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

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Abstract

Blood pressure (BP) is a heritable trait[1] 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 events[3]. 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 pathways[4]. 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* locus[28].

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 $P < 5\times10^{-9}$, 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 reported[6] 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 BP[9].

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 SNPsat 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 ($P=1.1\times10^{-40}$ in East Asian, $P=2.9\times10^{-13}$ in South Asian, $P=9.8\times10^{-4}$ in African ancestry individuals) and DBP ($P=2.9\times10^{-48}$, $P=9.5\times10^{-15}$, and $P=5.3\times10^{-5}$, 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 women[10], 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 agent[11]. 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 risk[3]. 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 ($P=6.0\times10^{-6}$), occurrence of stroke ($P=3.3\times10^{-5}$) and CAD ($P=8.1\times10^{-29}$). 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 hypertension[14]. 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≈56,000) and validation (N≈14,000) subsets, we found robust evidence for the existence of such undetected common variants (Supplementary Fig. 5, Supplementary Materials Section 12).

We estimate[15] that there are 116 (95% CI 57–174) independent BP variants with effect sizes similar to those reported here, which collectively explain ≈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 BP[16]. 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 BP[16] (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 BP[19]. 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 hypertension[20].

Another locus contains *ADM*, encoding adrenomedullin, which has natriuretic, vasodilatory, and BP-lowering properties[21]. 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 muscle[22]. 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 disease[23].

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 hemochromatosis[24]. The second is an Ala/Thr polymorphism located in exon 7 of *SLC39A8*, which encodes a zinc transporter that also transports cadmium and manganese[25]. The same allele of *SLC39A8* associated with BP in our study has recently been associated with high-density lipoprotein (HDL) cholesterol levels[26] and BMI[27] (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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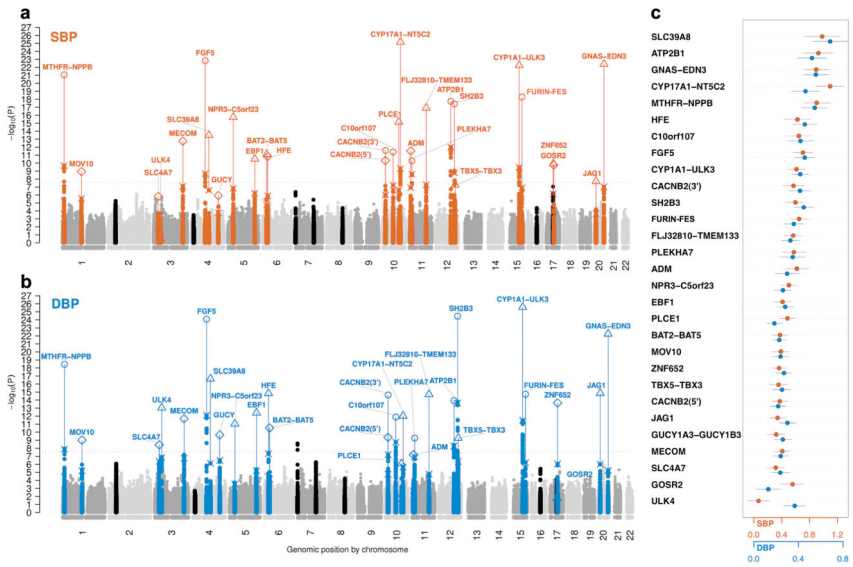

Fig. 1.

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 (±2.5Mb 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 = *GUCY1A3-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
MOV10	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	$2.9^{*}10^{-7}$
SLC4A7	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	$3.6^{*}10^{-4}$
MECOM	rs419076	3	170,583,580	T/C	0.47	-	-	0.409	$1.8^{*}10^{-13}$	+/+/+	0.241	$2.1^{*}10^{-12}$	+/+/−	0.031	$3.1^{*}10^{-4}$
SLC39A8	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	$4.9^{*}10^{-7}$
GUCY1A3-GUCY1B3	rs13139571	4	156,864,963	C/A	0.76	-	-	0.321	$1.2^{*}10^{-6}$	+/−/+	0.26	$2.2^{*}10^{-10}$	+/−/+	0.042	$2.5^{*}10^{-5}$
EPR3-C5orf23	rs1173771	5	32,850,785	G/A	0.6	-	-	0.504	$1.8^{*}10^{-16}$	+*/+/+	0.261	$9.1^{*}10^{-12}$	+*/+/−	0.062	$3.2^{*}10^{-10}$
EBF1	rs11953630	5	157,777,980	T/C	0.37	-	-	−0.412	$3.0^{*}10^{-11}$	+/+/+	−0.281	$3.8^{*}10^{-13}$	+/+/+	−0.052	$1.7^{*}10^{-7}$
HFE	rs1799945	6	26,199,158	G/C	0.14	Y	-	0.627	$7.7^{*}10^{-12}$	+/+/−	0.457	$1.5^{*}10^{-15}$	+/+/−	0.095	$1.8^{*}10^{-10}$
BAT2-BAT5	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	$1.1^{*}10^{-10}$
CACNB2(5′)	rs4373814	10	18,459,978	G/C	0.55	-	-	−0.373	$4.8^{*}10^{-11}$	+/+/−	−0.218	$4.4^{*}10^{-10}$	−/+/−	−0.046	$8.5^{*}10^{-8}$
PLCE1	rs932764	10	95,885,930	G/A	0.44	-	-	0.484	$7.1^{*}10^{-16}$	+/+/−	0.185	$8.1^{*}10^{-7}$	+/+/−	0.055	$9.4^{*}10^{-9}$
ADM	rs7129220	11	10,307,114	G/A	0.89	-	-	−0.619	$3.0^{*}10^{-12}$	?/−/+	−0.299	$6.4^{*}10^{-8}$	?/−/+	−0.044	$1.1^{*}10^{-3}$
FLJ32810-TMEM133	rs633185	11	100,098,748	G/C	0.28	-	-	−0.565	$1.2^{*}10^{-17}$	+*/+/+	−0.328	$2.0^{*}10^{-15}$	+*/+/−	−0.07	$5.4^{*}10^{-11}$
FURIN-FES	rs2521501	15	89,238,392	T/A	0.31	-	Y(−)	0.65	$5.2^{*}10^{-19}$	+*/+/+	0.359	$1.9^{*}10^{-15}$	+*/+/+	0.059	$7.0^{*}10^{-7}$
GOSR2	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
JAG1	rs1327235	20	10,917,030	G/A	0.46	-	-	0.34	$1.9^{*}10^{-8}$	$+^{*}/+/+$	0.302	$1.4^{*}10^{-15}$	$+^{*}/+^{*}/+$	0.034	$4.6^{*}10^{-4}$
GNAS-EDN3	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	$4.2^{*}10^{-14}$
MTHFR-NPPB	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	$2.3^{*}10^{-10}$
ULK4	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
FGF5	rs1458038	4	81,383,747	T/C	0.29	-	-	0.706	$1.5^{*}10^{-23}$	$+^{*}/+/+$	0.457	$8.5^{*}10^{-25}$	$+^{*}/+^{*}/+$	0.072	$1.9^{*}10^{-7}$
CACNB2(3′)	rs1813353	10	18,747,454	T/C	0.68	-	-	0.569	$2.6^{*}10^{-12}$	+/+/+	0.415	$2.3^{*}10^{-15}$	+/+/+	0.078	$6.2^{*}10^{-10}$
C10orf107	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	$9.8^{*}10^{-9}$
CYP17A1-NT5C2	rs11191548	10	104,836,168	T/C	0.91	-	Y(−)	1.095	$6.9^{*}10^{-26}$	$+^{*}/+^{*}/+$	0.464	$9.4^{*}10^{-13}$	$+^{*}/+^{*}/+$	0.097	$1.4^{*}10^{-5}$
PLEKHA7	rs381815	11	16,858,844	T/C	0.26	-	-	0.575	$5.3^{*}10^{-11}$	$+^{*}/+/+$	0.348	$5.3^{*}10^{-10}$	$+^{*}/-/+$	0.062	$3.4^{*}10^{-6}$
ATP2B1	rs17249754	12	88,584,717	G/A	0.84	-	-	0.928	$1.8^{*}10^{-18}$	$+^{*}/+^{*}/-$	0.522	$1.2^{*}10^{-14}$	$+^{*}/+^{*}/-$	0.126	$1.1^{*}10^{-14}$
SH2B3	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	$2.6^{*}10^{-6}$
TBX5-TBX3	rs10850411	12	113,872,179	T/C	0.7	-	-	0.354	$5.4^{*}10^{-8}$	−/+/−	0.253	$5.4^{*}10^{-10}$	−/−/−	0.045	$5.2^{*}10^{-6}$
CYP1A1-ULK3	rs1378942	15	72,864,420	C/A	0.35	-	Y(+)	0.613	$5.7^{*}10^{-23}$	$+^{*}/+/+$	0.416	$2.7^{*}10^{-26}$	$+^{*}/+/-$	0.073	$1.0^{*}10^{-8}$
ZNF652	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(+): indicatesBP 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.

		Effect	SE				Contrast top vs. bottom			
Phenotype	**Source**	**(per SD of genetic risk score)**			***P*-value**	**# SNPs**	**quintiles**	**deciles**		**N case/control or total**
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	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 oftarget organ damage										

Phenotype	Source	Effect (per SD of genetic risk score)	SE (per SD of genetic risk score)		*P*-value	# SNPs	Contrast top vs. bottom quintiles	Contrast top vs. bottom deciles		N case/control or total
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.