

Discovery analyses

242,296 SNVs tested for association with HTN, transformed SBP, DBP, PP in two meta-analyses:

1. Europeans (EUR) N = 165,276
2. EUR and South Asians (EUR_SAS) N = 192,763

SNV Selection

SNVs were selected for replication if $MAF \geq 0.05$ and $P < 1 \times 10^{-5}$ or $MAF < 0.05$ and $P < 1 \times 10^{-4}$ *

81 SNVs (26 SBP, 30 DBP, 19 PP, 6 HTN) selected using the larger EUR_SAS meta-analyses (80 SNVs) and EUR meta-analyses (1 SNV)

Analysis of 81 SNVs selected for replication in independent samples

81 SNVs tested for replication with HTN, raw SBP, DBP and PP

Two meta-analyses 1. EUR N = 125,713

2. EUR, HIS, AFR, SAS (ALL): N = 155,063

using *independent* samples (16 CHARGE+ studies and 2 ExomeBP studies)

(1) Replication at Bonferroni adjusted significance ($P < 6.17 \times 10^{-4}$)

1. Identification in EUR
2. Additional evidence from ALL ancestry

Only consider the primary BP trait

17 SNVs replicated

EUR: 2 SBP + 9 DBP + 3 PP
ALL: 3 SBP

(2) Combined meta-analysis of discovery + replication results at GWS ($P < 5 \times 10^{-8}$)

1. Identification in EUR
2. Additional evidence from ALL ancestry

Consider all four BP traits

13 SNVs validated with overall GWS evidence

EUR: 3 SBP + 5 DBP + 2 PP
ALL: 1 SBP + 1 DBP + 1 PP

30 novel BP loci identified and validated