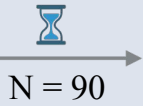


DISCOVERY POPULATION

Baseline (prepuberty)
N = 102 (48♂ 54♀)



Follow-up (puberty)
N = 138 (58♂ 71♀)



Discovery population

VALIDATION POPULATIONS

Pre-pubertal population
N = 113 (56♂ 57♀)

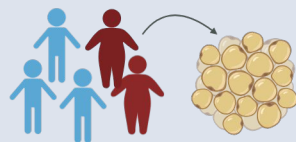


Validation population I

Pubertal population
N = 124 (63♂ 61♀)

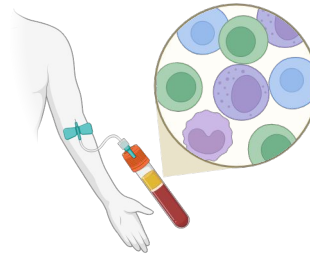


Pre-pubertal population
N = 13 (10♂ 3♀)



Validation population II

MULTI-OMIC ASSESSMENT

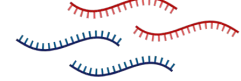


DNA methylation

Discovery population
(baseline & follow-up) and
validation population I



SNPs

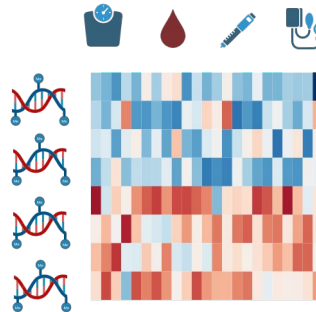


mRNA

Subset of 44 participants of
the discovery population
(follow-up)

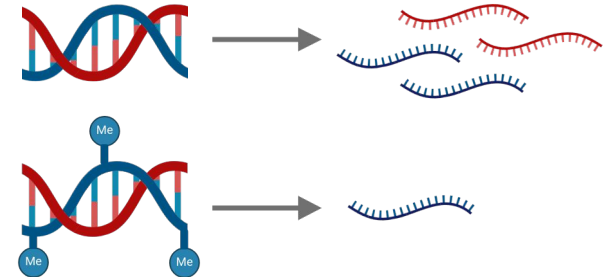
BIOINFORMATIC ANALYSES

Cardiometabolic outcomes



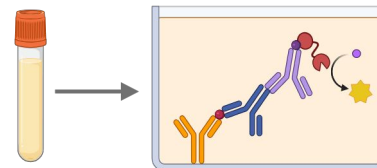
DNA methylation at the *VASN* locus
(cpg0041083) is positively associated
with BMI and blood pressure z-scores

Expression quantitative trait methylation (eQTMs)

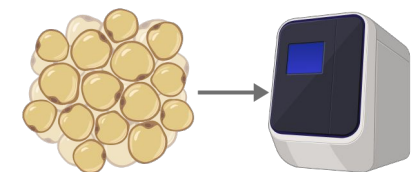


DNA methylation at the *VASN* locus (cpg0041083)
is negatively associated with gene expression levels

BIOMARKER VALIDATION



Circulating *VASN* levels are negatively
associated with FMI and HOMA-IR, and
positively associated with HDL-c



VASN expression in VAT was
downregulated in children with obesity
compared with normal-weight children