Journal of the American Heart Association

BRIEF COMMUNICATION

Estimating the Population Benefits of Blood Pressure Lowering: A Wide-Angled Mendelian Randomization Study in UK Biobank

Hannah Higgins , MPhil; Amy M. Mason , PhD; Susanna C. Larsson , PhD; Dipender Gill , BMBCh, PhD; Claudia Langenberg , MD, PhD; Stephen Burgess , PhD

BACKGROUND: The causal relevance of elevated blood pressure for several cardiovascular diseases (CVDs) is uncertain, as is the population impact of blood pressure lowering. This study systematically assesses evidence of causality for various CVDs in a 2-sample Mendelian randomization framework, and estimates the potential reduction in the prevalence of these diseases attributable to long-term population shifts in the distribution of systolic blood pressure (SBP).

METHODS AND RESULTS: We investigated associations of genetically predicted SBP as predicted by 256 genetic variants with 21 CVDs in UK Biobank, a population-based cohort of UK residents. The sample consisted of 376 703 participants of European ancestry, aged 40 to 69 years at recruitment. Genetically predicted SBP was positively associated with 14 of the outcomes (P<0.002), including dilated cardiomyopathy, endocarditis, peripheral vascular disease, and rheumatic heart disease. Using genetic variation to estimate the long-term impact of blood pressure lowering on disease in a middle-aged to early late-aged UK-based population, population reductions in SBP were predicted to result in an overall 16.9% (95% CI, 12.2%–21.3%) decrease in morbidity for a 5-mm Hg decrease from a population mean of 137.7 mm Hg, 30.8% (95% CI, 22.8%–38.0%) decrease for a 10-mm Hg decrease, and 56.2% (95% CI, 43.7%–65.9%) decrease for a 22.7-mm Hg decrease in SBP (22.7 mm Hg represents a shift from the current mean SBP to 115 mm Hg).

CONCLUSIONS: Risk of many CVDs is influenced by long-term differences in SBP. The burden of a broad range of CVDs could be substantially reduced by long-term population-wide reductions in the distribution of blood pressure.

Key Words: cardiovascular disease ■ genetic epidemiology ■ high blood pressure ■ hypertension ■ Mendelian randomization

igh blood pressure has severe, costly consequences largely through increased cardiovascular disease (CVD) risk.¹ For many CVDs, a causal relationship with blood pressure that is reversible through treatment has been demonstrated in randomized controlled trials (RCTs).² However, for diseases such as dilated cardiomyopathy, endocarditis, peripheral vascular disease, and aortic valve stenosis, RCT evidence demonstrating a causal effect of blood pressure lowering is lacking. Despite this, these outcomes

have been used to estimate the population impact of increased blood pressure.³ In addition, quantitative evidence for the benefit of reducing blood pressure has not been assessed for several CVD outcomes in a primary prevention setting.

In the absence of RCT evidence, Mendelian randomization (MR) can circumvent several limitations of observational epidemiology, allowing unconfounded inferences from observational data. 4 MR uses selected genetic variants related to an exposure to provide

Correspondence to: Stephen Burgess, PhD, Department of Public Health and Primary Care, University of Cambridge, 2 Worts Causeway, Cambridge CB1 8RN, United Kingdom. E-mail: sb452@medschl.cam.ac.uk

Preprint posted on medRxiv February 9, 2021. doi: https://doi.org/10.1101/2021.02.02.21250515.

Supplementary Material for this article is available at https://www.ahajournals.org/doi/suppl/10.1161/JAHA.121.021098

For Sources of Funding and Disclosures, see page 7.

© 2021 The Authors. Published on behalf of the American Heart Association, Inc., by Wiley. This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited. JAHA is available at: www.ahajournals.org/journal/jaha

J Am Heart Assoc. 2021;10:e021098. DOI: 10.1161/JAHA.121.021098

evidence supporting a causal hypothesis. The independent segregation of alleles at conception means that genetically defined subgroups of the population with increased or decreased average blood pressure levels should not differ systematically with respect to confounding variables, creating a natural experiment analogous to an RCT. Life-long average differences in the exposure between subgroups compared in an MR analysis provide evidence on the potential impact of long-term interventions on the exposure, in contrast to the short-term interventions usually evaluated by RCTs.⁵

Herein, we use MR to assess evidence for causality between systolic blood pressure (SBP) and a broad range of CVDs in UK Biobank, a population-based cohort of UK residents. We then use these estimates to predict the potential reduction in CVD burden in the UK population attributable to distributional shifts in SBP. We focus on SBP as a measure of blood pressure because it is a better predictor of health outcomes than diastolic blood pressure. However, as the genetic variants used in this investigation are associated with both SBP and diastolic blood pressure, estimates relate generally to blood pressure lowering and are not specific to SBP.

METHODS

Summarized genetic data used in this investigation have been made publicly available and can be accessed at https://doi.org/10.6084/m9.figshare.14417594.v1. The UK Biobank study was approved by the UK's North West Multi-Centre Research Ethics Committee. All participants provided written informed consent.

We performed 2-sample MR analyses using summarized data (Figure S1). Genetic associations with blood pressure were obtained in an analysis of 299 024 European ancestry participants from the International Consortium for Blood Pressure, which excluded UK Biobank participants.⁶ Genetic associations with 21 CVDs were estimated in 376 703 European ancestry participants from UK Biobank by logistic regression with adjustment for age, sex, and 10 genomic principal components (Table S1). Derivation of the analytic subset followed quality control steps described previously⁷: after filtering genetic variants (call rate ≥99%, information score >0.9, and Hardy-Weinberg equilibrium $P \ge 10^{-5}$) and participants (removal of genetic sex mismatches), we excluded participants having non-European ancestries (self-report or inferred by genetics) or excess heterozygosity (>3 SDs from the mean), and included only one of each set of related participants (third-degree relatives or closer).

As genetic instruments, we selected 256 variants previously associated with blood pressure at a genome-wide level of significance in the International Consortium for Blood Pressure data set, excluding UK

Biobank participants (Table S2). As the International Consortium for Blood Pressure and UK Biobank samples do not overlap, bias attributable to winner's curse is avoided. The variants explained 2.1% of variance in SBP in International Consortium for Blood Pressure, corresponding to an F-statistic of 23.1. Associations between a weighted genetic risk score and potential confounders (sex, age, body mass index [BMI], smoking status, low-density lipoprotein [LDL] cholesterol, alcohol drinker status, glycated hemoglobin, history of diabetes mellitus at recruitment, and physical activity) were assessed in UK Biobank.

Statistical analysis

MR estimates for the casual effect of SBP on the odds of 21 CVD outcomes were obtained using the inverse variance weighted (IVW) method.⁴ Estimates are odds ratios per 10-mm Hg increase in genetically predicted SBP. Sensitivity analyses were performed using the MR-Egger, weighted median, and Mendelian Randomization-Pleiotropy Residual Sum and Outlier (MR-PRESSO) methods.⁴

The plausibility of estimates derived from MR having a causal interpretation relies on genetic variants satisfying 3 assumptions: the genetic variant is associated with the exposure of interest (the relevance assumption); the genetic variant can only influence the outcome through its effect on the exposure (the exclusion restriction assumption); and the genetic variant is not associated with the outcome via a confounding pathway (the exchangeability assumption). The IVW method assumes that all genetic variants satisfy these assumptions, or that the average pleiotropic effect across genetic variants is zero.4 The additional methods provide reliable inferences when some genetic variants violate these assumptions, allowing investigation of the robustness of results. The MR-Egger method relaxes the IVW assumption that the average pleiotropic effect is zero, allowing for directional pleiotropy when the pleiotropic effects of the genetic variants on the outcome are not correlated with their associations with the exposure. The weighted median method takes a median (instead of a weighted mean) of the variant-specific estimates. providing an estimate robust to outlying variants. In the MR-PRESSO method, variants with heterogeneous estimates (which may be pleiotropic variants) are excluded from the analysis, and the IVW method is subsequently performed, omitting such variants.

Outcomes with consistent evidence for causality (P<0.05/21=0.002 in either the IVW or the MR-PRESSO method and concordant direction of estimates across all methods) were used to estimate the change in disease burden that would occur under interventions in the distribution of SBP. Assuming a linear model, we estimated the population impact fraction,³ representing

the relative reduction in disease risk if mean SBP was set to a given value for all individuals in the population. We also estimated the absolute reduction in events from a population shift in the distribution of SBP using disease prevalence estimates from surveys relevant to a middle-aged to early late-aged UK-based population (Table S3).

All analyses were performed in R version 3.6.3 ("Holding the Windsock").

RESULTS

SBP was approximately normally distributed, with a mean of 137.7 mm Hg (SD, 18.6 mm Hg) (Figure S2). There was no association between the genetic risk score and age, sex, smoking, physical activity, glycated hemoglobin, or alcohol consumption (Table). The genetic risk score was associated with SBP, BMI, LDL cholesterol, and history of diabetes mellitus, but the absolute magnitude of associations other than with SBP was small (mean difference between top versus bottom 50%: 4.1 mm Hg for SBP, -0.1 kg/m² for BMI, -0.04 mmol/L for LDL cholesterol, and 0.4% for prevalence of diabetes mellitus history). Indeed, any pleiotropic influence of BMI or LDL cholesterol would generally result in underestimation of

the effect of SBP as both BMI and LDL cholesterol increase the risk of most CVDs.

Fourteen outcomes satisfied the criteria of consistent evidence for causality: P<0.002 in either the IVW or the MR-PRESSO method and concordance of estimates across methods (Figure 1 and Table S4). In decreasing order of the IVW estimate, these were: aortic valve stenosis, ischemic stroke, dilated cardiomyopathy, coronary artery disease, subarachnoid hemorrhage, ischemic cerebrovascular disease, endocarditis, hemorrhagic stroke (all), chronic kidney disease, heart failure, transient ischemic attack, atrial fibrillation, rheumatic heart disease, and peripheral vascular disease (Figure S3). Two further outcomes (intracerebral hemorrhage and aortic aneurysm) had a positive IVW estimate at a conventional level of statistical significance (P<0.05). Deep vein thrombosis had an inverse IVW estimate at a conventional level of statistical significance (P<0.05).

Figure 2 shows the estimated changes in the absolute prevalence of outcomes with consistent evidence for causality resulting from a population shift in the distribution of SBP. Population impact fractions for these outcomes are provided in Table S5. Aggregating across these outcomes, reductions

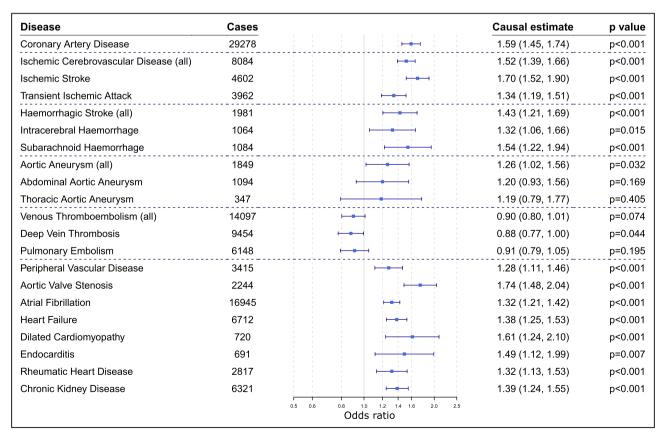


Figure 1. Mendelian randomization estimates (odds ratio with 95% CI per 10-mm Hg increase in genetically predicted systolic blood pressure) from the inverse variance weighted method.

To account for multiple testing, P<0.002 (0.05/21) is considered as the threshold for statistical significance.

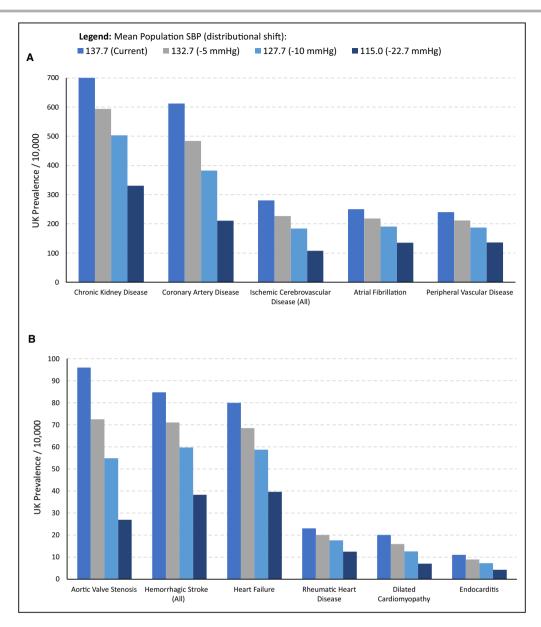


Figure 2. Bar chart showing the prevalence and estimated changes if lifelong systolic blood pressure (SBP) decreased across its distribution by 5, 10, or 22.7 mm Hg (22.7 mm Hg represents a shift from the current mean of 137.7 to 115 mm Hg) separately for each cardiovascular outcome and for high-prevalence outcomes (current UK prevalence >200 per 10 000) (A) and lower-prevalence outcomes (current UK prevalence <200 per 10 000) (B).

Ischemic cerebrovascular disease (all) comprises ischemic stroke and transient ischemic attack. Hemorrhagic stroke (all) comprises subarachnoid hemorrhage and intracerebral hemorrhage.

in SBP were predicted to result in an overall 16.9% (95% CI, 12.2%–21.3%) decrease in CVD morbidity for a 5-mm Hg SBP decrease from a population mean of 137.7 mm Hg, 30.8% (95% CI, 22.8%–38.0%) decrease for a 10-mm Hg SBP decrease, and 56.2% (95% CI, 43.7%–65.9%) decrease for a 22.7-mm Hg SBP decrease. The value of 22.7 mm Hg represents a shift from the current mean SBP in the population to 115 mm Hg, a value that has been proposed as a theoretical minimum risk target.³

DISCUSSION

Although for many CVDs, the causal effect of blood pressure lowering has been demonstrated convincingly in RCTs, several outcomes (dilated cardiomyopathy, endocarditis, peripheral vascular disease, and rheumatic heart disease) had previously only been shown to be associated with SBP in observational studies.^{1,3} Our analysis adds evidential weight to blood pressure as a causal risk factor for these outcomes

Table 1. Characteristics of Participants in the Analytic Subset of the UK Biobank Study

		Genetic r	isk score percentile	
Characteristics	Overall	Lower 50%	Upper 50%	P value
No. of participants	367 703	183 822	183 821	
Age at survey, mean (SD), y	57.2 (8.0)	57.2 (8.0)	57.2 (8.0)	0.26
Women, n (%)	198 902 (54.1)	99 564 (54.2)	99 307 (54.0)	0.39
Body mass index, mean (SD), kg/m ²	27.4 (4.8)	27.4 (4.8)	27.3 (4.7)	<0.001
Low-density lipoprotein, mean (SD), mmol/L	3.57 (0.87)	3.59 (0.87)	3.55 (0.87)	<0.001
HbA1c, mean (SD), mmol/mol	35.9 (6.4)	35.9 (6.4)	35.9 (6.5)	0.10
History of diabetes mellitus at recruitment, n (%)	16 927 (4.6)	8082 (4.4)	8843 (4.8)	<0.001
Physical activity, mean (SD), MET min/wk	2660 (2710)	2650 (2710)	2669 (2709)	0.06
Deaths, n (%)	8033 (2.2)	3925 (2.1)	4105 (2.2)	0.04
Cardiovascular events, n (%)	7145 (1.9)	3291 (1.8)	3853 (2.1)	<0.001
Cardiovascular events (fatal), n (%)	1422 (0.4)	682 (0.4)	740 (0.4)	0.12
Cardiovascular events (nonfatal), n (%)	5723 (1.6)	2609 (1.4)	3113 (1.7)	<0.001
Cerebrovascular events (fatal), n (%)	2714 (0.7)	1217 (0.7)	1497 (0.8)	<0.001
Current smokers, n (%)	37 866 (10.3)	19 099 (10.4)	18 763 (10.2)	0.07
Current alcohol drinkers, n (%)	342 797 (93.4)	171 486 (93.4)	171 260 (93.3)	0.25
Participants taking antihypertensives, n (%)	74 556 (20.4)	29 841 (16.4)	44 702 (24.5)	<0.001
Systolic blood pressure, mean (SD), mm Hg	137.7 (18.6)	135.6 (18.2)	139.7 (18.8)	<0.001
Diastolic blood pressure, mean (SD), mm Hg	82.0 (10.1)	81.1 (10.0)	82.8 (10.2)	<0.001

Genetic risk score was calculated from 256 variants previously associated with a blood pressure trait at $P < 5 \times 10^{-8}$ in data from the International Consortium for Blood Pressure, excluding UK Biobank participants. Physical activity is measured in MET minutes per week, and is taken from Data Field 22 040. HbA1c indicates glycated hemoglobin; and MET, metabolic equivalent task.

and to their inclusion in other SBP population impact studies.

Although most of the outcomes associated with genetically predicted SBP are chronic diseases, some have infectious origins (eg, endocarditis and rheumatic heart disease). Elevated SBP may therefore increase susceptibility to, or damage from, infection. A notable finding was the inverse association between genetically predicted SBP and deep vein thrombosis. Although this association did not achieve statistical significance after accounting for multiple testing, some evidence for an inverse association between SBP and venous thromboembolism has been found in previous observational studies.⁸

The MR estimates obtained herein were generally larger than those from RCTs and conventional observational analyses. For example, the MR estimate for the risk of ischemic stroke per 10–mm Hg increase in SBP was an odds ratio of 1.70 (95% CI, 1.52–1.90). This contrasts with relative risk estimates of 1.37 (95% CI, 1.30–1.47) from a recent meta-analysis of RCTs,² and 1.53 (95% CI, 1.49–1.56) for stroke in 60- to 69-year-old people in the observational analysis of the Prospective Studies Collaboration. Although some difference between estimates is expected as MR estimates represent the lifelong impact of elevated blood pressure, whereas RCTs vary blood pressure for a shorter period, other factors, such as trial setting and inclusion criteria, may also contribute to differences.

This study has many strengths, but also limitations. The large sample size and wide range of outcomes enable systematic cross-comparisons of unconfounded estimates in a single cohort. This is important from a public health perspective when comparing the impact of the same genetic change on different diseases. The genome-wide genotypic data available from the UK Biobank cohort absolved any need to use proxy variants in the instrument. However, the results should be interpreted in the context of several limitations.

First, the UK Biobank cohort is somewhat unrepresentative of the UK population and experiences a "healthy volunteer" selection bias. 10 Analyses were conducted in participants of European descent to avoid population stratification. Estimates may therefore not be fully relevant for the whole UK population. Whether the findings are applicable to other races/ethnicities warrants investigation, particularly because hypertension disproportionately affects Black African and Caribbean ancestry racial/ethnic groups in both the UK and abroad. 11 Given large global disparities in hypertension prevalence, generalizability of the public health modeling beyond the United Kingdom may be limited.

The MR approach is underpinned by assumptions that cannot be completely empirically validated. However, the genetic risk score for SBP was not strongly associated with major confounders, and estimates were generally similar across robust methods.

Although the principles of MR seek to emulate an RCT, the approach differs fundamentally in certain aspects, which are relevant when using MR in public health modeling. First, the results presented herein reflect lifelong differences in SBP relating to genetic variants that are determined at conception. The reversibility of these long-term effects is unknown; however, reversibility is assumed in the population impact fraction calculations. Although SBP-associated risks have demonstrated reversibility in RCTs for most cardiovascular outcomes, it is unknown whether this applies to the full spectrum of outcomes studied herein. There may be no existing intervention applicable to a mature cohort that can imitate the genetic effect, and if such an intervention does exist, the time lag or age at treatment onset required to produce the predicted effects is unknown. For context, antihypertensive drug treatment reduced SBP by 8.3 mm Hg in patients aged 30 to 49 years, 10.7 mm Hg in patients aged 60 to 79 years, and 9.4 mm Hg in patients aged >80 years in a meta-analysis of RCTs of patients with isolated systolic hypertension (SBP >160 mm Hg).¹² Population-wide shifts in the distribution of SBP using nonclinical interventions are generally much smaller in magnitude and occur over much larger time frames: for example, the UK population's average SBP has decreased by ≈3 mm Hg between 2003 and 2017.11

There are several limitations to use of the population impact factors. First, our results are tailored to a middle-aged to early late-aged UK-based population. We focus on this group as the estimates obtained from UK Biobank are most relevant to this population. We did not attempt subgroup or interaction analyses to investigate the impact of blood pressure lowering in different subgroups of the population, or in groups with comorbidities. The population impact fraction measure used herein assumes independence of effects on different outcomes; in reality, the outcomes considered are frequently consequential or coincident in patients. However, although dependence between the outcomes would inflate CIs for the public health modeling estimates, it would not affect the estimates themselves as the expected value of the sum of estimates is equal to the sum of the expectations of the estimates, even if the estimates are correlated. Finally, these analyses assume linearity of effects. Estimates are likely to be reliable for shifts in SBP of similar magnitude to the genetic associations with SBP, which are around 8 to 10 mm Hg.⁴ The appropriateness of extrapolation to larger changes in SBP cannot be assessed in this current study.

The evidence presented herein suggests that incidence of CVDs is influenced by long-term differences in the distribution of SBP, even in a population-based sample. Therefore, confining blood pressure—lowering interventions to older age groups and individuals over

a certain risk threshold will likely only partially address the totality of disease burden. Although these estimates constitute a modeling exercise and not an intervention analysis, they do provide evidence to support a life course approach to lowering population SBP. Several other publications support this stance. A recent MR study found evidence indicating a linear relationship of genetically predicted SBP with coronary artery disease. further supporting the conclusion that even individuals with SBP in the normal range can benefit from public health interventions achieving persistent SBP reduction for the primary prevention of CVD.¹³ In another MR investigation, naturally occurring random allocation to higher SBP instrumented by multiple common genetic variants was associated with a significantly faster increase in SBP with age, and this increased exposure to elevated blood pressure had a cumulative detrimental effect on the risk of coronary heart disease greater than that observed in RCTs.14 Further work has used the observation that some genetic predictors of blood pressure more strongly predict midlife blood pressure, whereas others more strongly predict later-life blood pressure. Genetically predicted midlife blood pressure was shown to be independently associated with coronary artery disease risk when conditioning on laterlife blood pressure, suggesting that these represent distinct risk factors.¹⁵ Interventions that target the determinants of high blood pressure at early stages in the life course, and earlier identification and treatment of those with high blood pressure, are therefore more likely to yield the large effect sizes observed herein than those that only target people already in a later stage of life. This provides an important opportunity to reduce the inequality in health outcomes along the socioeconomic gradient. Interventions that may replicate the lifelong reduction in exposure to elevated SBP evaluated herein include nonpharmacologic interventions, such as increased physical activity, weight control, and sodium reductions, as well as community-wide programs, such as consumer awareness campaigns and industry collaboration for food reformulation.

In conclusion, reducing SBP by 10 mm Hg could reduce the overall burden of a broad range of CVDs by around 30%. These findings contribute to an everexpanding body of evidence advocating targeted and population-based strategies for management of high blood pressure across the life course.

ARTICLE INFORMATION

Received January 29, 2021; accepted July 13, 2021.

Affiliations

Department of Public Health and Primary Care, University of Cambridge, United Kingdom (H.H., A.M.M., S.B.); Department of Surgical Sciences, Uppsala University, Uppsala, Sweden (S.C.L.); Unit of Cardiovascular and Nutritional Epidemiology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden (S.C.L.); Department of Epidemiology and

Biostatistics, School of Public Health, Imperial College London, London, United Kingdom (D.G.); Department of Genetics, Novo Nordisk Research Centre Oxford, Oxford, United Kingdom (D.G.); Clinical Pharmacology and Therapeutics Section, Institute of Medical and Biomedical Education and Institute for Infection and Immunity, St George's, University of London, London, United Kingdom (D.G.); Clinical Pharmacology Group, Pharmacy and Medicines Directorate, St George's University Hospitals National Health Service Foundation Trust, London, United Kingdom (D.G.); Medical Research Council Epidemiology Unit, University of Cambridge, United Kingdom (C.L.); Computational Medicine, Berlin Institute of Health, Charité Universitätsmedizin, Berlin, Germany (C.L.); and Medical Research Council Biostatistics Unit, University of Cambridge, Cambridge, United Kingdom (S.B.).

Acknowledgments

This research was conducted using the UK Biobank study under application number 29202. For the purpose of open access, the authors have applied a CC-BY public copyright license to any author accepted manuscript version arising from this submission.

Sources of Funding

Dr Mason is funded by the National Institute for Health Research (Cambridge Biomedical Research Centre at the Cambridge University Hospitals National Health Service Foundation Trust) and by a European Council Innovative Medicines Initiative (BigData@Heart). Dr Larsson has received grants from the Swedish Research Council for Health, Working Life and Welfare (Forte; grant No. 2018-00123), the Swedish Research Council (Vetenskapsrådet; grant No. 2019-00977), and the Swedish Heart-Lung Foundation (Hjärt-Lungfonden; grant No. 20190247). Dr Burgess is supported by Sir Henry Dale Fellowship jointly funded by the Wellcome Trust and the Royal Society (204623/Z/16/Z). Dr Gill is supported by the Wellcome Trust 4i Programme (203928/Z/16/Z) and British Heart Foundation Centre of Research Excellence (RE/18/4/34215) at Imperial College London, and a National Institute for Health Research Clinical Lectureship at St. George's, University of London (CL-2020-16-001). Dr Langenberg is funded by the Medical Research Council. This research was supported by the National Institute for Health Research Cambridge Biomedical Research Centre (BRC-1215-20014).

Disclosures

Dr Gill is employed part-time by Novo Nordisk outside the submitted work. Hannah Higgins is employed full-time by Public Health England outside the submitted work. The remaining authors have no disclosures to report.

Supplementary Material

Tables S1-S5 Figures S1-S3

REFERENCES

- Forouzanfar MH, Liu P, Roth GA, Ng M, Biryukov S, Marczak L, Alexander L, Estep K, Hassen Abate K, Akinyemiju TF, et al. Global burden of hypertension and systolic blood pressure of at least 110 to 115 mm Hg, 1990–2015. *JAMA*. 2017;317:165–182. doi: 10.1001/jama.2016.19043
- Ettehad D, Emdin CA, Kiran A, Anderson SG, Callender T, Emberson J, Chalmers J, Rodgers A, Rahimi K. Blood pressure lowering for prevention of cardiovascular disease and death: a systematic review and meta-analysis. *Lancet*. 2016;387:957–967. doi: 10.1016/S0140-6736(15)01225-8

- GBD Risk Factor Collaborators. Global, regional, and national comparative risk assessment of 84 behavioural, environmental and occupational, and metabolic risks or clusters of risks for 195 countries and territories, 1990–2017: a systematic analysis for the Global Burden of Disease Study 2017. Lancet. 2018;392:1923–1994. doi: 10.1016/S0140-6736(18)32225-6
- Burgess S, Davey Smith G, Davies N, Dudbridge F, Gill D, Glymour M, Hartwig F, Holmes M, Minelli C, Relton C, et al. Guidelines for performing Mendelian randomization investigations [version 2; peer review: 2 approved]. Wellcome Open Res. 2020;4:186. doi: 10.12688/wellcomeopenres.15555.2
- Ference BA, Bhatt DL, Catapano AL, Packard CJ, Graham I, Kaptoge S, Ference TB, Guo QI, Laufs U, Ruff CT, et al. Association of genetic variants related to combined exposure to lower low-density lipoproteins and lower systolic blood pressure with lifetime risk of cardiovascular disease. JAMA. 2019;322:1381–1391. doi: 10.1001/jama.2019.14120
- Evangelou E, Warren HR, Mosen-Ansorena D, Mifsud B, Pazoki R, Gao HE, Ntritsos G, Dimou N, Cabrera CP, Karaman I, et al. Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nat Genet*. 2018;50:1412–1425. doi: 10.1038/s4158 8-018-0205-x
- Astle WJ, Elding H, Jiang T, Allen D, Ruklisa D, Mann AL, Mead D, Bouman H, Riveros-Mckay F, Kostadima MA, et al. The allelic landscape of human blood cell trait variation and links to common complex disease. Cell. 2016;167:1415–1429. doi: 10.1016/j.cell.2016.10.042
- Gregson J, Kaptoge S, Bolton T, Pennells L, Willeit P, Burgess S, Bell S, Sweeting M, Rimm EB, Kabrhel C, et al. Cardiovascular risk factors associated with venous thromboembolism. *JAMA Cardiol*. 2019;4:163– 173. doi: 10.1001/jamacardio.2018.4537
- Lewington S, Clarke R, Qizilbash N, Peto R, Collins R, Prospective Studies Collaboration. 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. doi: 10.1016/s0140-6736(02)11911-8
- Fry A, Littlejohns TJ, Sudlow C, Doherty N, Adamska L, Sprosen T, Collins R, Allen NE. Comparison of sociodemographic and healthrelated characteristics of UK Biobank participants with those of the general population. *Am J Epidemiol*. 2017;186:1026–1034. doi: 10.1093/ aje/kwx246
- Public Health England Health matters: combating high blood pressure. 2017. https://www.gov.uk/government/publications/health-matters-combating-high-blood-pressure/health-matters-combating-high-blood-pressure. Accessed July 14, 2021.
- Wang J-G, Staessen JA, Franklin SS, Fagard R, Gueyffier F. Systolic and diastolic blood pressure lowering as determinants of cardiovascular outcome. *Hypertension*. 2005;45:907–913. doi: 10.1161/01.HYP.00001 65020.14745.79
- Malik R, Georgakis MK, Vujkovic M, Damrauer SM, Elliott P, Karhunen V, Giontella A, Fava C, Hellwege JN, Shuey MM, et al. Relationship between blood pressure and incident cardiovascular disease: linear and nonlinear mendelian randomization analyses. *Hypertension*. 2021;77:2004–2013. doi: 10.1161/HYPERTENSIONAHA.120.16534
- Ference BA, Julius S, Mahajan N, Levy PD, Williams KA Sr, Flack JM. Clinical effect of naturally random allocation to lower systolic blood pressure beginning before the development of hypertension. *Hypertension*. 2014;63:1182–1188. doi: 10.1161/HYPERTENSIONAHA.113.02734
- Gill D, Georgakis MK, Zuber V, Karhunen V, Burgess S, Malik R, Dichgans M. Genetically predicted midlife blood pressure and coronary artery disease risk: Mendelian randomization analysis. *J Am Heart Assoc*. 2020;9:e016773. doi: 10.1161/JAHA.120.016773

Supplemental Material

Table S1. Summary of disease outcomes considered, definitions, and sources of information within UK Biobank

Outcome name	ICD-9 Diagnosis or death	ICD-10 Diagnosis or death	OPCS procedure code	Self-report ^a
Coronary Artery Disease	410.X, 411.X, 412.X, 414.0, 414.8, 414.9	I21.X, I22.X, I23.X, I24.X, I25.1, I25.2, I25.5, I25.6, I25.8, I25.9	K40.X, K41.X, K42.X, K43.X, K44.X, K45.X, K46.X, K49.X, K50.1, K50.2, K50.4, K75.X	Non-cancer illness code (20002), Surgical operation code (20004), Health condition diagnosed by doctor (6150)
Ischemic Cerebrovascular Disease (all)	434.X, 435.X, 436.X	G45.X, I63.X, I64.X		Non-cancer illness code (20002)
Ischemic Stroke	433.X, 434.X	163.X, 164.X		Non-cancer illness code (20002)
Transient Ischemic Attack	435.X	G45.X		Non-cancer illness code (20002)
Hemorrhagic Stroke (all)	430.X, 431.X	I60.X, I61.X		Non-cancer illness code (20002)
Intracerebral Hemorrhage	431.X	I61.X		Non-cancer illness code (20002)
Subarachnoid Hemorrhage	430.X	160.X		Non-cancer illness code (20002)
Aortic Aneurysm (all)	441.X	171.X	L19.4, L19.5	Non-cancer illness code (20002), Surgical operation code (20004)
Abdominal Aortic Aneurysm	441.3, 441.4	171.3, 171.4	L19.4, L19.5	Non-cancer illness code (20002)
Thoracic Aortic Aneurysm	441.1, 441.2	l71.1, l71.2		Non-cancer illness code (20002)
Venous Thromboembolism (all)	415.1, 451.1, 452.X, 453.0, 453.4, 453.9,	I26.X, I80.1, I80.2, I81.X, I82.0	L90.2	Non-cancer illness code (20002), Health condition diagnosed by doctor (6152)
Deep Vein Thrombosis	451.1	180.2	L90.2	Non-cancer illness code (20002), Health condition diagnosed by doctor (6152)
Pulmonary Embolism	415.1	I26.X		Non-cancer illness code (20002), Health condition diagnosed by doctor (6152)

Outcome name	ICD-9 Diagnosis or death	ICD-10 Diagnosis or death	OPCS procedure code	Self-report [*]
Peripheral Vascular Disease	443.8, 443.9	173.8, 173.9		Non-cancer illness code (20002)
Aortic Valve Stenosis	424.1	135.0, 135.2		Non-cancer illness code (20002)
Atrial Fibrillation	427.3	148		Non-cancer illness code (20002)
Heart Failure	402.01, 402.11, 402.91, 404.01, 404.11, 404.91, 404.03, 404.13, 404.93, 428.X	I11.0, I13.0, I13.2, I50.X		Non-cancer illness code (20002)
Dilated Cardiomyopathy		142.0		
Endocarditis	391.1, 421.0, 421.9, 421.1	I33.X, I38, I39.8, I01.1		
Rheumatic Heart Disease	391.X, 397.9, 398.0, 394.1, 398.90, 397.1	I01.X, I02.0, I05.X, I06.X, I07.X, I08.X, I09.X		
Chronic Kidney Disease Note that X means that all suit	585.X	N18.X		Non-cancer illness code (20002)

Note that .X means that all sub-codes are matched.

Abbreviations: ICD, International Classification of Disease; OPCS, Office of Population Censuses and Surveys Classification of Surgical Operations and Procedures.

Health condition diagnosed by doctor (6150/6152) and Medication for health condition (6177) were self-reported from touchscreen; Non-cancer illness code (20002) and Surgical operation code (20004) were self-reported from interview with trained nurse.

Table S2. Details of the 256 single nucleotide polymorphisms (SNPs) from the International Consortium for Blood Pressure (ICBP) genome-wide association study (GWAS) included in the genetic instrument. β_{xj} corresponds to the variant-SBP association estimates (beta-coefficients in mmHg units). These variants are taken from Supplementary Table 24 of Evangelou et al, Nat Genet 2018, and represent variants that were published prior to the inclusion of UK Biobank in the ICBP.

SNP	Chromosome number	Chromosome position	Effect allele	Other allele	Effect allele frequency	R-squared	F-statistic	β_{xj}	eta_{xj} Standard error	eta_{xj} P-value
rs10057188	5	77837789	Α	G	0.4516	5.0E-05	5.5E-02	-1.9E-01	4.8E-02	4.4E-05
rs10059921	5	87514515	Т	G	0.0846	5.8E-05	6.3E-02	-3.7E-01	9.2E-02	4.9E-05
rs10077885	5	114390121	Α	С	0.498	8.2E-05	8.9E-02	-2.5E-01	4.8E-02	3.5E-07
rs10078021	5	75038431	G	Т	0.3744	4.8E-06	5.3E-03	6.2E-02	4.9E-02	2.1E-01
rs10224002	7	151415041	G	Α	0.2814	6.1E-05	6.7E-02	2.4E-01	5.3E-02	6.0E-06
rs1036477	15	48914926	G	Α	0.1044	5.8E-05	6.3E-02	-3.4E-01	7.4E-02	4.1E-06
rs10418305	19	15278808	G	С	0.897	3.0E-06	3.3E-03	7.8E-02	7.5E-02	3.0E-01
rs1055144	7	25871109	Т	С	0.1925	9.7E-06	1.1E-02	1.1E-01	5.8E-02	6.3E-02
rs1060105	12	123806219	T	С	0.2021	8.8E-06	9.6E-03	-1.0E-01	5.7E-02	7.9E-02
rs1063281	2	218668732	T	С	0.6045	7.3E-05	8.0E-02	-2.4E-01	4.8E-02	7.1E-07
rs10818775	9	125755571	Т	С	0.1236	4.3E-05	4.7E-02	-2.7E-01	7.0E-02	8.7E-05
rs10826995	10	32082658	C	T	0.1230	8.7E-06	9.5E-03	9.0E-02	5.1E-02	8.1E-02
rs10850411	12		С	T	0.3006	1.0E-04		-3.0E-02	4.9E-02	8.1E-10
rs10922502	1	115387796	G	A	0.3593	6.4E-05	1.1E-01 7.0E-02			2.3E-06
rs10943605		89360158		G			4.5E-02	2.3E-01	4.8E-02	
	6	79655477	A		0.4886	4.1E-05		1.7E-01	4.6E-02	1.6E-04
rs11008355	10	31412561	C	G	0.2369	7.1E-06	7.7E-03	-8.6E-02	5.4E-02	1.1E-01
rs11030119	11	27728102	A	G	0.2944	3.2E-05	3.5E-02	-1.7E-01	5.1E-02	8.5E-04
rs110419	11	8252853	G	Α	0.5071	8.8E-06	9.6E-03	-8.1E-02	4.7E-02	8.5E-02
rs11067763	12	116198341	G	Α	0.1031	1.8E-05	2.0E-02	-1.9E-01	7.5E-02	1.1E-02
rs111245230	9	113169775	С	Т	0.0338	8.4E-05	9.2E-02	6.9E-01	1.3E-01	1.0E-07
rs11128722	3	14958126	Α	G	0.5628	8.4E-05	9.1E-02	-2.5E-01	4.7E-02	8.5E-08
rs11154027	6	121781390	С	Т	0.5513	1.1E-07	1.2E-04	9.0E-03	4.8E-02	8.5E-01
rs11191548	10	104846178	С	Т	0.0871	4.5E-04	4.9E-01	-1.0E+00	8.2E-02	6.2E-36
rs112184198	10	102604514	Α	G	0.1058	1.4E-04	1.6E-01	-5.3E-01	7.6E-02	2.4E-12
rs11229457	11	58207203	Т	С	0.2144	7.5E-05	8.2E-02	-2.9E-01	5.6E-02	3.0E-07
rs112557609	1	56576924	Α	G	0.3414	6.9E-05	7.5E-02	2.4E-01	4.9E-02	1.1E-06
rs1126464	16	89704365	С	G	0.245	3.4E-05	3.7E-02	1.8E-01	5.7E-02	1.1E-03
rs1126930	12	49399132	С	G	0.0343	5.9E-05	6.4E-02	5.8E-01	1.4E-01	3.9E-05
rs11537751	11	47587452	Т	С	0.0521	4.1E-05	4.5E-02	3.9E-01	1.1E-01	2.6E-04
rs11556924	7	129663496	Т	С	0.3713	7.8E-05	8.5E-02	-2.5E-01	5.0E-02	5.9E-07
rs11639856	16	24788645	Α	Т	0.1902	4.3E-05	4.7E-02	-2.3E-01	5.8E-02	6.8E-05
rs11689667	2	85491365	С	Т	0.4536	1.9E-05	2.1E-02	-1.2E-01	4.7E-02	1.1E-02
rs11690961	2	46363336	С	Α	0.116	2.9E-07	3.1E-04	-2.3E-02	7.2E-02	7.5E-01
rs11701033	21	33788341	G	С	0.1831	4.9E-05	5.3E-02	2.5E-01	5.9E-02	3.2E-05
rs1173771	5	32815028	G	Α	0.6024	3.5E-04	3.8E-01	5.2E-01	4.7E-02	6.0E-29
rs11953630	5	157845402	Т	С	0.3694	2.5E-04	2.7E-01	-4.5E-01	5.0E-02	5.2E-19
rs11977526	7	46008110	Α	G	0.3993	8.3E-05	9.0E-02	-2.5E-01	4.8E-02	1.6E-07
rs12374077	3	185317674	С	G	0.3452	3.5E-05	3.8E-02	1.7E-01	4.8E-02	4.6E-04
rs12405515	1	172357441	Т	G	0.5741	3.9E-05	4.2E-02	-1.7E-01	4.6E-02	2.0E-04
rs12408022	1	217718789	Т	С	0.2611	6.5E-05	7.1E-02	2.5E-01	5.3E-02	2.4E-06
rs12521868	5	131784393	Т	G	0.4156	2.0E-05	2.2E-02	-1.2E-01	4.8E-02	9.7E-03
rs12579720	12	20173764	G	С	0.7621	8.9E-05	9.7E-02	3.0E-01	5.4E-02	2.5E-08
rs12627651	21	44760603	A	G	0.2944	1.9E-04	2.1E-01	4.2E-01	5.3E-02	3.3E-15
rs12628032	22	19967980	T	С	0.3152	4.5E-05	4.9E-02	2.0E-01	5.0E-02	7.7E-05
rs1275988	2	26914364	T	С	0.6055	3.4E-04	3.7E-01	-5.2E-01	4.7E-02	1.8E-28
rs12906962	15 16	95312071	С	T T	0.3293	8.4E-05	9.2E-02	2.7E-01	4.9E-02	6.4E-08
rs12921187	16	4943019	G	T	0.5726	7.7E-05	8.4E-02	2.4E-01	4.6E-02	1.3E-07
rs12940887	17	47402807	T	C	0.3727	8.9E-05	9.7E-02	2.7E-01	4.7E-02	1.4E-08
rs12941318	17	1333598	C	T	0.5018	5.8E-05	6.3E-02	2.1E-01	4.8E-02	1.7E-05
rs12946454	17	43208121	Т	A	0.261	1.1E-04	1.2E-01	3.2E-01	5.2E-02	7.3E-10
rs12958173	18	42141977	С	Α	0.7	1.4E-04	1.5E-01	-3.5E-01	5.0E-02	1.2E-12
rs13082711	3	27537909	С	Т	0.231	7.5E-05	8.2E-02	2.8E-01	5.5E-02	2.8E-07
rs13107325	4	103188709	Т	С	0.0722	2.8E-04	3.0E-01	-8.8E-01	9.5E-02	1.8E-20
rs13112725	4	106911742	С	G	0.7682	1.5E-04	1.6E-01	4.0E-01	5.6E-02	1.0E-12

SNP	Chromosome number	Chromosome position	Effect allele	Other allele	Effect allele frequency	R-squared	F-statistic	$oldsymbol{eta}_{xj}$	eta_{xj} Standard error	$oldsymbol{eta}_{xj}$ P-value
rs13139571	4	156645513	Α	С	0.2393	8.6E-05	9.3E-02	-3.0E-01	5.4E-02	3.7E-08
rs13205180	6	51832494	Т	С	0.4808	2.3E-06	2.5E-03	4.1E-02	4.6E-02	3.8E-01
rs13209747	6	127115454	Т	С	0.4465	2.2E-04	2.5E-01	4.1E-01	4.7E-02	9.8E-19
rs1322639	6	169587103	Α	G	0.7711	7.5E-06	8.2E-03	8.9E-02	5.6E-02	1.1E-01
rs13238550	7	131059056	Α	G	0.3909	3.7E-05	4.0E-02	1.7E-01	4.7E-02	3.3E-04
rs1327235	20	10969030	G	Α	0.4631	1.7E-04	1.8E-01	3.5E-01	4.5E-02	3.2E-15
rs13303	3	52558008	С	Т	0.5697	1.6E-05	1.7E-02	1.1E-01	4.7E-02	2.1E-02
rs13333226	16	20365654	G	Α	0.186	9.2E-05	1.0E-01	-3.4E-01	5.8E-02	7.0E-09
rs13359291	5	122476457	Α	G	0.1654	1.2E-04	1.3E-01	4.0E-01	6.2E-02	1.1E-10
rs13420463	2	37517566	G	Α	0.2225	7.0E-05	7.7E-02	-2.8E-01	5.6E-02	7.2E-07
rs1344653	2	19730845	G	Α	0.5039	3.3E-05	3.6E-02	1.6E-01	4.6E-02	5.8E-04
rs1378942	15	75077367	Α	С	0.6563	2.9E-04	3.1E-01	-4.9E-01	4.8E-02	5.0E-24
rs143112823	3	154707967	Α	G	0.076	6.1E-05	6.6E-02	-4.0E-01	9.5E-02	2.3E-05
rs1438896	2	145646072	С	Т	0.7001	5.8E-05	6.4E-02	-2.3E-01	5.0E-02	5.4E-06
rs1446468	2	164963486	С	Т	0.5488	3.2E-04	3.4E-01	4.9E-01	4.7E-02	2.3E-25
rs1449544	8	76591880	С	Α	0.4584	6.5E-05	7.1E-02	-2.2E-01	4.6E-02	1.4E-06
rs1458038	4	81164723	Т	С	0.2971	4.9E-04	5.4E-01	6.6E-01	5.1E-02	6.1E-39
rs1475130	14	100225144	С	Т	0.6571	3.2E-05	3.5E-02	1.6E-01	4.9E-02	7.4E-04
rs147696085	1	51021867	Α	G	0.1011	2.7E-06	2.9E-03	-7.4E-02	8.0E-02	3.5E-01
rs1530440	10	63524591	Т	С	0.1874	2.0E-04	2.2E-01	-5.0E-01	5.9E-02	2.0E-17
rs1563788	6	43308363	Т	С	0.2937	1.0E-04	1.1E-01	3.1E-01	5.0E-02	9.8E-10
rs167479	19	11526765	Т	G	0.4732	2.5E-04	2.7E-01	-4.3E-01	5.6E-02	2.5E-14
rs16823124	2	183224127	Α	G	0.303	6.1E-05	6.7E-02	2.3E-01	5.0E-02	3.1E-06
rs16851397	3	141134818	G	Α	0.0467	8.3E-05	9.1E-02	5.9E-01	1.1E-01	1.9E-07
rs17030613	1	113190807	С	Α	0.2191	1.4E-04	1.5E-01	3.9E-01	5.6E-02	2.5E-12
rs17080102	6	151004770	С	G	0.0677	1.7E-04	1.9E-01	-7.2E-01	9.2E-02	4.9E-15
rs17249754	12	90060586	A	G	0.1637	4.7E-04	5.2E-01	-8.0E-01	6.2E-02	2.2E-38
rs17367504	1	11862778	G	A	0.1556	4.3E-04	4.7E-01	-7.8E-01	6.4E-02	4.8E-34
rs17477177	7	106411858	С	T	0.2094	2.8E-04	3.1E-01	5.6E-01	5.6E-02	1.6E-23
rs17608766	17	45013271	С	T	0.1433	2.5E-04	2.7E-01	6.2E-01	6.7E-02	3.9E-20
rs17638167	19	11584818	T	C	0.047	6.6E-05	7.2E-02	-5.2E-01	1.1E-01	1.8E-06
rs1799945	6	26091179	G	С	0.1479	2.0E-04	2.2E-01	5.4E-01	6.6E-02	1.3E-16
rs1813353	10	18707448	С	Т	0.3411	2.3E-04	2.5E-01	-4.3E-01	4.8E-02	3.0E-19
rs1876487	2	73114352	С	A	0.7122	7.5E-06	8.2E-03	8.3E-02	5.5E-02	1.3E-01
rs1925153	6	56102780	Т	C	0.7122	3.5E-06	3.8E-03	-5.1E-02	4.9E-02	3.0E-01
rs1953126	9	123640500	C	Т	0.6453	4.2E-05	4.5E-02	-1.8E-01	4.9E-02 4.8E-02	1.2E-04
rs1975487	2	55809054	G	A	0.5124	6.5E-05	7.1E-02	2.2E-01	4.7E-02	2.9E-06
rs2004776	1	230848702	T	C	0.2381	1.1E-04	1.2E-01	3.4E-01	5.4E-02	5.3E-10
rs2014912	4	86715670	C	T	0.8485	1.8E-04	2.0E-01	-5.1E-01	6.4E-02	1.8E-15
rs2034618	15	83799632	T 	С	0.2231	2.1E-07	2.3E-04	-1.5E-02	5.5E-02	7.8E-01
rs2071518	8	120435812	T 	С	0.2571	4.9E-05	5.3E-02	2.2E-01	5.2E-02	3.1E-05
rs2076328	1	1687482	T	G	0.4748	1.1E-04	1.2E-01	-2.8E-01	5.0E-02	1.4E-08
rs2107595	7	19049388	Α -	G	0.166	6.8E-05	7.4E-02	3.0E-01	6.2E-02	1.2E-06
rs2157597	1	169201567	T _	С	0.3468	8.9E-06	9.7E-03	-8.6E-02	4.9E-02	8.1E-02
rs2240736	17	59485393	Т	С	0.7328	1.9E-04	2.1E-01	4.3E-01	5.3E-02	4.5E-16
rs2246438	10	45273079	Α	G	0.2779	5.1E-07	5.5E-04	-2.2E-02	5.1E-02	6.7E-01
rs2282978	7	92264410	С	Т	0.342	6.0E-06	6.5E-03	-7.0E-02	4.9E-02	1.5E-01
rs2289125	11	89224453	С	Α	0.7697	3.6E-05	3.9E-02	1.9E-01	5.8E-02	8.5E-04
rs2291435	4	38387395	Т	С	0.5248	7.8E-05	8.6E-02	-2.4E-01	4.6E-02	1.7E-07
rs2304130	19	19789528	G	Α	0.0833	3.9E-05	4.2E-02	3.1E-01	8.6E-02	3.6E-04
rs2306374	3	138119952	С	Т	0.1619	3.7E-05	4.1E-02	2.3E-01	6.3E-02	3.0E-04
rs2404715	1	57008778	Т	С	0.0925	1.8E-05	2.0E-02	-2.0E-01	8.0E-02	1.2E-02
rs2467099	17	73949045	Т	С	0.2204	3.4E-05	3.7E-02	-1.9E-01	5.5E-02	4.8E-04
rs2493292	1	3328659	Т	С	0.1501	4.9E-05	5.4E-02	2.7E-01	6.8E-02	7.8E-05
rs2521501	15	91437388	Т	Α	0.3301	3.7E-04	4.0E-01	5.6E-01	5.2E-02	4.8E-27
rs2579519	2	96675166	С	Т	0.3949	3.7E-08	4.1E-05	5.4E-03	4.8E-02	9.1E-01
rs2645466	17	57853214	С	Α	0.3018	4.4E-05	4.8E-02	2.0E-01	4.9E-02	7.1E-05
rs2759308	15	81016227	Α	G	0.4758	9.0E-05	9.8E-02	2.6E-01	4.6E-02	1.8E-08
rs2761436	1	207919748	Т	С	0.5276	5.0E-05	5.4E-02	1.9E-01	4.6E-02	2.9E-05

SNP	Chromosome number	Chromosome position	Effect allele	Other allele	Effect allele frequency	R-squared	F-statistic	β_{xj}	eta_{xj} Standard error	$oldsymbol{eta}_{xj}$ P-value
rs28427409	17	6473882	Т	С	0.4133	3.5E-05	3.8E-02	1.6E-01	4.6E-02	4.0E-04
rs2898290	8	11433909	С	Т	0.5165	1.6E-04	1.7E-01	-3.4E-01	4.7E-02	2.1E-13
rs2932538	1	113216543	G	Α	0.7414	1.2E-04	1.3E-01	3.4E-01	5.3E-02	7.2E-11
rs2969070	7	2512545	Α	G	0.6369	9.4E-05	1.0E-01	-2.8E-01	4.8E-02	8.4E-09
rs2972146	2	227100698	Т	G	0.6362	7.7E-05	8.4E-02	2.5E-01	4.8E-02	1.8E-07
rs2978098	8	101676675	С	Α	0.442	2.9E-05	3.2E-02	-1.5E-01	4.7E-02	1.7E-03
rs2978456	8	42324765	С	Т	0.4442	1.5E-05	1.7E-02	1.1E-01	5.0E-02	3.2E-02
rs3184504	12	111884608	С	Т	0.5244	4.5E-04	4.9E-01	-5.8E-01	4.7E-02	2.6E-35
rs33063	16	69640217	G	Α	0.856	2.1E-05	2.3E-02	-1.8E-01	6.5E-02	6.0E-03
rs34591516	8	142367087	Т	С	0.0533	8.5E-05	9.3E-02	5.6E-01	1.1E-01	1.5E-07
rs347591	3	11290122	Т	G	0.6625	9.7E-05	1.1E-01	2.8E-01	4.9E-02	6.3E-09
rs34872471	10	114754071	С	Т	0.2936	3.6E-05	3.9E-02	1.8E-01	5.1E-02	4.2E-04
rs35261357	16	75444572	Т	С	0.5698	1.0E-04	1.1E-01	2.8E-01	4.7E-02	2.7E-09
rs35410524	6	96885405	Т	С	0.1917	7.5E-05	8.2E-02	3.0E-01	5.9E-02	3.4E-07
rs35444	12	115552437	G	Α	0.3921	1.4E-04	1.5E-01	-3.3E-01	4.7E-02	1.8E-12
rs35783704	8	105966258	Α	G	0.1092	1.4E-04	1.6E-01	-5.2E-01	7.7E-02	1.5E-11
rs36010659	18	48283949	С	Т	0.1391	2.4E-05	2.7E-02	-2.0E-01	6.6E-02	3.0E-03
rs36022378	3	49913705	С	Т	0.1926	2.0E-05	2.2E-02	1.6E-01	6.0E-02	9.3E-03
rs3741378	11	65408937	Т	С	0.1328	1.1E-04	1.2E-01	-4.2E-01	7.0E-02	2.2E-09
rs3771371	2	71627539	Т	С	0.5658	4.3E-05	4.7E-02	-1.8E-01	4.6E-02	9.2E-05
rs381815	11	16902268	T	С	0.2705	1.4E-04	1.5E-01	3.6E-01	5.2E-02	1.5E-12
rs3820068	1	15798197	G	A	0.2023	9.8E-05	1.1E-01	-3.4E-01	6.0E-02	1.7E-08
rs3918226	7	150690176	T	C	0.0811	1.2E-04	1.3E-01	5.5E-01	9.1E-02	1.8E-09
rs409558	6	31708147	C	T	0.0011	1.5E-04	1.7E-01	-4.5E-01	6.4E-02	2.6E-12
rs419076	3	169100886	С	T	0.1712					5.4E-18
	1		A	C		2.1E-04	2.3E-01	-3.9E-01	4.6E-02	1.2E-03
rs4245739		204518842		С	0.7326	3.0E-05	3.3E-02	1.7E-01	5.3E-02	
rs4247374	19	7252756	T	T	0.1355	1.6E-04	1.8E-01	-5.1E-01	7.5E-02	1.8E-11
rs4292285	4	145271954	A		0.3994	2.1E-05	2.3E-02	-1.3E-01	4.7E-02	5.8E-03
rs4308	17	61559625	G	A	0.6178	9.4E-05	1.0E-01	-2.7E-01	4.8E-02	1.1E-08
rs4364717	9	21801530	G	A	0.4534	1.5E-05	1.6E-02	1.1E-01	4.6E-02	1.9E-02
rs4373814	10	18419972	С	G	0.441	8.4E-05	9.2E-02	2.5E-01	4.7E-02	6.2E-08
rs4387287	10	105677897	C	A	0.8262	2.9E-05	3.2E-02	-2.0E-01	6.2E-02	1.8E-03
rs4454254	8	141060027	Α	G	0.6346	6.1E-05	6.7E-02	-2.2E-01	4.8E-02	3.2E-06
rs4494250	10	96563757	Α	G	0.3611	8.1E-05	8.9E-02	2.6E-01	4.9E-02	1.3E-07
rs449789	6	159699125	G	С	0.8652	1.8E-05	1.9E-02	-1.7E-01	6.8E-02	1.3E-02
rs452036	14	23865885	Α	G	0.3492	2.5E-05	2.8E-02	-1.4E-01	4.8E-02	2.7E-03
rs470113	22	40729614	G	Α	0.188	5.0E-06	5.5E-03	7.8E-02	5.8E-02	1.8E-01
rs4728142	7	128573967	Α	G	0.4383	6.1E-05	6.7E-02	-2.2E-01	4.7E-02	3.9E-06
rs4757391	11	16302939	Т	С	0.8013	2.1E-04	2.3E-01	-4.9E-01	5.7E-02	8.3E-18
rs4823006	22	29451671	G	Α	0.4384	2.6E-05	2.9E-02	-1.4E-01	4.6E-02	2.0E-03
rs4952611	2	40567743	Т	С	0.5834	5.9E-05	6.5E-02	-2.1E-01	4.9E-02	1.2E-05
rs5219	11	17409572	С	Т	0.6245	1.3E-04	1.4E-01	-3.2E-01	4.7E-02	1.1E-11
rs55701159	2	25139596	G	Т	0.113	4.8E-05	5.3E-02	-3.0E-01	7.4E-02	5.3E-05
rs55780018	2	208526140	С	Т	0.452	1.4E-04	1.6E-01	3.3E-01	4.9E-02	1.9E-11
rs57927100	17	75317300	G	С	0.259	1.2E-04	1.4E-01	-3.5E-01	5.4E-02	8.4E-11
rs6015450	20	57751117	G	Α	0.1287	2.6E-04	2.8E-01	6.6E-01	6.9E-02	2.4E-21
rs60199046	1	59663341	G	Α	0.2868	3.5E-05	3.8E-02	-1.8E-01	5.1E-02	4.3E-04
rs6031435	20	42797358	G	Α	0.4612	6.9E-05	7.5E-02	2.3E-01	4.6E-02	6.7E-07
rs6060114	20	30169673	С	Т	0.162	5.8E-05	6.3E-02	-2.8E-01	6.2E-02	5.9E-06
rs6081613	20	19465907	Α	G	0.2722	2.0E-05	2.1E-02	1.4E-01	5.1E-02	7.3E-03
rs6095241	20	47308798	Α	G	0.4363	4.7E-05	5.1E-02	-1.9E-01	4.5E-02	3.3E-05
rs6108168	20	8626271	Α	С	0.2541	4.2E-05	4.6E-02	-2.0E-01	5.2E-02	8.8E-05
rs62011052	15	79156983	С	Т	0.1497	1.9E-07	2.0E-04	1.7E-02	6.4E-02	8.0E-01
rs62104477	19	30294991	Т	G	0.3313	9.0E-06	9.8E-03	8.7E-02	4.9E-02	7.4E-02
rs62270945	3	128201889	T	С	0.0302	3.9E-06	4.3E-03	1.6E-01	1.6E-01	3.2E-01
rs62524579	8	144060955	A	G	0.5307	4.4E-05	4.8E-02	-1.8E-01	5.3E-02	6.9E-04
rs6271	9	136522274	T	С	0.5307	6.8E-05	7.4E-02	-1.6E-01 -4.3E-01	1.0E-01	2.1E-05
rs633185			C	G						
	11	100593538			0.7096	2.7E-04	3.0E-01	5.0E-01	5.1E-02	9.8E-23
rs6429422	1	243472801	G ^	T	0.3289	2.4E-05	2.7E-02	1.4E-01	4.9E-02	3.6E-03
rs6487543	12	26438189	Α	G	0.7655	3.0E-05	3.2E-02	1.8E-01	5.6E-02	1.9E-03

SNP	Chromosome number	Chromosome position	Effect allele	Other allele	Effect allele frequency	R-squared	F-statistic	$oldsymbol{eta}_{xj}$	eta_{xj} Standard error	β _{xj} P-value
rs6557876	8	25900675	Т	С	0.2511	1.4E-04	1.5E-01	-3.7E-01	5.3E-02	6.0E-12
rs6595838	5	127868199	Α	G	0.2891	6.2E-05	6.7E-02	2.4E-01	5.1E-02	3.1E-06
rs661348	11	1905292	С	Т	0.4368	1.5E-04	1.7E-01	3.4E-01	5.0E-02	9.6E-12
rs6686889	1	25030470	Т	С	0.2581	7.5E-06	8.2E-03	8.5E-02	5.3E-02	1.1E-01
rs66887589	4	120509279	С	Т	0.4814	4.4E-05	4.8E-02	1.8E-01	4.6E-02	9.0E-05
rs67330701	11	69079707	Т	С	0.0958	3.6E-05	3.9E-02	-2.8E-01	9.1E-02	2.4E-03
rs6783086	3	133959552	Т	С	0.409	8.6E-05	9.4E-02	2.6E-01	4.7E-02	3.9E-08
rs6797587	3	48197614	G	Α	0.6797	9.2E-05	1.0E-01	2.8E-01	5.0E-02	1.5E-08
rs6825911	4	111381638	Т	С	0.787	5.1E-05	5.5E-02	-2.4E-01	5.8E-02	3.7E-05
rs687621	9	136137065	G	Α	0.3392	1.2E-05	1.3E-02	-9.8E-02	4.8E-02	4.3E-02
rs6891344	5	123136656	G	Α	0.1856	6.5E-05	7.1E-02	-2.8E-01	6.0E-02	2.2E-06
rs6911827	6	22130601	Т	С	0.4623	3.1E-05	3.4E-02	1.5E-01	4.7E-02	1.3E-03
rs6969780	7	27159136	С	G	0.0961	6.4E-05	7.0E-02	3.7E-01	7.9E-02	3.1E-06
rs709209	1	6278414	G	Α	0.3421	1.1E-05	1.2E-02	-9.4E-02	5.3E-02	7.6E-02
rs7103648	11	47461783	G	Α	0.3844	1.2E-04	1.3E-01	3.1E-01	4.7E-02	6.2E-11
rs7126805	11	828916	Α	G	0.7292	1.5E-05	1.7E-02	1.2E-01	5.6E-02	3.1E-02
rs7129220	11	10350538	Α	G	0.1233	8.9E-05	9.7E-02	3.9E-01	7.2E-02	6.3E-08
rs7178615	15	66869072	G	Α	0.6085	2.6E-05	2.8E-02	1.4E-01	4.7E-02	2.8E-03
rs7236548	18	43097750	Α	С	0.1857	5.7E-05	6.2E-02	2.6E-01	5.8E-02	5.5E-06
rs7248104	19	7224431	Α	G	0.4085	3.3E-05	3.6E-02	-1.6E-01	4.6E-02	6.0E-04
rs7255	2	20878820	С	Т	0.5345	6.7E-06	7.3E-03	7.1E-02	4.7E-02	1.3E-01
rs72765298	9	127900996	С	Т	0.1179	6.8E-05	7.4E-02	3.5E-01	7.3E-02	1.7E-06
rs72799341	16	30936743	Α	G	0.2392	8.8E-06	9.6E-03	9.5E-02	5.4E-02	7.9E-02
rs72812846	5	173377636	Α	Т	0.278	6.1E-05	6.7E-02	-2.4E-01	5.3E-02	8.2E-06
rs7297416	12	54443090	С	A	0.3133	9.2E-05	1.0E-01	-2.8E-01	5.0E-02	1.8E-08
rs7302981	12	50537815	G	Α	0.6131	1.8E-04	2.0E-01	-3.7E-01	4.6E-02	4.4E-16
rs73030266	6	166179459	Т	Α	0.0674	3.3E-05	3.6E-02	-3.1E-01	9.8E-02	1.4E-03
rs73091767	1	227250775	c	T	0.2654	8.6E-06	9.4E-03	9.1E-02	5.2E-02	7.9E-02
rs73099903	12	53440779	T	C	0.0794	7.0E-05	7.6E-02	4.2E-01	8.8E-02	1.6E-06
rs73161324	22	42038786	T.	С	0.0591	1.3E-05	1.5E-02	2.1E-01	1.2E-01	6.7E-02
rs740406	19	2232221	G	A	0.0631	9.6E-05	1.0E-01	5.5E-01	1.0E-01	6.9E-08
rs7406910	17	46688256	С	T	0.9107	1.0E-04	1.1E-01	4.9E-01	8.1E-02	1.9E-09
rs740698	17		T	C	0.5726	2.8E-05	3.0E-02	-1.5E-01	4.8E-02	2.2E-03
		60767151		Т						
rs745821	18	48142854	G	G G	0.2509	3.2E-05	3.5E-02	-1.8E-01	5.3E-02	7.5E-04
rs7480089	11	45207851	A		0.1222	3.1E-05	3.4E-02	-2.3E-01	7.2E-02	1.1E-03
rs7500448	16	83045790	G	A	0.2531	5.1E-05	5.6E-02	-2.3E-01	5.3E-02	2.4E-05
rs7515635	1	42408070	С	T 	0.5316	7.6E-05	8.3E-02	-2.4E-01	4.6E-02	2.7E-07
rs751984	11	61278246	С	T 	0.1211	1.1E-04	1.2E-01	-4.3E-01	7.4E-02	4.1E-09
rs7562	2	28635740	С	T _	0.4703	3.2E-05	3.5E-02	-1.6E-01	4.7E-02	9.3E-04
rs7592578	2	191439591	G	Т	0.7926	1.0E-04	1.1E-01	3.4E-01	6.0E-02	1.5E-08
rs76206723	7	40447971	A	G	0.1097	5.9E-05	6.4E-02	-3.4E-01	7.4E-02	6.4E-06
rs76326501	2	43167878	С	A	0.0891	1.3E-04	1.4E-01	-5.5E-01	8.3E-02	3.1E-11
rs76452347	9	35906471	Т	С	0.2058	2.6E-05	2.8E-02	-1.7E-01	6.2E-02	5.8E-03
rs76785029	12	94882905	Т	С	0.0717	2.2E-06	2.5E-03	-7.9E-02	9.7E-02	4.2E-01
rs7777128	7	27337113	С	G	0.0816	1.2E-04	1.3E-01	5.5E-01	8.4E-02	4.7E-11
rs7810028	7	139461616	G	С	0.1945	4.1E-05	4.5E-02	-2.2E-01	5.8E-02	1.5E-04
rs78378222	17	7571752	G	Т	0.0164	2.9E-06	3.2E-03	-1.8E-01	2.1E-01	3.8E-01
rs78648104	6	50683009	С	Т	0.1015	6.2E-05	6.8E-02	3.6E-01	8.3E-02	1.7E-05
rs79089478	17	40317241	С	Т	0.0278	2.8E-06	3.1E-03	-1.4E-01	1.5E-01	3.4E-01
rs7914287	10	69350563	С	Т	0.2303	2.1E-05	2.3E-02	1.5E-01	5.6E-02	7.8E-03
rs79146658	2	179786068	С	Т	0.0821	8.2E-09	8.9E-06	4.5E-03	8.6E-02	9.6E-01
rs7927515	11	76125330	Α	С	0.3455	3.5E-05	3.9E-02	1.7E-01	4.9E-02	4.8E-04
rs7977389	12	49981722	С	Т	0.1065	1.4E-05	1.5E-02	-1.6E-01	7.5E-02	2.8E-02
rs8059962	16	81574197	С	Т	0.5764	3.7E-05	4.1E-02	1.7E-01	4.7E-02	3.0E-04
rs8105753	19	31927547	С	Α	0.3745	4.5E-05	4.9E-02	-1.9E-01	4.9E-02	9.9E-05
rs8258	11	117283676	С	Т	0.6324	3.9E-06	4.3E-03	-5.6E-02	4.8E-02	2.4E-01
rs869396	4	169688000	Α	С	0.4668	4.3E-05	4.7E-02	-1.8E-01	4.7E-02	1.1E-04
rs871606	4	54799245	С	Т	0.1058	6.6E-05	7.2E-02	-3.6E-01	7.6E-02	2.2E-06
	1	10796866	С	Т	0.348	3.3E-04	3.6E-01	5.2E-01	5.0E-02	1.3E-25
rs880315		1010000	0					0.22	0.00	1.00 20

SNP	Chromosome number	Chromosome position	Effect allele	Other allele	Effect allele frequency	R-squared	F-statistic	$oldsymbol{eta}_{xj}$	eta_{xj} Standard error	eta_{xj} P-value
rs891511	7	150704843	Α	G	0.3518	7.8E-05	8.5E-02	-2.5E-01	5.2E-02	1.2E-06
rs894344	8	135612745	G	Α	0.4105	2.8E-05	3.0E-02	1.5E-01	4.7E-02	1.8E-03
rs900145	11	13293905	Т	С	0.7041	1.4E-05	1.6E-02	1.1E-01	5.0E-02	2.3E-02
rs917275	7	28658522	G	Α	0.3892	1.6E-05	1.8E-02	1.1E-01	4.8E-02	1.8E-02
rs918466	3	64710253	Α	G	0.4105	2.5E-05	2.7E-02	-1.4E-01	4.8E-02	3.6E-03
rs9306160	21	45107562	С	Т	0.6026	5.5E-05	6.0E-02	2.1E-01	4.7E-02	1.3E-05
rs9323988	14	98587630	С	Т	0.3896	7.2E-05	7.9E-02	2.4E-01	4.6E-02	3.1E-07
rs932764	10	95895940	G	Α	0.4439	1.8E-04	1.9E-01	3.7E-01	4.7E-02	4.8E-15
rs9337951	10	30317073	Α	G	0.337	1.0E-05	1.1E-02	9.3E-02	5.3E-02	7.8E-02
rs9349379	6	12903957	G	Α	0.4088	8.9E-05	9.8E-02	-2.6E-01	4.9E-02	6.4E-08
rs9372498	6	118572486	Α	Т	0.0848	5.4E-05	5.9E-02	3.6E-01	8.3E-02	1.4E-05
rs9479200	6	152398505	G	Α	0.1231	5.6E-06	6.1E-03	9.9E-02	7.1E-02	1.7E-01
rs9549328	13	113636156	Т	С	0.2345	4.6E-05	5.0E-02	2.2E-01	5.5E-02	8.6E-05
rs956006	15	62808539	Т	С	0.336	5.8E-06	6.4E-03	-7.0E-02	4.9E-02	1.6E-01
rs9662255	1	9441949	Α	С	0.4307	4.7E-05	5.1E-02	-1.9E-01	4.8E-02	9.4E-05
rs9678851	2	27887034	Α	С	0.559	1.7E-05	1.9E-02	-1.1E-01	4.7E-02	1.7E-02
rs9687065	5	148391140	G	Α	0.1957	5.3E-05	5.8E-02	-2.5E-01	5.9E-02	2.3E-05
rs9729719	1	38298207	Α	G	0.2946	1.1E-05	1.3E-02	1.0E-01	5.3E-02	5.6E-02
rs9810888	3	53635595	G	Т	0.5024	3.0E-05	3.3E-02	1.5E-01	4.6E-02	1.2E-03
rs9815354	3	41912651	Α	G	0.1711	3.0E-06	3.3E-03	-6.3E-02	6.3E-02	3.2E-01
rs9827472	3	56726646	Т	С	0.3577	3.3E-05	3.6E-02	-1.6E-01	4.9E-02	7.2E-04
rs9888615	14	53377540	С	Т	0.7064	6.2E-05	6.7E-02	2.4E-01	5.0E-02	2.3E-06

Table S3. UK prevalence estimates used to calculate population impact of distributional shifts in blood pressure.

Outcome	UK prevalence (per 10,000)	Age group (years)	Year	Source of prevalence estimate
Coronary Artery Disease	612	45-64	2017	Health Survey for England ¹
Ischemic Cerebrovascular Disease (AII)	280	45-64	2017	Health Survey for England ¹
Hemorrhagic Stroke (All)	84.7	50-69	2010	Global Burden of Disease ²
Peripheral Vascular Disease	240	50-89	2014	The Health Improvement Network ³
Aortic Valve Stenosis	96.0	45-64	2017	Health Survey for England ¹
Atrial Fibrillation	250	45-69	2017	Public Health England ⁴
Heart failure	80.0	45-74	2017	Quality and Outcomes Framework ⁵
Dilated Cardiomyopathy	20.0	45-75	2014	British Heart Foundation ⁶
Endocarditis	11	All ages ^a	2013	Hospital Episode Statistics ⁷
Rheumatic Heart Disease	23.0	All ages ^a	2013	Hospital Episode Statistics ⁸
Chronic Kidney Disease	700	45-64	2017	Health Survey for England ¹

^a When no age group-specific estimates could be obtained, the total population prevalence was used.

- NHS Digital. Health Survey for England 2017. https://digital.nhs.uk/data-and-information/publications/statistical/health-survey-for-england/2017.
- Global Burden of Disease Collaborative Network. Global Burden of Disease Study 2017 (GBD 2017) Results. http://ghdx.healthdata.org/gbd-results-tool. Published 2018.
- 3. Cea-Soriano L, Fowkes FGR, Johansson S, Allum AM, García Rodriguez LA. Time trends in peripheral artery disease incidence, prevalence and secondary preventive therapy: a cohort study in The Health Improvement Network in the UK. *BMJ Open.* 2018;8(1):e018184. doi:10.1136/bmjopen-2017-018184
- 4. Public Health England. Atrial fibrillation prevalence estimates in England: Application of recent population estimates of AF. *PHE Publ Gateway number 2014778*. 2015;August:1-4.
- NHS Digital. Quality and Outcomes Framework, Achievement, prevalence and exceptions data 2017-18. https://digital.nhs.uk/data-and-information/publications/statistical/quality-and-outcomes-framework-achievement-prevalence-and-exceptions-data/2017-18.
- 6. Cardiomyopathy British Heart Foundation. https://www.bhf.org.uk/informationsupport/conditions/cardiomyopathy.
- Dayer MJ, Jones S, Prendergast B, Baddour LM, Lockhart PB, Thornhill MH. Incidence of infective endocarditis in England, 2000-13: a secular trend, interrupted time-series analysis. *Lancet*. 2015;385(9974):1219-1228. doi:10.1016/S0140-6736(14)62007-9
- 8. Bhatnagar P, Wickramasinghe K, Williams J, Rayner M, Townsend N. The epidemiology of cardiovascular disease in the UK 2014. *Heart*. 2015;101(15):1182-1189. doi:10.1136/heartjnl-2015-307516.

Jownloaded from http://ahajournals.org by on September 17, 2

Table S4. Mendelian randomization estimates (odds ratio with 95% confidence interval per 10 mmHg increase in genetically-predicted systolic blood pressure) using the inverse-variance weighted, MR-Egger, weighted median, and MR-PRESSO methods for 21 disease outcomes.

Outcome	Inverse-weiç variance		MR-Egg	er	Weighted me	edian	MR-PRES	so
Outcome	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value
Coronary Artery Disease	1.59 (1.45-1.74)	<0.001	1.44 (1.20-1.73)	<0.001	1.61 (1.48-1.75)	<0.001	1.59 (1.45-1.75)	<0.001
Ischemic Cerebrovascular Disease (all)	1.52 (1.39-1.66)	<0.001	1.66 (1.40-1.98)	<0.001	1.50 (1.33-1.70)	<0.001	1.52 (1.39-1.66)	<0.001
Ischemic Stroke	1.70 (1.52-1.90)	<0.001	1.86 (1.48-2.32)	<0.001	1.78 (1.51-2.09)	<0.001	1.71 (1.52-1.91)	<0.001
Transient Ischemic Attack	1.34 (1.19-1.51)	<0.001	1.40 (1.10-1.79)	0.006	1.38 (1.15-1.64)	<0.001	1.35 (1.19-1.52)	<0.001
Hemorrhagic Stroke (all)	1.43 (1.21-1.69)	<0.001	1.39 (0.99-1.95)	0.05	1.33 (1.04-1.71)	0.02	1.42 (1.20-1.68)	<0.001
Intracerebral Hemorrhage	1.32 (1.06-1.66)	0.02	1.22 (0.78-1.91)	0.39	1.24 (0.88-1.74)	0.21	1.31 (1.04-1.64)	0.02
Subarachnoid Hemorrhage	1.54 (1.22-1.94)	<0.001	1.72 (1.09-2.72)	0.02	1.65 (1.17-2.32)	0.004	1.53 (1.22-1.94)	<0.001
Aortic Aneurysm (all)	1.26 (1.02-1.56)	0.03	1.51 (0.99-2.31)	0.06	1.39 (1.06-1.82)	0.02	1.28 (1.03-1.58)	0.02
Abdominal Aortic Aneurysm	1.20 (0.93-1.56)	0.17	1.07 (0.64-1.79)	0.80	1.34 (0.95-1.88)	0.10	1.22 (0.94-1.58)	0.15
Thoracic Aortic Aneurysm	1.19 (0.79-1.77)	0.41	1.99 (0.90-4.41)	0.09	1.34 (0.75-2.40)	0.33	1.23 (0.82-1.84)	0.31
Venous Thromboembolism (all)	0.90 (0.80-1.01)	0.07	1.00 (0.79-1.25)	0.98	0.87 (0.78-0.96)	0.005	0.90 (0.80-1.01)	0.07
Deep Vein Thrombosis	0.88 (0.77-1.00)	0.04	0.95 (0.74-1.22)	0.67	0.90 (0.80-1.02)	0.09	0.87 (0.77-0.99)	0.04
Pulmonary Embolism	0.91 (0.79-1.05)	0.20	1.05 (0.79-1.38)	0.75	0.96 (0.83-1.11)	0.57	0.92 (0.80-1.05)	0.22
Peripheral Vascular Disease	1.28 (1.11-1.46)	<0.001	1.01 (0.77-1.32)	0.96	1.18 (0.98-1.43)	0.09	1.28 (1.11-1.47)	<0.001
Aortic Valve Stenosis	1.74 (1.48-2.04)	<0.001	1.90 (1.38-2.62)	<0.001	1.81 (1.43-2.29)	<0.001	1.75 (1.49-2.05)	<0.001
Atrial Fibrillation	1.32 (1.21-1.42)	<0.001	1.35 (1.15-1.58)	< 0.001	1.29 (1.17-1.42)	<0.001	1.32 (1.21-1.43)	<0.001
Heart Failure	1.38 (1.25-1.53)	<0.001	1.36 (1.12-1.67)	0.002	1.47 (1.28-1.69)	<0.001	1.37 (1.24-1.51)	<0.001
Dilated Cardiomyopathy	1.61 (1.24-2.10)	<0.001	2.57 (1.52-4.35)	<0.001	1.60 (1.07-2.40)	0.02	1.58 (1.23-2.03)	<0.001
Endocarditis	1.49 (1.12-1.99)	0.007	1.41 (0.79-2.52)	0.24	1.47 (0.97-2.24)	0.07	1.52 (1.14-2.03)	<0.001
Rheumatic Heart Disease	1.32 (1.13-1.53)	<0.001	1.55 (1.15-2.09)	0.004	1.43 (1.16-1.77)	0.001	1.31 (1.13-1.52)	<0.001
Chronic Kidney Disease	1.39 (1.24-1.55)	<0.001	1.17 (0.95-1.46)	0.14	1.38 (1.19-1.59)	<0.001	1.39 (1.24-1.55)	<0.001

Table S5. Population impact fractions (PIFs) for outcomes with strong evidence of causality for systolic blood pressure. The PIF represents the percentage reduction (with 95% confidence interval) in events if systolic blood pressure was 132.7 mmHg, 127.7 mmHg, and 115.0 mmHg for all individuals in the UK Biobank study sample, instead of the current mean systolic blood pressure of 137.7 mmHg.

	_	luction in number of e	
Outcomes	132.7 mmHg (-5 mmHg)	127.7 mmHg (-10 mmHg)	115.0 mmHg (-22.7 mmHg)
Coronary Artery Disease	20.9 (17.3-24.4)	37.5 (31.6-42.9)	65.6 (57.8-72.0)
Ischemic Cerebrovascular Disease (all) ^a	18.9 (15.2-22.5)	34.3 (28.1-40.0)	61.5 (52.7-68.6)
Hemorrhagic Stroke (all) ^a	16.1 (8.6-22.9)	29.5 (16.5-40.5)	54.8 (33.5-69.3)
Peripheral Vascular Disease	11.8 (5.4-17.7)	22.1 (10.4-32.3)	43.3 (22.1-58.7)
Aortic Valve Stenosis	24.4 (18.1-30.2)	42.9 (33.0-51.3)	72.0 (59.7-80.5)
Atrial Fibrillation	12.6 (9.1-16.5)	23.7 (17.3-30.2)	45.8 (35.0-55.8)
Heart Failure	14.4 (10.0-18.5)	26.7 (18.9-33.6)	50.5 (37.9-60.6)
Dilated Cardiomyopathy	20.5 (9.1-30.2)	36.9 (17.3-51.3)	64.8 (35.0-80.5)
Endocarditis	18.9 (6.3-29.9)	34.2 (12.2-50.8)	61.4 (25.6-80.0)
Rheumatic Heart Disease	12.6 (5.8-18.9)	23.7 (11.3-34.3)	45.8 (23.9-61.5)
Chronic Kidney Disease	15.2 (10.4-19.8)	28.1 (19.8-35.7)	52.7 (39.3-63.2)
Total	16.9 (12.2-21.3)	30.8 (22.8-38.0)	56.2 (43.7-65.9)

^a To minimize double counting, we present single estimates for both ischemic cerebrovascular disease and hemorrhagic stroke

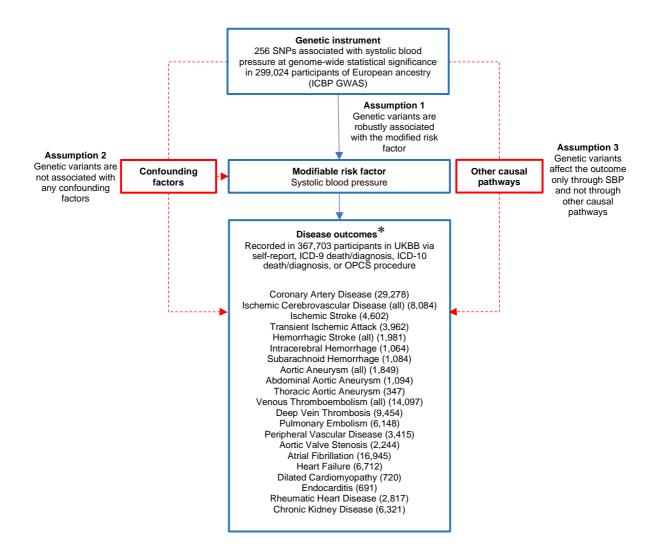


Figure S1. Summary of the data sources for this study and the assumptions of the Mendelian randomization design. Broken lines represent potential pleiotropic or direct causal effects between variables that would violate the Mendelian randomization assumptions.

*The number of cases for each outcome is reported in parentheses.

GWAS, Genome-wide association study; ICBP, International Blood Pressure Consortium; ICD, International Classification of Disease; OPCS, Office of Population Censuses and Surveys Classification of Surgical Operations and Procedures; SBP, systolic blood pressure; SNP, single nucleotide polymorphism; UKBB, UK Biobank.

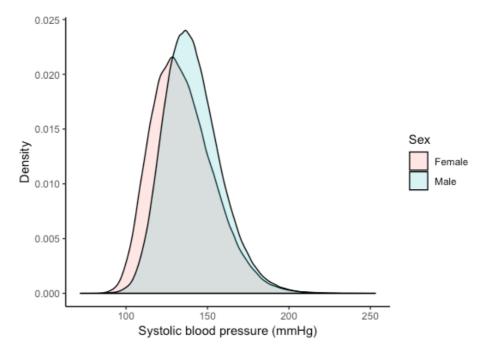


Figure S2. Distribution of systolic blood pressure in UK Biobank. Overall mean systolic blood pressure is 137.7 mmHg (standard deviation 18.6 mmHg); female mean systolic blood pressure is 135.0 mmHg (standard deviation 19.2); male mean systolic blood pressure is 140.8 (standard deviation is 17.4 mmHg).

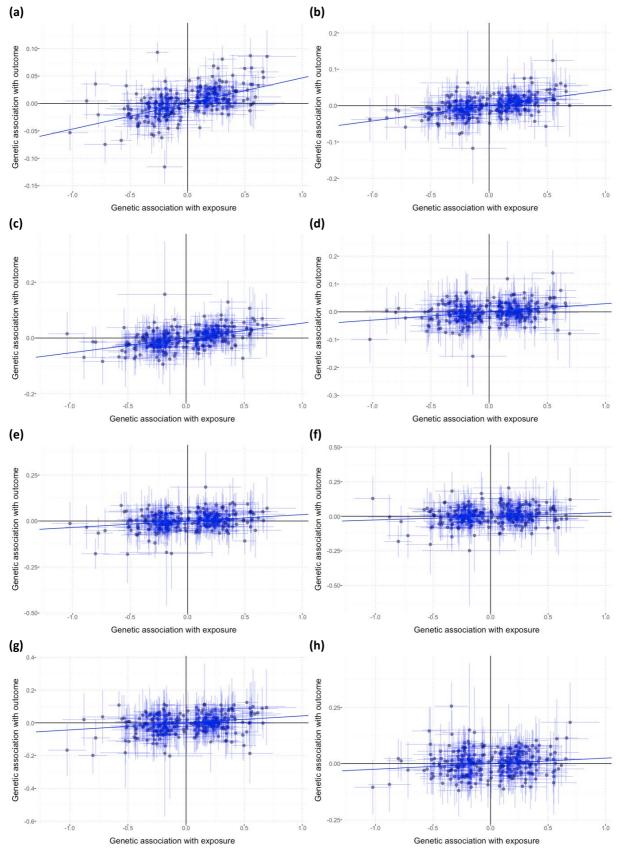


Figure S3 (a)-(m). Scatter plots of the beta-coefficients for the exposure plotted against the beta-coefficients for the outcome for each of the 256 SNPs in the instrument. Each dot corresponds to a SNP. Lines represent the 95% CI for each SNP's beta-coefficient. Each scatter plot corresponds to one outcome: (a) Coronary artery disease; (b) Ischemic cerebrovascular disease (all); (c) Ischemic stroke; (d) Transient ischemic attack; (e) Hemorrhagic stroke (all); (f) Intracerebral hemorrhage; (g) Subarachnoid hemorrhage; (h) Aortic aneurysm (all); (i) Abdominal aortic aneurysm; (j) Thoracic aortic aneurysm; (k) Venous thromboembolism (all); (l) Deep vein thrombosis; (m) Pulmonary embolism; (n) Peripheral vascular disease; (o) Aortic valve stenosis; (p) Atrial fibrillation; (q) Heart failure; (r) Dilated cardiomyopathy; (s) Endocarditis; (t) Rheumatic heart disease; (u) Chronic kidney disease.

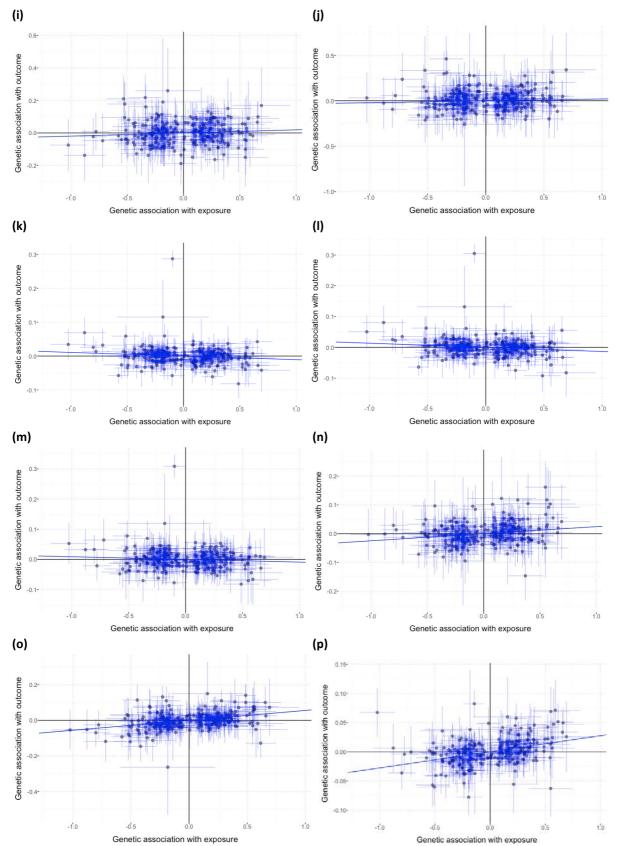


Figure S3 (contd.) (a)-(m). Scatter plots of the beta-coefficients for the exposure plotted against the beta-coefficients for the outcome for each of the 256 SNPs in the instrument. Each dot corresponds to a SNP. Lines represent the 95% CI for each SNP's beta-coefficient. Each scatter plot corresponds to one outcome: (a) Coronary artery disease; (b) Ischemic cerebrovascular disease (all); (c) Ischemic stroke; (d) Transient ischemic attack; (e) Hemorrhagic stroke (all); (f) Intracerebral hemorrhage; (g) Subarachnoid hemorrhage; (h) Aortic aneurysm (all); (i) Abdominal aortic aneurysm; (j) Thoracic aortic aneurysm; (k) Venous thromboembolism (all); (l) Deep vein thrombosis; (m) Pulmonary embolism; (n) Peripheral vascular disease; (o) Aortic valve stenosis; (p) Atrial fibrillation; (q) Heart failure; (r) Dilated cardiomyopathy; (s) Endocarditis; (t) Rheumatic heart disease; (u) Chronic kidney disease.

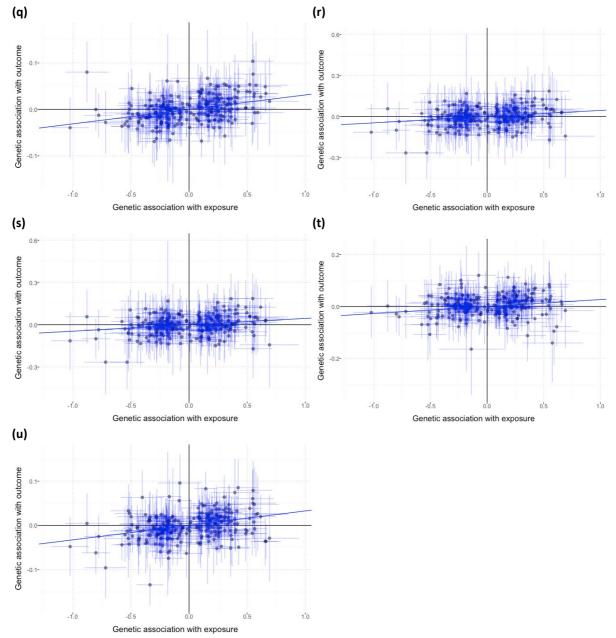


Figure S3 (contd.) (a)-(m). Scatter plots of the beta-coefficients for the exposure plotted against the beta-coefficients for the outcome for each of the 256 SNPs in the instrument. Each dot corresponds to a SNP. Lines represent the 95% CI for each SNP's beta-coefficient. Each scatter plot corresponds to one outcome: (a) Coronary artery disease; (b) Ischemic cerebrovascular disease (all); (c) Ischemic stroke; (d) Transient ischemic attack; (e) Hemorrhagic stroke (all); (f) Intracerebral hemorrhage; (g) Subarachnoid hemorrhage; (h) Aortic aneurysm (all); (i) Abdominal aortic aneurysm; (j) Thoracic aortic aneurysm; (k) Venous thromboembolism (all); (l) Deep vein thrombosis; (m) Pulmonary embolism; (n) Peripheral vascular disease; (o) Aortic valve stenosis; (p) Atrial fibrillation; (q) Heart failure; (r) Dilated cardiomyopathy; (s) Endocarditis; (t) Rheumatic heart disease; (u) Chronic kidney disease.