⁰, an increase of 1 standard deviation in the genetic risk score was associated with a 21% increase in the odds of hypertension (95% CI 19%–28%; Table 2, Supplementary Table 14). Among individuals in the top decile of the risk score, the prevalence of hypertension was 29% compared with 16% in the bottom decile (odds ratio 2.09, 95% CI 1.86–2.36). Similar results were observed in an independent hypertension case-control sample (Table 2). In our study, individuals in the top compared to bottom quintiles of genetic risk score differed by 4.6 mm Hg SBP and 3.0 mm Hg DBP, differences that approach population-averaged BP treatment effects for a single antihypertensive agent¹¹. Epidemiologic data have shown that differences in SBP and DBP of this magnitude, across the population range of BP, are associated with an increase in cardiovascular disease risk³. Consistent with this and in line with findings from randomized trials of BP-lowering medication in hypertensive patients^{12,13}, the genetic risk score was positively associated with left ventricular wall thickness ($P=6.0\times 10^{-6}$), occurrence of stroke ($P=3.3\times 10^{-5}$) and CAD ($P=8.1\times 10^{-29}$). The same genetic risk score was not, however, significantly associated with chronic kidney disease or measures of kidney function, even though these renal outcomes were available in a similar sample size as for the other outcomes (Table 2). The absence of association with kidney phenotypes could be explained by a weaker causal relation of BP with kidney phenotypes than with CAD and stroke. This finding is consistent with the mismatch between observational data that show a positive association of BP with kidney disease, and clinical trial data that show inconsistent evidence of benefit of BP lowering on kidney disease prevention in patients with hypertension¹⁴. Thus, several lines of evidence converge to suggest that BP elevation may in part be a consequence rather than a cause of sub-clinical kidney disease.

Our discovery meta-analysis (Supplementary Fig. 2) suggests an excess of modestly significant ($10^{-5} < P < 10^{-2}$) associations likely arising from common BP variants of small effect. By dividing our principal GWAS dataset into non-overlapping discovery ($N\approx 56,000$) and validation ($N\approx 14,000$) subsets, we found robust evidence for the existence of such undetected common variants (Supplementary Fig. 5, Supplementary Materials Section 12).

We estimate¹⁵ that there are 116 (95% CI 57–174) independent BP variants with effect sizes similar to those reported here, which collectively explain $\approx 2.2\%$ of the phenotypic variance for SBP and DBP, compared with 0.9% explained by the 29 associations discovered thus far (Supplementary Fig. 6, Supplementary Materials Section 13).

Most of the 28 BP loci harbour multiple genes (Supplementary Table 15, Supplementary Fig. 4), and although substantial research is required to identify the specific genes and variants responsible for these associations, several loci contain highly plausible biological candidates. The *NPPA* and *NPPB* genes at the *MTHFR-NPPB* locus encode precursors for atrial- and B-type natriuretic peptides (ANP, BNP), and previous work has identified SNPs, modestly correlated with our index SNP at this locus, that are associated with plasma ANP, BNP, and BP¹⁶. We found the index SNP at this locus was associated with opposite effects on BP and on ANP/BNP levels, consistent with a model in which the variants act through increased ANP/BNP production to lower BP¹⁶ (Supplementary Materials Section 14).

Two other loci identified in the current study harbour genes involved in natriuretic peptide and related nitric oxide signalling pathways,^{17,18} both of which act to regulate cyclic guanosine monophosphate (cGMP). The first locus contains *NPR3*, which encodes the natriuretic peptide clearance receptor (NPR-C). *NPR3* knockout mice exhibit reduced clearance of circulating natriuretic peptides and lower BP¹⁹. The second locus includes *GUCY1A3* and *GUCY1B3*, encoding the alpha and beta subunits of soluble guanylatecyclase (sGC); knockout of either gene in murine models results in hypertension²⁰.

Another locus contains *ADM*, encoding adrenomedullin, which has natriuretic, vasodilatory, and BP-lowering properties²¹. At the *GNAS-EDN3* locus, *ZNF831* is closest to the index SNP, but *GNAS* and *EDN3* are two nearby compelling biological candidates (Supplementary Fig. 4, Supplementary Table 15).

We identified two loci with plausible connections to BP via genes implicated in renal physiology or kidney disease. At the first locus, *SLC4A7* is an electro-neutral sodium bicarbonate co-transporter expressed in the nephron and in vascular smooth muscle²². At the second locus, *PLCE1* (phospholipase-C-epsilon-1 isoform) is important for normal podocyte development in the glomerulus; sequence variation in *PLCE1* has been implicated in familial nephrotic syndromes and end-stage kidney disease²³.

Missense variants in two genes involved in metal ion transport were associated with BP in our study. The first encodes a His/Asp change at amino acid 63 (*H63D*) in *HFE* and is a low penetrance allele for hereditary hemochromatosis²⁴. The second is an Ala/Thr polymorphism located in exon 7 of *SLC39A8*, which encodes a zinc transporter that also transports cadmium and manganese²⁵. The same allele of *SLC39A8* associated with BP in our study has recently been associated with high-density lipoprotein (HDL) cholesterol levels²⁶ and BMI²⁷ (Supplementary Table 15).

In conclusion, we have shown that 29 independent genetic variants influence BP in people of European ancestry. The variants reside in 28 loci, 16 of which were novel, and we confirmed association of several of them in individuals of non-European ancestry. A risk score derived from the 29 variants was significantly associated with BP-related organ

damage and clinical cardiovascular disease, but not kidney disease. These loci improve our understanding of the genetic architecture of BP, provide new biological insights into BP control and may identify novel targets for the treatment of hypertension and the prevention of cardiovascular disease.

Methods summary

Supplementary Materials provide complete methods and include the following sections: study recruitment and phenotyping, adjustment for antihypertensive medications, genotyping, data quality control, genotype imputation, within-cohort association analyses, meta-analyses of discovery and validation stages, stratified analyses by sex and BMI, identification of eSNPs and nsSNPs, metabolomic and lipidomic analyses, CNV analyses, pathway analyses, analyses for non-European ancestries, association of a risk score with hypertension and cardiovascular disease, estimation of numbers of undiscovered variants, measurement of natriuretic peptides, and brief literature reviews and GWAS database lookups of all validated BP loci.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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References

1. Levy D, et al. Evidence for a gene influencing blood pressure on chromosome 17. Genome scan linkage results for longitudinal blood pressure phenotypes in subjects from the framingham heart study. *Hypertension*. 2000; 36:477–483. [PubMed: 11040222]
2. Kearney PM, et al. Global burden of hypertension: analysis of worldwide data. *Lancet*. 2005; 365:217–223. [PubMed: 15652604]
3. Lewington S, Clarke R, Qizilbash N, Peto R, Collins R. Age-specific relevance of usual blood pressure to vascular mortality: a meta-analysis of individual data for one million adults in 61 prospective studies. *Lancet*. 2002; 360:1903–1913. [PubMed: 12493255]
4. Lifton RP, Gharavi AG, Geller DS. Molecular mechanisms of human hypertension. *Cell*. 2001; 104:545–556. [PubMed: 11239411]
5. Newton-Cheh C, et al. Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet*. 2009; 41:666–676. [PubMed: 19430483]
6. Levy D, et al. Genome-wide association study of blood pressure and hypertension. *Nat Genet*. 2009; 41:677–687. [PubMed: 19430479]
7. Meyer TE, et al. GOSR2 Lys67Arg is associated with hypertension in whites. *Am J Hypertens*. 2009; 22:163–168. [PubMed: 19057520]
8. Li N, et al. Associations between genetic variations in the FURIN gene and hypertension. *BMC Med Genet*. 2010; 11:124. [PubMed: 20707915]
9. Mussig K, et al. 17alpha-hydroxylase/17,20-lyase deficiency caused by a novel homozygous mutation (Y27Stop) in the cytochrome CYP17 gene. *J Clin Endocrinol Metab*. 2005; 90:4362–4365. [PubMed: 15811924]

10. Ridker PM, et al. Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy american women. *Clin Chem*. 2008; 54:249–255. [PubMed: 18070814]
11. Burt VL, et al. Trends in the prevalence, awareness, treatment, and control of hypertension in the adult US population. Data from the health examination surveys, 1960 to 1991. *Hypertension*. 1995; 26:60–69. [PubMed: 7607734]
12. Turnbull F, et al. Effects of different regimens to lower blood pressure on major cardiovascular events in older and younger adults: meta-analysis of randomised trials. *BMJ*. 2008; 336:1121–1123. [PubMed: 18480116]
13. Law MR, Morris JK, Wald NJ. Use of blood pressure lowering drugs in the prevention of cardiovascular disease: meta-analysis of 147 randomised trials in the context of expectations from prospective epidemiological studies. *BMJ*. 2009; 338:b1665. [PubMed: 19454737]
14. Lewis JB. Blood pressure control in chronic kidney disease: is less really more? *J Am Soc Nephrol*. 2010; 21:1086–1092. [PubMed: 20576804]
15. Park JH, et al. Estimation of effect size distribution from genome-wide association studies and implications for future discoveries. *Nat Genet*. 2010; 42:570–575. [PubMed: 20562874]
16. Newton-Cheh C, et al. Association of common variants in NPPA and NPPB with circulating natriuretic peptides and blood pressure. *Nat Genet*. 2009; 41:348–353. [PubMed: 19219041]
17. Schenk DB, et al. Purification and subunit composition of atrial natriuretic peptide receptor. *Proc Natl Acad Sci U S A*. 1987; 84:1521–1525. [PubMed: 2882506]
18. Schmidt HH, Walter U. NO at work. *Cell*. 1994; 78:919–925. [PubMed: 7923361]
19. Matsukawa N, et al. The natriuretic peptide clearance receptor locally modulates the physiological effects of the natriuretic peptide system. *Proc Natl Acad Sci U S A*. 1999; 96:7403–7408. [PubMed: 10377427]
20. Friebe A, Mergia E, Dangel O, Lange A, Koesling D. Fatal gastrointestinal obstruction and hypertension in mice lacking nitric oxide-sensitive guanylyl cyclase. *Proc Natl Acad Sci U S A*. 2007; 104:7699–7704. [PubMed: 17452643]
21. Ishimitsu T, Ono H, Minami J, Matsuoka H. Pathophysiologic and therapeutic implications of adrenomedullin in cardiovascular disorders. *Pharmacol Ther*. 2006; 111:909–927. [PubMed: 16616959]
22. Pushkin A, et al. Cloning, tissue distribution, genomic organization, and functional characterization of NBC3, a new member of the sodium bicarbonate cotransporter family. *J Biol Chem*. 1999; 274:16569–16575. [PubMed: 10347222]
23. Hinkes B, et al. Positional cloning uncovers mutations in PLCE1 responsible for a nephrotic syndrome variant that may be reversible. *Nat Genet*. 2006; 38:1397–1405. [PubMed: 17086182]
24. Feder JN, et al. A novel MHC class I-like gene is mutated in patients with hereditary haemochromatosis. *Nat Genet*. 1996; 13:399–408. [PubMed: 8696333]
25. He L, Wang B, Hay EB, Nebert DW. Discovery of ZIP transporters that participate in cadmium damage to testis and kidney. *Toxicology and applied pharmacology*. 2009; 238:250–257. [PubMed: 19265717]
26. Teslovich TM, et al. Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*. 2010; 466:707–713. [PubMed: 20686565]
27. Speliotes EK, et al. Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nat Genet*. 2010; 42:937–948. [PubMed: 20935630]
28. Kato N, et al. Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. *Nat Genet*. 2011; 43:531–538. [PubMed: 21572416]

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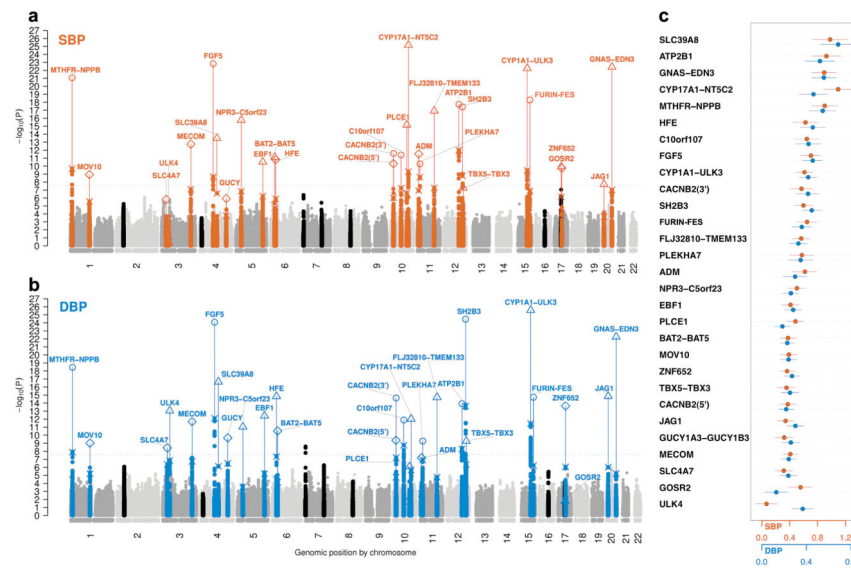


Fig. 1. Genome-wide $-\log_{10} P$ -value plots and effects for significant loci. Genome-wide $-\log_{10} P$ -value plots are shown for systolic (SBP: panel a) and diastolic (DBP: panel b). SNPs within loci reaching genome-wide significance are labeled in red for SBP and blue for DBP (± 2.5 Mb of lowest P -value) and lowest P -values in the initial genome-wide analysis as well as the results of analysis including validation data are labeled separately. The lowest P -values in the initial GWAS are denoted as an X. The range of different sample sizes in the final meta-analysis including the validation data are indicated as: circle (96–140k), triangle (>140 –180k), and diamond (>180 –220k). SNPs near unconfirmed loci are in black. The horizontal dotted line is $P=2.5 \times 10^{-8}$. Panel c shows the effect size estimates and 95% confidence bars per BP-increasing allele of the 29 significant variants for SBP (red) and DBP (blue). Effect sizes are expressed in mmHg/allele. GUCY = *GUCYA3-GUCY1B3*.

Table 1

Summary association results for 29 BP SNPs

Summary association statistics, based on combined discovery and follow-up data, for 29 independent SNPs in individuals of European ancestry are shown. New genome-wide significant findings (17 SNPs) are presented in the top half of the table, data on 12 previously published signals are presented in the lower half.

| Locus | Index SNP | Chr | Position | CA/NCA | CAF | nsSNP | eSNP | SBP | | | DBP | | | HTN | |
|-------------------------|------------|-----|-------------|--------|------|-------|------|--------|-----------------------|-------------------|--------|-----------------------|-------------------|--------|-----------------------|
| | | | | | | | | Beta | P-value | Effect in EA/SA/A | Beta | P-value | Effect in EA/SA/A | Beta | P-value |
| <i>MOV10</i> | rs2932538 | 1 | 113,018,066 | G/A | 0.75 | Y(p) | Y(p) | 0.388 | 1.2×10^{-9} | +/+/- | 0.24 | 9.9×10^{-10} | +/+*/- | 0.049 | 2.9×10^{-7} |
| <i>SLC44A7</i> | rs13082711 | 3 | 27,512,913 | T/C | 0.78 | Y(p) | Y(p) | -0.315 | 1.5×10^{-6} | -/-/+ | -0.238 | 3.8×10^{-9} | -/-/+ | -0.035 | 3.6×10^{-4} |
| <i>EP300</i> | rs419076 | 3 | 170,583,580 | T/C | 0.47 | - | - | 0.409 | 1.8×10^{-13} | +/++ | 0.241 | 2.1×10^{-12} | +/+/- | 0.031 | 3.1×10^{-4} |
| <i>SLC39A8</i> | rs13107325 | 4 | 103,407,732 | T/C | 0.05 | Y | Y(+) | -0.981 | 3.3×10^{-14} | ?/+ | -0.684 | 2.3×10^{-17} | ?/+ | -0.105 | 4.9×10^{-7} |
| <i>GUCY1A3-GUCY1B3</i> | rs13139571 | 4 | 156,864,963 | C/A | 0.76 | - | - | 0.321 | 1.2×10^{-6} | +/-/+ | 0.26 | 2.2×10^{-10} | +/-/+ | 0.042 | 2.5×10^{-5} |
| <i>SPR3-C5orf23</i> | rs1173771 | 5 | 32,850,785 | G/A | 0.6 | - | - | 0.504 | 1.8×10^{-16} | +*/++ | 0.261 | 9.1×10^{-12} | +*/+/- | 0.062 | 3.2×10^{-10} |
| <i>EPF1</i> | rs11953630 | 5 | 157,777,980 | T/C | 0.37 | - | - | -0.412 | 3.0×10^{-11} | +/+ | -0.281 | 3.8×10^{-13} | +/+ | -0.052 | 1.7×10^{-7} |
| <i>EPF2</i> | rs1799945 | 6 | 26,199,158 | G/C | 0.14 | Y | - | 0.627 | 7.7×10^{-12} | +/+/- | 0.457 | 1.5×10^{-15} | +/+/- | 0.095 | 1.8×10^{-10} |
| <i>BAT2-BAT5</i> | rs805303 | 6 | 31,724,345 | G/A | 0.61 | Y(p) | Y(+) | 0.376 | 1.5×10^{-11} | -/-/? | 0.228 | 3.0×10^{-11} | -/-/+ | 0.054 | 1.1×10^{-10} |
| <i>CACNB2(5)</i> | rs4373814 | 10 | 18,459,978 | G/C | 0.55 | - | - | -0.373 | 4.8×10^{-11} | +/+/- | -0.218 | 4.4×10^{-10} | -/+/- | -0.046 | 8.5×10^{-8} |
| <i>PLCE1</i> | rs932764 | 10 | 95,885,930 | G/A | 0.44 | - | - | 0.484 | 7.1×10^{-16} | +/+/- | 0.185 | 8.1×10^{-7} | +/+/- | 0.055 | 9.4×10^{-9} |
| <i>ADM</i> | rs7129220 | 11 | 10,307,114 | G/A | 0.89 | - | - | -0.619 | 3.0×10^{-12} | ?/-/+ | -0.299 | 6.4×10^{-8} | ?/-/+ | -0.044 | 1.1×10^{-3} |
| <i>FLJ32810-TMEM133</i> | rs633185 | 11 | 100,098,748 | G/C | 0.28 | - | - | -0.565 | 1.2×10^{-17} | +*/++ | -0.328 | 2.0×10^{-15} | +*/+/- | -0.07 | 5.4×10^{-11} |
| <i>FURIN-FES</i> | rs2521501 | 15 | 89,238,392 | T/A | 0.31 | - | Y(-) | 0.65 | 5.2×10^{-19} | +*/++ | 0.359 | 1.9×10^{-15} | +*/+/- | 0.059 | 7.0×10^{-7} |
| <i>GOSR2</i> | rs17608766 | 17 | 42,368,270 | T/C | 0.86 | - | Y(+) | -0.556 | 1.1×10^{-10} | +/-/+ | -0.129 | 0.017 | +/-/+ | -0.025 | 0.08 |

| Locus | Index SNP | Chr | Position | CA/NCA | CAF | nsSNP | eSNP | SBP | | DBP | | HTN | | | |
|----------------------|------------|-----|-------------|--------|------|-------|--------|--------|-----------------------|-------------------|--------|-----------------------|-------------------|--------|-----------------------|
| | | | | | | | | Beta | P-value | Effect in EA/SA/A | Beta | P-value | Effect in EA/SA/A | Beta | P-value |
| <i>JAG1</i> | rs1327235 | 20 | 10,917,030 | G/A | 0.46 | - | - | 0.34 | 1.9×10^{-8} | +*/+/+ | 0.302 | 1.4×10^{-15} | +*/+/+ | 0.034 | 4.6×10^{-4} |
| <i>GNAS-EDN3</i> | rs6015450 | 20 | 57,184,512 | G/A | 0.12 | Y(p) | - | 0.896 | 3.9×10^{-23} | ?/+/+ | 0.557 | 5.6×10^{-23} | ?/+/+ | 0.11 | 4.2×10^{-14} |
| <i>MTHFR-NPPB</i> | rs17367504 | 1 | 11,785,365 | G/A | 0.15 | - | Y(-/r) | -0.903 | 8.7×10^{-22} | +*/+/+ | -0.547 | 3.5×10^{-19} | +*/+/+ | -0.103 | 2.3×10^{-10} |
| <i>ULK4</i> | rs3774372 | 3 | 41,852,418 | T/C | 0.83 | Y | Y(r/p) | -0.067 | 0.39 | -*/+/+ | -0.367 | 9.0×10^{-14} | +*/+/+ | -0.017 | 0.18 |
| <i>FGF5</i> | rs1458038 | 4 | 81,383,747 | T/C | 0.29 | - | - | 0.706 | 1.5×10^{-23} | +*/+/+ | 0.457 | 8.5×10^{-25} | +*/+/+ | 0.072 | 1.9×10^{-7} |
| <i>CACNB2(3')</i> | rs1813353 | 10 | 18,747,454 | T/C | 0.68 | - | - | 0.569 | 2.6×10^{-12} | +*/+/+ | 0.415 | 2.3×10^{-15} | +*/+/+ | 0.078 | 6.2×10^{-10} |
| <i>C10orf107</i> | rs4590817 | 10 | 63,137,559 | G/C | 0.84 | - | Y(r) | 0.646 | 4.0×10^{-12} | -*/+/+ | 0.419 | 1.3×10^{-12} | -*/+/+ | 0.096 | 9.8×10^{-9} |
| <i>CYP17A1-NT5C2</i> | rs11191548 | 10 | 104,836,168 | T/C | 0.91 | - | Y(-) | 1.095 | 6.9×10^{-26} | +*/+/+ | 0.464 | 9.4×10^{-13} | +*/+/+ | 0.097 | 1.4×10^{-5} |
| <i>PLEKHA7</i> | rs381815 | 11 | 16,858,844 | T/C | 0.26 | - | - | 0.575 | 5.3×10^{-11} | +*/+/+ | 0.348 | 5.3×10^{-10} | +*/+/+ | 0.062 | 3.4×10^{-6} |
| <i>ATP2B1</i> | rs17249754 | 12 | 88,584,717 | G/A | 0.84 | - | - | 0.928 | 1.8×10^{-18} | +*/+/+ | 0.522 | 1.2×10^{-14} | +*/+/+ | 0.126 | 1.1×10^{-14} |
| <i>SH2B3</i> | rs3184504 | 12 | 110,368,991 | T/C | 0.47 | Y | Y(+) | 0.598 | 3.8×10^{-18} | -*/+/+ | 0.448 | 3.6×10^{-25} | -*/+/+ | 0.056 | 2.6×10^{-6} |
| <i>TBX5-TBX3</i> | rs10850411 | 12 | 113,872,179 | T/C | 0.7 | - | - | 0.354 | 5.4×10^{-8} | -*/+/+ | 0.253 | 5.4×10^{-10} | -*/+/+ | 0.045 | 5.2×10^{-6} |
| <i>CYP17A1-ULK3</i> | rs1378942 | 15 | 72,864,420 | C/A | 0.35 | - | Y(+) | 0.613 | 5.7×10^{-23} | +*/+/+ | 0.416 | 2.7×10^{-26} | +*/+/+ | 0.073 | 1.0×10^{-8} |
| <i>ZNF652</i> | rs12940887 | 17 | 44,757,806 | T/C | 0.38 | - | Y(-) | 0.362 | 1.8×10^{-10} | +*/+/+ | 0.27 | 2.3×10^{-14} | +*/+/+ | 0.046 | 1.2×10^{-7} |

Y indicates the BP index SNP is a nsSNP, Y(p) indicates a proxy SNP is a nsSNP, Y(+): indicates BP index SNP is the strongest known eSNP for a transcript; Y(-): indicates BP index SNP is an eSNP but not strongest known eSNP for any transcript. Y(r): indicates BP index SNP is strongest known eSNP in a regional SNP-RTPCR experiment. Y(p): indicates a proxy SNP ($r^2 > 0.8$) to BP SNP is an eSNP but not the strongest known eSNP. Observed effect directions in East Asian (EA), South Asian (SA), and African (A) ancestry individuals are coded + or - if concordant or discordant with directions in European ancestry results;

* denotes significance controlling the FDR at 5% over 58 tests per ancestry (Supplementary Tables 5 and 12). Effect size estimates (beta) correspond to mmHg per coded allele for SBP and DBP and ln(odds) per coded allele for HTN.

CA = coded allele; NCA = non-coded allele; CAF = coded allele frequency; ? denotes missing data. Genomic positions use NCBI Build 36 coordinates.

Table 2
Genetic risk score and cardiovascular outcome association results

Association of genetic risk score (using all 29 SNPs at 28 loci, parameterised using the average of SBP and DBP effects [= (SBP effect + DBP effect)/2] from the discovery analysis), tested in results from other GWAS consortia.

| Phenotype | Source | Effect (per SD of genetic risk score) | SE | P-value | # SNPs | Contrast top vs. bottom | | | N case/control or total |
|---|---------------------------------------|--|-----------|-----------------------|--------|-------------------------|----------|----|-------------------------|
| | | | | | | quintiles | deciles | | |
| Blood pressure phenotypes | | | | | | | | | |
| SBP [mmHg] | WGHs | 1.645 | 0.098 (a) | 6.5*10 ⁻⁶³ | 29 | 4.61 | 5.77 (a) | | 23,294 |
| DBP [mmHg] | WGHs | 1.057 | 0.067 (a) | 8.4*10 ⁻⁵⁷ | 29 | 2.96 | 3.71 (a) | | 23,294 |
| Prevalent hypertension | WGHs | 0.211 | 0.018 (b) | 3.1*10 ⁻³³ | 29 | 1.80 | 2.09 (b) | | 5,018/18,276 |
| Prevalent hypertension | BRIGHT | 0.287 | 0.031 (b) | 7.7*10 ⁻²¹ | 29 | 2.23 | 2.74 (b) | | 2,406/1,990 |
| Dichotomous endpoints | | | | | | | | | |
| Incident heart failure | CHARGE-HF | 0.035 | 0.021 (c) | 0.10 | 29 | 1.10 | 1.13 (c) | | 2,526/18,400 |
| Incident stroke | NEURO-CHARGE | 0.103 | 0.028 (c) | 0.0002 | 28 | 1.34 | 1.44 (c) | | 1,544/18,058 |
| Prevalent stroke | UK-US Stroke Collaborative Group(SCG) | 0.075 | 0.037 (b) | 0.05 | 29 | 1.23 | 1.30 (b) | | 1,473/1,482 |
| Stroke (combined, incident and prevalent) | CHARGE & SCG | NA | NA | 3.3*10 ⁻⁵ | NA | NA | NA | NA | 3,017/19,540 |
| Prevalent CAD | CARDIoGRAM | 0.092 | 0.010 (b) | 1.6*10 ⁻¹⁹ | 28 | 1.29 | 1.38 (b) | | 22,233/64,726 |
| Prevalent CAD | C4D ProCARDIS | 0.132 | 0.022 (b) | 2.2*10 ⁻⁹ | 29 | 1.45 | 1.59 (b) | | 5,720/4,381 |
| Prevalent CAD | C4D HPS | 0.083 | 0.027 (b) | 0.002 | 29 | 1.26 | 1.34 (b) | | 2,704/2,804 |
| Prevalent CAD (combined) | CARDIoGRAM & C4D | 0.100 | 0.009 (b) | 8.1*10 ⁻²⁹ | 29 | 1.32 | 1.42 (b) | | 30,657/71,911 |
| Prevalent chronic kidney disease | CKDGen | 0.014 | 0.015 (b) | 0.35 | 29 | 1.04 | 1.05 (b) | | 5,807/61,286 |
| Prevalent microalbuminuria | CKDGen | 0.008 | 0.019 (b) | 0.68 | 29 | 1.02 | 1.03 (b) | | 3,698/27,882 |
| Continuous measures of target organ damage | | | | | | | | | |

| Phenotype | Source | Effect | | P-value | # SNPs | Contrast top vs. bottom | | N case/control or total |
|-------------------------------------|-----------|--------------------------------|------------|----------------------|--------|-------------------------|----------|-------------------------|
| | | (per SD of genetic risk score) | SE | | | quintiles | deciles | |
| Blood pressure phenotypes | | | | | | | | |
| Left ventricular mass [g] | EchoGen | 0.822 | 0.317 (a) | 0.01 | 29 | 2.30 | 2.89 (a) | 12,612 |
| Left ventricular wall thickness[cm] | EchoGen | 0.009 | 0.002 (a) | 6.0*10 ⁻⁶ | 29 | 0.03 | 0.03 (a) | 12,612 |
| Serum creatinine | KidneyGen | -0.001 | 0.001 (d) | 0.24 | 29 | 1.00 | 1.00 (d) | 23,812 |
| eGFR (4 parameter MDRD equation) | CKDGen | -0.0001 | 0.0009 (d) | 0.93 | 29 | 1.00 | 1.00 (d) | 67,093 |
| Urinary albumin/creatinine ratio | CKDGen | 0.005 | 0.007 (d) | 0.43 | 29 | 1.01 | 1.02 (d) | 31,580 |

(a) Units are the unit of phenotypic measurement, either per SD of genetic risk score, or as a difference between top/bottom quintiles or deciles.

(b) Units are ln(odds) per SD of genetic risk score, or odds ratio between top/bottom quintiles or deciles.

(c) Units are ln(hazard) per SD of genetic risk score, or hazard ratio between top/bottom quintiles or deciles.

(d) Units are ln(phenotype) per SD of genetic risk score, or phenotypic ratio between top/bottom quintiles or deciles.