

Online Supplemental Figures 1-2

A Multi-Omics Approach to Defining Target Organ Injury in Youth with Primary Hypertension

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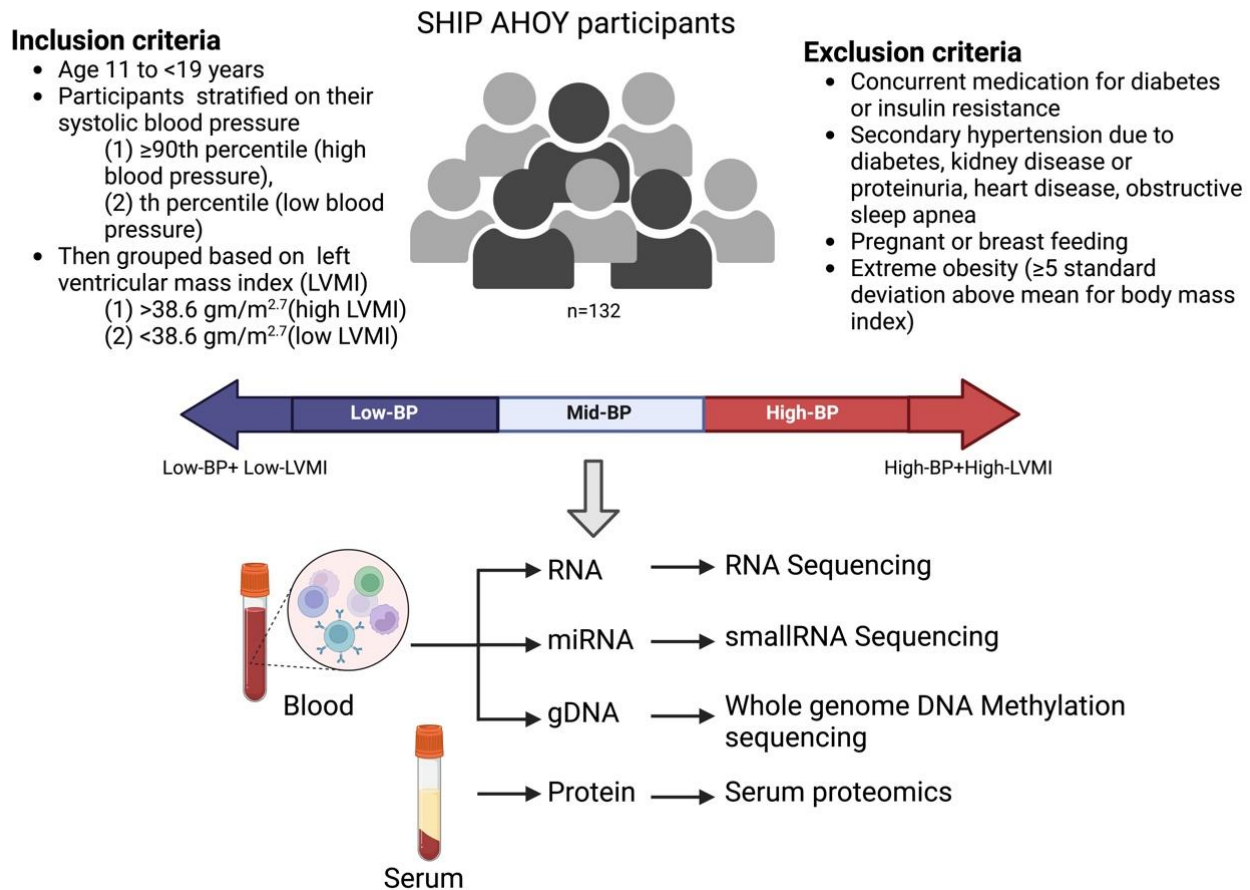
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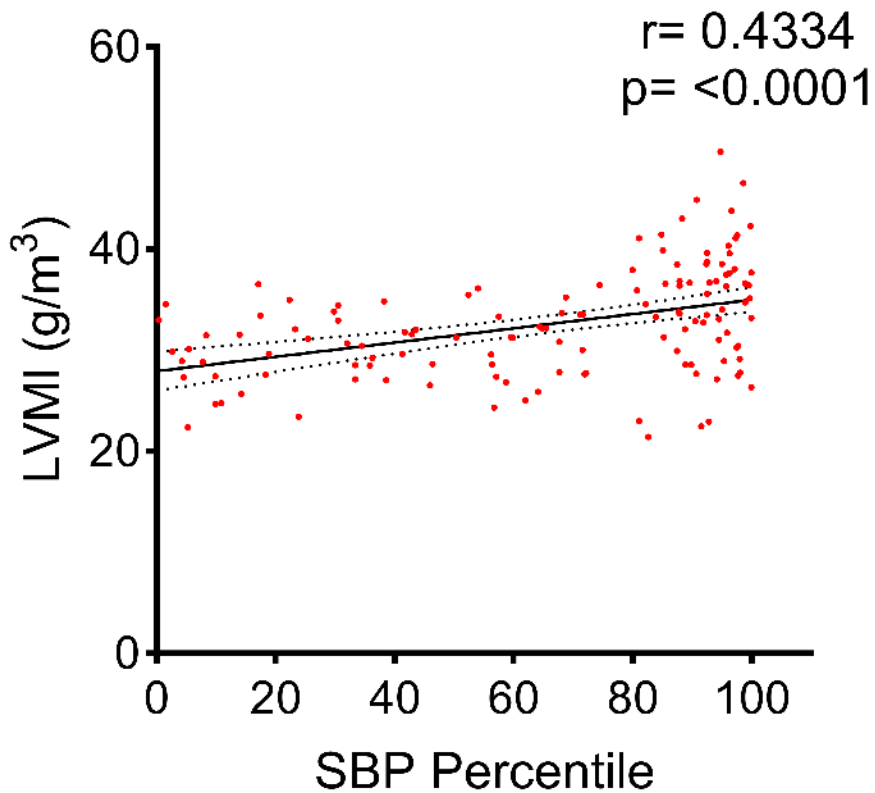
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Supplemental Figure S1. Human study experimental approach. This schematic depicts the methodology and study approach in the present study. We examined a SHIP AHOY cohort of youths with the indicated inclusion and exclusion criteria. The study participants were stratified based on their blood pressure and 132 adolescents (mean age ~15 years, male-57.58%) were included for this cross-sectional study (Table 1, Methods section) and grouped based on their left ventricular mass index (Table 2, Methods section). Blood and serum samples collected from the participants were utilized to isolate total RNA, miRNA, genomic DNA and protein samples that were later utilized to perform RNA sequencing, miRNA sequencing, whole-genome DNA methylation sequencing and serum proteomics analyses. The sequencing and proteomics data were further analyzed and correlated to identify the candidate genes and pathways involved in the early cardiovascular target organ injury (Figure Created with BioRender.com). **gDNA**: genomic DNA, **miRNA**: microRNA.



Supplemental Figure S2. Correlation of LVMI with systolic blood pressure percentile in adolescents of SHIP AHOY participants. Each data point represents an individual participant's SBP Percentile values against their LVMI (n=132). The Spearman correlation coefficient and its significant value are 0.4334 and $p < 0.0001$ respectively, indicating a significant positive correlation between SBP percentile and LVMI.

LVMI: Left Ventricular Mass Index; SBP: systolic blood pressure.