

Meta-analyses using RMW of samples from ExomeBP, T2D and CHD Exome+ consortia

4 BP traits: HTN, transformed SBP, DBP and PP

Two ancestry meta-analyses:

1. Europeans (EUR) N = 147,402
2. EUR and South Asians (EUR_SAS) N = 173,329

Conditional analyses

Gene-Based Analyses
(SKAT)
MAF < 5% and MAF < 1%

Novel Loci:

4 loci: 2 independent signals
1 locus: 3 independent signals
($P_{\text{cond}} < 1 \times 10^{-4}$)

Known Loci:

5 loci: 2 independent signals
($P_{\text{cond}} < 1 \times 10^{-4}$)

1 new BP gene identified with
multiple rare variant signals
($P < 2.8 \times 10^{-6}$)