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New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals

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We analyzed 77 single nucleotide variants (SNVs) that remained of interest, but did not achieve genome-wide significance with blood pressure (BP) traits from a prior analysis of Exome chip genotypes. A meta-analysis of results from the CHARGE Exome BP and European led consortia in combination with association results from UK Biobank samples (pan-ancestry sample of ~475,000 and European only sample of ~423,000) indicated 21 genome wide significant loci. Four of these are novel BP loci: rs9678851 (missense, *SLC4A1AP*), rs7437940 (*AFAP1*), rs13303 (missense, *STAB1*) and rs1055144 (7p15.2). We also identified a potentially independent novel BP-associated SNV, rs3416322 (missense, *SYNPO2L*) at a known locus. Two of the BP-associated SNVs influence expression levels of nearby genes. These new findings add to the growing number of BP loci and could potentially facilitate an improved understanding of BP regulation, and identify novel therapeutic targets to reduce the burden of cardiovascular disease.