

1 Trans-ancestry meta-analyses identify novel rare and common variants associated with blood

2 pressure and hypertension

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298 **Abstract**

299 High blood pressure is a major risk factor for cardiovascular disease and premature death. However, there is
300 limited knowledge on specific causal genes and pathways. To better understand the genetics of blood
301 pressure, we genotyped 242,296 rare, low-frequency and common genetic variants in up to ~192,000
302 individuals, and used ~155,063 samples for independent replication. We identified 31 novel blood pressure
303 or hypertension associated genetic regions in the general population, including three rare missense variants
304 in *RBM47*, *COL21A1* and *RRAS* with larger effects (>1.5mmHg/allele) than common variants. Multiple rare,
305 nonsense and missense variant associations were found in *A2ML1* and a low-frequency nonsense variant in
306 *ENPEP* was identified. Our data extend the spectrum of allelic variation underlying blood pressure traits and
307 hypertension, provide new insights into the pathophysiology of hypertension and indicate new targets for
308 clinical intervention.

309

310 **Introduction**

311 High blood pressure (BP) or hypertension is a highly prevalent chronic disorder. It is estimated to be
312 responsible for a larger proportion of global disease burden and premature mortality than any other disease
313 risk factor¹. Elevated systolic and/or diastolic BP increases the risk of several cardiovascular disorders
314 including stroke, coronary heart disease (CHD), heart failure, peripheral arterial disease and abdominal
315 aortic aneurysms². BP is a complex, heritable, polygenic phenotype for which genome-wide association
316 studies (GWAS) have identified over 67 genetic regions associated with BP and/or hypertension to date³⁻¹¹.
317 These variants are common (minor allele frequency, $MAF \geq 0.05$), mostly map to intronic or intergenic
318 regions, with the causal alleles and genes not readily identified due to linkage disequilibrium (LD)^{4,5}, and
319 explain only ~2% of trait variance¹². Low-frequency ($0.01 < MAF < 0.05$) and rare ($MAF \leq 0.01$) single
320 nucleotide variants (SNVs), predominantly unexplored by GWAS may have larger phenotypic effects than
321 common SNVs¹³, and may help to explain the missing heritability, and identify causative genes as
322 demonstrated previously¹⁴.

323 To identify novel coding variants and loci influencing BP traits and hypertension we performed the largest
324 meta-analysis to date that included a total of ~350,000 individuals, directly genotyped with the Exome chip.
325 The Exome chip contains ~240,000 mostly rare and low-frequency variants (Methods). A single-variant
326 discovery analysis was performed, and candidate SNVs were taken forward for validation using independent
327 replication samples. Gene-based tests were used to identify BP associated genes harboring multiple rare
328 variant associations. We next assessed whether the newly identified BP associated SNVs were associated
329 with expression levels of nearby genes, and tested these variants in aggregate for a causal association of BP
330 with other cardiovascular traits and risk factors. Our findings highlight the contribution of rare variants in
331 the aetiology of blood pressure in the general population, and provide new insights into the pathophysiology
332 of hypertension.

333

334 **Results**

335 **Discovery of single variant BP associations**

336 We genotyped 192,763 individuals from 51 studies, and assessed association of 242,296 SNVs with
337 diastolic BP (DBP), systolic BP (SBP), pulse pressure (PP) and hypertension (HTN; Supplementary Tables
338 1, 2 and 3; Methods). An overview of the SNV discovery study design is given in Figure 1. A fixed effects
339 meta-analysis for each trait was performed using study-level association summary statistics from i) samples
340 of European (EUR) ancestry (up to 165,276 individuals), and ii) a trans-ethnic meta-analysis of the EUR and
341 additional South Asian (SAS) ancestry samples (EUR_SAS; up to 192,763 individuals). Two analyses of
342 DBP, SBP and PP were performed, one in which the trait was inverse normal transformed and a second in
343 which the raw phenotype was analysed. Both sets of results were consistent (Methods), therefore to
344 minimise sensitivity to deviations from normality in the analysis of rare variants, the results from the
345 analyses of the transformed traits were used for discovery. Strong correlations between the BP traits were
346 observed across studies (Methods), hence no adjustment of significance thresholds for independent trait
347 testing was applied.

348 The discovery meta-analyses identified 50 genomic regions with genome-wide significant (GWS) evidence
349 of association with at least one of the four BP traits tested ($P < 5 \times 10^{-8}$; Supplementary Table 4). There were
350 45 regions associated in the EUR_SAS samples, of which 13 were novel (Figure 2). An additional five
351 regions were GWS in the EUR only meta-analyses of which two were novel (Supplementary Figure 1). In
352 total, 16 genomic regions were identified that were GWS for at least one BP trait that have not been
353 previously reported.

354 **Replication of single variant BP associations**

355 Next we sought support for our findings, in an independent replication dataset comprising of 18 studies, 16
356 of which were from the Cohorts for Heart and Aging Research in Genomic Epidemiology+ (CHARGE+)
357 exome chip blood pressure consortium (Figure 1; Liu *et al.* Nature Genetics, *submitted*). Variants were
358 selected for replication first using the larger (transformed) EUR_SAS data, with additional variants from the
359 (transformed) EUR data also selected. SNVs were selected if they mapped outside of known BP genomic
360 regions and had $MAF \geq 0.05$ and $P < 1 \times 10^{-5}$ or $MAF < 0.05$ and $P < 1 \times 10^{-4}$ with at least one BP trait, *i.e.*
361 choosing a lower significance threshold for the selection of rare variants (full details of the selection criteria
362 are provided in the Methods). In total 81 candidate SNVs were selected for replication (Supplementary

363 Table 5). Eighty variants were selected from EUR_SAS (transformed) results and one SNV at the *ZNF101*
364 locus from the EUR (transformed) analyses. The results for EUR_SAS and EUR were consistent
365 (association statistics were correlated, $\rho=0.9$ across ancestries for each of the traits). Of the 81 variants, 30
366 SNVs were selected for association with DBP as the primary trait, 26 for SBP, 19 for PP and 6 for HTN,
367 with the primary trait defined as the BP trait with the smallest association *P*-value in the EUR-SAS
368 discovery analyses.

369 Meta-analyses were performed on results from analyses of untransformed DBP, SBP, PP and HTN (as only
370 results of untransformed traits were available from CHARGE+) in (i) up to 125,713 individuals of EUR
371 descent, and (ii) up to 155,063 individuals of multiple ethnicities (4,632 of Hispanic descent, 22,077 of
372 African American descent, 2,641 SAS samples with the remainder EUR; Figure 1). Given that a large
373 proportion of the ancestries in the trans-ethnic meta-analyses were not included in our discovery samples,
374 we used the EUR meta-analyses as the main data set for replication, but we also report any additional
375 associations identified within the larger trans-ethnic dataset.

376 Novel BP-SNV associations were identified based on two criteria (Figure 1; Methods). Firstly, replication of
377 the primary BP trait-SNV association was sought at a Bonferroni adjusted *P*-value threshold in the
378 replication data ($P \leq 6.17 \times 10^{-4}$, assuming $\alpha=0.05$ for 81 SNVs tested and same direction of effect; Methods)
379 without the need for GWS. Secondly, meta-analyses of discovery and replication results across all four
380 (untransformed) BP traits were performed to assess the overall level of support across all samples for the 81
381 candidate SNVs; those BP-SNV associations that were GWS (with statistical support in the replication
382 studies; $P < 0.05$ and the same direction of effect) were also declared as novel.

383

384 Seventeen SNV-BP associations formally replicated with concordant direction of effect at a Bonferroni
385 adjusted significance level for the primary trait. Fourteen were in the EUR meta-analyses, and amongst these
386 was a rare non-synonymous (ns) SNV mapping to *COL21A1* (Table 1, Supplementary Table 6). Three
387 associations were in the trans-ethnic meta-analyses, these included two rare nsSNVs in *RBM47* and *RRAS*
388 (Table 1, Supplementary Table 7; Methods).

389

390 In addition to the 17 SNV-BP trait associations that formally replicated, we identified 13 further SNV-
391 associations that were GWS in the combined (discovery and replication) meta-analyses. Ten of these were
392 GWS in the combined EUR analyses, (Table 2; Supplementary Tables 6 and 8a), and three were GWS in the
393 combined trans-ethnic meta-analyses (Table 2; Supplementary Tables 7 and 8b).

394

395 This gives a total of 30 novel SNV-BP associations (15 SNV-DBP, 9 SNV-SBP and 6 SNV-PP; Tables 1
396 and 2; Supplementary Figures 2 and 3). Five of the SNVs were GWS with more than one BP trait (Figure 3:
397 Tables 1 and 2; Supplementary Table 8). Four loci (*CERS5*, *TBX2*, *RGL3* and *OBFC1*) had GWS
398 associations with HTN in addition to GWS associations with DBP and SBP. The *PRKAG1* locus had GWS
399 associations with both SBP and PP.

400

401 Conditional analyses were performed to identify secondary signals of association within the novel BP loci.
402 The RAREMETALWORKER (RMW) package (Methods)¹⁵ allows conditional analyses to be performed
403 using summary level data. Hence, analyses of the transformed primary traits and HTN were re-run in RMW
404 across the discovery studies (Figure 4). The results of the RMW single variant tests were consistent with the
405 initial discovery analyses (Supplementary Information). Given the RMW analyses were based on our
406 discovery samples, the larger EUR-SAS data was used as the main analysis to increase power, but we also
407 report any additional associations with evidence in EUR.

408

409 We identified secondary independent signals of association in four loci, *PREX1*, *PRKAG1* and *RRP1B*
410 within the EUR_SAS analyses and *COL21A1* in the EUR analyses ($P_{\text{conditional}} < 1 \times 10^{-4}$, Bonferroni adjusted
411 for ~500 variants within each region; Methods; Supplementary Tables 9 and 10). Three independent
412 association signals were identified in the *MYH6* locus in the EUR_SAS analyses (Supplementary Table 11).

413

414 **Gene-based BP associations**

415 To improve statistical power to detect associations in genes harbouring rare variants, analytical methods that
416 combine effects of variants across a gene into a single test have been devised and are implemented in the

417 RMW package¹⁵. We applied the gene-based sequence kernel association test (SKAT)¹⁶ and Burden tests¹⁷
418 to the RMW dataset (MAF<0.05 or MAF<0.01; Figure 4; Methods). One previously unidentified BP gene
419 (*A2ML1*) was associated with HTN ($P=7.73 \times 10^{-7}$) in the EUR_SAS studies and also in EUR studies
420 (Supplementary Table 12; Bonferroni-corrected threshold of significance $P < 2.8 \times 10^{-6}$, after adjusting for
421 17,996 genes tested, Methods). The gene showed residual association with the primary BP trait after
422 conditioning on the most associated SNV in the gene ($P_{\text{conditional}} = 5.00 \times 10^{-4}$; Supplementary Table 12),
423 suggesting that the association is due to multiple rare variants in the gene. One nonsense variant
424 (rs199651558, p.Arg893*, MAF= 3.5×10^{-4}) was observed, and there were multiple missense variants (Figure
425 5). *A2ML1* encodes alpha-2-macroglobulin-like 1 protein, and is a member of the alpha macroglobulin
426 superfamily, which comprises protease inhibitors targeting a wide range of substrates. Mutations in this gene
427 are associated with a disorder clinically related to Noonan syndrome, a developmental disorder which
428 involves cardiac abnormalities¹⁸. We sought replication in the CHARGE+ studies for this gene, however
429 there was no evidence of association with HTN ($P=0.45$). Given the very low frequencies of the variants
430 involved, however, studies in which the variants are polymorphic will be required to replicate the
431 association with HTN. The DBH gene was found to be associated with DBP using the SKAT test
432 ($P=2.88 \times 10^{-6}$). However, this was not due to multiple rare variants as the association was driven by
433 rs77273740 (Supplementary Table 5) and the SNV was not validated in the replication samples.

434

435 **Rare and common variant associations in established BP loci**

436 Of the 67 established BP loci, 35 loci were on the Exome chip (N=43 SNVs or close proxies $r^2 > 0.7$). All 43
437 SNVs had at least nominal evidence of association with BP in our discovery samples ($P < 0.01$;
438 Supplementary Table 13). We also assessed if any of the established BP loci contained coding variants that
439 are associated with BP traits and in LD ($r^2 > 0.2$) with the known BP variants on the Exome chip
440 (Supplementary Table 13), using the 1000G phase 3 release for LD annotation. Focusing on SNVs that were
441 GWS for any BP trait from our transformed discovery data for either ancestry, there were 25 coding
442 variants, of which 6 were predicted to be damaging at loci labelled *CDC25A*, *SLC39A8*, *HFE*, *ULK4*, *ST7L*-
443 *CAPZA1-MOV10* and *CYP11A1-ULK3*. Three of these are published variants at loci labelled *SLC39A8*, *HFE*
444 and *ST7-CAPZA1-MOV10*. At *CYP11A1-ULK3*, the coding variant was in moderate LD with the reported

445 variant, but was less significantly associated with DBP in our EUR_SAS dataset ($P=2.24\times 10^{-8}$ compared to
446 $P=1.68\times 10^{-15}$ for the published variant). At the *ULK4* locus the predicted damaging coding variant had
447 similar association as the published coding variant (predicted to be benign), and prior work has already
448 indicated several associated nsSNVs in strong LD in *ULK4*¹⁹. The nsSNV within the *CDC25A* locus
449 (rs11718350 in *SPINK8*) had similar association with DBP as the intergenic published SNV in our
450 EUR_SAS dataset ($P=2.00\times 10^{-8}$ compared to $P=2.27\times 10^{-8}$ for the published variant). Overall at least 5 of
451 the known loci are consistent with having a coding causal variant.

452 Gene-based SKAT tests of all genes that map within 1 Mb of a previously reported SNV association
453 (Supplementary Table 14), indicated no genes with multiple rare or low-frequency variant associations.
454 Single variant conditional analyses showed that rs33966350, a rare nonsense variant in *ENPEP* (MAF=0.01)
455 was associated with SBP ($P_{\text{conditional}}=1.61\times 10^{-5}$) in the EUR_SAS samples (Supplementary Tables 14 and 15;
456 Methods) independently of the known SNV (rs6825911). *ENPEP* encodes aminopeptidase A (APA) an
457 enzyme of the renin-angiotensin-aldosterone system (RAAS) that converts angiotensin II (AngII) to AngIII.
458 There were no other established loci with convincing low-frequency or rare SNV associations in the
459 EUR_SAS samples. However, *HOXC4*, had evidence of a second independent signal with a rare missense
460 SNV in EUR samples (rs78731604; MAF=0.005, $P_{\text{conditional}}=5.76\times 10^{-5}$; Supplementary Table 15). The
461 secondary signal in the *HOXC4* region, mapped to *CALCOCO1*, ~300kb from the known SNV. The gene
462 association (MAF \leq 0.01, $P=2.37\times 10^{-5}$) was below the required significance threshold and attributable to
463 rs78731604, which is not predicted to have detrimental effects on protein structure. Therefore, replication of
464 this association is required. Three loci (*ST7L-CAPZA1-MOV10*, *FIGN-GRB14*, and *TBX5-TBX3*) had
465 evidence of a second independent signal in the region in EUR_SAS samples with a common variant
466 ($P_{\text{conditional}}<1\times 10^{-4}$; Supplementary Table 15) that has not been previously reported.

467 Having identified 30 novel loci associated with BP traits, as well as additional new independent SNVs at
468 four novel loci and five known loci, we calculated the percent of the trait variance explained (Methods).
469 This was 2.08%/2.11%/1.15% for SBP/DBP/PP for the 43 previously reported BP-SNVs covered in our
470 dataset, increasing to 3.38%/3.41%/2.08% respectively with the inclusion of the 30 lead SNVs from novel
471 loci, plus new independent SNV-BP associations identified from novel and known loci.

473 **Effect of BP SNVs on cardiovascular traits & risk factors**

474 Amongst our novel BP-SNV associations, some have previously been reported to be associated with other
475 cardiovascular traits and risk factors (Supplementary Table 16); these include coronary heart disease (CHD:
476 *PHACTR1*, *ABO*)^{20,21}, QT interval (*RNF207*)²², heart rate (*MYH6*)²³, and cholesterol levels (2q36.3, *ABO*,
477 *ZNF101*)²⁴.

478 To test the impact of BP variants on cardiovascular endpoints and risk factors we created three weighted
479 genetic risk scores (GRS) according to SBP/DBP/PP based on the newly identified and previously published
480 BP variants (up to N=125; Methods). The GRS models were used to test the causal effect of BP on the
481 following traits: ischemic stroke (including the subtypes, cardiometabolic, large and small vessel²⁵), CHD,
482 heart failure,²⁶ left ventricular mass²⁷, left ventricular wall thickness²⁷, high-density lipoprotein cholesterol
483 (HDL-c), low-density lipoprotein (LDL-c), triglycerides, total cholesterol, body mass index (BMI), waist-
484 hip ratio adjusted BMI, height and estimated glomerular filtration rate (eGFR) (Methods). As expected, BP
485 was positively associated with increased CHD risk (OR [95% CI]=1.39[1.22-1.59] per 10mmHg increase in
486 SBP, $P=6.07 \times 10^{-7}$; 1.62[1.28-2.05] per 10mmHg increase in DBP, $P=5.99 \times 10^{-5}$; 1.70[1.34-2.16] per
487 10mmHg increase in PP, $P=1.20 \times 10^{-5}$; Table 3), and increased risk of ischemic stroke (OR [95%
488 CI]=1.93[1.47-2.55] per 10mmHg increase in DBP, $P=2.81 \times 10^{-6}$; 1.57[1.35-1.84] per 10mmHg increase in
489 SBP, $P=1.16 \times 10^{-8}$; 2.12[1.58-2.84] per 10mmHg increase in PP, $P=5.35 \times 10^{-7}$). The positive association with
490 ischemic stroke was primarily due to large vessel stroke (Table 3). DBP and SBP were also positively
491 associated with left ventricular mass (9.57 [3.98-15.17] gram increase per 10mmHg increase in DBP,
492 $P=8.02 \times 10^{-4}$ and 5.13 [1.77-8.48] gram increase per 10mmHg increase in SBP, $P=0.0027$) and left
493 ventricular wall thickness (0.10 [0.06-0.13] cm increase per 10mmHg increase in DBP, $P=1.88 \times 10^{-8}$ and
494 0.05 [0.03-0.07] cm increase per 10mmHg increase in SBP, $P=5.52 \times 10^{-6}$, Table 3). There was no convincing
495 evidence to support the BP associated variants having an effect on lipid levels ($P>0.1$), BMI ($P>0.005$),
496 waist hip ratio adjusted BMI ($P>0.1$), height ($P>0.06$), eGFR ($P>0.02$) or heart failure ($P>0.04$). The causal
497 associations with CHD, stroke, and left ventricular measures augment the results from a previous association
498 analysis using 29 BP variants²⁸. Our data strongly support the previous observations of no causal

499 relationship between BP and eGFR. Lack of evidence of a BP effect with heart failure may only be due to
500 lack of power, as the association was in the expected direction.

501 502 503 **Possible functional variants at BP loci and candidate genes**

504 Twenty-six of our newly discovered BP associated SNVs had $MAF \geq 0.05$ and therefore due to extensive LD
505 with other SNVs not genotyped on the Exome array, identifying the causal genes requires additional
506 information. If a SNV is associated with increased or decreased expression of a particular gene, *i.e.* it is an
507 expression quantitative trait locus (eQTL) this suggests the gene on which the SNV acts could be in the
508 causal pathway. To help identify potential candidate causal genes in the novel BP loci (Supplementary Table
509 9), information from publicly available eQTL databases was investigated (MuTHER for LCL, adipose and
510 skin and GTEx for nine tissues including the heart and tibial artery; Methods).

511 The DBP increasing allele of the nsSNV, rs7302981-A, was associated with increased expression of *CERS5*
512 in: LCLs ($P_{MuTHER}=3.13 \times 10^{-72}$) skin ($P_{MuTHER}=2.40 \times 10^{-58}$) adipose ($P_{MuTHER}=2.87 \times 10^{-54}$) and nerve
513 ($P_{GTEx}=4.5 \times 10^{-12}$) (Supplementary Figure 4). Additional testing (Methods) provided no evidence against
514 colocalisation of the eQTL and DBP association signals, implicating *CERS5* as a candidate causal gene for
515 this DBP locus. *CERS5* (LAG1 homolog, ceramide synthase 5) is involved in the synthesis of ceramide, a
516 lipid molecule involved in several cellular signaling pathways. *Cers5* knockdown has been shown to reduce
517 cardiomyocyte hypertrophy in mouse models²⁹. However, it is unclear whether the blood pressure raising
518 effects at this locus are the cause or result of any potential effects on cardiac hypertrophy. Future studies
519 investigating this locus in relation to parameters of cardiac hypertrophy and function (*e.g.* ventricular wall
520 thickness) should help address this question.

521 The DBP raising allele of the nsSNV (rs867186-A) was associated with increased expression of *PROCR* in
522 adipose tissue ($P_{MuTHER}=3.24 \times 10^{-15}$) and skin ($P_{MuTHER}=1.01 \times 10^{-11}$) (Supplementary Figure 4). There was no
523 evidence against colocalisation of the eQTL and DBP association thus supporting *PROCR* as a candidate
524 causal gene. *PROCR* encodes the Endothelial Protein C receptor, a serine protease involved in the blood

525 coagulation pathway, and rs867186 has previously been associated with coagulation and haematological
526 factors.^{30,31} The PP decreasing allele of, rs10407022-T, which is predicted to have detrimental effects on
527 protein structure (Methods) was associated with increased expression of *AMH* in muscle ($P_{\text{GTEX}}=9.95 \times 10^{-15}$),
528 thyroid ($P_{\text{GTEX}}=8.54 \times 10^{-7}$), nerve ($P_{\text{GTEX}}=7.15 \times 10^{-8}$), tibial artery ($P_{\text{GTEX}}=6.46 \times 10^{-9}$), adipose
529 ($P_{\text{GTEX}}=4.69 \times 10^{-7}$), and skin ($P_{\text{GTEX}}=5.88 \times 10^{-8}$) (Supplementary Figure 4). There was no evidence against
530 colocalisation of the eQTL and PP association, which supports *AMH* as a candidate causal gene for PP. Low
531 *AMH* levels have been previously associated with hypertensive status in women with the protein acting as a
532 marker of ovarian reserve³². The intergenic SBP raising allele of rs4728142-A was associated with reduced
533 expression of *IRF5* in skin ($P_{\text{MUTHER}}=5.24 \times 10^{-31}$) and LCLs ($P_{\text{MUTHER}}=1.39 \times 10^{-34}$), whole blood
534 ($P_{\text{GTEX}}=3.12 \times 10^{-7}$) and tibial artery ($P_{\text{GTEX}}=1.71 \times 10^{-7}$).

535

536 Three novel rare nsSNVs were identified that map to *RBM47*, *RRAS* (both associated with SBP) and
537 *COL21A1* (associated with PP). They had larger effect sizes than common variant associations (>1.5mmHg
538 per allele; Supplementary Figure 5) and were predicted to have detrimental effects on protein structure
539 (Supplementary Table 16; Methods). In *RBM47*, rs35529250 (p.Gly538Arg) is located in a highly conserved
540 region of the gene and was most strongly associated with SBP (MAF=0.008; +1.59 mmHg per T allele;
541 $P=5.90 \times 10^{-9}$). *RBM47* encodes the RNA binding motif protein 47 and is responsible for post-transcriptional
542 regulation of RNA, through its direct and selective binding with the molecule.³³ In *RRAS*, rs61760904
543 (p.Asp133Asn) was most strongly associated with SBP (MAF=0.007; +1.51 mmHg per T allele; $P=8.45 \times 10^{-8}$).
544 *RRAS* encodes a small GTPase belonging to the Ras subfamily of proteins H-RAS, N-RAS, and K-RAS
545 and has been implicated in actin cytoskeleton remodelling, and controlling cell proliferation, migration and
546 cycle processes³⁴. The nsSNV in *COL21A1* (rs200999181, p.Gly665Val) was most strongly associated with
547 PP (MAF=0.001; +3.14 mmHg per A allele; $P=1.93 \times 10^{-9}$). *COL21A1* encodes the collagen alpha-1 chain
548 precursor of type XXI collagen, a member of the FACIT (fibril-associated collagens with an interrupted
549 triple helix) family of proteins³⁵. The gene is detected in many tissues, including the heart and aorta. Based
550 on our results, these three genes represent good candidates for functional follow-up. However, due to the
551 incomplete coverage of all SNVs across the region on the Exome chip, it is possible that other non-
552 genotyped SNVs may better explain some of these associations. We therefore checked for variants in LD

553 ($r^2 > 0.3$) with these three rare nsSNVs in the UK10K + 1000G dataset³⁶ to ascertain if there are other
554 candidate SNVs at these loci (Supplementary Table 17). There were no SNVs within 1Mb of the *RBM47*
555 locus in LD with the BP associated SNV. At the *COL21A1* locus there were only SNVs in moderate LD, and
556 these were annotated as intronic, intergenic or in the 5'UTR. At the *RRAS* locus, there were two SNVs in
557 strong LD with the BP associated SNV, which both mapped to introns of *SCAF1* and are not predicted to be
558 damaging. All SNVs in LD at both loci were rare as expected (Supplementary Table 17) supporting a role
559 for rare variants. Hence, the rare BP associated nsSNVs at *RBM47*, *COL21A1* and *RRAS* remain the best
560 causal candidates.

561

562 **Pathway and network analyses**

563 To identify connected gene sets and pathways implicated by the BP associated genes we used Meta-Analysis
564 Gene-set Enrichment of variant Associations (MAGENTA)³⁷ and GeneGo MetaCore (Thomson Reuters,
565 UK). MAGENTA tests for over-representation of BP associated genes in pre-annotated pathways (gene
566 sets) (Methods and Supplementary Table 18a). GeneGo Metacore identifies potential gene networks. The
567 MAGENTA analysis was used for hypothesis generation and results were compared with the GeneGo
568 Metacore outputs to cross-validate findings.

569 Using MAGENTA there was an enrichment ($P < 0.01$ and $FDR < 5\%$ in either the EUR_SAS or the EUR
570 participants) of six gene sets with DBP, three gene sets with HTN and two gene sets for SBP
571 (Supplementary Table 18b). The RNA polymerase I promoter clearance (chromatin modification) pathway
572 showed the most evidence of enrichment with genes associated with DBP ($P_{\text{Reactome}} = 8.4 \times 10^{-5}$, $FDR = 2.48\%$).
573 NOTCH signalling was the most associated pathway with SBP ($P_{\text{Reactome}} = 3.00 \times 10^{-4}$, $FDR = 5\%$) driven by
574 associations at the *FURIN* gene. The inorganic cation anion solute carrier (SLC) transporter pathway had
575 the most evidence of enrichment by HTN associated genes ($P_{\text{Reactome}} = 8.00 \times 10^{-6}$, $FDR = 2.13\%$).

576 Using GeneGo MetaCore, five network processes were enriched ($FDR < 5\%$; Methods; Supplementary
577 Tables 19 and 20). These included several networks with genes known to influence vascular tone and BP:
578 inflammation signalling, $P = 1.14 \times 10^{-4}$ and blood vessel development $P = 2.34 \times 10^{-4}$. The transcription and
579 chromatin modification network ($P = 2.85 \times 10^{-4}$) was also enriched, a pathway that was also highlighted in the

580 MAGENTA analysis, with overlap of the same histone genes (*HIST1H4C*, *HIST1H2AC*, *HIST1H2BC*,
581 *HIST1H1T*) and has also been recently reported in an integrative network analysis of published BP loci and
582 whole blood expression profiling³⁸. Two cardiac development pathways were enriched: the oxidative stress-
583 driven (ROS/NADPH) ($P=4.12 \times 10^{-4}$) and the Wnt/ β -catenin/integrin-driven ($P=0.0010$). Both these cardiac
584 development pathways include the *MYH6*, *MYH7*, and *TBX2* genes, revealing a potential overlap with
585 cardiomyopathies and hypertension, and suggesting some similarity in the underlying biological
586 mechanisms.

587

588 Discussion

589 By conducting the largest ever genetic study of BP, we identified further novel common variants with small
590 effects on BP traits, similar to what has been observed for obesity and height^{39,40}. More importantly, our
591 study identified some of the first rare coding variants of strong effect (>1.5 mmHg) that are robustly
592 associated with BP traits in the general population, complementing and extending the previous discovery
593 and characterisation of variants underlying rare Mendelian disorders of blood pressure regulation⁴¹. Using
594 SNV associations in 17 genes reported to be associated with monogenic disorders of blood pressure
595 (Methods) we found no convincing evidence of enrichment ($P_{\text{enrichment}}=0.044$). This suggests that BP control
596 in the general population may occur through different pathways to monogenic disorders of BP re-enforcing
597 the importance of our study findings. The identification of 30 novel BP loci plus further new independent
598 secondary signals within four novel and five known loci (Methods) has augmented the trait variance
599 explained by 1.3%, 1.2% and 0.93% for SBP, DBP and PP respectively within our data-set. This suggests
600 that with substantially larger sample sizes, for example through UK BioBank⁴², we expect to identify 1000s
601 more loci associated with BP traits, and replicate more of our discovery SNV associations that are not yet
602 validated in the current report.

603 The discovery of rare missense variants has implicated several interesting candidate genes, which are often
604 difficult to identify from common variant GWAS, and should therefore lead to more rapidly actionable
605 biology. *A2ML1*, *COL21A1*, *RRAS* and *RBM47* all warrant further follow-up studies to define the role of

606 these genes in regulation of BP traits, as well as functional studies to understand their mechanisms of action.
607 *COL21A1* and *RRAS* warrant particular interest since both are involved in blood vessel remodelling, a
608 pathway of known aetiological relevance to hypertension.

609 We observed a rare nonsense SBP associated variant in *ENPEP* (rs33966350; p.Trp317*): this overlaps a
610 highly conserved region of both the gene and protein and is predicted to result in either a truncated protein
611 with reduced catalytic function or is subject to nonsense mediated RNA decay. ENPEP converts angiotensin
612 II (AngII) to Ang-III. AngII activates the angiotensin 1 (AT1) receptor resulting in vasoconstriction, while
613 AngIII activates the angiotensin 2 (AT2) receptor that promotes vasodilation and protects against
614 hypertension.⁴³ The predicted truncated protein may lead to predominant AngII signaling in the body, and
615 increases in BP. This new observation could potentially inform therapeutic strategies. Of note, angiotensin-
616 converting-enzyme (ACE) inhibitors are commonly used in the treatment of hypertension. However, patients
617 who suffer from adverse reactions to ACE inhibitors, such as dry cough and skin rash, would benefit from
618 alternative drugs that target RAAS. Murine studies have shown that in the brain, AngIII is the preferred AT1
619 agonist that promotes vasoconstriction and increases blood pressure, as opposed to AngII in the peripheral
620 system. These results have motivated the development of brain specific APA inhibitors to treat
621 hypertension⁴⁴. Our results confirm APAs, such as ENPEP, as a valid target to modify blood pressure, but
622 suggest that long-term systemic reduction in APA activity may lead to an increase in blood pressure. Future
623 studies are needed to examine the effects of the p.Trp317* variant on the RAAS system, specifically in the
624 brain and peripheral vasculature, in order to test the benefits of the proposed therapeutic strategy in humans.

625 In addition to highlighting new genes in pathways of established relevance to BP and hypertension, and
626 identifying new pathways, we have also identified multiple signals at new loci. For example, there are three
627 distinct signals at the locus containing the *MYH6/MYH7* genes, and we note that *TBX2* maps to one of the
628 novel regions. These genes are related to cardiac development and/or cardiomyopathies, and provide an
629 insight into the shared inheritance of multiple complex traits. Unravelling the causal networks within these
630 polygenic pathways may provide opportunities for novel therapies to treat or prevent both hypertension and
631 cardiomyopathies.

632

633 **URLs**

634 Exome chip design information: http://genome.sph.umich.edu/wiki/Exome_Chip_Design

635 [RareMetalWorker](http://genome.sph.umich.edu/wiki/RAREMETALWORKER) information: <http://genome.sph.umich.edu/wiki/RAREMETALWORKER>

636 [Summary SNV association results: http://www.phenoscanter.medschl.cam.ac.uk](http://www.phenoscanter.medschl.cam.ac.uk)

637 [Databases used for variant annotation: http://www.ncbi.nlm.nih.gov/SNP/](http://www.ncbi.nlm.nih.gov/SNP/)

638 <http://www.ensembl.org/info/docs/tools/index.html> and <http://evs.gs.washington.edu/EVS/>

639 UCSC reference file used for annotation of variants with gene and exon information:

640 <http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/refFlat.txt.gz>

641 Databases used for pathway analysis: MAGENTA (<https://www.broadinstitute.org/mpg/magenta/>) and

642 THOMSON REUTERS MetaCore™ Single Experiment Analysis workflow tool

643 ([http://thomsonreuters.com/en/products-services/pharma-life-sciences/pharmaceutical-](http://thomsonreuters.com/en/products-services/pharma-life-sciences/pharmaceutical-research/metacore.html)

644 [research/metacore.html](http://thomsonreuters.com/en/products-services/pharma-life-sciences/pharmaceutical-research/metacore.html)).

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996 NSa, JV, FWA, PIWB, MJB, MJC, JCC, JMC, IJD, GD, AFD, PE, TE, PWF, GG, PH, CH, KH, EI, MJ,
997 FKa, SK, JSK, LLi, MIM, OM, AMe, ADM, APM, PBM, MEN, SP, CP, OPo, DP, SR, OR, IR, VS, NJS,
998 PSe, TDS, JMS, NJW, CJW, EZ, MB, IB, FSC, LG, TH, EKH, PJ, JKu, ML, TAL, AL, KLM, HO, OPe,
999 RR, JT, MU. **Study Phenotyping in alphabetical order by consortium (CHD Exome+, ExomeBP and**
000 **GoT2D):** PA, DA, SBI, MC, JF, JWJ, FKe, KK, SFN, BGN, CJP, AR, MS, NSa, JV, WZo, RAB, MJB,
001 MJC, JCC, JMC, AFD, ASFD, LAD, TE, AF, GG, GH, PH, AS H, OLH, EI, MJ, FK, JSK, LLi, LLa, GM,
002 AMc, PM, AMe, RMg, MJN, MEN, OPo, NP, FR, VS, NJS, TDS, AVS, JMS, MT, AV, NV, NJW, TiT,
003 CC, LLH, MEJ, AK, PK, JL DPS, SM, ERBP, AS, TS, HMS, BT. **Study Data QC and analysis in**
004 **alphabetical order by consortium (CHD Exome+, ExomeBP and GoT2D):** ASB, AJMC, JMMH, JK,
005 SFN, BGN, MMN, SP, MP, PSu, ST, GV, SMW, RY, FWA, JPC, FD, AF, TF, CH, AMc, AMj, APM,
006 PBM, CP, WR, FR, NJS, MT, VT, HW, HY, NG, AKM, XS. **Exome chip data QC in alphabetical order**
007 **by consortium (CHD Exome+, ExomeBP and GoT2D):** ASB, JMMH, SFN, BGN, PSu, RY, FWA,
008 PIWB, AIFB, JCC, JPC, PD, LAD, FD, EE, CF, TF, SEH, PH, SSH, KH, JEH, EK, AMj, GM, JM, NM,
009 EMI, AMo, APM, PBM, CPN, MJN, CP, AP, WR, NRR, RAS, NS, LS, KES, MDT, VT, TVV, TVV, NV,
010 HW, HY, AMY, EZ, WZg, NG, CML, AKM, XS. **Exome chip Data analysis in alphabetical order by**
011 **consortium (CHD Exome+, ExomeBP and GoT2D):** JMMH, PSu, RY, FWA, PIWB, AIFB, RAB, MJC,
012 JCC, JPC, PD, LAD, PE, EE, CF, TF, PWF, SF, CG, SEH, PH, ASH, CH, OLH, JEH, EI, MJ, FKa, JSK,
013 DCML, LLi, JL, GM, RMr, JM, NM, MIM, PM, OM, CM, EMI, AMo, APM, RMg, PBM, CPN, MJN, TO,
014 APo, APa, WR, NRR, NJS, RAS, NS, LS, TDS, KES, MDT, ET, VT, TVV, NV, LVW, NJW, HW, HY,
015 AMY, EZ, HZ, WZg, LLB, APG, NG, MHs, JRH, AUJ, JBJ, CML, AKM, NN, XS, AS, AJS. **GRS**
016 **lookups:** AEJ, EMa, HFM, HL, HMH, JFF, MTr, RSV, WL.

017

018 **Conflict of interests**

019 N. P. has received financial support from several pharmaceutical companies that manufacture either blood
020 pressure lowering or lipid lowering agents, or both, and consultancy fees.

021 S. K. has received Research Grant-Merck, Bayer, Aegerion; SAB-Catabasis, Regeneron Genetics Center,
022 Merck, Celera; Equity-San Therapeutics, Catabasis; Consulting-Novartis, Aegerion, Bristol Myers-Squibb,
023 Sanofi, AstraZeneca, Alnylam.

024 P. Sever has received research awards from Pfizer Inc.

025 A. Malarstig and M. Uria-Nickelsen are full time employees of Pfizer.

026 D. Reily and M. Hoek are full time employees of Merck and co Inc.

027 M.J. Caulfield is Chief Scientist for Genomics England a UK Government company.

028 The authors declare no competing financial interest.

029

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137 **Figure Legends**

138 **Figure 1 Study design and work flow diagram of single variant discovery analyses.** EUR=European, SAS=South
139 Asian, HIS=Hispanic, AA=African American, HTN=hypertension, BP=blood pressure, SBP=systolic blood pressure,
140 DBP= diastolic blood pressure, PP=pulse pressure, N=sample size, MAF=minor allele frequency, P = P -value
141 significance threshold, SNV=single-nucleotide variant, GWS=genome-wide significance *Further details of the selection
142 criteria are provided in the methods.

143 **Figure 2 Discovery SNV-BP associations.** Results are provided for (a) transformed SBP (b) transformed DBP (c)
144 transformed PP and (d) HTN in the European and South Asian (EUR_SAS) discovery samples. The y-axis represents –
145 $\log_{10}P$ for association. Red triangles represent variants that map to one of the 81 regions selected for replication, blue
146 triangles represent SNVs that map to previously published BP regions, and grey triangles represent all remaining SNVs.
147 SNVs are ordered according to chromosome (black lines on the outside of the plot) and physical position. Genes that
148 SNVs map to are given in the outer blocks.

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150 **Figure 3 Overlap of the 30 novel loci associations across SBP, DBP, PP and HTN.** The Venn diagram shows which
151 of the 30 newly identified BP loci are associated with multiple BP traits. Only SNV-BP trait associations that were
152 genome-wide significant ($P < 5 \times 10^{-8}$) in the combined discovery and replication meta-analyses are listed for any given
153 BP trait, within the corresponding ancestry dataset that the given locus was validated for (see Tables 1 and 2). The
154 association of *RRAS* variant with SBP was replicated in the independent samples, but did not achieve GWS in the
155 combined discovery and replication meta-analysis and is therefore only included for SBP. HTN=hypertension,
156 SBP=systolic blood pressure, DBP= diastolic blood pressure, PP=pulse pressure.

157 **Figure 4 Study design for conditional analyses and rare variant gene-based discovery analyses.**

158 RMW=RareMetalWorker, EUR=European, SAS = South Asian, HTN=hypertension, BP=blood pressure, SBP=systolic
159 blood pressure, DBP= diastolic blood pressure, PP=pulse pressure. N=sample size, MAF=minor allele frequency, P = P -
160 value significance threshold, P_{cond} =conditional P -value significance threshold

161 **Figure 5 Locus plot for *A2ML1* and secondary amino acid structure of the gene product.** (a) Locus plot for *A2ML1*
162 associated with HTN identified through gene based tests. The variants' positions along the gene (x axis, based on

163 human genome build 37) and the $-\log_{10}(P\text{-value of association})$ (y axis) are indicated. The variants are colour coded:
164 nonsense (black), missense, predicted damaging (blue), and missense (orange). The schematic above the x-axis
165 represents the intron / exon (black vertical bars) structure, the untranslated regions are shown as grey vertical bars.

(b) The white box denotes the full-length amino acid sequence for each of the two gene products. Black numbers
166 denote amino acid residue positions of note. Coloured boxes depict putative functional domains (see below). Coloured
167 vertical lines indicate the amino acid substitutions corresponding to the variants depicted in the locus plots above using
168 the same colour coding. Bold, italic indicates the SNV association with smallest *P*-value.

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170 Dark grey – signal peptide sequence. Brown – regions of intramolecular disulfide bonds. For simplicity only those
171 regions coinciding with variants described were indicated. Black – bait region described to interact with proteases.
172 Purple – thiol ester sequence region aiding in interaction with proteases. Light grey – alpha helical regions thought to
173 mediate A2ML1 interaction with LRP1, facilitating receptor-mediated endocytosis.

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Table 1 Novel blood pressure trait associated loci. Variants with formal replication

| Locus | Variant information | | | Discovery | | Replication | | | Combined | | |
|---------------------|---------------------|---------------------|-------|------------------------|------------------------|-------------|---------|------------------------|----------|---------|------------------------|
| | rsID | Chr:Pos (EA:EAF) | Trait | P_t | P_u | N | β | P | N | β | P |
| EUR | | | | | | | | | | | |
| <i>RNF207</i> | rs709209 | 1:6.28 (A:0.655) | PP | 4.57×10^{-6} | 1.60×10^{-6} | 122,780 | 0.17 | 5.83×10^{-4} | 284,683 | 0.20 | 9.62×10^{-9} |
| <i>C5orf56</i> | rs12521868 | 5:131.78 (T:0.373) | DBP | 1.59×10^{-6} | 3.03×10^{-7} | 122,795 | -0.18 | 2.29×10^{-5} | 282,023 | -0.19 | 6.12×10^{-11} |
| <i>PHACTR1</i> | rs9349379 | 6:12.90 (A:0.566) | SBP | 2.11×10^{-8} | 1.78×10^{-7} | 122,809 | 0.24 | 4.06×10^{-4} | 284,673 | 0.29 | 8.84×10^{-10} |
| <i>COL21A1</i> | rs200999181† | 6:55.94 (A:0.002) | PP | 3.08×10^{-8} | 2.46×10^{-7} | 121,487 | 2.70 | 1.90×10^{-4} | 242,486 | 3.25 | 6.27×10^{-10} |
| <i>ABO</i> | rs687621 | 9:136.14 (A:0.615) | DBP | 8.80×10^{-8} | 2.55×10^{-7} | 122,798 | 0.16 | 1.96×10^{-4} | 276,014 | 0.19 | 5.45×10^{-10} |
| <i>ADO</i> | rs10995311 | 10:64.56 (C:0.567) | DBP | 1.86×10^{-6} | 1.14×10^{-6} | 122,798 | 0.23 | 8.47×10^{-8} | 266,456 | 0.21 | 1.12×10^{-12} |
| <i>LMO1</i> | rs110419 | 11:8.25 (A:0.48) | DBP | 9.41×10^{-6} | 2.22×10^{-5} | 122,798 | 0.16 | 1.81×10^{-4} | 279,935 | 0.16 | 3.04×10^{-8} |
| <i>OR5B12</i> | rs11229457 | 11:58.21 (T:0.236) | SBP | 1.58×10^{-6} | 4.62×10^{-5} | 122,809 | -0.32 | 7.53×10^{-5} | 284,680 | -0.31 | 2.70×10^{-8} |
| <i>CERS5</i> | rs7302981 | 12:50.54 (A:0.361) | DBP | 1.35×10^{-13} | 4.60×10^{-11} | 122,798 | 0.24 | 2.64×10^{-8} | 284,718 | 0.25 | 1.38×10^{-17} |
| <i>MYH6</i> | rs452036 | 14:23.87 (A:0.327) | PP | 4.59×10^{-11} | 2.80×10^{-13} | 122,780 | -0.21 | 1.81×10^{-5} | 284,672 | -0.28 | 2.96×10^{-16} |
| <i>DPEP1</i> | rs1126464 | 16:89.70 (C:0.256) | DBP | 1.19×10^{-9} | 4.35×10^{-11} | 118,677 | 0.24 | 1.68×10^{-6} | 261,564 | 0.28 | 1.02×10^{-15} |
| <i>TBX2</i> | rs8068318† | 17:59.48 (T:0.698) | DBP | 7.46×10^{-13} | 5.71×10^{-10} | 122,798 | 0.26 | 3.23×10^{-8} | 281,978 | 0.26 | 1.95×10^{-16} |
| <i>RGL3</i> | rs167479 | 19:11.53 (T:0.486) | DBP | 2.22×10^{-23} | 1.97×10^{-22} | 122,797 | -0.29 | 3.01×10^{-11} | 283,332 | -0.33 | 1.99×10^{-31} |
| <i>PREX1</i> | rs6095241 | 20:47.31 (A:0.452) | DBP | 5.65×10^{-6} | 2.29×10^{-5} | 122,798 | -0.18 | 2.56×10^{-5} | 281,322 | -0.17 | 4.75×10^{-9} |
| ALL ancestry | | | | | | | | | | | |
| <i>RBM47</i> | rs35529250† | 4:40.43 (T:0.01) | SBP | 6.56×10^{-7} | 6.15×10^{-6} | 148,878 | -1.43 | 5.02×10^{-4} | 306,352 | -1.55 | 2.42×10^{-8} |
| <i>OBFC1</i> | rs4387287 | 10:105.68 (A:0.157) | SBP | 2.23×10^{-8} | 1.32×10^{-7} | 147,791 | 0.28 | 3.37×10^{-4} | 320,494 | 0.36 | 9.12×10^{-10} |
| <i>RRAS</i> | rs61760904† | 19:50.14 (T:0.008) | SBP | 1.96×10^{-6} | 1.90×10^{-5} | 148,878 | 1.38 | 5.70×10^{-4} | 322,664 | 1.50 | 8.45×10^{-8} |

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SNV-BP associations are reported for the newly identified BP loci that replicated at $P < 6.2 \times 10^{-4}$ (Bonferroni correction for the 81 variants selected for replication for a primary blood pressure trait; Methods). Loci are categorised into EUR and ALL ancestry based on the meta-analysis used to replicate the variants for the primary BP trait shown in columns labelled 'Trait'. In the columns that contains the discovery meta-analyses results, P_t represents the P -value for association of the variant with the transformed primary BP trait in the EUR_SAS discovery meta-analyses (which was also used to select the variant for replication) and P_u represents the P -value for association with the untransformed primary BP trait in the ancestry in which the variant replicated. N, β and P , which denote the number of samples, estimated allelic effect and P -value for association with the primary BP trait, are provided for the untransformed primary BP trait in the replication data and also from the combined (discovery and replication) meta-analyses. NB: ALL ancestry corresponds to all ancestries in the combined (discovery + replication) meta-analyses

Locus – Gene or region containing the SNV, rsID – dbSNP rsID. Chr:Pos (EA:EAF) – Chromosome:NCBI Build 37 position in Mb (effect allele:effect allele frequency), Trait – primary blood pressure trait for which the variant was and also replicated, β – effect estimate, N:sample size, EUR – European.

† indicates it is a non-synonymous SNV (nsSNV) or is in linkage disequilibrium with a nsSNV ($r^2 > 0.8$) that is predicted to be damaging

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Table 2 Novel blood pressure trait associated loci. Variants with GWS evidence of association in combined meta-analyses

| Locus | Variant information | | | Discovery | | Replication | | | Combined | | |
|---------------------|-------------------------|---------------------|---------------------------|------------------------|-----------------------|-------------|---------|-----------------------|----------|---------|------------------------|
| | rsID | Chr:Pos (EA:EAF) | Trait | P_t | P_u | N | β | P | N | β | P |
| EUR | | | | | | | | | | | |
| 2q36.3 | rs2972146 | 2:227.10 (T:0.652) | DBP [§] (HTN) | 1.51×10^{-9} | 2.47×10^{-7} | 122,798 | 0.13 | 2.20×10^{-3} | 275,610 | 0.17 | 8.40×10^{-9} |
| ZBTB38 | rs16851397 | 3:141.13 (A:0.953) | DBP [§] (SBP) | 6.87×10^{-6} | 3.20×10^{-5} | 122,798 | -0.38 | 1.20×10^{-4} | 284,717 | -0.38 | 3.01×10^{-8} |
| PRDM6 | rs1008058 | 5:122.44 (A:0.135) | SBP | 5.09×10^{-7} | 1.01×10^{-8} | 43,109 | 0.46 | 3.61×10^{-3} | 176,362 | 0.55 | 2.99×10^{-10} |
| GPR20 | rs34591516 | 8:142.37 (T:0.055) | SBP [§] (DBP) | 1.54×10^{-6} | 1.01×10^{-7} | 122,807 | 0.51 | 4.20×10^{-4} | 282,009 | 0.64 | 6.10×10^{-10} |
| HOXB7 | rs7406910 | 17:46.69 (T:0.118) | SBP | 6.07×10^{-10} | 2.74×10^{-9} | 122,809 | -0.20 | 4.89×10^{-2} | 284,690 | -0.46 | 3.80×10^{-8} |
| AMH | rs10407022 [†] | 19:2.25 (T:0.82) | PP | 1.63×10^{-7} | 1.73×10^{-7} | 118,656 | -0.19 | 1.62×10^{-3} | 252,525 | -0.26 | 5.94×10^{-9} |
| ZNF101 | rs2304130 | 19:19.79 (A:0.914) | DBP | 1.66×10^{-8} | 1.92×10^{-8} | 122,798 | -0.17 | 1.71×10^{-2} | 284,705 | -0.29 | 1.53×10^{-8} |
| PROCR | rs867186 | 20:33.76 (A:0.873) | DBP | 1.44×10^{-6} | 4.15×10^{-7} | 122,798 | 0.21 | 2.48×10^{-3} | 284,722 | 0.26 | 1.19×10^{-8} |
| RRP1B | rs9306160 | 21:45.11 (T:0.374) | DBP [§] (SBP) | 1.04×10^{-8} | 1.90×10^{-6} | 100,489 | -0.16 | 4.30×10^{-4} | 249,817 | -0.18 | 6.80×10^{-9} |
| TNRC6B | rs470113 | 22:40.73 (A:0.804) | PP | 1.48×10^{-10} | 1.31×10^{-9} | 122,780 | -0.14 | 1.37×10^{-2} | 284,683 | -0.25 | 1.67×10^{-9} |
| ALL ancestry | | | | | | | | | | | |
| 7q32.1 | rs4728142 | 7:128.57 (A:0.433) | SBP | 8.10×10^{-6} | 4.21×10^{-6} | 150,542 | -0.21 | 8.62×10^{-4} | 338,338 | -0.24 | 3.45×10^{-8} |
| PRKAG1 | rs1126930 [†] | 12:49.40 (C:0.036) | PP | 2.12×10^{-6} | 4.62×10^{-7} | 151,481 | 0.36 | 3.74×10^{-3} | 314,894 | 0.50 | 3.34×10^{-8} |
| SBNO1 | rs1060105 | 12:123.81 (T:0.209) | DBP | 6.66×10^{-7} | 1.09×10^{-6} | 150,532 | -0.15 | 2.67×10^{-3} | 336,413 | -0.18 | 3.07×10^{-8} |

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SNV-BP associations are reported for the newly identified BP loci that showed genome-wide significant association ($P < 5 \times 10^{-8}$) in the combined discovery and replication meta-analyses. In the columns that contain results from the discovery meta-analyses, P_t represents the P -value for association of the variant with the transformed *primary* BP trait in the EUR_SAS discovery meta-analyses (used to select the variant for replication) and P_u represents the P -value for association with the untransformed BP trait in the ancestry in which the variant was validated. Loci are categorised into EUR and ALL ancestry based on the ancestry in which the variant showed association with a blood pressure trait at $P < 5 \times 10^{-8}$. N, β and P , which denote the number of samples, estimated allelic effect and P -value for association with the validated BP trait, are provided for the untransformed BP trait in the replication data and also from the combined (discovery and replication) meta-analyses. NB: ALL ancestry corresponds to all ancestries in the combined (discovery + replication) meta-analyses.

Locus – Gene or region containing the SNV, rsID - dbSNP rsID. Chr:Pos (EA:EAF) – Chromosome:NCBI Build 37 position in Mb (effect allele:effect allele frequency), Trait - blood pressure trait for which association is reported, EUR - European.

§ At four loci (2q36.3, ZBTB38, GPR20 and RRP1B) the primary trait used to select the variants for replication is given in parentheses because the variant associations were validated in the combined meta-analysis for the listed secondary trait. For these variants, P_t denotes the P -value for association with the primary trait, the other P -values provided are for the secondary trait.

† indicates it is a non-synonymous SNV (nsSNV) or is linkage disequilibrium with a nsSNV ($r^2 > 0.8$) that is predicted to be damaging

Table 3 Results of the genetic risk score analyses across CVD traits and risk factors.

| Outcome | Units | N | DBP (per 10mmHg increase) | | SBP (per 10mmHg increase) | | PP (per 10mmHg increase) | |
|---------------------------------|-------|---------|---------------------------|-------------------------|---------------------------|-------------------------|--------------------------|-------------------------|
| | | | Effect [95% CI] | <i>P</i> | Effect [95% CI] | <i>P</i> | Effect [95% CI] | <i>P</i> |
| CHD | OR | 82,056 | 1.62 [1.28, 2.05] | 5.99 x 10 ⁻⁵ | 1.39 [1.22, 1.59] | 6.07 x 10 ⁻⁷ | 1.70 [1.34, 2.16] | 1.20 x 10 ⁻⁵ |
| Ischemic stroke | OR | 25,799 | 1.93 [1.47, 2.55] | 2.81 x 10 ⁻⁶ | 1.57 [1.35, 1.84] | 1.16 x 10 ⁻⁸ | 2.12 [1.58, 2.84] | 5.35 x 10 ⁻⁷ |
| Cardioembolic stroke | OR | 16,113 | 1.43 [0.86, 2.39] | 0.1683 | 1.33 [0.99, 1.80] | 0.0584 | 1.73 [1.00, 3.02] | 0.0518 |
| Large vessel stroke | OR | 13,903 | 2.26 [1.25, 4.08] | 0.0068 | 1.85 [1.32, 2.59] | 3.61 x 10 ⁻⁴ | 3.05 [1.64, 5.68] | 4.37 x 10 ⁻⁴ |
| Small vessel stroke | OR | 15,617 | 1.96 [1.13, 3.41] | 0.0168 | 1.56 [1.13, 2.16] | 0.0064 | 1.98 [1.09, 3.61] | 0.0248 |
| Heart failure | OR | 13,282 | 1.48 [1.02, 2.17] | 0.0409 | 1.25 [1.00, 1.57] | 0.0512 | 1.33 [0.88, 2.02] | 0.1757 |
| Left ventricular mass | g | 11,273 | 9.57 [3.98, 15.17] | 8.02 x 10 ⁻⁴ | 5.13 [1.77, 8.48] | 0.0027 | 5.97 [-0.38, 12.31] | 0.0653 |
| Left ventricular wall thickness | cm | 11,311 | 0.10 [0.06, 0.13] | 1.88 x 10 ⁻⁸ | 0.05 [0.03, 0.07] | 5.52 x 10 ⁻⁶ | 0.05 [0.01, 0.09] | 0.0187 |
| HDL | mg/dl | 80,395 | 0.25 [-1.00, 1.51] | 0.6930 | 0.21 [-0.50, 0.92] | 0.5622 | 0.47 [-0.79, 1.73] | 0.4668 |
| LDL | mg/dl | 77,021 | -1.57 [-5.20, 2.06] | 0.3972 | 0.07 [-2.03, 2.16] | 0.9498 | 1.87 [-1.86, 5.59] | 0.3255 |
| Total cholesterol | mg/dl | 80,455 | -1.34 [-5.90, 3.22] | 0.5639 | 0.70 [-1.93, 3.32] | 0.6029 | 3.68 [-0.97, 8.33] | 0.1209 |
| Triglycerides | mg/dl | 77,779 | 0.02 [-0.03, 0.08] | 0.3859 | 0.02 [-0.01, 0.05] | 0.2697 | 0.03 [-0.03, 0.08] | 0.3025 |
| BMI | INVT | 526,508 | -0.10 [-0.18, -0.01] | 0.0342 | -0.07 [-0.13, -0.02] | 0.0058 | -0.12 [-0.23, -0.02] | 0.0165 |
| WHRadjBMI | INVT | 344,369 | 0.03 [-0.04, 0.11] | 0.4025 | 0.03 [-0.02, 0.08] | 0.2170 | 0.06 [-0.03, 0.15] | 0.1885 |
| Height | INVT | 458,927 | 0.02 [-0.15, 0.18] | 0.8592 | -0.04 [-0.15, 0.06] | 0.4170 | -0.18 [-0.37, 0.01] | 0.0683 |
| eGFR | INVT | 51,039 | -0.02 [-0.15, 0.11] | 0.7810 | -0.03 [-0.10, 0.04] | 0.4080 | -0.07 [-0.20, 0.06] | 0.2741 |

CHD, coronary heart disease; HDL, high density lipoprotein; LDL, low density lipoprotein; eGFR, estimated glomerular filtration rate; DBP, diastolic blood pressure; SBP systolic blood pressure; PP, pulse pressure; OR, odds ratio; g, grams; INVT, inverse normally

transformed (hence no units); N, sample size; *P*, *P*-value of association of BP with the trait listed; CI, confidence interval. Results are considered significant if *P* < 0.0038, which corresponds to a Bonferroni correction for 13 phenotypes tested.

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210

211 **Online Methods**

212 **Overview of discovery studies**

213 The cohorts contributing to the discovery meta-analyses comprise studies from three consortia (CHD
214 Exome+, ExomeBP, and GoT2D/T2D-GENES) with a total number of 192,763 unique samples. All
215 participants provided written informed consent and the studies were approved by their local Research Ethics
216 Committees and/or Institutional Review Boards.

217 The CHD Exome+ consortium comprised 77,385 samples: eight studies (49,898 samples) of European
218 (EUR) ancestry, two studies (27,487 samples) of South Asian (SAS) ancestry (Supplementary Table 1). The
219 ExomeBP consortium included 25 studies (75,620 samples) of EUR ancestry (Supplementary Table 1). The
220 GoT2D consortium comprised 14 studies (39,758 samples) of Northern EUR ancestry from Denmark,
221 Finland, and Sweden (Supplementary Table 1). The participating studies and their characteristics including
222 BP phenotypes are detailed in Supplementary Tables 1 and 2. Note, any studies contributing to multiple
223 consortia were only included once in all meta-analyses.

224 **Phenotypes**

225 Four blood pressure (BP) traits were analysed: systolic blood pressure (SBP), diastolic blood pressure
226 (DBP), pulse pressure (PP) and hypertension (HTN). For individuals known to be taking BP lowering
227 medication, 15/10 mmHg was added to the raw SBP/DBP values, respectively, to obtain medication-
228 adjusted SBP/DBP values⁴⁵. PP was defined as SBP minus DBP, post-adjustment. For HTN, individuals
229 were classified as hypertensive cases if they satisfied at least one of: (i) $SBP \geq 140$ mmHg, (ii) $DBP \geq 90$
230 mmHg, (iii) taking anti-hypertensive or BP lowering medication. All other individuals were included as
231 controls. The four BP traits were correlated (SBP:DBP correlations were between 0.6 and 0.8, and SBP:PP
232 correlations were ~ 0.8). However, they measure partly distinct physiological features including, cardiac
233 output, vascular resistance, and arterial stiffness, all measures for determining a cardiovascular risk profile.
234 Therefore the genetic architecture of the individual phenotypes are of interest, and a multi-phenotype
235 mapping approach was not adopted.

238 **Genotyping**

239 All samples were genotyped using one of the Illumina HumanExome Beadchip arrays (Supplementary Table
240 3). An Exome chip quality control Standard Operating Procedure (SOP) developed by Anubha Mahajan,
241 Neil Robertson and Will Rayner at the Wellcome Trust Centre for Human Genetics, University of Oxford
242 was used by most studies for genotype calling and QC⁴⁶ (Supplementary Table 3). All genotypes were
243 aligned to the plus strand of the human genome reference sequence (Build37) prior to any analyses and any
244 unresolved mappings were removed. Genotype cluster plots were reviewed for all the novel rare variants
245 (both lead and secondary signals) and for rare variants that contributed to the gene-based testing.

246 **Meta-analyses**

247 Meta-analyses were performed using METAL⁴⁷, for both discovery and replication analyses, using inverse
248 variance weighted fixed effect meta-analysis for the continuous traits (SBP, DBP and PP) and sample size
249 weighted meta-analysis for the binary trait (HTN).

250 **Discovery SNV analyses**

251 Analyses of both untransformed and inverse normal transformed SBP, DBP and PP were conducted within
252 each contributing study. The analyses of the transformed traits were performed in order to minimise
253 sensitivity to deviations from normality in the analysis of rare variants and for discovery of new SNV-BP
254 associations. The residuals from the null model obtained after regressing the medication-adjusted trait on the
255 covariates (age, age², sex, BMI, and disease status for CHD) within a linear regression model, were ranked
256 and inverse normalised. These normalised residuals were used to test trait-SNV associations. All SNVs that
257 passed QC were analysed for association, without any further filtering by MAF, but a minor allele count of
258 10 was used for the analysis of HTN. An additive allelic effects model was assumed.

259 Two meta-analyses were performed for each trait, one with EUR and SAS ancestries combined (EUR_SAS)
260 and another for EUR ancestry alone. Contributing studies used principal components (PCs) to adjust for
261 population stratification. Consequently minimal inflation in the association test statistics, λ , was observed (

262 $\lambda = 1.07$ for SBP, 1.10 for DBP, 1.04 for PP and <1 for HTN in the transformed discovery meta-analysis in
263 EUR_SAS; $\lambda = 1.06$ for SBP, 1.09 for DBP, 1.05 for PP and <1 for HTN in the transformed discovery
264 meta-analysis in EUR; Supplementary Figure 6). The meta-analyses were performed independently in two
265 centres and results were found to be concordant between centres. Given the studies contributing to the
266 discovery analyses were ascertained on CHD or T2D, we tested potential systematic bias in calculated effect
267 estimates amongst these studies. No evidence of bias in the overall effect estimates was obtained.

268 The results for the transformed traits were taken forward and used to select candidate SNVs for replication.
269 Results (P -values) from the transformed and untransformed analyses were strongly correlated ($r^2 > 0.9$).

270 **Replication SNV analyses**

271 SNVs associated with any of the transformed traits (SBP, DBP, PP) or HTN were annotated using the
272 Illumina SNV annotation file, humanexome-12v1_a_gene_annotation.txt, independently across two centres.
273 Given the difference in power to detect common versus low frequency and rare variant associations, two
274 different significance thresholds were chosen for SNV selection. For SNVs with $MAF \geq 0.05$, $P \leq 1 \times 10^{-5}$ was
275 selected, while, $P \leq 1 \times 10^{-4}$ was used for SNVs with $MAF < 0.05$. By choosing a significance threshold of
276 $P < 1 \times 10^{-4}$ we maximized the opportunity to follow-up rare variants (making the assumption that any true
277 signals at this threshold could replicate at Bonferroni adjusted significance, $P \leq 6.17 \times 10^{-4}$, assuming $\alpha = 0.05$
278 for 81 SNVs). All previously published BP associated SNVs and any variants in LD with them ($r^2 > 0.2$),
279 were removed from the list of associated SNVs as we aimed to replicate new findings only. SNVs for which
280 only one study contributed to the association result or showed evidence of heterogeneity ($P_{het} < 0.0001$) were
281 removed from the list as they were likely to be an artefact. Where SNVs were associated with multiple traits,
282 to minimise the number of tests performed, only the trait with the smallest P -value was selected as the
283 primary trait in which replication was sought. Where multiple SNVs fitted these selection criteria for a
284 single region, only the SNV with the smallest P -value was selected. In total, 81 SNVs were selected for
285 validation in independent samples. These 81 SNVs had concordant association results for both transformed
286 and non-transformed traits. Eighty SNVs were selected from EUR_SAS results (with consistent support in
287 EUR), and one SNV from EUR results only. In the next step, we looked up the 81 SNV-BP associations
288 using data from a separate consortium, the CHARGE+ exome chip blood pressure consortium (who had

289 analysed untransformed SBP, DBP, PP and HTN), and UHP and Lolipop (ExomeBP consortium;
290 Supplementary Tables 2 and 3). The analysed residuals from CHARGE+ were approximately normally
291 distributed in their largest studies (Supplementary Figure 7).

292 Two meta-analyses of the replication datasets were performed: one of EUR samples, and a second of EUR,
293 African American, Hispanics and SAS ancestries (“ALL”). Replication was confirmed if P (1-tailed) <
294 $0.05/81=6.17 \times 10^{-4}$ and the effect (beta) was in the direction observed in discovery meta-analyses for the
295 selected trait. A combined meta-analysis was performed of discovery (untransformed results as only
296 untransformed data was available from CHARGE+ exome chip blood pressure consortium) and replication
297 results across the four traits to assess the overall support for each locus. For the combined meta-analyses, a
298 GWS threshold of, $P \leq 5 \times 10^{-8}$, was used to declare a SNV as novel rather than a less stringent experiment
299 wide threshold, as GWS is used to declare significance in GWAS and we wish to minimise the possibility of
300 false positive associations. (Note that GWS is equivalent to an exome-wide threshold of $P \leq 2 \times 10^{-7}$ adjusted
301 for four traits).

302

303 Note: all validated BP-associated variants were associated at $P < 10^{-5}$ in the discovery dataset (for the primary
304 trait). Hence, we could have used the same inclusion criteria for both common and rare SNVs. Therefore the
305 optimal threshold to choose for future experiments may need further consideration.

306 **Conditional analyses and gene-based tests**

307 The RAREMETALWORKER (RMW) tool¹⁵ (version 4.13.3) that does not require individual level data to
308 perform conditional analyses and gene-based tests was used for conditional analyses. All studies that
309 contributed to the SNV discovery analyses were re-contacted and asked to run RMW. Only FENLAND,
310 GoDARTS, HELIC-MANOLIS, UKHLS and EPIC-InterAct were unable to run RMW, while two new
311 studies were included, INCIPE and NFBC1966 (Supplementary Table 1 and 2). In total, 43 studies (147,402
312 samples) were included in the EUR analyses and 45 studies (173,329 samples) in the EUR_SAS analyses
313 (Supplementary Tables 2 and 3). Comparison of discovery and RMW study level results were made
314 (Supplementary Information).

315 For each novel locus, the genomic coordinates and size of the region were defined according to
316 recombination rates (Supplementary Table 9) around the lead variant. For known loci, a 1 Mb window was
317 used (Supplementary Table 14). Conditional analyses were performed across each region, in both EUR and
318 EUR_SAS samples, for the transformed phenotype corresponding to the validated BP trait for novel loci and
319 the published BP trait for known loci.

320 Gene based tests were performed in both the EUR and EUR_SAS datasets using the Sequence Kernel
321 Association Test (SKAT)¹⁶ method implemented in RMW as it allows for the SNVs to have different
322 directions and magnitudes of effect. Burden tests were also performed but are not presented as only SKAT
323 provided significant results. The variants in the gene-based tests using SKAT were weighted using the
324 default settings, *i.e.* a beta distribution density function to up-weight rare variants, $\text{Beta}(\text{MAF}_j, 1, 25)$ where
325 MAF_j represents the pooled MAF for variant j across all studies. Analyses were restricted to coding SNVs
326 with $\text{MAF} < 5\%$ and $< 1\%$. Genes were deemed to be associated if $P < 2.8 \times 10^{-6}$ (Bonferroni adjusted for
327 17,996 genes). To confirm the gene associations were not attributable to a solitary SNV, a gene-based test
328 conditional on the most associated SNV was performed ($P_{\text{conditional}} < 0.001$). The QC of all SNVs
329 contributing to the gene based tests including the number of samples and studies were checked prior to
330 claiming association. We sought replication of associated genes in the CHARGE+ exome chip blood
331 pressure consortium.

332

333 **Pathway analyses with MAGENTA**

334 We tested seven databases in MAGENTA³⁷ (BioCarta, Kyoto Encyclopedia of Genes and Genomes,
335 Ingenuity, Panther, Panther Biological Processes, Panther Molecular Functions and Reactome) for
336 overrepresentation of the SNV discovery results from both EUR and EUR_SAS ancestries. Each of the four
337 BP phenotypes were tested. Pathways exhibiting $P < 0.01$ and $\text{FDR} < 5\%$ were considered statistically
338 significant.

339 **GeneGo MetaCore Network analyses**

340 A set of BP genes based on previously published studies and our current results (locus defined as $r^2 > 0.4$ and
 341 500kb on either side of the lead SNV; Supplementary Table 19) were tested for enrichment using the
 342 THOMSON REUTERS MetaCore™ Single Experiment Analysis workflow tool. The data were mapped
 343 onto selected MetaCore ontology databases: pathway maps, process networks, GO processes and diseases /
 344 biomarkers, for which functional information is derived from experimental literature. Outputs were sorted
 345 based on P - and FDR-values. A gene set was considered enriched for a particular process if $P < 0.05$ and
 346 $FDR < 5\%$.

347
 348 **Genetic Risk Score**
 349

350 To assess the effect of BP on CHD, ischemic stroke (and subtypes: large vessel, small vessel and
 351 cardioembolic stroke) left ventricular mass, left ventricular wall thickness, heart failure, HDL-c, LDL-c,
 352 total cholesterol, triglycerides and eGFR, we performed a weighted generalized linear regression of the
 353 genetic associations with each outcome variable on the genetic associations with BP.

354 When genetic variants are uncorrelated, the estimates from such a weighted linear regression analysis using
 355 summarized data, and a genetic risk score analysis using individual-level data, are equal⁴⁸. We refer to the
 356 analysis as a genetic risk score (also known as a polygenic risk score) analysis as this is likely to be more
 357 familiar to applied readers. As some of the genetic variants in our analysis are correlated, a generalized
 358 weighted linear regression model is fitted that accounts for the correlations between variants, as follows:

359 If β_X are the genetic associations (beta-coefficients) with the risk factor (here, BP) and β_Y are the genetic
 360 associations with the outcome, then the causal estimate from a weighted generalized linear regression is $(\beta_X^T$
 361 $\Omega^{-1}\beta_X)^{-1} \beta_X^T \Omega^{-1}\beta_Y$, with standard error,

$$\hat{\sigma} \sqrt{(\beta_X^T \Omega^{-1} \beta_X)^{-1}},$$

363 where T is a matrix transpose, $\hat{\sigma}$ is the estimate of the residual standard error from the regression model, and
 364 the weighting matrix Ω has terms

$$\Omega_{j_1 j_2} = \sigma_{Y j_1} \sigma_{Y j_2} \rho_{j_1 j_2}$$

366 , where $\sigma_{Y j}$ is the standard error of the genetic association with the outcome for the j th SNV, and $\rho_{j_1 j_2}$ is the
 367 correlation between the j_1 th and j_2 th SNVs. The presence of the estimated residual standard error allows for

368 heterogeneity between the causal estimates from the individual SNVs as overdispersion in the regression
369 model (in the case of underdispersion, the residual standard error estimate is set to unity). This is equivalent
370 to combining the causal estimates from each SNV using a multiplicative random-effects model⁴⁹.

371

372 For each of SBP, DBP and PP, the score was created using both the novel and known BP SNVs or a close
373 proxy ($r^2 > 0.8$). Both the sentinel SNV association and any secondary SNV associations that remained after
374 adjusting for the sentinel SNV were included in the genetic risk score. For the 30 validated novel SNV-BP
375 associations, β s were taken from the independent replication analyses (Table 1 and 2) to weight the SNV in
376 the genetic risk score. For the secondary SNVs from the seven novel loci and five known loci, β s were taken
377 from the discovery analyses (Supplementary Tables 10 and 15). For the 82 known SNVs, 43 were either
378 genotyped or had proxies on the Exome chip and the β s were taken from discovery results (Supplementary
379 Table 13), the remaining β s were taken from published effect estimates. This strategy for selecting betas for
380 use in the GRS was taken to minimize the influence of winner's curse. The associations between the BP
381 variants with CHD, HDL-c, LDL-c, total cholesterol, log(triglycerides) and log(eGFR) were obtained using
382 the CHD Exome+ Consortium studies, the associations with BMI, waist-hip ratio adjusted BMI and height
383 from the GIANT consortium (unpublished data), ischemic stroke from METASTROKE²⁵, and left
384 ventricular mass, left ventricular wall thickness and heart failure from EchoGen²⁷ and CHARGE-HF²⁶. A
385 causal interpretation of the association of GRS with the outcome as the effect of BP on the outcome assumes
386 that the effects of genetic variants on the outcome are mediated via blood pressure and not via alternate
387 causal pathways, for example via LV thickness. There are also limitations of the Mendelian randomization
388 approach in distinguishing between the causal effects of different measures of blood pressure, due to the
389 paucity of genetic variants associated with only one measure of blood pressure.

390

391 **eQTL analyses**

392 The MuTHER dataset contains gene expression data from 850 UK twins for 23,596 probes and 2,029,988
393 (HapMap 2 imputed) SNVs. All cis-associated SNVs with FDR < 1%, within each of the 30 novel regions
394 (IMPUTE info score > 0.8) were extracted from the MuTHER project dataset for, LCL (n=777), adipose

395 (n=776) and skin (n=667)⁵⁰. The pilot phase of the GTEx Project (dbGaP Accession phs000424.v3.p1)
396 provides expression data from up to 156 individuals for 52,576 genes and 6,820,472 genotyped SNVs
397 (imputed to 1000 Genomes project, MAF \geq 5%)⁵¹. The eQTL analysis was focused on subcutaneous adipose
398 tissue (n=94), tibial artery (n=112), heart (left ventricle) (n=83), lung (n=119), skeletal muscle (n=138),
399 tibial nerve (n=88), skin (sun exposed, lower leg) (n=96), thyroid (n=105) and whole blood (n=156) which
400 have >80 samples and genes expressed at least 0.1 RPKM in 10 or more individuals in a given tissue. All
401 transcripts with a transcription start site (TSS) within one of the 30 new BP loci and for which there was a
402 cis-associated SNV (IMPUTE info score >0.4) within 1Mb of the TSS at FDR<5%, were identified. Kidney
403 was not evaluated because the sample size was too small (n=8). From each resource, we report eQTL
404 signals, which reach the resource-specific thresholds for significance described above, for SNVs that are in
405 LD ($r^2>0.8$) with our sentinel SNV.

406 For identified eQTLs, we tested whether they colocalised with the BP associated SNV⁵². Colocalisation
407 analyses were considered to be significant if the posterior probability of colocalisation was greater than 0.95.

408 **Annotation of variants**

409 *In silico* prediction of the functional effect of associated variants was based on the annotation from dbSNP,
410 the Ensembl Variant Effect Predictor tool and the Exome Variant Server, NHLBI GO Exome Sequencing
411 Project (ESP), Seattle, WA.

412 **Trait variance explained**

413 The percentage trait variance explained for SBP, DBP, PP was assessed with 5,861 individuals with
414 complete information for all phenotypes and covariates from the population-based cohort, 1958BC.

415 Two genetic models were investigated: one containing the 43 previously known BP associated SNVs
416 covered on the Exome chip; the other additionally including the 30 novel lead SNVs and 9 conditionally
417 independent SNVs from both novel and known loci. These nine conditionally independent SNVs were
418 taken from the EUR results, as 1958BC is EUR. They included four from novel loci (*PREX1*, *COL21A1*,
419 *PRKAG1* and *MYH6* (there was only 1 in EUR); Supplementary Table 10) and five from known loci (*ST7L*-
420 *CAPZA1-MOV10*, *FIGN-GRB14*, *ENPEP*, *TBX5-TBX3* and *HOXC4*; Supplementary Table 15).

421 The residual trait was obtained by adjusting each of the BP traits in a regression model with sex and BMI
422 variables (not age or age² as all 1958BC individuals were aged 44 years). The residual trait was regressed
423 on all SNVs within the corresponding model and adjusted for the first ten PCs. The R² calculated from this
424 regression model was used as the percentage trait variance explained.

426 Monogenic Enrichment analyses

427 To determine if sub-significant signals of association were present in a set of genes associated with
428 monogenic forms of disease, we performed an enrichment analysis of the discovery single variant meta-
429 analyses association results for all four traits, both for EUR and EUR_SAS datasets.

430 The monogenic gene set included: *WNK1*, *WNK4*, *KLHL3*, *CUL3*, *PPARG*, *NR3C2*, *CYP11B1*, *CYP11B2*,
431 *CYP17A1*, *HSD11B2*, *SCNNIA*, *SCNN1B*, *SCNN1G*, *CLCNKB*, *KCNJ1*, *SLC12A1*, *SLC12A3*³. The
432 association results of coding SNVs in these genes were extracted and the number of tests with $P < 0.001$
433 observed. In order to determine how often such an observation would be observed by chance, we
434 constructed 1,000 matched gene sets. The matching criteria for each monogenic gene was the intersection of
435 all genes in the same exon length quintile and all genes in the same coding variant count decile. Within the
436 matched sets, the number of variants with $P < 0.001$ was observed. The empirical P -value was calculated as
437 the fraction of matched sets with an equal or larger number of variants less than 0.001.

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